

Transcription-based dissection of floral identity and trichome biosynthesis pathways in *Cannabis sativa* L.

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Sequence ID	Start	Alignment	End	Identity	Coverage
Risteovski.cs10_MADS_REF.XP_030499268.2	(+)	1 MSYSEPNNNI DTHHQYHYHHHEEDDHHDENSSNKQKKIRGKTQIKFIENQTNRVTFSKRRNKAGELSVLCDAKVSLIPNNNKLHETKEMIDLYQTKGVLD	245	100.00	100.00
JL_Mother_Y_protein_KAF4383261.1	(+)	1 MSYSEPNNNI DTHHQYHYHHHEEDDHHDENSSNKQKKIRGKTQIKFIENQTNRVTFSKRRNKAGELSVLCDAKVSLIPNNNKLHETKEMIDLYQTKGVLD	179	91.67	73.06
Chemdog91.pep.CsCD91_00G0095450	(+)	1 MSYSEPNNNI DTHHQYHYHHHEEDDHHDENSSNKQKKIRGKTQIKFIENQTNRVTFSKRRNKAGELSVLCDAKVSLIPNNNKLHETKEMIDLYQTKGVLD	245	99.59	100.00
CBDRx-18.pep.CsCBD_04G0027110	(+)	1 MSYSEPNNNI DTHHQYHYHHHEEDDHHDENSSNKQKKIRGKTQIKFIENQTNRVTFSKRRNKAGELSVLCDAKVSLIPNNNKLHETKEMIDLYQTKGVLD	245	100.00	100.00
LAConfidential.pep.CsLAC_00G0003590	(+)	1 MSYSEPNNNI DTHHQYHYHHHEEDDHHDENSSNKQKKIRGKTQIKFIENQTNRVTFSKRRNKAGELSVLCDAKVSLIPNNNKLHETKEMIDLYQTKGVLD	245	100.00	100.00
PBBKush.pep.CsPBB_00G0001540	(+)	1 MSYSEPNNNI DTHHQYHYHHHEEDDHHDENSSNKQKKIRGKTQIKFIENQTNRVTFSKRRNKAGELSVLCDAKVSLIPNNNKLHETKEMIDLYQTKGVLD	245	100.00	100.00
PurpleKush.pep.CsPKP_09G0005340	(+)	1 MSYSEPNNNI DTHHQYHYHHHEEDDHHDENSSNKQKKIRGKTQIKFIENQTNRVTFSKRRNKAGELSVLCDAKVSLIPNNNKLHETKEMIDLYQTKGVLD	245	100.00	100.00
pink_pepper_XP_030499268.2	(+)	1 MSYSEPNNNI DTHHQYHYHHHEEDDHHDENSSNKQKKIRGKTQIKFIENQTNRVTFSKRRNKAGELSVLCDAKVSLIPNNNKLHETKEMIDLYQTKGVLD	245	100.00	100.00

Figure S1 - Multiple Sequence Alignment Visualization of Clade AP3 from OG0000033

Sequence ID	Start	Alignment	End	Identity	Coverage	Mismatches	
Risteovski.cs10.MADS.REF.XP_030480504.1	(+)	1	MAYNNNNNNNNNNVNSISMSMSMSVSSPGRKMRGKI EI KRI ENITNMQVTFCKRRNGLKKAYELSVLCDAEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	297	100.00	100.00	0
CBDRx-18.pep.CsCBD_09G0023430	(+)	1	MAYNNNNNNNNNNVNSISMSMSMSVSSPGRKMRGKI EI KRI ENITNMQVTFCKRRNGLKKAYELSVLCDAEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	297	100.00	100.00	0
pink_pepper.XP_030480504.1	(+)	1	MAYNNNNNNNNNNVNSISMSMSMSVSSPGRKMRGKI EI KRI ENITNMQVTFCKRRNGLKKAYELSVLCDAEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	297	100.00	100.00	0
PurpleKush.pep.CsPKP_07G0028690	(+)	1	MAYNNNNNNNNNNVNSISMSMSMSVSSPGRKMRGKI EI KRI ENITNMQVTFCKRRNGLKKAYELSVLCDAEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	298	99.66	100.00	0
Finola.pep.CsFN_06G0064570	(+)	1	MAYNNNNNNNNNNVNSISMSMSMSVSSPGRKMRGKI EI KRI ENITNMQVTFCKRRNGLKKAYELSVLCDAEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	290	94.63	97.31	7
PBBKush.pep.CsPBB_00G0012070	(+)	1	MAYNNNNNNNNNNVNSISMSMSMSVSSPGRKMRGKI EI KRI ENITNMQVTFCKRRNGLKKAYELSVLCDAEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	295	91.00	97.31	16
Finola.pep.CsFN_06G0001290	(+)	1	MAYNNNNNNNNNNVNSISMSMSMSVSSPGRKMRGKI EI KRI ENITNMQVTFCKRRNGLKKAYELSVLCDAEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	276	85.67	91.92	16
Finola.pep.CsFN_00G0064000	(+)	1	MEFGSNNNNEEEGGSSSRKMRGKI EI KRI ENITNMQVTFCKRRNGLKKAYELSVLCDAEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	83	70.53	27.95	16
LAConfidential.pep.CsLAC_00G0052990	(+)	1	MEFGSNNNNEEEGGSSSRKMRGKI EI KRI ENITNMQVTFCKRRNGLKKAYELSVLCDAEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	83	70.53	27.95	16
JL_Mother_Y_protein.KAF4365251.1	(+)	1	MAYNNNNNNNNNNVNSISMSMSMSVSSPGRKMRGKI EI KRI ENITNMQVTFCKRRNGLKKAYELSVLCDAEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	209	69.70	70.37	2
PBBKush.pep.CsPBB_00G0179580	(+)	1	MEFGSNNNNEEEGGSSSRKMRGKI EI KRI ENITNMQVTFCKRRNGLKKAYELSVLCDAEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	179	64.95	57.91	46
Chemdog91.pep.CsCD91_00G0128130	(+)	1	MRGKI EI KRI ENITNMQVTFCKRRNGLKKAYELSVLCDAEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	180	64.74	60.27	56
Cannatonic.pep.CsCAN_00G0145860	(+)	1	MRGKI EI KRI ENITNMQVTFCKRRNGLKKAYELSVLCDAEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	258	60.59	85.86	92
pink_pepper.XP_030481705.2	(+)	1	MEFGSNNNNEEEGGSSSRKMRGKI EI KRI ENITNMQVTFCKRRNGLKKAYELSVLCDAEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	281	57.14	93.27	105
Risteovski.cs10.MADS.REF.XP_030481705.2	(+)	1	MEFGSNNNNEEEGGSSSRKMRGKI EI KRI ENITNMQVTFCKRRNGLKKAYELSVLCDAEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	281	57.14	93.27	105
CBDRx-18.pep.CsCBD_10G0025940	(+)	1	MEFGSNNNNEEEGGSSSRKMRGKI EI KRI ENITNMQVTFCKRRNGLKKAYELSVLCDAEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	279	57.00	92.93	105
PBBKush.pep.CsPBB_00G0038630	(+)	1	MRGKI EI KRI ENITNMQVTFCKRRNGLKKAYELSVLCDAEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	227	55.47	75.76	88
pink_pepper.XP_060961491.1	(+)	1	MRGKI EI KRI ENITNMQVTFCKRRNGLKKAYELSVLCDAEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	227	55.47	75.76	88
pink_pepper.XP_060961490.1	(+)	1	MRGKI EI KRI ENITNMQVTFCKRRNGLKKAYELSVLCDAEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	227	55.47	75.76	88
PurpleKush.pep.CsPKP_06G0018600	(+)	1	MRGKI EI KRI ENITNMQVTFCKRRNGLKKAYELSVLCDAEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	227	55.47	75.76	88
Cannatonic.pep.CsCAN_00G0137570	(+)	1	MRGKI EI KRI ENITNMQVTFCKRRNGLKKAYELSVLCDAEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	227	55.47	75.76	88
pink_pepper.XP_060961494.1	(+)	1	MRGKI EI KRI ENITNMQVTFCKRRNGLKKAYELSVLCDAEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	226	55.06	75.42	88
pink_pepper.XP_060961493.1	(+)	1	MRGKI EI KRI ENITNMQVTFCKRRNGLKKAYELSVLCDAEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	226	55.06	75.42	88
pink_pepper.XP_060961492.1	(+)	1	MRGKI EI KRI ENITNMQVTFCKRRNGLKKAYELSVLCDAEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	226	55.06	75.42	88
Finola.pep.CsFN_09G0025020	(+)	1	MEFGSNNNNEEEGGSSSRKMRGKI EI KRI ENITNMQVTFCKRRNGLKKAYELSVLCDAEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	283	54.90	92.26	106
JL_Mother_Y_protein.KAF4377298.1	(+)	1	MRGKI EI KRI ENITNMQVTFCKRRNGLKKAYELSVLCDAEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	197	49.39	65.66	73
Finola.pep.CsFN_00G0078470	(+)	1	MRGKI EI KRI ENITNMQVTFCKRRNGLKKAYELSVLCDAEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	229	43.62	71.72	90
JL_Mother_Y_protein.KAF4376524.1	(+)	1	MEFGSNNNNEEEGGSSSRKMRGKI EI KRI ENITNMQVTFCKRRNGLKKAYELSVLCDAEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	238	43.27	75.08	88
Finola.pep.CsFN_00G0063990	(+)	1	MEFGSNNNNEEEGGSSSRKMRGKI EI KRI ENITNMQVTFCKRRNGLKKAYELSVLCDAEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	136	43.02	45.45	61
PurpleKush.pep.CsPKP_00G0048440	(+)	1	MAYGKATISLLLRKKMMRNGKRLMSNSLSKKEISLEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	259	43.00	86.20	127
LAConfidential.pep.CsLAC_00G0195700	(+)	1	MAYGKATISLLLRKKMMRNGKRLMSNSLSKKEISLEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	114	40.00	37.37	61
Chemdog91.pep.CsCD91_00G0033630	(+)	1	MAYGKATISLLLRKKMMRNGKRLMSNSLSKKEISLEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	112	37.37	37.71	1
CBDRx-18.pep.CsCBD_00G0006340	(+)	1	MAYGKATISLLLRKKMMRNGKRLMSNSLSKKEISLEVALI VFSRRGRLYEYANQSVKSTI DRYKKASSDTSNTGVSVEVNAQFYQQEAAKLRGQ ESLOKQ RELLGECI DSAKPRDLKNLESKLERGI SRI RSKKNELLFAE	68	18.87	22.56	27

Figure S2 - Multiple Sequence Alignment Visualization of Clade AG from OG0000096

Sequence ID	Start	Alignment	End	Identity	Coverage	Mismatches	
Risteovski.cs10.MADS.REF.XP_030510457.1	(+)	1	MGRGKQVEMKLIENKQSRQVTFQAKRRSSGLMKKKAHEL SVLC DVEI GLI VFSGNGRLYEFCSGHSLGNTIERYKTKGKEEKSSNELENC D Y DGLWEDVDLLKG	192	100.00	100.00	0
CBDRx-18.pep.CsCBD_08G0023490	(+)	1	MGRGKQVEMKLIENKQSRQVTFQAKRRSSGLMKKKAHEL SVLC DVEI GLI VFSGNGRLYEFCSGHSLGNTIERYKTKGKEEKSSNELENC D Y DGLWEDVDLLKG	141	69.27	73.44	8
CsCBD_18.pep.CsCBD_08G0023510	(+)	1	MGRGKQVEMKLIENKQSRQVTFQAKRRSSGLMKKKAHEL SVLC DVEI GLI VFSGNGRLYEFCSGHSLGNTIERYKTKGKEEKSSNELENC D Y DGLWEDVDLLKG	216	31.93	83.33	84
Cannatonic.pep.CsCAN_00G0069840	(+)	1	MGRGKQVEMKLIENKQSRQVTFQAKRRSSGLMKKKAHEL SVLC DVEI GLI VFSGNGRLYEFCSGHSLGNTIERYKTKGKEEKSSNELENC D Y DGLWEDVDLLKG	135	76.47	66.15	10
Finola.pep.CsFN_02G0035420	(+)	1	MGRGKQVEMKLIENKQSRQVTFQAKRRSSGLMKKKAHEL SVLC DVEI GLI VFSGNGRLYEFCSGHSLGNTIERYKTKGKEEKSSNELENC D Y DGLWEDVDLLKG	135	89.19	70.31	3
JL_Mother_Y_protein.KAF4348876.1	(+)	1	MGRGKQVEMKLIENKQSRQVTFQAKRRSSGLMKKKAHEL SVLC DVEI GLI VFSGNGRLYEFCSGHSLGNTIERYKTKGKEEKSSNELENC D Y DGLWEDVDLLKG	151	47.40	67.19	56
LACConfidential.pep.CsLAC_00G0012730	(+)	1	MGRGKQVEMKLIENKQSRQVTFQAKRRSSGLMKKKAHEL SVLC DVEI GLI VFSGNGRLYEFCSGHSLGNTIERYKTKGKEEKSSNELENC D Y DGLWEDVDLLKG	77	80.00	40.10	5
PurpleKush.pep.CsPKP_02G0005400	(+)	1	MGRGKQVEMKLIENKQSRQVTFQAKRRSSGLMKKKAHEL SVLC DVEI GLI VFSGNGRLYEFCSGHSLGNTIERYKTKGKEEKSSNELENC D Y DGLWEDVDLLKG	135	89.19	70.31	3
pink_pepper.XP_030510457.1	(+)	1	MGRGKQVEMKLIENKQSRQVTFQAKRRSSGLMKKKAHEL SVLC DVEI GLI VFSGNGRLYEFCSGHSLGNTIERYKTKGKEEKSSNELENC D Y DGLWEDVDLLKG	192	100.00	100.00	0
pink_pepper.XP_060973467.1	(+)	1	MGRGKQVEMKLIENKQSRQVTFQAKRRSSGLMKKKAHEL SVLC DVEI GLI VFSGNGRLYEFCSGHSLGNTIERYKTKGKEEKSSNELENC D Y DGLWEDVDLLKG	192	100.00	100.00	0

Figure S3 - Multiple Sequence Alignment Visualization of Clade FLC from OG0000096

Sequence ID	Start	Alignment	End	Identity	Coverage	Mismatches	
Ristevski_cs10_MADS_REF_XP_030484711.2	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	260	100.00	100.00	0
LAConfidential_pep_CsLAC_00G0190040	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	83	26.87	31.92	47
LAConfidential_pep_CsLAC_00G0071310	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	88	67.71	33.85	23
Finola_pep_CsFN_07G0011180	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	91	56.20	35.00	23
PurpleKush_pep_CsPK_08G0012930	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	101	96.04	38.85	4
PBBKush_pep_CsPBB_00G0253870	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	112	11.67	39.23	74
LAConfidential_pep_CsLAC_00G0197970	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	116	10.23	40.77	79
JL_Mother_Y_protein_KAF4353554.1	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	113	69.43	43.46	4
CBDRx-18_pep_CsCBD_10G0009770	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	114	97.37	43.85	3
Finola_pep_CsFN_09G0019230	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	114	97.37	43.85	3
Cannatonic_pep_CsCAN_00G0023830	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	114	100.00	43.85	0
Finola_pep_CsFN_09G0018310	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	121	40.93	46.54	15
PBBKush_pep_CsPBB_00G0249120	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	131	51.01	49.62	53
Finola_pep_CsFN_07G0011170	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	140	22.89	50.38	85
PurpleKush_pep_CsPK_08G0012950	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	154	71.86	52.69	17
Finola_pep_CsFN_00G0037410	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	138	55.24	53.08	59
Finola_pep_CsFN_09G0019220	(+)	3	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	140	99.28	53.08	1
JL_Mother_Y_protein_KAF4390551.1	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	163	57.99	61.92	63
Cannatonic_pep_CsCAN_00G0083430	(+)	3	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	181	76.56	62.31	15
PurpleKush_pep_CsPK_08G0026940	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	168	29.41	62.31	102
Finola_pep_CsFN_04G0014590	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	176	26.14	63.85	97
PBBKush_pep_CsPBB_00G0124390	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	181	30.05	65.38	109
Chemdog91_pep_CsCD91_00G0034500	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	181	32.02	65.38	105
CBDRx-18_pep_CsCBD_10G0009760	(+)	3	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	216	69.63	66.92	25
pink_pepper_XP_060957998.1	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	175	64.57	66.92	61
PurpleKush_pep_CsPK_00G0107280	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	179	75.92	68.85	34
PurpleKush_pep_CsPK_00G0122050	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	179	75.92	68.85	34
pink_pepper_XP_060962641.1	(+)	13	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	206	26.04	70.38	114
LAConfidential_pep_CsLAC_00G0141940	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	192	35.50	70.38	112
Chemdog91_pep_CsCD91_00G0066140	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	223	52.99	80.77	68
CBDRx-18_pep_CsCBD_10G0009780	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	223	52.99	80.77	68
PurpleKush_pep_CsPK_08G0012880	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	223	52.99	80.77	68
PurpleKush_pep_CsPK_09G0022210	(+)	16	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	281	25.08	81.92	136
PurpleKush_pep_CsPK_06G0022280	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	233	40.75	85.38	114
pink_pepper_XP_030492903.2	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	236	45.28	86.54	105
Ristevski_cs10_MADS_REF_XP_030492903.2	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	236	45.28	86.54	105
pink_pepper_XP_060968229.1	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	235	45.45	86.54	105
JL_Mother_Y_protein_KAF4382065.1	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	235	43.18	86.54	111
Cannatonic_pep_CsCAN_00G0023790	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	238	66.42	88.46	52
CBDRx-18_pep_CsCBD_04G0008320	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	243	46.04	89.23	110
pink_pepper_XP_030496177.1	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	243	46.04	89.23	110
PBBKush_pep_CsPBB_00G0096760	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	243	46.04	89.23	110
Ristevski_cs10_MADS_REF_XP_030496177.1	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	243	46.04	89.23	110
PurpleKush_pep_CsPK_09G0022150	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	243	46.04	89.23	110
pink_pepper_XP_030492902.2	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	249	46.21	91.92	117
pink_pepper_XP_030492901.2	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	250	46.04	91.92	117
CBDRx-18_pep_CsCBD_03G0018590	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	249	45.45	91.92	119
Ristevski_cs10_MADS_REF_XP_030492901.2	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	250	46.04	91.92	117
PurpleKush_pep_CsPK_04G0013630	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	249	45.45	91.92	119
Cannatonic_pep_CsCAN_00G0002440	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	249	45.45	91.92	119
Finola_pep_CsFN_09G0004710	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	248	47.91	91.92	113
pink_pepper_XP_060958690.1	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	255	67.03	93.08	59
pink_pepper_XP_060958689.1	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	255	67.03	93.08	59
pink_pepper_XP_030484352.2	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	253	48.86	93.46	114
JL_Mother_Y_protein_KAF4385536.1	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	252	49.05	93.46	114
pink_pepper_XP_060957999.1	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	253	48.86	93.46	114
pink_pepper_XP_030484353.2	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	252	49.05	93.46	114
Cannatonic_pep_CsCAN_00G0178460	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	252	49.05	93.46	114
CBDRx-18_pep_CsCBD_10G0021460	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	252	49.05	93.46	114
Ristevski_cs10_MADS_REF_XP_030484352.2	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	253	48.86	93.46	114
pink_pepper_XP_030484349.1	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	256	48.50	93.85	115
CBDRx-18_pep_CsCBD_10G0021450	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	255	48.68	93.85	115
Ristevski_cs10_MADS_REF_XP_030484349.1	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	256	48.50	93.85	115
Cannatonic_pep_CsCAN_00G0178450	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	255	48.68	93.85	115
pink_pepper_XP_030484020.1	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	258	67.77	94.23	60
Ristevski_cs10_MADS_REF_XP_030484020.1	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	258	67.77	94.23	60
pink_pepper_XP_060958688.1	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	258	67.77	94.23	60
PBBKush_pep_CsPBB_00G0054540	(+)	5	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	446	34.30	98.46	103
JL_Mother_Y_protein_KAF4353552.1	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	269	70.33	98.46	64
pink_pepper_XP_060958687.1	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	269	70.33	98.46	64
JL_Mother_Y_protein_KAF4353551.1	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	269	70.33	98.46	64
Finola_pep_CsFN_09G0018330	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	269	70.33	98.46	64
Ristevski_cs10_MADS_REF_XP_030484019.1	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	269	70.33	98.46	64
PBBKush_pep_CsPBB_00G0054550	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	277	68.33	98.46	64
pink_pepper_XP_030484019.1	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	269	70.33	98.46	64
pink_pepper_XP_030484711.2	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	260	100.00	100.00	0
Ristevski_cs10_MADS_REF_XP_030484710.2	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	267	97.38	100.00	0
pink_pepper_XP_030484710.2	(+)	1	MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLF EFCSGPSITKTTLERYEKCCYAEQESKLLSGKDIESTYQEYLKLKE	267	97.38	100.00	0

Figure S4 - Multiple Sequence Alignment Visualization of Clade SEP from OG0000096

Sequence ID	Start	Alignment	End	Identity	Coverage	Mismatches	
Ristevski.cs10_MADS_REF_XP_030480518.1	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRNGLLKKAKELAI LCDAEVGV M FSSTGKLYDFSSTSMKTI I DRYNKAKE DHHPGNPTSEVKFWQREAA MLRQQLQSLQENHRQMMGEELSGLNVKELQNLNQLMSLRGVRMKKDOI LMHEI Q	249	100.00	100.00	0
JL_Mother_Y_protein_KAF4353427.1	(+)	14	DFKLSIKITF	27	22.22	5.62	10
PBBKush.pep.CsPBB_00G0119430	(+)	31	LCR I I KLSLSIKSRNYPFKLRWREWKYVM	155	2.55	12.45	23
LAConfidential.pep.CsLAC_00G0147020	(+)	21	GL I I VPKLSLSIKSRNYPFKLRWREWKYVM	134	3.01	12.85	23
Chemdog91.pep.CsCD91_00G0040530	(+)	6	GL I I KLSLSIKSRNYPFKLRWREWKYVM	119	3.68	12.85	21
PurpleKush.pep.CsPK_09G0011800	(+)	1	MR I I I KLSLSIKSRNYPFKLRWREWKYVM	146	3.00	13.25	23
PurpleKush.pep.CsPK_09G0030130	(+)	35	MRGCV I VPKLSLSIKSRNYPFKLRWREWKYVM	183	3.29	14.06	24
pink_pepper_XP_030507718.2	(+)	43	MRGCV I VPKLSLSIKSRNYPFKLRWREWKYVM	191	3.29	14.06	24
JL_Mother_Y_protein_KAF4355296.1	(+)	59	MRGCV I VPKLSLSIKSRNYPFKLRWREWKYVM	207	3.29	14.06	24
PurpleKush.pep.CsPK_05G0002120	(+)	43	MRGCV I VPKLSLSIKSRNYPFKLRWREWKYVM	191	3.29	14.06	24
Finola.pep.CsFN_08G0001150	(+)	3	KHK I VAVFLSLI DLPQVYTS HQANEWRLYKMDA AIV	167	4.74	20.48	39
pink_pepper_XP_060959818.1	(+)	10	MRGCV I VVEFLSLI DLPQVYTS HQANEWRLYKMDA D E	175	5.14	20.88	39
PurpleKush.pep.CsPK_09G0030140	(+)	9	MRGCV I VVEFLSLI DLPQVYTS HQANEWRLYKMDA D E	174	5.14	20.88	39
PurpleKush.pep.CsPK_05G0002140	(+)	9	MRGCV I VVEFLSLI DLPQVYTS HQANEWRLYKMDA D E	174	5.14	20.88	39
PBBKush.pep.CsPBB_00G0203680	(+)	9	MRGCV I VVEFLSLI DLPQVYTS HQANEWRLYKMDA D E	174	5.14	20.88	39
pink_pepper_XP_030507538.2	(+)	9	MRGCV I VVEFLSLI DLPQVYTS HQANEWRLYKMDA D E	174	5.14	20.88	39
Cannatonic.pep.CsCAN_00G0143830	(+)	9	MRGCV I VVEFLSLI DLPQVYTS HQANEWRLYKMDA D E	174	5.14	20.88	39
CBDRx-18.pep.CsCBD_07G0002070	(+)	9	MRGCV I VVEFLSLI DLPQVYTS HQANEWRLYKMDA D E	174	5.14	20.88	39
CBDRx-18.pep.CsCBD_07G0002030	(+)	9	MRGCV I VVEFLSLI DLPQVYTS HQANEWRLYKMDA D E	174	5.14	20.88	39
LAConfidential.pep.CsLAC_00G0213070	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRNGLLKKAKELSI LCDAVG I I FSSTGKLYDFSSTRL	67	23.11	26.51	11
JL_Mother_Y_protein_KAF4381059.1	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRNGLLKKAKELSI LCDAVG I I FSSTGKLYDFSSTRL	68	64.37	27.31	12
JL_Mother_Y_protein_KAF4377227.1	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRNGLLKKAKELAI LCDAEVGV M FSSTGKLYDFSSTSP E	71	64.21	28.51	10
JL_Mother_Y_protein_KAF4353425.1	(+)	1					
Chemdog91.pep.CsCD91_00G0124020	(+)	1					
PBBKush.pep.CsPBB_00G0256530	(+)	1					
JL_Mother_Y_protein_KAF4381058.1	(+)	1					
Finola.pep.CsFN_00G0075040	(+)	53	MGRGKI VI RRI DNSTSRQVTF SKRRNGLLKKAKELAI LCDAEVGV M FSSTGKLYDFSSTRV FVINYK K KERRREL I P LLS F L S F K K K	144	69.47	36.95	26
JL_Mother_Y_protein_KAF4353426.1	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRGL K KAKELAI LCDAEVGV I FSSTGKLYE FANTSMKSI I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	110	32.23	43.78	31
PBBKush.pep.CsPBB_00G0119440	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRGL K KAKELAI LCDAEVGV I FSSTGKLYE FANTSMKSI I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	121	55.28	48.19	31
LAConfidential.pep.CsLAC_00G0123710	(+)	1					
Cannatonic.pep.CsCAN_00G0060700	(+)	30	MRGCV I I KLSLSIKSRNYPFKLRWREWKYVM L VNRSVRSI GEGTGKLYE FANTSMKSI I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	154	50.00	51.00	44
Finola.pep.CsFN_03G0003970	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRNGLLKKAKELSI LCDAVG I I FSSTGKLYDFSSTSMKSV I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	274	16.96	51.00	70
Finola.pep.CsFN_03G000410	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRNGLLKKAKELSI LCDAVG I I FSSTGKLYDFSSTSMKSV I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	146	30.62	51.41	49
JL_Mother_Y_protein_KAF4371276.1	(+)	17	MRGKI GMR I DNSTSRQVTF SKRRGL LKKA QELAI LCDVGV I I FSSTGKLYE FANTSMKSI I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	129	66.89	51.81	28
PurpleKush.pep.CsPK_00G0117890	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRNGLLKKAKELSI LCDAVG I I FSSTGKLYDFSSTSMKSV I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	150	23.18	52.21	76
Ristevski.cs10_MADS_REF_XP_030505853.1	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRNGLLKKAKELSI LCDAVG I I FSSTGKLYDFSSTSMKSV I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	160	30.37	55.82	57
pink_pepper_XP_030505853.1	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRNGLLKKAKELSI LCDAVG I I FSSTGKLYDFSSTSMKSV I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	145	45.49	58.23	34
Finola.pep.CsFN_03G0002820	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRNGLLKKAKELSI LCDAVG I I FSSTGKLYDFSSTSMKSV I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	145	45.49	58.23	34
CBDRx-18.pep.CsCBD_06G0003980	(+)	1					
PurpleKush.pep.CsPK_00G0054150	(+)	1	MKSV I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	196	46.92	65.46	64
pink_pepper_XP_060970360.1	(+)	1	MKSV I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	206	47.96	69.48	67
pink_pepper_XP_030496685.1	(+)	1	MKSV I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	203	55.81	70.68	56
Ristevski.cs10_MADS_REF_XP_030496685.1	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRGL K KAKELAI LCDAEVGV I FSSTGKLYE FANTSMKSI I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	184	67.72	73.49	55
pink_pepper_XP_030480533.1	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRGL K KAKELAI LCDAEVGV I FSSTGKLYE FANTSMKSI I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	184	67.72	73.49	55
Ristevski.cs10_MADS_REF_XP_030496685.1	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRGL K KAKELAI LCDAEVGV I FSSTGKLYE FANTSMKSI I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	184	67.72	73.49	55
pink_pepper_XP_030480533.1	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRNGLLKKAKELAI LCDAEVGV M FSSTGKLYDFSSTSMKTI I DRYNKAKE DHHPGNPTSEVKFWQREAA MLRQQLQSLQENHRQMMGEELSGLNVKELQNLNQLMSLRGVRMKKDOI LMHEI Q	186	98.92	74.70	2
Ristevski.cs10_MADS_REF_XP_030480533.1	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRNGLLKKAKELAI LCDAEVGV M FSSTGKLYDFSSTSMKTI I DRYNKAKE DHHPGNPTSEVKFWQREAA MLRQQLQSLQENHRQMMGEELSGLNVKELQNLNQLMSLRGVRMKKDOI LMHEI Q	186	98.92	74.70	2
pink_pepper_XP_060962849.1	(+)	1	MKTI I DRYNKAKE DHHPGNPTSEVKFWQREAA MLRQQLQSLQENHRQMMGEELSGLNVKELQNLNQLMSLRGVRMKKDOI LMHEI Q	192	96.35	75.50	3
pink_pepper_XP_030496684.2	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRGL K KAKELAI LCDAEVGV I FSSTGKLYE FANTSMKSI I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	204	55.28	76.71	55
Ristevski.cs10_MADS_REF_XP_030496684.2	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRGL K KAKELAI LCDAEVGV I FSSTGKLYE FANTSMKSI I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	204	55.28	76.71	55
JL_Mother_Y_protein_KAF4379552.1	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRNGLLKKAKELSI LCDAVG I I FSSTGKLYDFSSTSMKSV I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	195	69.41	77.91	42
CBDRx-18.pep.CsCBD_04G0020520	(+)	6	GL I I KLSLSIKSRNYPFKLRWREWKYVM L VNRSVRSI GEGTGKLYE FANTSMKSI I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	318	37.61	86.75	93
pink_pepper_XP_030496683.2	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRGL K KAKELAI LCDAEVGV I FSSTGKLYE FANTSMKSI I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	232	63.01	87.95	64
pink_pepper_XP_060970359.1	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRGL K KAKELAI LCDAEVGV I FSSTGKLYE FANTSMKSI I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	232	63.01	87.95	64
Finola.pep.CsFN_07G0027970	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRGL K KAKELAI LCDAEVGV I FSSTGKLYE FANTSMKSI I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	232	63.01	87.95	64
Ristevski.cs10_MADS_REF_XP_030496683.2	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRGL K KAKELAI LCDAEVGV I FSSTGKLYE FANTSMKSI I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	232	63.01	87.95	64
Finola.pep.CsFN_00G0077650	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRGL K KAKELAI LCDAEVGV I FSSTGKLYE FANTSMKSI I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	232	63.41	87.95	63
pink_pepper_XP_060965911.1	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRNGLLKKAKELSI LCDAVG I I FSSTGKLYDFSSTSMKSV I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	250	60.51	89.56	56
PurpleKush.pep.CsPK_09G0011810	(+)	5	EEODLE I RLROOGAPAYVPAAQAEI VVAANLEPL YEREARLVI GEGTGKLYE FANTSMKSI I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	266	41.70	91.57	110
PBBKush.pep.CsPBB_00G0198070	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRNGLLKKAKELSI LCDAVG I I FSSTGKLYDFSSTSMKSV I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	267	57.09	93.98	73
pink_pepper_XP_030480525.1	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRNGLLKKAKELAI LCDAEVGV M FSSTGKLYDFSSTSMKTI I DRYNKAKE DHHPGNPTSEVKFWQREAA MLRQQLQSLQENHRQMMGEELSGLNVKELQNLNQLMSLRGVRMKKDOI LMHEI Q	239	91.70	94.38	3
pink_pepper_XP_060962848.1	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRNGLLKKAKELAI LCDAEVGV M FSSTGKLYDFSSTSMKTI I DRYNKAKE DHHPGNPTSEVKFWQREAA MLRQQLQSLQENHRQMMGEELSGLNVKELQNLNQLMSLRGVRMKKDOI LMHEI Q	235	94.38	94.38	0
Ristevski.cs10_MADS_REF_XP_030480525.1	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRNGLLKKAKELAI LCDAEVGV M FSSTGKLYDFSSTSMKTI I DRYNKAKE DHHPGNPTSEVKFWQREAA MLRQQLQSLQENHRQMMGEELSGLNVKELQNLNQLMSLRGVRMKKDOI LMHEI Q	239	91.70	94.38	3
pink_pepper_XP_030503511.1	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRNGLLKKAKELSI LCDAVG I I FSSTGKLYDFSSTSMKSV I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	264	63.41	95.18	62
Finola.pep.CsFN_03G0002560	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRNGLLKKAKELSI LCDAVG I I FSSTGKLYDFSSTSMKSV I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	264	63.41	95.18	62
Cannatonic.pep.CsCAN_00G0237870	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRNGLLKKAKELSI LCDAVG I I FSSTGKLYDFSSTSMKSV I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	264	61.96	95.18	66
CBDRx-18.pep.CsCBD_06G0004040	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRNGLLKKAKELSI LCDAVG I I FSSTGKLYDFSSTSMKSV I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	264	63.41	95.18	62
Ristevski.cs10_MADS_REF_XP_030503511.1	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRNGLLKKAKELSI LCDAVG I I FSSTGKLYDFSSTSMKSV I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	264	63.41	95.18	62
PBBKush.pep.CsPBB_00G0146150	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRNGLLKKAKELSI LCDAVG I I FSSTGKLYDFSSTSMKSV I ERYNKAKEE HQOLNP TSEIK LST AKGGGNL KAATA	264	63.41	95.18	62
pink_pepper_XP_030480518.1	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRNGLLKKAKELAI LCDAEVGV M FSSTGKLYDFSSTSMKTI I DRYNKAKE DHHPGNPTSEVKFWQREAA MLRQQLQSLQENHRQMMGEELSGLNVKELQNLNQLMSLRGVRMKKDOI LMHEI Q	249	100.00	100.00	0
pink_pepper_XP_030480508.1	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRNGLLKKAKELAI LCDAEVGV M FSSTGKLYDFSSTSMKTI I DRYNKAKE DHHPGNPTSEVKFWQREAA MLRQQLQSLQENHRQMMGEELSGLNVKELQNLNQLMSLRGVRMKKDOI LMHEI Q	253	97.23	100.00	3
Ristevski.cs10_MADS_REF_XP_030480508.1	(+)	1	MGRGKI VI RRI DNSTSRQVTF SKRRNGLLKKAKELAI LCDAEVGV M FSSTGKLYDFSSTSMKTI I DRYNKAKE DHHPGNPTSEVKFWQREAA MLRQQLQSLQENHRQMMGEELSGLNVKELQNLNQLMSLRGVRMKKDOI LMHEI Q	253	97.23	100.00	3

Figure S5 - Multiple Sequence Alignment Visualization of Clade AGL17 from OG0000207

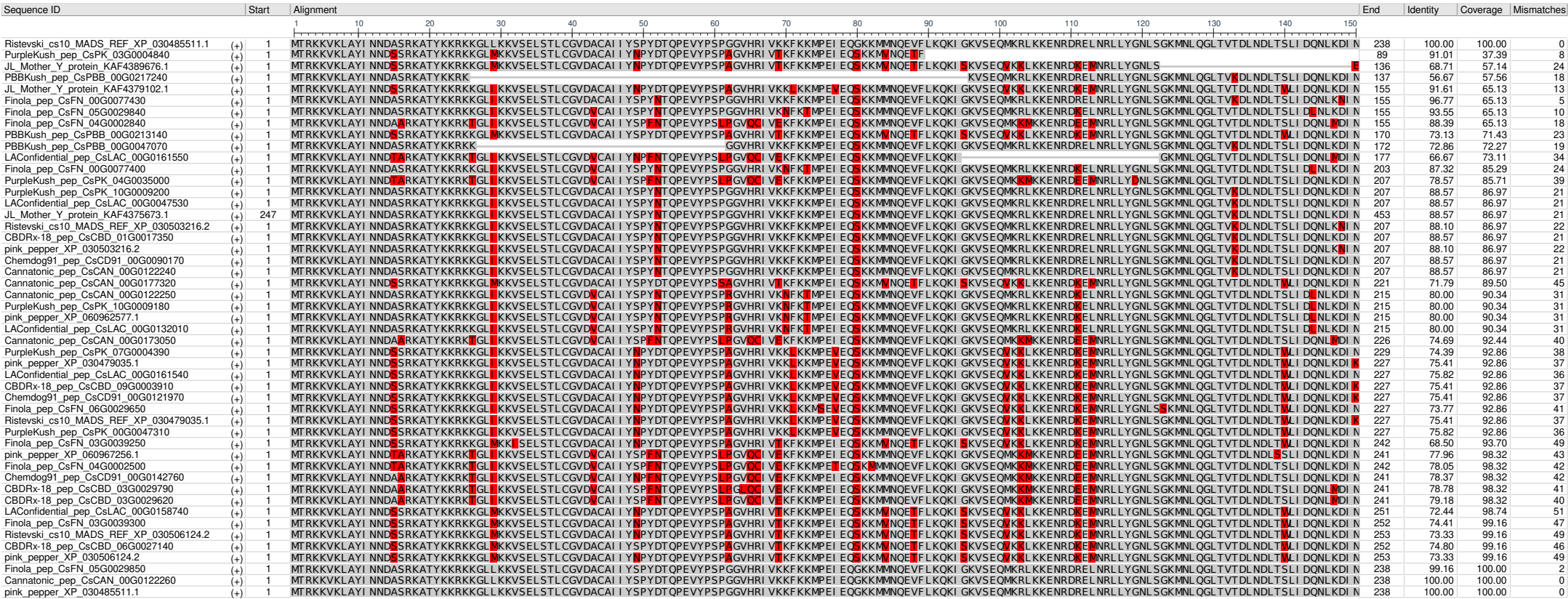


Figure S6 - Multiple Sequence Alignment Visualization of Clade Mg from OG0000366

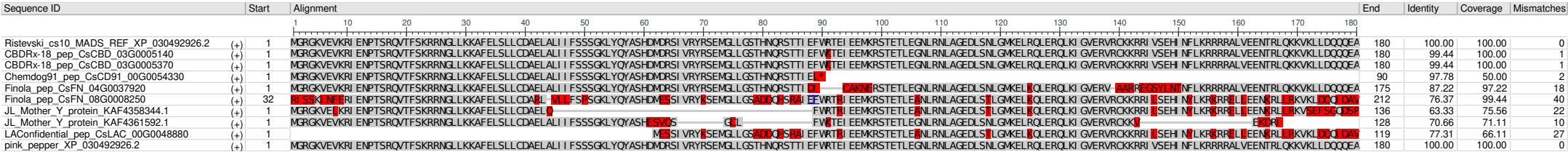


Figure S7 - Multiple Sequence Alignment Visualization of Clade FLC-like from OG0000433

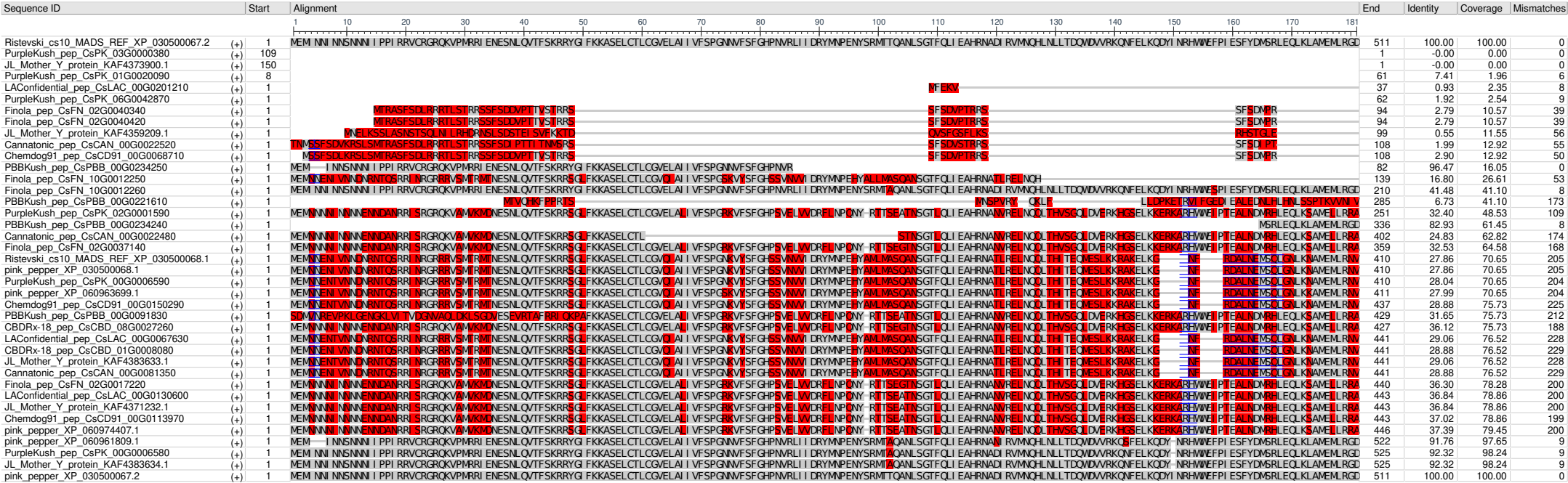


Figure S8 - Multiple Sequence Alignment Visualization of Clade Ma from OG0000580

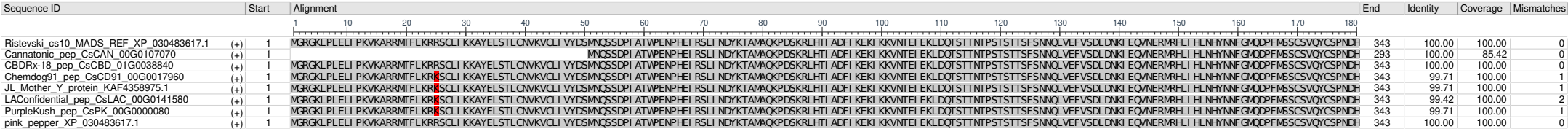


Figure S9 - Multiple Sequence Alignment Visualization of Clade Mb from OG0000736

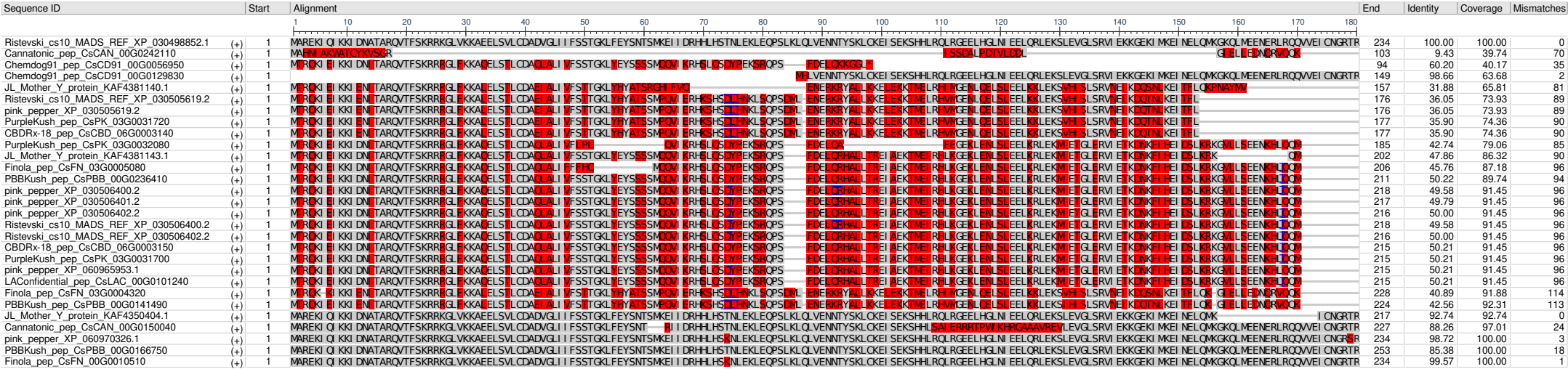


Figure S10 - Multiple Sequence Alignment Visualization of Clade SVP from OG0000955

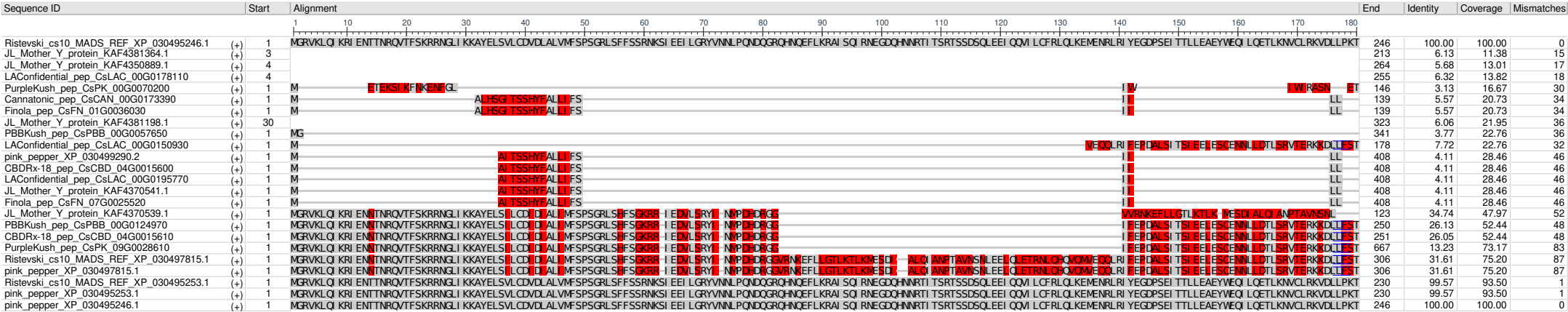


Figure S11 - Multiple Sequence Alignment Visualization of Clade MIKCS from OG0001105

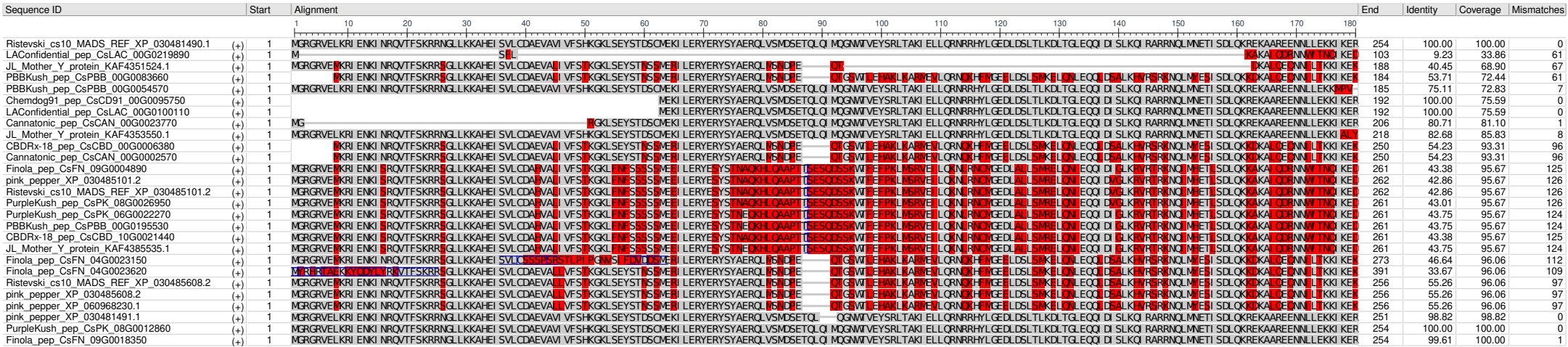


Figure S12 - Multiple Sequence Alignment Visualization of Clade SQUA from OG0001251

Sequence ID	Start	Alignment	End	Identity	Coverage	Mismatches	
		1 10 20 30 40 50 60 70 80 90 100 110 120 130 140 150 160 170 180					
Risteovski.cs10.MADS.REF.XP_030493305.2	(+)	1	MRLKLLKI QRLSEI SNRQVITYSKRRNG LKKAKELSL LCDI D ALLMFSPSGKPTLYQERSNFEEVI TKFSQLTCQERAKRKLLESLALKITFKKL DHDVNI QDFMGSSSQIT EDMSQV/RVLOAQL TGLQRRLSFVSNPDQI NDVENI I QI EDI LRESI NKI QI YKESFRKHQLLPLN	358	100.00	100.00	0
Chemdog91.pep.CsCD91_00G00163360	(+)	1	MRLKLLKI QRLSEI SNRQVITYSKRRNG LKKAKELSL LCDI D ALLMFSPSGKPTLYQERSNFEEVI TKFSQLTCQERAKRKLLESLALKITFKKL DHDVNI QDFMGSSSQIT EDMSQV/RVLOAQL TGLQRRLSFVSNPDQI NDVENI I QI EDI LRESI NKI QI YKESFRKHQLLPLN	124	31.82	34.08	80
pink_pepper.XP_060968155.1	(+)	2	MRLKLLKI QRLSEI SNRQVITYSKRRNG LKKAKELSL LCDI D ALLMFSPSGKPTLYQERSNFEEVI TKFSQLTCQERAKRKLLESLALKITFKKL DHDVNI QDFMGSSSQIT EDMSQV/RVLOAQL TGLQRRLSFVSNPDQI NDVENI I QI EDI LRESI NKI QI YKESFRKHQLLPLN	343	95.53	95.53	0
JL_Mother_Y_protein.KAF4394809.1	(+)	1	MRLKLLKI KXLENTG QRYTYAKRHG LKKAKELSL LCDI D ALLMFSP SGKPTLY QERSN FEVI TKF SQLTCQ ERAKRKLLESLALKITFKKL DHDVNI Q DFMGSSSQIT EDMSQV/RVLOAQL TGLQRRLSFVSNPDQI NDVENI I QI EDI LRESI NKI QI YKESFRKHQLLPLN	351	47.96	95.53	166
JL_Mother_Y_protein.KAF4396743.1	(+)	1	MRLKLLKI KXLENTG QRYTYAKRHG LKKAKELSL LCDI D ALLMFSP SGKPTLY QERSN FEVI TKF SQLTCQ ERAKRKLLESLALKITFKKL DHDVNI Q DFMGSSSQIT EDMSQV/RVLOAQL TGLQRRLSFVSNPDQI NDVENI I QI EDI LRESI NKI QI YKESFRKHQLLPLN	344	47.50	95.53	171
pink_pepper.XP_030484796.1	(+)	1	MRLKLLKI KXLENTG QRYTYAKRHG LKKAKELSL LCDI D ALLMFSP SGKPTLY QERSN FEVI TKF SQLTCQ ERAKRKLLESLALKITFKKL DHDVNI Q DFMGSSSQIT EDMSQV/RVLOAQL TGLQRRLSFVSNPDQI NDVENI I QI EDI LRESI NKI QI YKESFRKHQLLPLN	351	49.44	97.49	171
Risteovski.cs10.MADS.REF.XP_030484795.1	(+)	1	MRLKLLKI KXLENTG QRYTYAKRHG LKKAKELSL LCDI D ALLMFSP SGKPTLY QERSN FEVI TKF SQLTCQ ERAKRKLLESLALKITFKKL DHDVNI Q DFMGSSSQIT EDMSQV/RVLOAQL TGLQRRLSFVSNPDQI NDVENI I QI EDI LRESI NKI QI YKESFRKHQLLPLN	352	49.72	97.77	171
pink_pepper.XP_030484795.1	(+)	1	MRLKLLKI KXLENTG QRYTYAKRHG LKKAKELSL LCDI D ALLMFSP SGKPTLY QERSN FEVI TKF SQLTCQ ERAKRKLLESLALKITFKKL DHDVNI Q DFMGSSSQIT EDMSQV/RVLOAQL TGLQRRLSFVSNPDQI NDVENI I QI EDI LRESI NKI QI YKESFRKHQLLPLN	352	49.72	97.77	171
CBDRx-18.pep.CsCBD_10G0004940	(+)	1	MRLKLLKI KXLENTG QRYTYAKRHG LKKAKELSL LCDI D ALLMFSP SGKPTLY QERSN FEVI TKF SQLTCQ ERAKRKLLESLALKITFKKL DHDVNI Q DFMGSSSQIT EDMSQV/RVLOAQL TGLQRRLSFVSNPDQI NDVENI I QI EDI LRESI NKI QI YKESFRKHQLLPLN	352	49.72	97.77	171
PBBKush.pep.CsPBB_00G0070620	(+)	1	MRLKLLKI KXLENTG QRYTYAKRHG LKKAKELSL LCDI D ALLMFSP SGKPTLY QERSN FEVI TKF SQLTCQ ERAKRKLLESLALKITFKKL DHDVNI Q DFMGSSSQIT EDMSQV/RVLOAQL TGLQRRLSFVSNPDQI NDVENI I QI EDI LRESI NKI QI YKESFRKHQLLPLN	352	49.72	97.77	171
LAConfidential.pep.CsLAC_00G0082750	(+)	1	MRLKLLKI KXLENTG QRYTYAKRHG LKKAKELSL LCDI D ALLMFSP SGKPTLY QERSN FEVI TKF SQLTCQ ERAKRKLLESLALKITFKKL DHDVNI Q DFMGSSSQIT EDMSQV/RVLOAQL TGLQRRLSFVSNPDQI NDVENI I QI EDI LRESI NKI QI YKESFRKHQLLPLN	352	49.72	97.77	171
Finola.pep.CsFN_09G0031060	(+)	1	MRLKLLKI KXLENTG QRYTYAKRHG LKKAKELSL LCDI D ALLMFSP SGKPTLY QERSN FEVI TKF SQLTCQ ERAKRKLLESLALKITFKKL DHDVNI Q DFMGSSSQIT EDMSQV/RVLOAQL TGLQRRLSFVSNPDQI NDVENI I QI EDI LRESI NKI QI YKESFRKHQLLPLN	352	49.72	97.77	171
Cannatonic.pep.CsCAN_00G0020060	(+)	1	MRLKLLKI KXLENTG QRYTYAKRHG LKKAKELSL LCDI D ALLMFSP SGKPTLY QERSN FEVI TKF SQLTCQ ERAKRKLLESLALKITFKKL DHDVNI Q DFMGSSSQIT EDMSQV/RVLOAQL TGLQRRLSFVSNPDQI NDVENI I QI EDI LRESI NKI QI YKESFRKHQLLPLN	352	49.72	97.77	171
Finola.pep.CsFN_04G0017790	(+)	1	MRLKLLKI QRLSEI SNRQVITYSKRRNG LKKAKELSL LCDI D ALLMFSPSGKPTLYQERSNFEEVI TKFSQLTCQERAKRKLLESLALKITFKKL DHDVNI QDFMGSSSQIT EDMSQV/RVLOAQL TGLQRRLSFVSNPDQI NDVENI I QI EDI LRESI NKI QI YKESFRKHQLLPLN	358	99.16	100.00	3
pink_pepper.XP_030493305.2	(+)	1	MRLKLLKI QRLSEI SNRQVITYSKRRNG LKKAKELSL LCDI D ALLMFSPSGKPTLYQERSNFEEVI TKFSQLTCQERAKRKLLESLALKITFKKL DHDVNI QDFMGSSSQIT EDMSQV/RVLOAQL TGLQRRLSFVSNPDQI NDVENI I QI EDI LRESI NKI QI YKESFRKHQLLPLN	358	100.00	100.00	0
pink_pepper.XP_030493306.2	(+)	1	MRLKLLKI QRLSEI SNRQVITYSKRRNG LKKAKELSL LCDI D ALLMFSPSGKPTLYQERSNFEEVI TKFSQLTCQERAKRKLLESLALKITFKKL DHDVNI QDFMGSSSQIT EDMSQV/RVLOAQL TGLQRRLSFVSNPDQI NDVENI I QI EDI LRESI NKI QI YKESFRKHQLLPLN	358	100.00	100.00	0
pink_pepper.XP_060968152.1	(+)	2	MRLKLLKI QRLSEI SNRQVITYSKRRNG LKKAKELSL LCDI D ALLMFSPSGKPTLYQERSNFEEVI TKFSQLTCQERAKRKLLESLALKITFKKL DHDVNI QDFMGSSSQIT EDMSQV/RVLOAQL TGLQRRLSFVSNPDQI NDVENI I QI EDI LRESI NKI QI YKESFRKHQLLPLN	359	100.00	100.00	0
pink_pepper.XP_060968153.1	(+)	1	MRLKLLKI QRLSEI SNRQVITYSKRRNG LKKAKELSL LCDI D ALLMFSPSGKPTLYQERSNFEEVI TKFSQLTCQERAKRKLLESLALKITFKKL DHDVNI QDFMGSSSQIT EDMSQV/RVLOAQL TGLQRRLSFVSNPDQI NDVENI I QI EDI LRESI NKI QI YKESFRKHQLLPLN	358	100.00	100.00	0
pink_pepper.XP_060968154.1	(+)	1	MRLKLLKI QRLSEI SNRQVITYSKRRNG LKKAKELSL LCDI D ALLMFSPSGKPTLYQERSNFEEVI TKFSQLTCQERAKRKLLESLALKITFKKL DHDVNI QDFMGSSSQIT EDMSQV/RVLOAQL TGLQRRLSFVSNPDQI NDVENI I QI EDI LRESI NKI QI YKESFRKHQLLPLN	358	100.00	100.00	0

Figure S13 - Multiple Sequence Alignment Visualization of Clade MIKCS from OG0001495

Sequence ID	Start	Alignment	End	Identity	Coverage	Mismatches
		1 10 20 30 40 50 60 70 80 90 100 110 120 130 140 150 160 170 180				
Risteovski.cs10.MADS.REF.XP_030490980.2	(+)	1 MGRGKI KI SRI ENKI TRQVTFAKRRAGL LKKTHELAVL CDAQ GLI I FSANGKLYDFCS DPLSMQNI I QYQLTTGTIRI VEQNDTEQLHGE MRR I SETQNLQLSLQRYTGEDLSLTLGELNELEQVLVHSHNRARKFEI LQQQENLQRKI KEHQATAAAAYEEQNVHVTKI EEVE	242	100.00	100.00	0
JL_Mother_Y_protein.KAF4388994.1	(+)	1 MRR I SETQNLQLSLQRYTGEDLSLTLGELNELEQVLVHSHNRARKFEI LQQQENLQRKI KEHQATAAAAYEEQNVHVTKI EEVE	168	86.90	62.40	5
CBDRx-18.pep.CsCBD_10G0010840	(+)	1 MGRGKI KI SRI ENKI TRQVTFAKRRAGL LKKTHELAVL CDAQ GLI I FSANGKLYDFCS DPLSMQNI I QYQLTTGTIRI VEQNDTEQLHGE MRR I SETQNLQLSLQRYTGEDLSLTLGELNELEQVLVHSHNRARKFEI LQQQENLQRKI KEHQATAAAAYEEQNVHVTKI EEVE	250	72.59	96.28	45
Cannatonic.pep.CsCAN_00G0075010	(+)	1 MGRGKI KI SRI ENKI TRQVTFAKRRAGL LKKTHELAVL CDAQ GLI I FSANGKLYDFCS DPLSMQNI I QYQLTTGTIRI VEQNDTEQLHGE MRR I SETQNLQLSLQRYTGEDLSLTLGELNELEQVLVHSHNRARKFEI LQQQENLQRKI KEHQATAAAAYEEQNVHVTKI EEVE	250	72.20	96.28	46
Chemdog91.pep.CsCD91_00G0011680	(+)	1 MGRGKI KI SRI ENKI TRQVTFAKRRAGL LKKTHELAVL CDAQ GLI I FSANGKLYDFCS DPLSMQNI I QYQLTTGTIRI VEQNDTEQLHGE MRR I SETQNLQLSLQRYTGEDLSLTLGELNELEQVLVHSHNRARKFEI LQQQENLQRKI KEHQATAAAAYEEQNVHVTKI EEVE	250	72.20	96.28	46
Finola.pep.CsFN_09G0021140	(+)	1 MGRGKI KI SRI ENKI TRQVTFAKRRAGL LKKTHELAVL CDAQ GLI I FSANGKLYDFCS DPLSMQNI I QYQLTTGTIRI VEQNDTEQLHGE MRR I SETQNLQLSLQRYTGEDLSLTLGELNELEQVLVHSHNRARKFEI LQQQENLQRKI KEHQATAAAAYEEQNVHVTKI EEVE	251	72.31	96.28	45
JL_Mother_Y_protein.KAF4355770.1	(+)	1 MGRGKI KI SRI ENKI TRQVTFAKRRAGL LKKTHELAVL CDAQ GLI I FSANGKLYDFCS DPLSMQNI I QYQLTTGTIRI VEQNDTEQLHGE MRR I SETQNLQLSLQRYTGEDLSLTLGELNELEQVLVHSHNRARKFEI LQQQENLQRKI KEHQATAAAAYEEQNVHVTKI EEVE	250	72.20	96.28	46
LAConfidential.pep.CsLAC_00G0090280	(+)	1 MGRGKI KI SRI ENKI TRQVTFAKRRAGL LKKTHELAVL CDAQ GLI I FSANGKLYDFCS DPLSMQNI I QYQLTTGTIRI VEQNDTEQLHGE MRR I SETQNLQLSLQRYTGEDLSLTLGELNELEQVLVHSHNRARKFEI LQQQENLQRKI KEHQATAAAAYEEQNVHVTKI EEVE	251	72.31	96.28	45
PurpleKush.pep.CsPKP_08G0010530	(+)	1 MGRGKI KI SRI ENKI TRQVTFAKRRAGL LKKTHELAVL CDAQ GLI I FSANGKLYDFCS DPLSMQNI I QYQLTTGTIRI VEQNDTEQLHGE MRR I SETQNLQLSLQRYTGEDLSLTLGELNELEQVLVHSHNRARKFEI LQQQENLQRKI KEHQATAAAAYEEQNVHVTKI EEVE	250	72.59	96.28	45
Risteovski.cs10.MADS.REF.XP_030484436.2	(+)	1 MGRGKI KI SRI ENKI TRQVTFAKRRAGL LKKTHELAVL CDAQ GLI I FSANGKLYDFCS DPLSMQNI I QYQLTTGTIRI VEQNDTEQLHGE MRR I SETQNLQLSLQRYTGEDLSLTLGELNELEQVLVHSHNRARKFEI LQQQENLQRKI KEHQATAAAAYEEQNVHVTKI EEVE	251	72.31	96.28	45
pink_pepper.XP_030484436.2	(+)	1 MGRGKI KI SRI ENKI TRQVTFAKRRAGL LKKTHELAVL CDAQ GLI I FSANGKLYDFCS DPLSMQNI I QYQLTTGTIRI VEQNDTEQLHGE MRR I SETQNLQLSLQRYTGEDLSLTLGELNELEQVLVHSHNRARKFEI LQQQENLQRKI KEHQATAAAAYEEQNVHVTKI EEVE	251	72.31	96.28	45
Finola.pep.CsFN_05G0014890	(+)	1 MGRGKI KI SRI ENKI TRQVTFAKRRAGL LKKTHELAVL CDAQ GLI I FSANGKLYDFCS DPLSMQNI I QYQLTTGTIRI VEQNDTEQLHGE MRR I SETQNLQLSLQRYTGEDLSLTLGELNELEQVLVHSHNRARKFEI LQQQENLQRKI KEHQATAAAAYEEQNVHVTKI EEVE	262	87.40	100.00	13
PurpleKush.pep.CsPKP_06G0036280	(+)	1 MGRGKI KI SRI ENKI TRQVTFAKRRAGL LKKTHELAVL CDAQ GLI I FSANGKLYDFCS DPLSMQNI I QYQLTTGTIRI VEQNDTEQLHGE MRR I SETQNLQLSLQRYTGEDLSLTLGELNELEQVLVHSHNRARKFEI LQQQENLQRKI KEHQATAAAAYEEQNVHVTKI EEVE	258	91.86	100.00	5
Risteovski.cs10.MADS.REF.XP_030490979.2	(+)	1 MGRGKI KI SRI ENKI TRQVTFAKRRAGL LKKTHELAVL CDAQ GLI I FSANGKLYDFCS DPLSMQNI I QYQLTTGTIRI VEQNDTEQLHGE MRR I SETQNLQLSLQRYTGEDLSLTLGELNELEQVLVHSHNRARKFEI LQQQENLQRKI KEHQATAAAAYEEQNVHVTKI EEVE	256	94.53	100.00	0
pink_pepper.XP_030490979.2	(+)	1 MGRGKI KI SRI ENKI TRQVTFAKRRAGL LKKTHELAVL CDAQ GLI I FSANGKLYDFCS DPLSMQNI I QYQLTTGTIRI VEQNDTEQLHGE MRR I SETQNLQLSLQRYTGEDLSLTLGELNELEQVLVHSHNRARKFEI LQQQENLQRKI KEHQATAAAAYEEQNVHVTKI EEVE	256	94.53	100.00	0
pink_pepper.XP_030490980.2	(+)	1 MGRGKI KI SRI ENKI TRQVTFAKRRAGL LKKTHELAVL CDAQ GLI I FSANGKLYDFCS DPLSMQNI I QYQLTTGTIRI VEQNDTEQLHGE MRR I SETQNLQLSLQRYTGEDLSLTLGELNELEQVLVHSHNRARKFEI LQQQENLQRKI KEHQATAAAAYEEQNVHVTKI EEVE	242	100.00	100.00	0

Figure S14 - Multiple Sequence Alignment Visualization of Clade Bsister from OG0002194

Sequence ID	Start	Alignment	End	Identity	Coverage	Mismatches
		1 10 20 30 40 50 60 70 80 90 100 110 120 130 140 150 160 170 180				
Risteovski.cs10_MADS_REF.XP_030482855.1	(+)	1 MGRGKI EI KKI ENTISNRAVITYAKRRKAG FKKAKEI AI LCDKVSLI I VSGSGKDAMDSPDNLSTI CEEYHKHSKEKLPAPAKHENLHNEI EMVKKENENM I ELRHLNGQDI NLNHYELI PI EEALENG LI SVRARKSELVNI LRQNL EAKEEEHKRLI CELHQKMEWGDHGYHNHHI	213	100.00	100.00	0
Chemdog91.pep.CsCD91_00G00136580	(+)	1 MGRGKI EI KKI ENTISNRAVITYAKRRKAG FKKAKEI AI LCDKVSLI I VSGSGKDAMDSPDNLSTI CEEYHKHSKEKLPAPAKHENLHNEI EMVKKENENM I ELRHLNGQDI NLNHYELI PI EEALENG LI SVRARKSELVNI LRQNL EAKEEEHKRLI CELHQKMEWGDHGYHNHHI	141	97.87	66.20	3
Finola.pep.CsFN_08G0037140	(+)	1 MDAMCSPDNLSTI CEEYHKHSKEKLPAPAKHENLHNEI EMVKKENENM I ELRHLNGQDI NLNHYELI PI EEALENG LI SVRARKSELVNI LRQNL EAKEEEHKRLI CELHQKMEWGDHGYHNHHI	160	100.00	75.12	0
PurpleKush.pep.CsPKP_08G0032660	(+)	1 MGRGKI EI KKI ENTISNRAVITYAKRRKAG FKKAKEI AI LCDKVSLI I VSGSGKDAMDSPDNLSTI CEEYHKHSKEKLPAPAKHENLHNEI EMVKKENENM I ELRHLNGQDI NLNHYELI PI EEALENG LI SVRARKSELVNI LRQNL EAKEEEHKRLI CELHQKMEWGDHGYHNHHI	186	83.73	87.32	11
CBDRx-18.pep.CsCBD_10G0026750	(+)	1 MGRGKI EI KKI ENTISNRAVITYAKRRKAG FKKAKEI AI LCDKVSLI I VSGSGKDAMDSPDNLSTI CEEYHKHSKEKLPAPAKHENLHNEI EMVKKENENM I ELRHLNGQDI NLNHYELI PI EEALENG LI SVRARKSELVNI LRQNL EAKEEEHKRLI CELHQKMEWGDHGYHNHHI	213	100.00	100.00	0
JL_Mother_Y_protein.KAF4376578.1	(+)	1 MGRGKI EI KKI ENTISNRAVITYAKRRKAG FKKAKEI AI LCDKVSLI I VSGSGKDAMDSPDNLSTI CEEYHKHSKEKLPAPAKHENLHNEI EMVKKENENM I ELRHLNGQDI NLNHYELI PI EEALENG LI SVRARKSELVNI LRQNL EAKEEEHKRLI CELHQKMEWGDHGYHNHHI	216	98.61	100.00	0
PurpleKush.pep.CsPKP_00G0094330	(+)	1 MGRGKI EI KKI ENTISNRAVITYAKRRKAG FKKAKEI AI LCDKVSLI I VSGSGKDAMDSPDNLSTI CEEYHKHSKEKLPAPAKHENLHNEI EMVKKENENM I ELRHLNGQDI NLNHYELI PI EEALENG LI SVRARKSELVNI LRQNL EAKEEEHKRLI CELHQKMEWGDHGYHNHHI	213	99.53	100.00	1

Figure S15 - Multiple Sequence Alignment Visualization of Clade PI/GLO from OG0005875

Sequence ID	Start	Alignment	End	Identity	Coverage	Mismatches
		102030405060708090100110120130140150160170180				
Risteovski.cs10.MADS.REF.XP_030483127.1	(+)	1MARGVQLRRI ENPVHQRVTFCKRRAGL LKKAKELSVL CDAEI GLVI FSAHGKLYDLATKGTMGQI EKYMKSTKGSVLAQADQQQI LQTQSDQDAKNEI SMLKOEI EI LQKGLRYFMGGAGTNNLDEQI LEKNLELWYHIH RSAKMDI MSCEI QLLKNKEGI LKAANKYLODKI E	213	100.00	100.00	0
Finola.pep.CsFN_00G0041960	(+)	1MARGVQLRRI ENPVHRRLLGLVI FSAHGKLYDLATKGTMGQI EKYMKSTKGSVLAQADQQQI LQTQSDQDAKNEI AKI	84	73.33	39.44	7
Finola.pep.CsFN_00G0041970	(+)	1MARGVQLRRI ENPVHQRVTFCKRRAGL LKKAKELSVL CDAEI GLVI FSAHGKLYDLATKGTMGQI EKYMKSTKGSVLAQADQQQI LQTQSDQDAKNEI SMLKOEI EI LQKGLRYFMGGAGTNNLDEQI LEKNLELWYHIH RSAKMDI MSCEI QLLKNKEGI LKAANKYLODKI E	87	100.00	40.85	0
Chemdog91.pep.CsCD91_00G00081560	(+)	1MARGVQLRRI ENPVHQRVTFCKRRAGL LKKAKELSVL CDAEI GLVI FSAHGKLYDLATKGTMGQI EKYMKSTKGSVLAQADQQQI LQTQSDQDAKNEI SMLKOEI EI LQKGLRYFMGGAGTNNLDEQI LEKNLELWYHIH RSAKMDI MSCEI QLLKNKEGI LKAANKYLODKI E	95	100.00	44.60	0
LAConfidential.pep.CsLAC_00G0031180	(+)	1MARGVQLRRI ENPVHQRVTFCKRRAGL LKKAKELSVL CDAEI GLVI FSAHGKLYDLATKGTMGQI EKYMKSTKGSVLAQADQQQI LQTQSDQDAKNEI SMLKOEI EI LQKGLRYFMGGAGTNNLDEQI LEKNLELWYHIH RSAKMDI MSCEI QLLKNKEGI LKAANKYLODKI E	95	100.00	44.60	0
JL_Mother_Y_protein.KAF4373163.1	(+)	1MARGVQLRRI ENPVHQRVTFCKRRAGL LKKAKELSVL CDAEI GLVI FSAHGKLYDLATKGTMGQI EKYMKSTKGSVLAQADQQQI LQTQSDQDAKNEI SMLKOEI EI LQKGLRYFMGGAGTNNLDEQI LEKNLELWYHIH RSAKMDI MSCEI QLLKNKEGI LKAANKYLODKI E	167	80.49	78.40	2
CBDRx-18.pep.CsCBD_01G0038030	(+)	1MARGVQLRRI ENPVHQRVTFCKRRAGL LKKAKELSVL CDAEI GLVI FSAHGKLYDLATKGTMGQI EKYMKSTKGSVLAQADQQQI LQTQSDQDAKNEI SMLKOEI EI LQKGLRYFMGGAGTNNLDEQI LEKNLELWYHIH RSAKMDI MSCEI QLLKNKEGI LKAANKYLODKI E	213	100.00	100.00	0
Cannatonic.pep.CsCAN_00G0017120	(+)	1MARGVQLRRI ENPVHQRVTFCKRRAGL LKKAKELSVL CDAEI GLVI FSAHGKLYDLATKGTMGQI EKYMKSTKGSVLAQADQQQI LQTQSDQDAKNEI SMLKOEI EI LQKGLRYFMGGAGTNNLDEQI LEKNLELWYHIH RSAKMDI MSCEI QLLKNKEGI LKAANKYLODKI E	213	100.00	100.00	0
PBBKush.pep.CsPBB_00G0247520	(+)	1MARGVQLRRI ENPVHQRVTFCKRRAGL LKKAKELSVL CDAEI GLVI FSAHGKLYDLATKGTMGQI EKYMKSTKGSVLAQADQQQI LQTQSDQDAKNEI SMLKOEI EI LQKGLRYFMGGAGTNNLDEQI LEKNLELWYHIH RSAKMDI MSCEI QLLKNKEGI LKAANKYLODKI E	214	98.60	100.00	2
PurpleKush.pep.CsPKP_06G0028870	(+)	1MARGVQLRRI ENPVHQRVTFCKRRAGL LKKAKELSVL CDAEI GLVI FSAHGKLYDLATKGTMGQI EKYMKSTKGSVLAQADQQQI LQTQSDQDAKNEI SMLKOEI EI LQKGLRYFMGGAGTNNLDEQI LEKNLELWYHIH RSAKMDI MSCEI QLLKNKEGI LKAANKYLODKI E	213	100.00	100.00	0
pink_pepper.XP_030483127.1	(+)	1MARGVQLRRI ENPVHQRVTFCKRRAGL LKKAKELSVL CDAEI GLVI FSAHGKLYDLATKGTMGQI EKYMKSTKGSVLAQADQQQI LQTQSDQDAKNEI SMLKOEI EI LQKGLRYFMGGAGTNNLDEQI LEKNLELWYHIH RSAKMDI MSCEI QLLKNKEGI LKAANKYLODKI E	213	100.00	100.00	0

Figure S16 - Multiple Sequence Alignment Visualization of Clade AGL12 from OG0006023

Sequence ID	Start	Alignment	End	Identity	Coverage	Mismatches
		1102030405060708090100110120130140150160170180				
Ristevski_cs10_MADS_REF_XP_030494537.1	(+)	1MGRGKI EI KRI ENANSRQVTFISKRRAGLLKKAQELAI LCDAEVAMI I FSNTGKLF EYSSSGMKRTLARYNKVDYPEGAI VDKTEKQDSKEVDDLKDEI AKLQRKQSRLLGEDLSGMSKELQHLEHQLNDGLI SVKERKEKLLKEQLEQSRLQEQRAVLENETLRRQI EELRCLFPRAD	254	100.00	100.00	0
LACConfidential_pep_CsLAC_00G0085810	(+)	1MGRGKI EI KRI ENANSRQVTFISKRRAGLLKKAQELAI LCDAEVAMI I FSNTGKLF EYSSSGMKRTLARYNKVDYPEGAI VDKTEKQDSKEVDDLKDEI AKLQRKQSRLLGEDLSGMSKELQHLEHQLNDGLI SVKERKEKLLKEQLEQSRLQEQRAVLENETLRRQI EELRCLFPRAD	117	41.57	45.67	10
PurpleKush_pep_CsPK_00G0018340	(+)	1MGRGKI EI KRI ENANSRQVTFISKRRAGLLKKAQELAI LCDAEVAMI I FSNTGKLF EYSSSGMKRTLARYNKVDYPEGAI VDKTEKQDSKEVDDLKDEI AKLQRKQSRLLGEDLSGMSKELQHLEHQLNDGLI SVKERKEKLLKEQLEQSRLQEQRAVLENETLRRQI EELRCLFPRAD	225	77.47	88.19	28
Chemdog91_pep_CsCD91_00G0161240	(+)	1MGRGKI EI KRI ENANSRQVTFISKRRAGLLKKAQELAI LCDAEVAMI I FSNTGKLF EYSSSGMKRTLARYNKVDYPEGAI VDKTEKQDSKEVDDLKDEI AKLQRKQSRLLGEDLSGMSKELQHLEHQLNDGLI SVKERKEKLLKEQLEQSRLQEQRAVLENETLRRQI EELRCLFPRAD	254	100.00	100.00	0
PurpleKush_pep_CsPK_04G0000610	(+)	1MGRGKI EI KRI ENANSRQVTFISKRRAGLLKKAQELAI LCDAEVAMI I FSNTGKLF EYSSSGMKRTLARYNKVDYPEGAI VDKTEKQDSKEVDDLKDEI AKLQRKQSRLLGEDLSGMSKELQHLEHQLNDGLI SVKERKEKLLKEQLEQSRLQEQRAVLENETLRRQI EELRCLFPRAD	264	95.45	100.00	2

Figure S17- Multiple Sequence Alignment Visualization of Clade AGL15 from OG0007459