Supporting information:

Table A. Distribution and characteristics of SNP sites in five eIF4E genes and neighboring regions in 61 cassava accessions

Loci*	Total SNP	Up/Downstream (+/- 5kb)	Genes	Introns	mRNA	CDS	Synonymous	Non-synonymous
eIF(iso)4E_me1	986	835	151	92	59	22	9	13
nCBP_me2	666	499	167	127	40	15	13	2
nCBP_me1	858	637	221	147	74	22	7	15
eIF(iso)4E_me2	992	780	212	175	37	13	9	4
eIF4E_me	886	776	110	68	42	30	13	17
Total	4388	3527	861	609	252	102	51	51

Table B. Non-synonymous single nucleotide polymorphisms in five cassava eIF4E genes of 14 cassava accessions

Chromosome Position		AM560	Albert	AR37-80	Kibandameno*	Kiroba	MCOL22	Mkombozi	Muzege	Namikonga	Nachinyaya	TME3	TME7	TMS30572	TMS60444
Chr03	25396170	G/G	G/G	G/G	G/G	G/G	G/C	G/G	G/G	G/G	./.	G/G	G/G	G/G	G/G
Chr03	25396238	G/G	G/G	G/G	G/G	G/G	G/C	G/G	G/G	G/G	./.	G/G	G/G	G/C	G/C
Chr03	25396987	A/A	A/A	A/A	A/A	A/A	A/T	./.	A/A	A/A	./.	A/A	A/A	./.	A/T
Chr09	25948588	T/T	C/C	T/C	T/C	C/C	T/C	T/C	T/C	T/C	T/C	C/C	C/C	T/T	C/C
Chr15	3318172	C/C	C/T	C/T	./.	C/T	C/T	C/C	C/T	C/C	T/T	./.	C/C	C/C	C/C
Chr17	20187344	A/A	A/A	A/A	A/T	T/T	A/A	A/A	A/A	A/T	A/A	A/A	A/A	A/T	A/A
Chr17	20187753	T/T	T/T	T/T	T/T	T/C	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T
Chr17	20188018	A/A	A/A	A/A	A/A	A/C	A/A	A/A	A/A	A/A	./.	A/A	A/A	A/A	A/A
Chr17	20188026	C/C	C/C	C/C	C/C	C/G	C/C	C/C	C/C	C/C	./.	C/C	C/C	C/C	C/C
Chr17	20189389	C/C	C/C	C/C	C/C	C/T	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	./.
Chr17	20189407	T/T	T/T	T/T	T/T	T/A	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	./.
Chr17	20189457	T/T	./.	T/T	T/T	T/C	T/T	T/T	T/T	T/T	T/T	./.	T/T	T/T	T/T
Chr17	20189544	T/T	./.	T/T	T/T	T/A	T/T	T/A	T/T	T/A	T/T	T/A	T/A	A/A	T/T

*Accessions in red display tolerant responses to CBSD while accessions in white display susceptible response to CBSD. Missing data are represented by "./."

Table C. Association of SNPs upstream of *eIF4E_me* gene with CBSD disease responses.

CHR	BP	SNP	P value	Regions	Substitutions
Chr17	20190229	ss.94871927	0.004	Intergenic	G/A
Chr17	20190238	ss.94871930	0.007	Intergenic	TA/T
Chr17	20190251	ss.94871935	0.007	Intergenic	A/G
Chr17	20190252	ss.94871936	0.007	Intergenic	TC/T
Chr17	20192085	ss.94872078	0.007	Manes.17G063200	G/T, T187K

Table D. Information on Illumina RNAseq unpaired reads of two cassava accessions and Bowtie mapping statistics[1].

								Reads mapped to genes					
SRA accessions	Cassava accessions	CBSV Infection	Tissues	Phenotypes	Bases	Total reads[2]	%mapped to genome	eIF4E	eIF(iso)4E1	eIF(iso)4E2	nCBP1	nCBP2	Actin
SRR1213744	Albert	Healthy	leaf	Susceptible	2628M	42768937	0.8765	1676	98	1041	351	4136	6497
SRR1213745	Albert	Infected	leaf	Susceptible	2921M	47596602	0.886	2203	154	1558	490	6171	8700
SRR1213746	Kaleso	Healthy	leaf	Tolerant	1894M	30730846	0.8634	1224	77	804	254	2744	3927
SRR1213747	Kaleso	Infected	leaf	Tolerant	2416M	47596602	0.886	2352	191	1536	422	2825	9677

[1] Raw sequencing reads were generated by Maruthi et al. in 2014 [1] and retrieved from http://www.ncbi.nlm.nih.gov/sra.

[2] Average read lengths are 51 bp.

Table E. Differential expression analysis of five cassava eIF4E genes in healthy and CBSV infected Albert and Kaleso accessions.

Genes	Cassava lines	Healthy (FPKM)	Infected (FPKM)	log2	test_stat	p[1]	q[2]
eIF4E	Albert	67.4627	80.5457	0.255717	0.447822	0.6613	0.998506
	Kaleso	68.9774	87.6125	0.345012	0.596169	0.54455	0.998506
eIF(iso)4E1	Albert	6.18663	8.75624	0.501157	0.599087	0.5463	0.998506
	Kaleso	6.74423	11.0195	0.708338	0.878567	0.36865	0.998506
eIF(iso)4E2	Albert	39.6478	53.6243	0.435647	0.752701	0.44975	0.998506
	Kaleso	42.7417	53.4709	0.32311	0.560435	0.5804	0.998506
nCBP1	Albert	9.56893	11.9476	0.320294	0.474463	0.6357	0.998506
	Kaleso	9.70205	10.443	0.106175	0.157073	0.87315	0.998506
nCBP2	Albert	135.035	181.42	0.426	0.720313	0.4565	0.998506
	Kaleso	125.056	83.9671	-0.574679	-0.990581	0.32255	0.998506

[1] The uncorrected p-value of the test statistic.

[2] The FDR-adjusted p-value of the test statistic. FDR is set at 0.05.

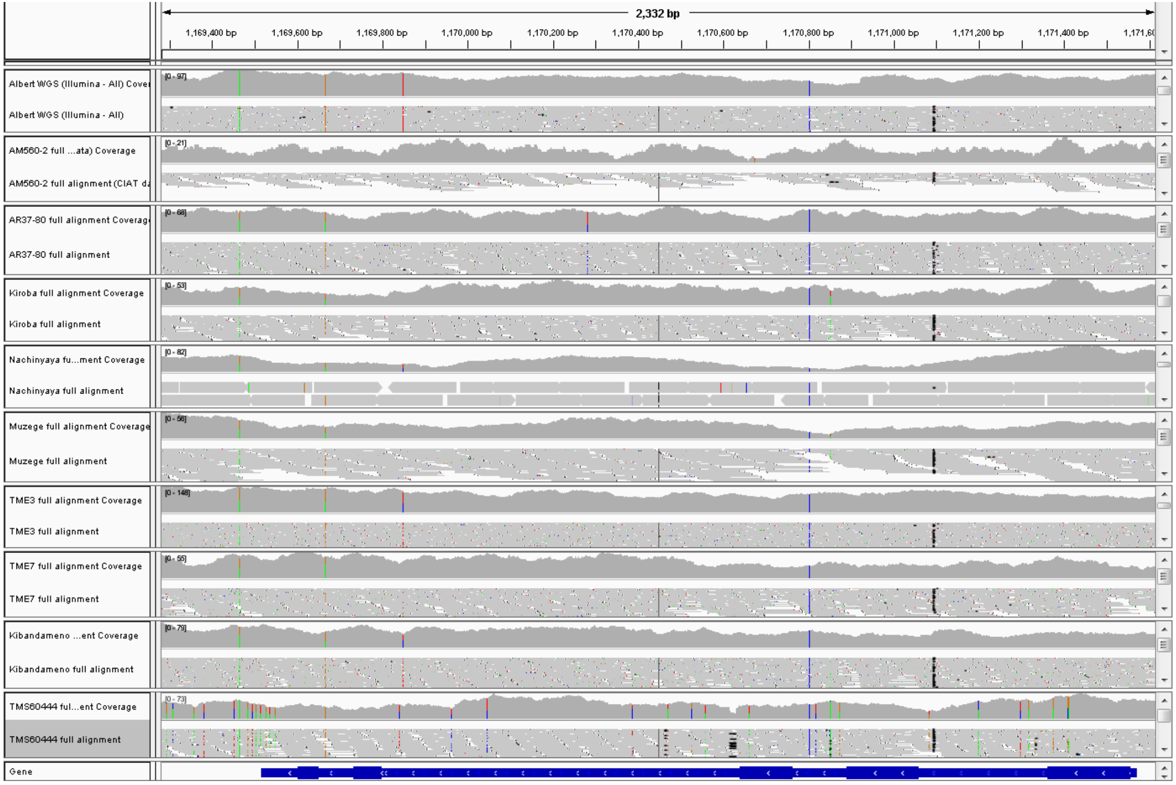
Table F. Information on 454 GS FLX Titanium RNAseq reads of six cassava accessions and Bowtie mapping statistics[1].

							Reads mapped to genes					
SRA accessions	Cassava accessions	Tissues	Phenotypes	Bases	Total reads[2]	%mapped to genome	eIF4E	eIF(iso)4E1	eIF(iso)4E2	nCBP1	nCBP2	Actin
SRR955450	AR37-80	leaf, stem	Susceptible	88M	190325	70.84%	19	2	5	8	4	32
SRR955446	AR40-6	leaf, stem	Susceptible	101M	208365	64.21%	17	2	15	7	0	68
SRR955445	Mkombozi	leaf, stem	Susceptible	168M	346000	66.89%	22	3	19	10	3	85
SRR955449	Kiroba	leaf, stem	Tolerant	123M	291436	60.83%	7	2	6	N/A	2	54
SRR955447	Nachinyaya	leaf, stem	Tolerant	141M	261139	68.06%	5	4	13	17	1	46
SRR955444	Namikonga	leaf, stem	Tolerant	99M	205405	61.29%	14	1	5	2	3	49

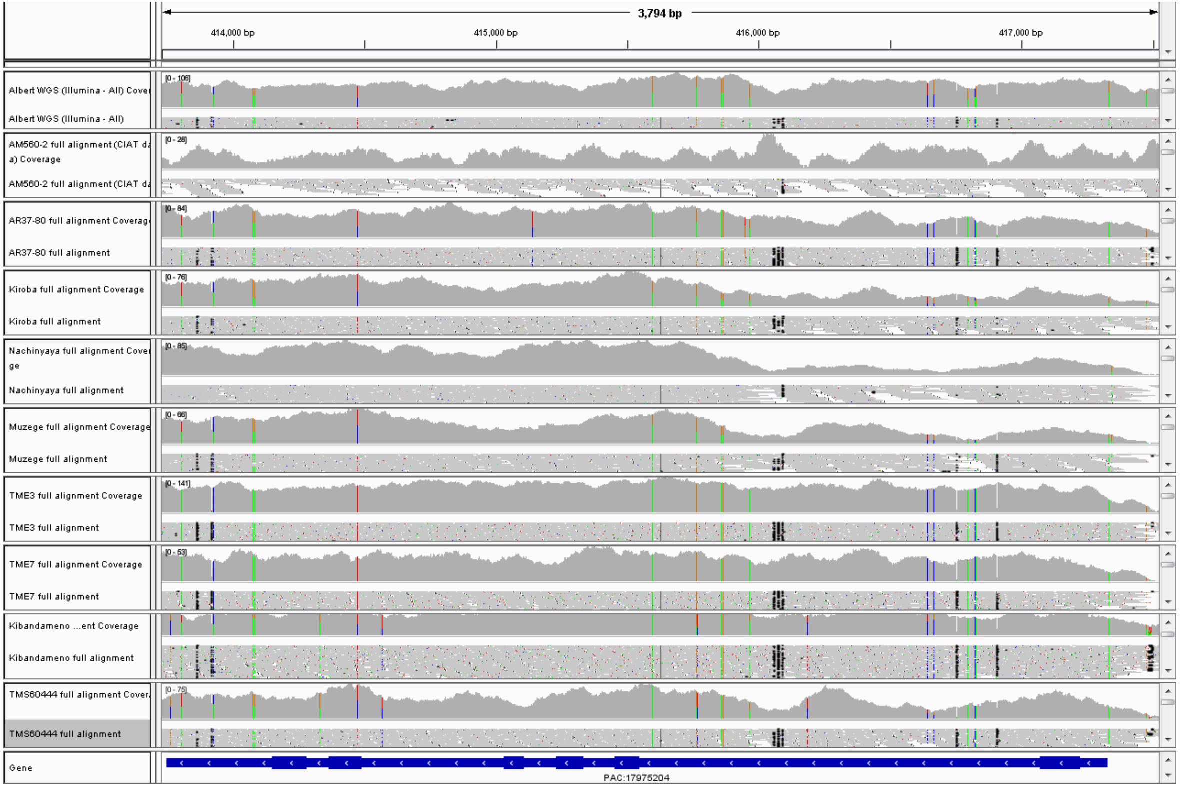
[1] Raw sequencing reads were generated by Ferguson et al in 2015 [2] and retrieved from http://www.ncbi.nlm.nih.gov/sra.

[2] Average read lengths are 500 bp.

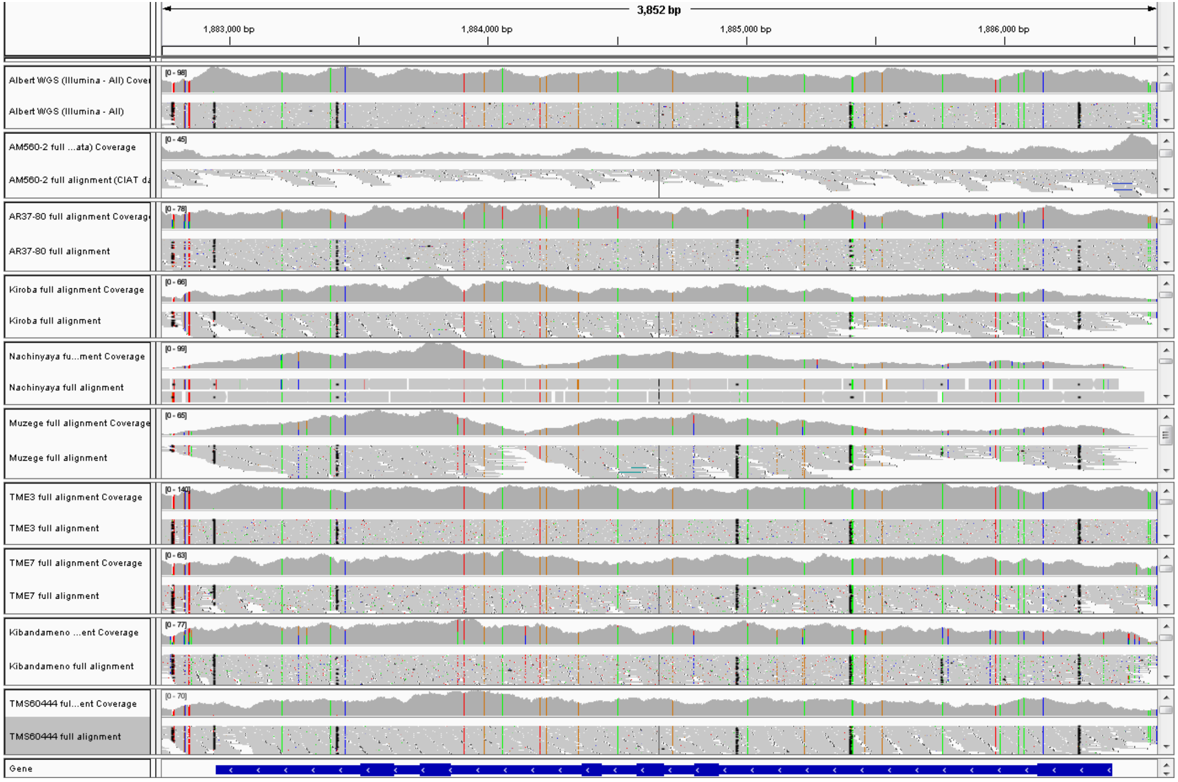
A. eIF(iso)4E_me1 (Locus: Manes.03G160000)



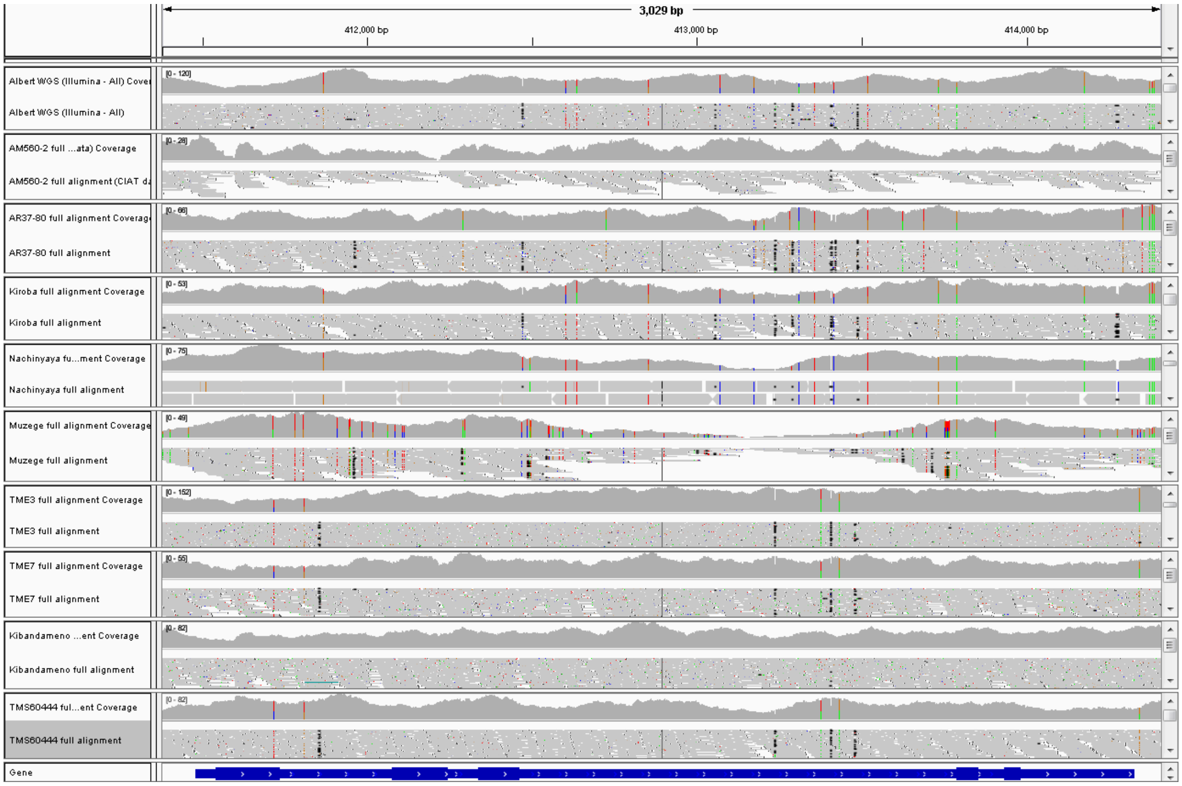
B. nCBP_me2 (Locus: Manes.08G145200)



C. nCBP_me1 (Locus: Manes.09G140300)



D. eIF(iso)4E_me2 (Locus: Manes.15G044900)



E. eIF4E_me (Locus: Manes.17G063100)

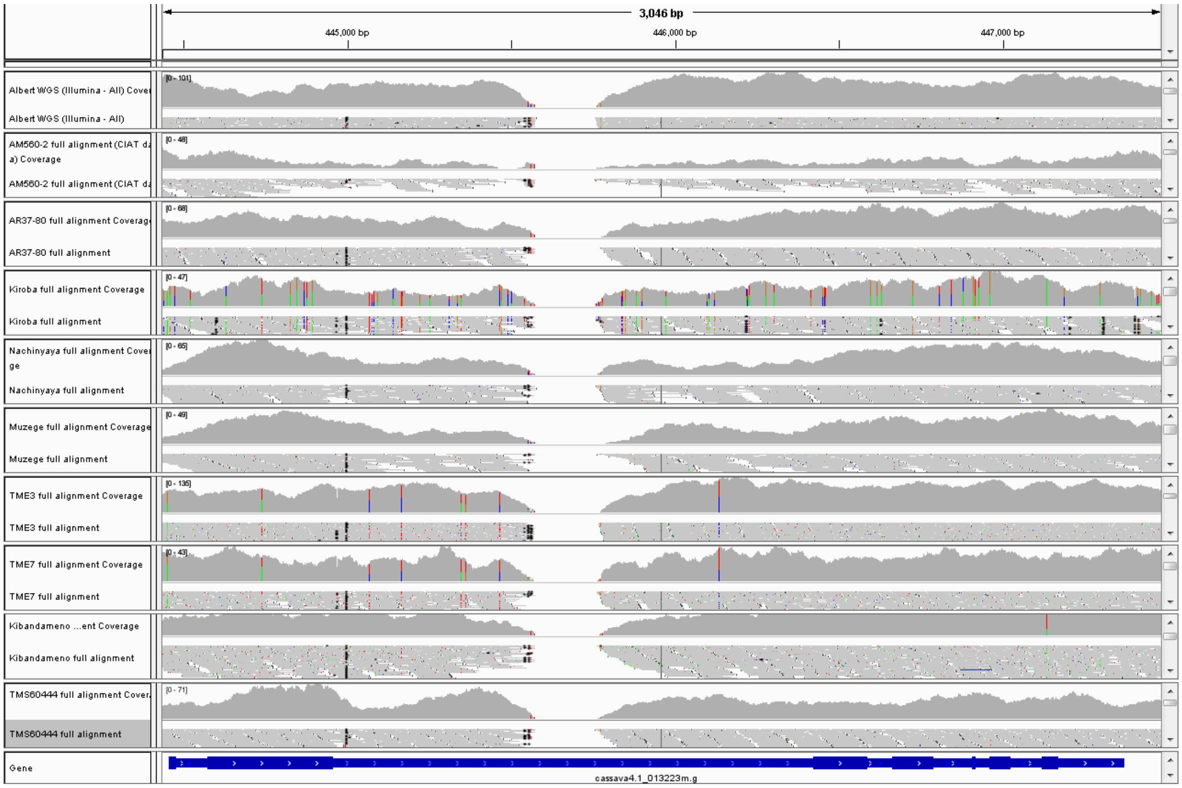
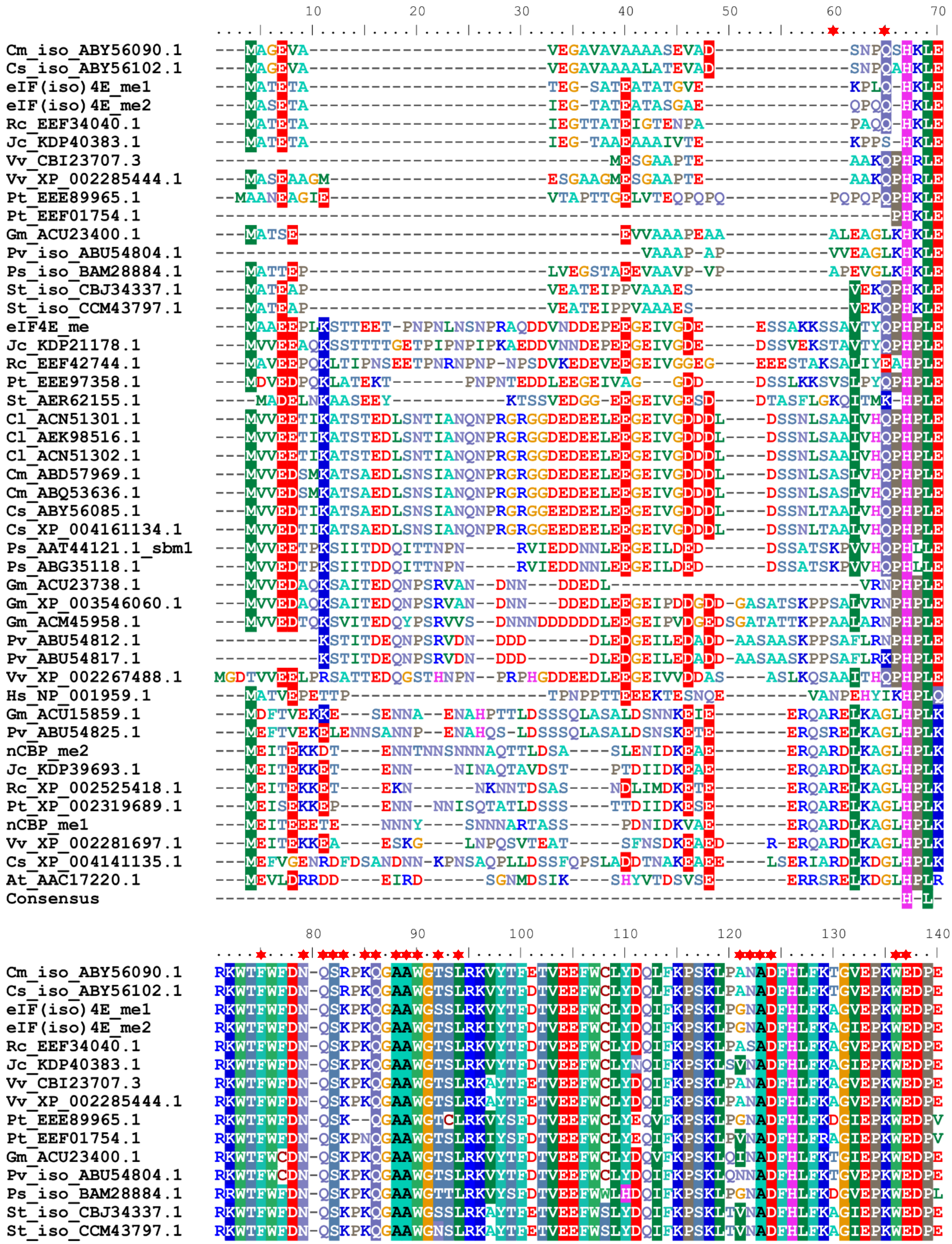


Figure A. Distribution of nucleotide polymorphisms in five cassava eIF4E genes across 10 landraces. High quality Illumina reads of 10 cassava genomes are anchor-aligned to the cassava genome and viewed in IGV [3]. Vertical colored lines indicate nucleotide polymorphisms. Each color represents a different nucleotide substitution. Black dots indicate deletions or missing data. Biallelic variations are clearly visible in certain genes of cassava lines.



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                                  10        20        30        40        50        60        70
Cm_iso_ABY56090.1        ---MAGEVA-----------------------VEGAVAVAAAASEVAD-------------SNPQSHKLE
Cs_iso_ABY56102.1        ---MAGEVA-----------------------VEGAVAAAALATEVAD-------------SNPQAHKLE
eIF(iso)4E_me1           ---MATETA-----------------------TEG-SATEATATGVE--------------KPLQ-HKLE
eIF(iso)4E_me2           ---MASETA-----------------------IEG-TATEATASGAE--------------QPQQ-HKLE
Rc_EEF34040.1            ---MATETA-----------------------IEGTTATEIGTENPA--------------PAQQ-HKLE
Jc_KDP40383.1            ---MATETA-----------------------IEG-TAAEAAAIVTE--------------KPPS-HKLE
Vv_CBI23707.3            --------------------------------------MESGAAPTE--------------AAKQPHRLE
Vv_XP_002285444.1        ---MASEAAGM---------------------ESGAAGMESGAAPTE--------------AAKQPHRLE
Pt_EEE89965.1            --MAANEAGIE---------------------VTAPTTGELVTEQPQPQ----------PQPQPQPHKLE
Pt_EEF01754.1            -----------------------------------------------------------------PHKLE
Gm_ACU23400.1            ---MATSE-------------------------------EVVAAAPEAA----------ALEAGLKHKLE
Pv_iso_ABU54804.1        -----------------------------------------VAAAP-AP----------VVEAGLKHKLE
Ps_iso_BAM28884.1        ---MATTEP-----------------------LVEGSTAEEVAAVP-VP----------APEVGLKHKLE
St_iso_CBJ34337.1        ---MATEAP-----------------------VEATEIPPVAAAES---------------VEKQPHKLE
St_iso_CCM43797.1        ---MATEAP-----------------------VEATEIPPVAAAES---------------VEKQPHKLE
eIF4E_me                 ---MAAEEPLKSTTEET-PNPNLNSNPRAQDDVNDDEPEEGEIVGDE-----ESSAKKSSAVTYQPHPLE
Jc_KDP21178.1            ---MVVEEAQKSSTTTTGETPIPNPIPKAEDDVNNDEPEEGEIVGDE-----DSSVEKSTAVTYQPHPLE
Rc_EEF42744.1            ---MAVEEPQKLTIPNSEETPNRNPNP-NPSDVKEDEVEEGEIVGGEG----EEESTAKSALIYEAHPLE
Pt_EEE97358.1            ---MDVEDPQKLATEKT-------PNPNTEDDLEEGEIVAG---GDD-----DSSLKKSVSLPYQPHPLE
St_AER62155.1            ----MADELNKAASEEY-----------KTSSVEDGG-EEGEIVGESD----DTASFLGKQITMK-HPLE
Cl_ACN51301.1            ---MVVEETIKATSTEDLSNTIANQNPRGRGGDEDEELEEGEIVGDDDL----DSSNLSAAIVHQPHPLE
Cl_AEK98516.1            ---MVVEETIKATSTEDLSNTIANQNPRGRGGDEDEELEEGEIVGDDDL----DSSNLSAAIVHQPHPLE
Cl_ACN51302.1            ---MVVEETIKATSTEDLSNTIANQNPRGRGGDEDEELEEGEIVGDDDL----DSSNLSAAIVHQPHPLE
Cm_ABD57969.1            ---MVVEDSMKATSAEDLSNSIANQNPRGRGGDEDEELEEGEIVGDDDL----DSSNLSASLVHQPHPLE
Cm_ABQ53636.1            ---MVVEDSMKATSAEDLSNSIANQNPRGRGGDEDEELEEGEIVGDDDL----DSSNLSASLVHQPHPLE
Cs_ABY56085.1            ---MVVEDTIKATSAEDLSNSIANQNPRGRGGEEDEELEEGEIVGDDDL----DSSNLTAALVHQPHPLE
Cs_XP_004161134.1        ---MVVEDTIKATSAEDLSNSIANQNPRGRGGEEDEELEEGEIVGDDDL----DSSNLTAALVHQPHPLE
Ps_AAT44121.1_sbm1       ---MVVEETPKSIITDDQITTNPN-----RVIEDDNNLEEGEILDED------DSSATSKPVVHQPHLLE
Ps_ABG35118.1            ---MVVEDTPKSIITDDQITTNPN-----RVIEDDNNLEEGEILDED------DSSATSKPVVHQPHLLE
Gm_ACU23738.1            ---MVVEDAQKSAITEDQNPSRVAN--DNN---DDEDL------------------------VRNPHPLE
Gm_XP_003546060.1        ---MVVEDAQKSAITEDQNPSRVAN--DNN---DDEDLEEGEIPDDGDD-GASATSKPPSALVRNPHPLE
Gm_ACM45958.1            ---MVVEDTQKSVITEDQYPSRVVS--DNNNDDDDDDLEEGEIPVDGEDSGATATTKPPAALARNPHPLE
Pv_ABU54812.1            ----------KSTITDEQNPSRVDN--DDD------DLEDGEILEDADD-AASAASKPPSAFLRNPHPLE
Pv_ABU54817.1            ----------KSTITDEQNPSRVDN--DDD------DLEDGEILEDADD-AASAASKPPSAFLRKPHPLE
Vv_XP_002267488.1        MGDTVVEELPRSATTEDQGSTHNPN--PRPHGDDEEDLEEGEIVVDDAS----ASLKQSAAITHQPHPLE
Hs_NP_001959.1           ---MATVEPETTP-------------------TPNPPTTEEEKTESNQE--------VANPEHYIKHPLQ
Gm_ACU15859.1            ---MDFTVEKKE---SENNA--ENAHPTTLDSSSQLASALDSNNKEIE-------ERQARELKAGLHPLK
Pv_ABU54825.1            ---MEFTVEKELENNSANNP--ENAHQS-LDSSSQLASALDSNSKETE-------ERQSRELKAGLHPLK
nCBP_me2                 ---MEITEKKDT----ENNTNNSNNNAQTTLDSA----SLENIDKEAE-------ERQARDLKAGLHPLK
Jc_KDP39693.1            ---MEITEKKET----ENN----NINAQTAVDST----PTDIIDKEAE-------ERQARDLKAGLHPLK
Rc_XP_002525418.1        ---MEITEKKET----EKN------NKNNTDSAS----NDLIMDKETE-------ERQARELKAGLHPLK
Pt_XP_002319689.1        ---MEISEKKEP----ENN--NNISQTATLDSSS----TTDIIDKESE-------ERQARELKAGLHPLK
nCBP_me1                 ---MEITEEETE----NNNY----SNNNARTASS-----PDNIDKVAE-------ERQARDLKAGLHPLK
Vv_XP_002281697.1        ---MEITEKKEA----ESKG----LNPQSVTEAT-----SFNSDKEAED----R-ERQARDLKAGLHPLK
Cs_XP_004141135.1        ---MEFVGENRDFDSANDNN-KPNSAQPLLDSSFQPSLADDTNAKEAEE----LSERIARDLKDGLHPLK
At_AAC17220.1            ---MEVLDRRDD----EIRD------SGNMDSIK----SHYVTDSVSE-------ERRSRELKDGLHPLR
Consensus                ------------------------------------------------------------------H-L-

                                  80        90       100       110       120       130       140
Cm_iso_ABY56090.1        RKWTFWFDN-QSRPKQGAAWGTSLRKVYTFETVEEFWCLYDQLFKPSKLPANADFHLFKTGVEPKWEDPE
Cs_iso_ABY56102.1        RKWTFWFDN-QSRPKQGAAWGTSLRKVYTFDTVEEFWCLYDQLFKPSKLPANADFHLFKTGVEPKWEDPE
eIF(iso)4E_me1           RKWTFWFDN-QSKPKQGAAWGSSLRKVYTFDTVEEFWCLYDQIFKPSKLPGNADFHLFKAGVEPKWEDPE
eIF(iso)4E_me2           RKWTFWFDN-QSKPKQGAAWGTSLRKIYTFDTVEEFWCLYDQIFKPSKLPGNADFHLFKAGIEPKWEDPE
Rc_EEF34040.1            RKWTFWFDN-QSKPKQGAAWGTSLRKVYTFDTVEEFWCLYDQIFKPSKLPASADFHLFKAGVEPKWEDPE
Jc_KDP40383.1            RKWTFWFDN-QSKPKQGAAWGTSLRKVYTFDTVEEFWCLYNQIFKPSKLSVNADFHLFKAGIEPKWEDPE
Vv_CBI23707.3            RKWTFWFDN-QSKPKQGAAWGTSLRKAYTFETVEEFWCLYDQIFKPSKLPANADFHLFKAGVEPKWEDPE
Vv_XP_002285444.1        RKWTFWFDN-QSKPKQGAAWGTSLRKAYTFETVEEFWCLYDQIFKPSKLPANADFHLFKAGVEPKWEDPE
Pt_EEE89965.1            RKWTFWFDN-QSK--QGAAWGTCLRKVYSFDTVEEFWCLYEQVFKPSKLPGNADFHLFKDGIEPKWEDPV
Pt_EEF01754.1            RKWTFWFDN-QSKPNQGAAWGTSLRKIYSFDTVEEFWCLYEQIFKPSKLPVNADFHLFRAGIEPKWEDPV
Gm_ACU23400.1            RKWTFWCDN-QSKPKQGAAWGTSLRKVYTFDTVEEFWCLYDQVFKPSKLQINADFHLFKTGIEPKWEDPE
Pv_iso_ABU54804.1        RKWTFWCDN-QSKPKQGAAWGTSLRKVYTFDTVEEFWCLYDQIFKPSKLQNNADFHLFKTGVEPKWEDPE
Ps_iso_BAM28884.1        RRWTFWFDN-QSKPKQGAAWGTTLRKVYSFDTVEEFWWLHDQIFKPSKLPGNADFHLFKDGVEPKWEDPL
St_iso_CBJ34337.1        RKWTFWFDN-QSKPKQGAAWGSSLRKAYTFETVEEFWSLYDQIFKPSKLTVNADFHLFKAGIEPKWEDPE
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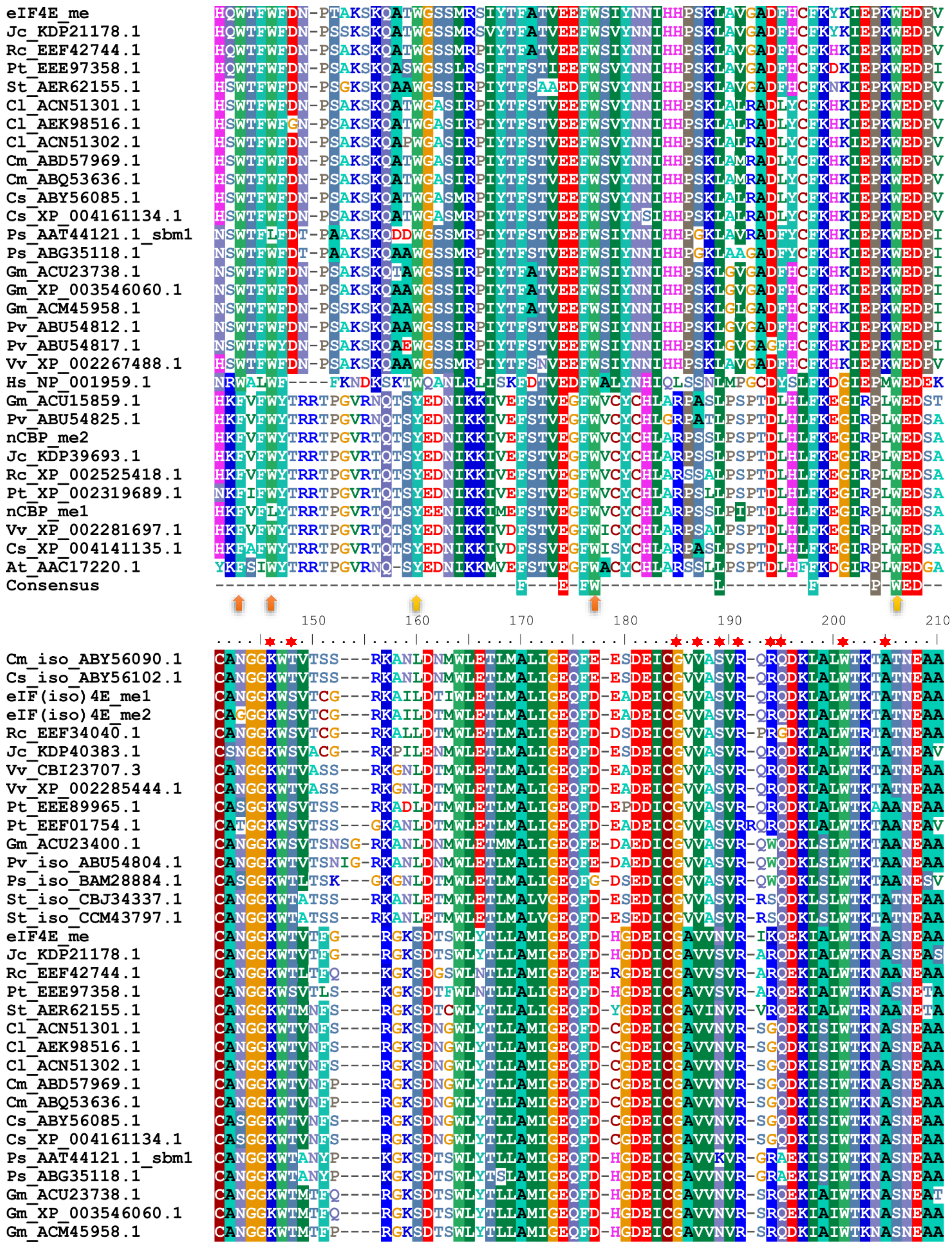

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Rc_EEF42744.1       HQWTFWFDN-PSAKSKQATWGSSMRPIYTFATVEEFWSIYNNIHHPSKLAVGADFHCFKHKIEPKWEDPV
Pt_EEE97358.1       HQWTFWFDN-PSAKSKQASWGSSLRSIFTFSTIEEFWSVYNNIHHPSKLAVGADFHCFKDKIEPKWEDPI
St_AER62155.1       HSWTFWFDN-PSGKSKQAAWGSSIRPIYTFSAAEDFWSVYNNIHHPSKLAVGADFHCFKNKIEPKWEDPV
Cl_ACN51301.1       HSWTFWFDN-PSAKSKQATWGASIRPIYTFSTVEEFWSVYNNIHHPSKLALRADLYCFKHKIEPKWEDPV
Cl_AEK98516.1       HSWTFWFGN-PSAKSKQATWGASIRPIYTFSTVEEFWSVYNNIHHPSKLALRADLYCFKHKIEPKWEDPV
Cl_ACN51302.1       HSWTFWFDN-PSAKSKQAPWGASIRPIYTFSTVEEFWSVYNNIHHPSKLALRADLYCFKHKIEPKWEDPV
Cm_ABD57969.1       HSWTFWFDN-PSAKSKQATWGASIRPIYTFSTVEEFWSVYNNIHHPSKLAMRADLYCFKHKIEPKWEDPV
Cm_ABQ53636.1       HSWTFWFDN-PSAKSKQATWGASIRPIYTFSTVEEFWSVYNNIHHPSKLAMRADLYCFKHKIEPKWEDPV
Cs_ABY56085.1       HSWTFWFDN-PSAKSKQATWGASMRPIYTFSTVEEFWSVYNNIHHPSKLALRADLYCFKHKIEPKWEDPV
Cs_XP_004161134.1   HSWTFWFDN-PSAKSKQATWGASMRPIYTFSTVEEFWSVYNSIHHPSKLALRADLYCFKHKIEPKWEDPV
Ps_AAT44121.1_sbm1  NSWTFLFDT-PAAKSKQDDWGSSMRPIYTFSTVEEFWSIYNNIHHPGKLAVRADFYCFKHKIEPKWEDPI
Ps_ABG35118.1       NSWTFWFDT-PAAKSKQAAWGSSMRPIYTFSTVEEFWSIYNNIHHPGKLAAGADFYCFKHKIEPKWEDPI
Gm_ACU23738.1       NSWTFWFDN-PSAKSKQTAWGSSIRPIYTFATVEEFWSIYNNIHHPSKLGVGADFHCFKHKIEPKWEDPI
Gm_XP_003546060.1   NSWTFWFDN-PSAKSKQAAWGSSIRPIYTFATVEEFWSIYNNIHHPSKLGVGADFHCFKHKIEPKWEDPI
Gm_ACM45958.1       NSWTFWFDN-PSSKSKQAAWGSSIRPIYTFATVEEFWSIYNNIHHPSKLGLGADFHCFKHKIEPKWEDPI
Pv_ABU54812.1       NSWTFWFDN-PSAKSKQAAWGSSIRPIYTFSTVEEFWSIYNNIHHPSKLGVGADFHCFKHKIEPKWEDPI
Pv_ABU54817.1       NSWTFWYDN-PSAKSKQAEWGSSIRPIYTFSTVEEFWSIYNNIHHPSKLGVGAGFHCFKHKIEPKWEDPI
Vv_XP_002267488.1   HSWTFWFDN-PSAKSKQAAWGSSMRPIYTFSNVEEFWSIYNNIHHPSKLAVGADFHCFKHKIEPKWEDPV
Hs_NP_001959.1      NRWALWF----FKNDKSKTWQANLRLISKFDTVEDFWALYNHIQLSSNLMPGCDYSLFKDGIEPMWEDEK
Gm_ACU15859.1       HKFVFWYTRRTPGVRNQTSYEDNIKKIVEFSTVEGFWVCYCHLARPASLPSPTDLHLFKEGIRPLWEDST
Pv_ABU54825.1       HKFVFWYTRRTPGVRNQTSYEDNIKKIVEFSTVEGFWVCYCHLGRPATLPSPTDLHLFKEGIRPLWEDSA
nCBP_me2            HKFVFWYTRRTPGVRTQTSYEDNIKKIVEFSTVEGFWVCYCHLARPSSLPSPTDLHLFKEGIRPLWEDSA
Jc_KDP39693.1       HKFVFWYTRRTPGVRTQTSYEDNIKKIVEFSTVEGFWVCYCHLARPSSLPSPTDLHLFKEGIRPLWEDSA
Rc_XP_002525418.1   HKFVFWYTRRTPGVRTQTSYEDNIKKIVEFSTVEGFWVCYCHLARSSALPSPTDLHLFKEGIRPLWEDSA
Pt_XP_002319689.1   NKFIFWYTRRTPGVRTQTSYEDNIKKIVEFSTVEGFWVCYCHLARPSLLPSPTDLHLFKEGIRPLWEDSA
nCBP_me1            HKFVFLYTRRTPGVRTQTSYEENIKKIMEFSTVEGFWVCYCHLARPSSLPIPTDLHLFKEGIRPLWEDSA
Vv_XP_002281697.1   HKFVFWYTRRTPGVRTQTSYEDNIKKIVDFSTVEGFWICYCHLARPSALPSPTDLHLFKEGIRPLWEDSA
Cs_XP_004141135.1   HKFAFWYTRRTPGVRTQTSYEDNIKKIVDFSSVEGFWISYCHLARPASLPSPTDLHLFKEGIRPLWEDSA
At_AAC17220.1       YKFSIWYTRRTPGVRNQ-SYEDNIKKMVEFSTVEGFWACYCHLARSSLLPSPTDLHFFKDGIRPLWEDGA
Consensus           -----------------------------F---E-FW-----------L--------F-----P-WED--

Cm_iso_ABY56090.1   CANGGKWTVTSS---RKANLDNMWLETLMALIGEQFE-ESDEICGVVASVR-QRQDKLALWTKTATNEAA
Cs_iso_ABY56102.1   CANGGKWTVTSS---RKANLDNMWLETLMALIGEQFE-ESDEICGVVASVR-QRQDKLALWTKTATNEAA
eIF(iso)4E_me1      CANGGKWSVTCG---RKAILDTIWLETLMALIGEQFD-EADEICGVVASVR-QRQDKLALWTKTATNEAA
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Gm_XP_003546060.1   CANGGKWTMTFQ----RGKSDTSWLYTLLAMIGEQFD-HGDEICGAVVNVR-SRQEKIAIWTKNASNEAA
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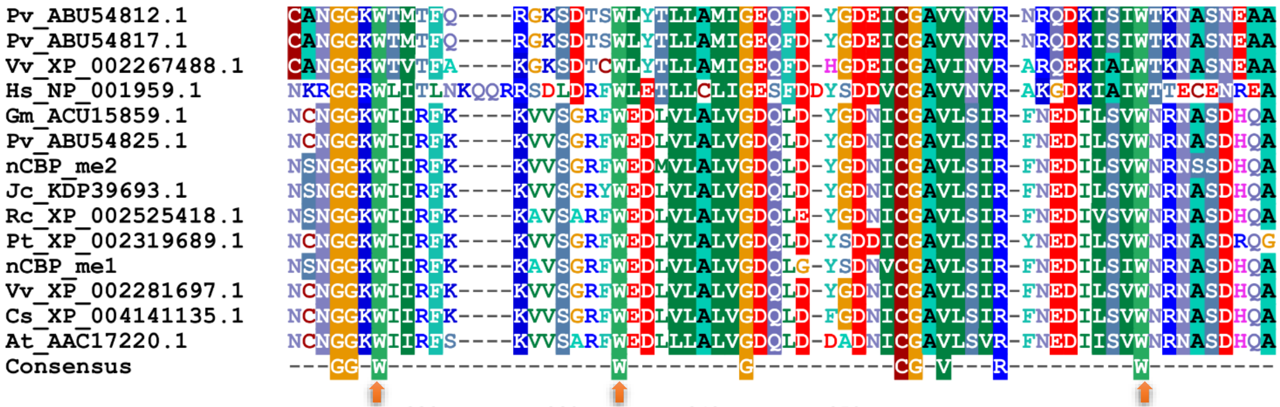

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Consensus           ---GG-W----------------W--------G----------CG-V---R---------W---------
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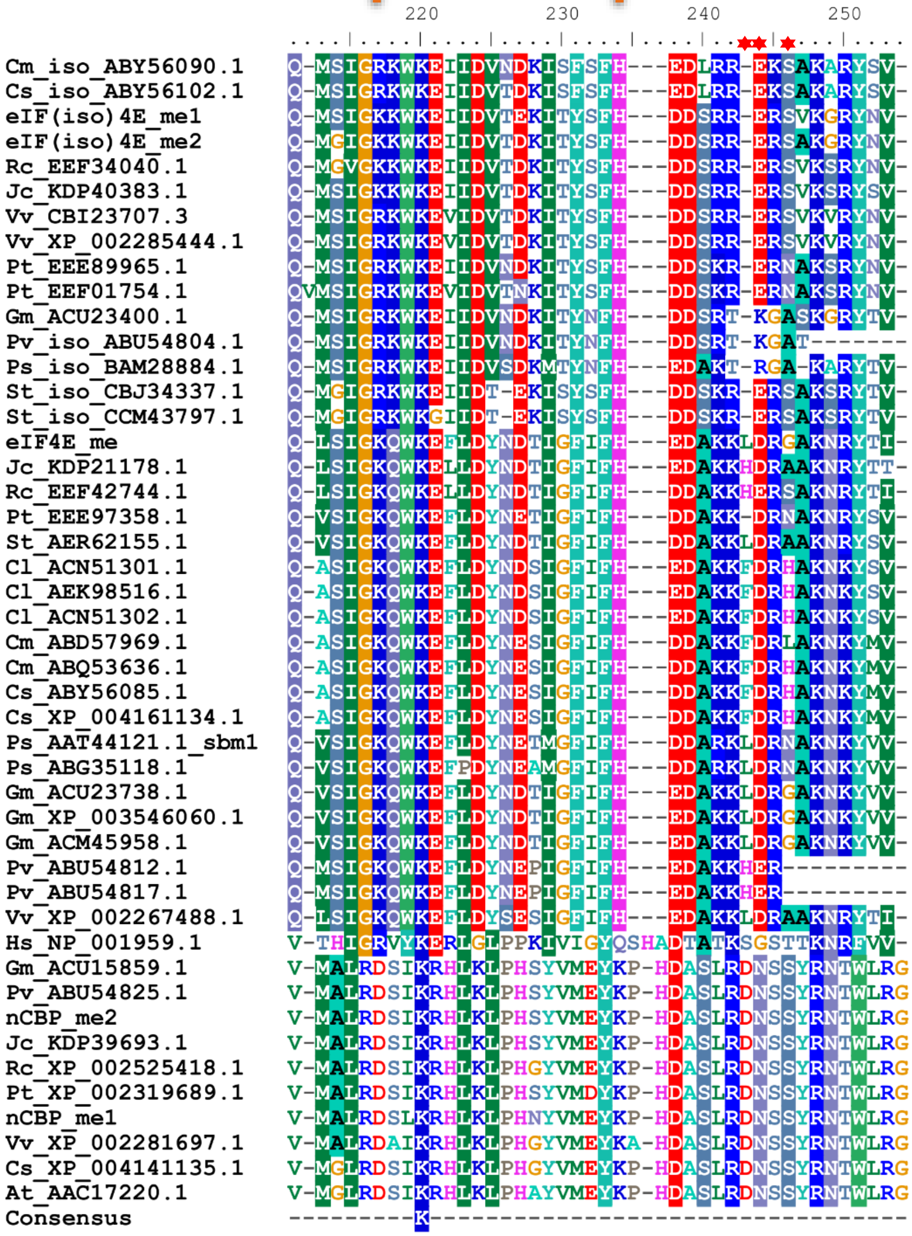

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Jc_KDP40383.1       Q-MSIGKKWKEIIDVTDKITYSFH---DDSRR-ERSVKSRYSV-
Vv_CBI23707.3       Q-MSIGRKWKEVIDVTDKITYSFH---DDSRR-ERSVKVRYNV-
Vv_XP_002285444.1   Q-MSIGRKWKEVIDVTDKITYSFH---DDSRR-ERSVKVRYNV-
Pt_EEE89965.1       Q-MSIGRKWKEIIDVNDKITYSFH---DDSKR-ERNAKSRYNV-
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St_iso_CCM43797.1   Q-MGIGRKWKGIIDT-EKISYSFH---DDSKR-ERSAKSRYTV-
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Jc_KDP21178.1       Q-LSIGKQWKELLDYNDTIGFIFH---EDAKKHDRAAKNRYTT-
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Pt_EEE97358.1       Q-VSIGKQWKEFLDYNETIGFIFH---DDAKK-DRNAKNRYSV-
St_AER62155.1       Q-VSIGKQWKEFLDYNDTIGFIFH---DDAKKLDRAAKNRYSV-
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Cl_AEK98516.1       Q-ASIGKQWKEFLDYNDSIGFIFH---EDAKKFDRHAKNKYSV-
Cl_ACN51302.1       Q-ASIGKQWKEFLDYNDSIGFIFH---EDAKKFDRHAKNKYSV-
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Pv_ABU54817.1       Q-MSIGKQWKEFLDYNEPIGFIFH---EDAKKHER---------
Vv_XP_002267488.1   Q-LSIGKQWKEFLDYSESIGFIFH---EDAKKLDRAAKNRYTI-
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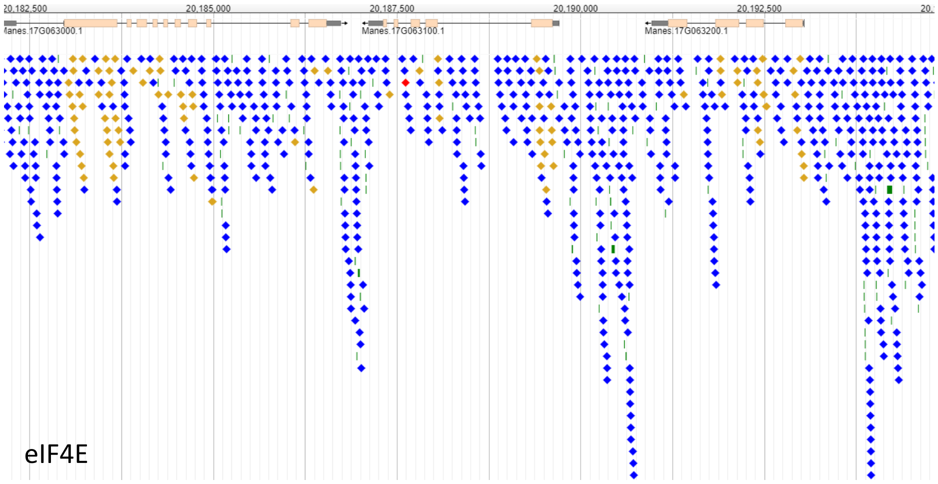
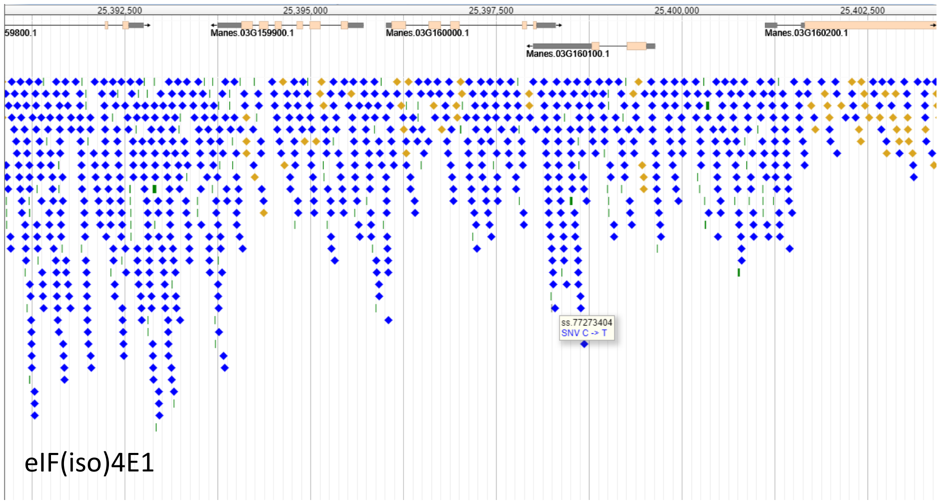
Cs_XP_004141135.1   V-MGLRDSIKRHLKLPHGYVMEYKP-HDASLRDNSSYRNTWLRG
At_AAC17220.1       V-MGLRDSIKRHLKLPHAYVMEYKP-HDASLRDNSSYRNTWLRG
Consensus           ---------K----------------------------------
```

Figure B. Alignment of cassava eIF4E proteins with representative plant and human eIF4E proteins. Proteins were aligned with ClustalX 2.0 [4] and manually inspected and adjusted. Shading of similar amino acids and display were performed with BioEdit 7.09 [5]. Amino acids conserved in all eIF4E proteins are noted in the consensus line. Eight conserved tryptophan (W) amino acids are indicated with arrows and two involved in cap-binding are indicated in red arrows. Positions of eIF4E proteins where amino acid substitutions resulted in recessive resistance to potyviruses in nature or experimentally [6,7] are indicated by red six-point stars. Protein sequences of additional eIF4E family proteins were retrieved from NCBI. Protein sources are identified with two letters representing the initials of genus and species, followed by NCBI accession number. At, *Arabidopsis thaliana*; Ca: *Capsicum annuum*; Cl, *Citrullus lanatus*; Cm, *Cucumis melo*; Cs, *Cucumis sativus*; Gm, *Glycine max*; Hs, *Homo sapiens*; Jc, *Jatropha curcas*; Ps, *Pisum sativum*; Pt, *Populus trichocarpal*; Pv, *Phaseolus vulgaris*; Rc, *Ricinus communis* ; St, *Solanum tuberosum*; and Vv, *Vitis vinifera*.



eIF4E



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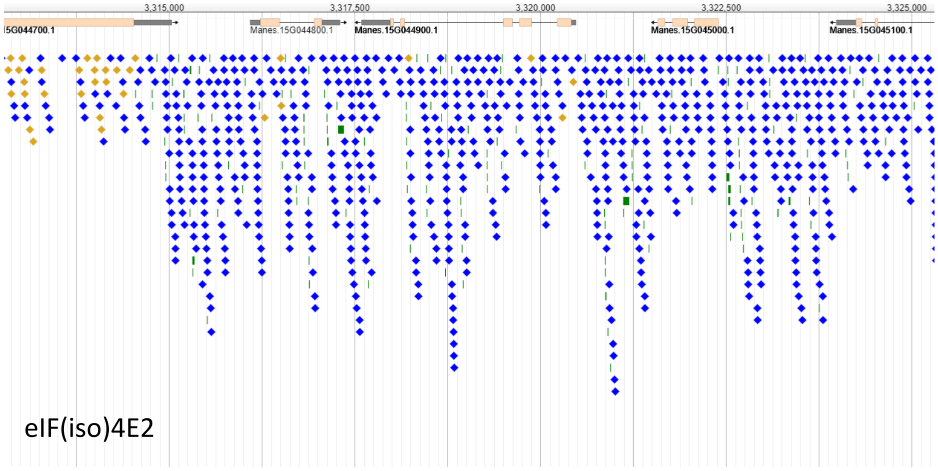

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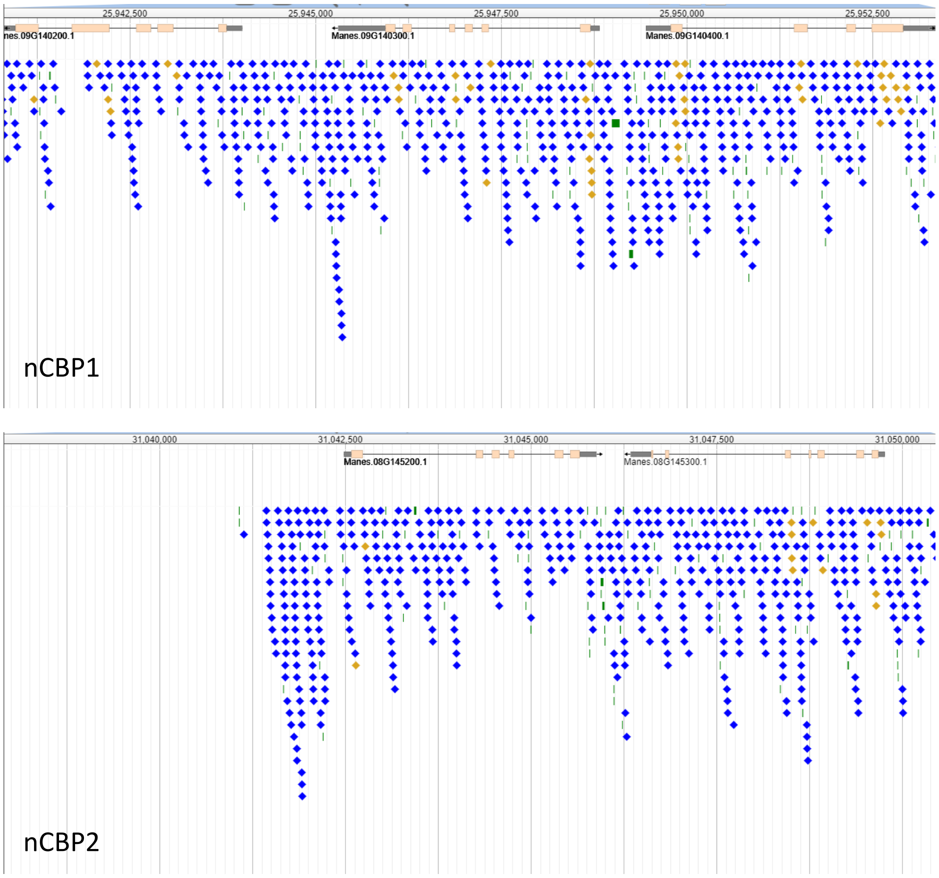

Figure C. Single nucleotide polymorphisms (SNPs) in the five cassava eIF4E genes and the upstream and downstream 5 kb regions. Data were obtained from combined SNPs and indels from 61 cassava accessions curated at Phytozome (phytozome.jgi.doe.gov). Images of SNPs were rendered in the Genome Browser implemented at the same site. Blue diamonds: synonymous nucleotide substitutions in coding regions or substitutions in non-coding regions; yellow diamonds: non-synonymous substitutions in coding regions; red diamonds: missense substitutions; vertical green lines: indels. Only a 2kb region upstream of nCBP2 is available from the genomic sequence.

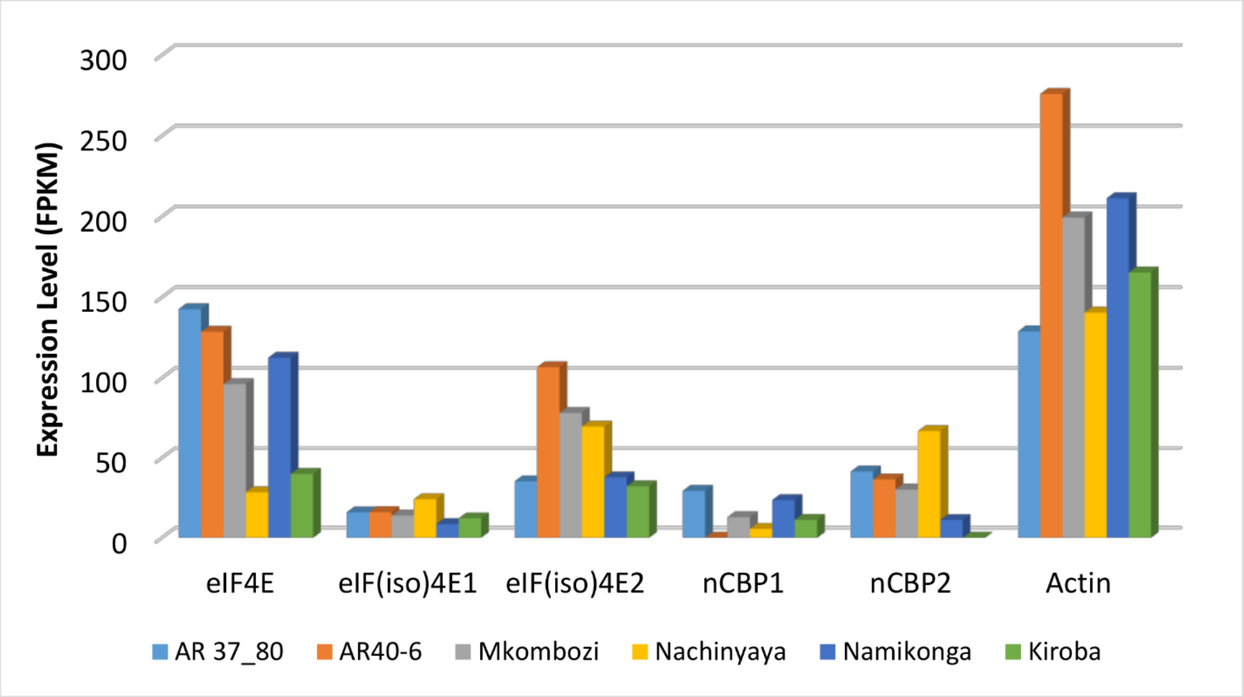

Figure D. Expression levels of five eIF4E genes in CBSD-susceptible and -tolerant lines. RNAseq long reads (0.5 kb) specific to each gene from each of the lines generated by the Life Sciences 454 sequencing were counted and normalized to total mapped reads from each sample to generate the FPKM counts. AR37-80, AR40-6, and Mkombozi were susceptible to CBSD while Kiroba, Nachinyaya, and Namikonga were tolerant to CBSD. Raw data were retrieved from NCBI SRA (accessions SRR955444-SRR955447, SRR955449, SRR955450, SRR955453, and SRR955456) [2].

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