

Supplementary Data File S4: Annotated alignment of aphid and planthopper UV-opsin protein sequences. See Figure 1 for species aphid and planthopper species abbreviations. Outgroup sequences: *Chrysochroa rajah* (Craj) UV1-anc (WCQ76393) and UV2-der (WCQ76394), *Frankliniella occidentalis* (Focc) (XP\_026279762).

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	12		345678901		23456	
Btau_rhodopsin	1	MN-----	GTEGPNFYV-----		PFSNK-----	16
Craj_UV2-anc	1	MHLTN-----Y--S-VKFP-----	EAR--VM---D---SGHQLIAWNVPAAD			31
Adif_UV2-anc	1	MVWSVSLSAVANPPTMMRLINW--T-DHTIL--A-----	EPR--IM---E---SRPGSMewnISPEN			49
Craj_UV1-der	1	MKEMM-----FNG--TFLDGPL--P-----	QAR--VL---S---EERRLLGWNVDNSD			36
Adif_UV1-der	1	ML-----LNW--TAIDRPL--P-----	QLG--GD--SG---HEVRLLGWNIPPSE			34
Focc_UV	1	MEYPESAD-C-----SNG--T-AWLpv--A-----	EARIGSGVSGP---SEQRLLGWNVPpDE			44
Dcit_UV	1	MESDFY-----LND--T-SIGPVALARVAAQQSFSVNEKLFVPIFSprVAAQQSF-SV---NGKRMLGWNVPpED				63
Pcel_UV	1	-----	-----			0
Apis_UV-anc	1	MSPTLIMD-----FNR--T-VSRPL--A-----	QLG--LME-NE--VGETHLGWNlQAED			41
Rmai_UV-anc	1	MSPTLIMD-----FNR--T-VSRPL--P-----	QLG--LME-NE--VGETHLGWNlPAED			41
Mper_UV-anc	1	MSPTMIMD-----FNR--T-VSRPL--Q-----	QLG--LME-NE--VGETHLGWNlPAED			41
Sfla_UV-anc	1	MFPALIMD-----FNR--T-VSRPL--P-----	QMG--SAD-DA--GGETHLGWNlGAED			41
Cced_UV-anc	1	MMM--MD-----FNR--T-VSKPL--P-----	ELG--LLE-NEPGETGRQLGWNlAAED			40
Apis_UV-der	1	MD-----FNR--S-VSRPL--S-----	QLGSSFME-NE--EELQLMGWNlTPED			36
Rmai_UV-der	1	MD-----FNR--S-VSRPL--S-----	QLGSSFME-NE--DELQLMGWNlTPED			36
Mperi_UV-der	1	MD-----FNR--S-VSRPL--S-----	QLGSSFME-NE--DELQLMGWNlTPED			36
Sfla_UV-der	1	MD-----FNR--S-ISRTL--S-----	QLG--FME-EE--PELHLMGWNlTPED			34
Cced_UV-der	1	MD-----FNG--S-VLRPL--P-----	QLG--PMD-ND--EEAHLMGWNlTPED			34
Ncin_UV	1	MEFFNGAS-----YNTSS----PVAMA-----	RMG--LG---A---GAPRMLGWNVPtED			38
Evit_UV	1	MEVFDGAN-----YNASAA-LFQPQALP-----	RLG--M---P---NGVQMLGWNVPTEE			41
Monu_UV	1	MEYLSGAD-----YNASAA-LFQPQALP-----	RLG--M---P---NGVQMLGWNVPTEE			41
Nlug_UV-anc	1	MEAFGGANNC-----PNG--T-VWGPQ--A-----	S---F---R---TAQRSLIWNVPtDE			37
Lstr_UV-anc	1	MDVFGGAKNC-----PNE--T-VWGPQ--A-----	S---F---R---TAQRSLIWNVPTEE			37
Sfur_UV-anc	1	MDVFGGAKNC-----PNE--T-VWGPQ--A-----	S---F---R---TAQRSLIWNVPTEE			37
Nlug_UV-der	1	MEVFRGASDC-----PNE--S-VWGPQ--V-----	S---F---R---TAERTLIWNVPLEE			37
Lstr_UV-der	1	MDVFGGAKNC-----PNE--T-VWGPQ--V-----	S---F---R---TAERTLIWNVPLEE			37
Sfur_UV-der	1	MDVFSGAKNC-----PNE--T-VWGPQ--A-----	S---F---R---TAERTLIWNVPLEE			37

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		789012345678901234---56789012345678901234567890123456789012345678901234567890123456		
Btau_rhodopsin	17	TGVVRSPEAPQYYLAEP---WQFSMLAAYMFLLIMLGFPINFLTLYVTVQHKKLRTPNLNLAVALDFMVFGGFTTTLY	96	
Craj_UV2-anc	32	--L---EHIPEHWLKYPAPEASLHLLGLLYIGLFMSILGNGLVLWIFSSAKCLRTPSNMFIVNLAFCDFVMML-KTPIFIY	108	
Adif_UV2-anc	50	--I---PYVPEHWLKFPPEMSLNLGLLYIVFFMSIIGNGLVIWIFSTAKSLRTPSNMFVVNLAFLDFVMML-KTPIFIF	126	
Craj_UV1-der	37	--L---VHIPEHWLKYPEPEASIHFLGLLYILYFLMSTIGNGLVLWIFSSKSLRTPSNLFVVNLAFCDLIMLL-KAPLFVY	113	
Adif_UV1-der	35	--L---VHIPEHWLKYPEPEASLHFLLLILLYLICFLLSTVGNGMVIWIFSTAKSLRTPSNMFVVNLAFLDFIMLS	111	
Focc_UV	45	--L---PHIPTHWLVPEDPLINYGLGVLYCFFFFFFAVMGNGIVIIYIFLTSKNLKTSPSNIFVVNLAICDFVMMA-KTPIFIY	121	
Dcit_UV	64	--R---FRIPEHWFQYEEIDPMYNYVLGCLYIVFTIFISICGNGMVIWVFIAAKSLRTPSNIFVLNLALMDFMMMV-KTPIFIY	140	
Pcel_UV	64	-----MNNYILGSLYCVFCAVSLIGNGLVIWIFLTAKALRTPSNLFVVNLAIMDFVMML-KTPIFIY	161	
Apis_UV-anc	42	--L---IHIPEHWLKYQEPSSLQHYYLAFMYTI	FMFVALFGNGLVIWVFCVAKPLRTPSNIFVINLALCDFVMMA-KAPIFIL	118
Rmai_UV-anc	42	--L---IHIPEHWLKYQEPSSALQHYYLAFMYTL	FTTIALFGNGLVIWIFCIAKPLRTPSNIFVINLALCDFVMMA-KAPIFIY	118
Mper_UV-anc	42	--L---IHIPEHWLKYQEPSSLQHYYLAFMYTI	FTTFVALFGNGLVIWIFCIAKPLRTPSNIFVINLALCDFVMMA-KSPIFIY	118
Sfla_UV-anc	42	--L---IHIPEHWLKYEEPSSALQHYYLAFMYTI	FTTIALVGNGGLVIWIFCISKSLRTPSNIFVINLALCDFLMMMA-KAPIFIY	118
Cced_UV-anc	41	--L---VHIPDHWNLYQEPSSLSHYYLAFMYSI	FTTIFALVGNGGLVIWIFCVAKPLRTPSNIFVINLALCDFCMMA-KAPIFIY	117
Apis_UV-der	37	--L---THIPEHWLSYPEVRSLYHYILAFSYTI	LFCLGVIGNGLVLWIFCVSKPLRTPSNLFVLNLALCDFSMVL-VLPILY	113
Rmai_UV-der	37	--L---THIPEHWLSYPEVRSLYHYILAFAYTI	LFSLGVIGNGLVLWIFCVSKPLRTPSNLFVLNLALCDFSMVL-VLPILY	113
Mper_UV-der	37	--L---THIPEHWLSYPEVRSLYHYILAFAYTI	LFCLGVIGNGLVLWIFCVSKPLRTPSNLFVLNLAMCDFSMVL-VLPILY	113
Sfla_UV-der	35	--L---IHIPEHWLSYPEVRSIYHYILAFMYSI	LFSLGVIGNGLVLWIFCVSKPLRTPSNLFVLNLALCDFSMVL-VLPILY	111
Cced_UV-der	35	--L---VHVPEHWLSYPEVRSMYHYIMAFSYSI	LFVIGIIGNGLVIWIFSLSKPLRTPSNLFVLNLALCDFSMVL-VLPILY	111
Ncin_UV	39	--L---VHIPQHHLKYQAPAMQHMYLGFYIYFFMIASLIGNGLVIWIFCGARNLRTPSNMFVINLAICDFMMML-KTPIFIY	115	
Evit_UV	42	--L---VHIPQHHLKYPAPEPIQHYVLGFLYIYFFMFAALFGNGLVIWIFCGAKNLRTPSNMFVINLALCDFLMMS-KTPIFIY	118	
Monu_UV	42	--L---VHIPQHHLKYPAPEPIQHYVLGFLYIYFFMFAALFGNGLVIWIFCGAKNLRTPSNMFVINLALCDFLMMS-KTPIFIY	118	
Nlug_UV-anc	38	--L---ANPEHWFNYPEPDMYNYVLGLLYVYFMFFSL	IGNGLVIWIFCSAKSLRTPSNMFVVNLAICDFMMMV-KTPIFIY	114
Lstr_UV-anc	38	--L---PHPEHWFNYPEPDMYNYVLGLLYVYFMFFSL	VGNGLVIWIFCSAKSLRTPSNMFVVNLAICDFLMML-KTPIFIY	114
Sfur_UV-anc	38	--L---PHPEHWFNYPEPDMYNYVLGLLYVYFMFFSL	VGNGLVIWIFCSAKSLRTPSNMFVVNLAICDFMMML-KTPIFIY	114
Nlug_UV-der	38	--L---EHVPEHWFNHPAPEPIYNYVLGLVYMFYMFSS	IGNGLVIWIFSSAKTLRTPSNMFVVNLAICDLLMMV-KIPIFIY	114
Lstr_UV-der	38	--L---EHVPEHWFNHPAPEPIYNYVLGLVYMFYMFSS	VGNGLVIWIFSSAKSLRTPSNMFVVNLAICDLLMMI-KIPIFIY	114
Sfur_UV-der	38	--L---EHVPEHWFNHPAPEPIYNYILGLVYMFYMFSS	VGNGLVIWIFSSAKSLRTPSNMFVVNLAICDLLMMV-KIPIFIY	114

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			9999000000000111111111122222222233333333334444444444555555555566666666777-7777777	
			7890123456789012345678901234567890123456789012345678901234567890123456789012-3456789	
Btau_rhodopsin	97	TSLHGYFVFGPTGCNLEGGFATLGGEIALWSLVLAIERYVVVCKPMSNFRFGENHAIMGVAFTWVMALACAAPPL-VGWSRYI	179	
Craj_UV2-anc	109	NSFNRGFAAGFVSCQVFVGMTLSGIGAGMSNACIAYDRYHTITNPLEG-KLTRTKALVMILFVWTYTTPWAILPLFEIWGKFV	191	
Adif_UV2-anc	127	NSFKQGFLYSMVWCYVFIAGTYSIGIGASMTNVCIAYDRYHTITNPMEG-RLTRTKALLMILFIYVYVTPFAILPYLKIWNFI	209	
Craj_UV1-der	114	NAFNRGYATGHIGCQIFAMVGSLSGIGAGTTNACIAYDRYTITNPLEG-RLSKTKAVILIIFVWMYTMPVWVLPLEIWSRFV	196	
Adif_UV1-der	112	NAFHRYGAAGHLGCQIFGTIGTLSSGIGAGMTDVCIAIDRYTITNPLEG-RMSKIKAIIMIIFFWLTYLPWIILPFTEVWNRFV	194	
Focc_UV	122	NSFNLGPASGPTACLVFATMGFSFGIGAGATNAVIAIDRYMTIAKPFGS-KMTRGKAIMIIFFLWMVWPVWVPATEIWGRFV	204	
Dcit_UV	141	NSFNQGYALGHQCQIFGLMGSISGIGQSATNVAIAYDRYRVIAKPMDG-RMSYSKALMILILICYVIPWAMPFPYLEKWSRFV	223	
Pcel_UV	162	NSFHQQYELGHQCQWFGLMGAITGIGQSATNVAIAYDRYRVIAKPMDG-RMSFSKAFIILIMIYAYVLPWALFPFYFEKWSRFV	144	
Apis_UV-anc	119	GSINR <b>G</b> Y-QGHFLCQLFGTAGAFSGIGA <b>S</b> ATNAAIAYDRFSTIAKPF <b>DG</b> -RMTY <b>G</b> R <b>A</b> FFLIICIWYTYLPWGLLPLTEKNWRYV	200	
Rmai_UV-anc	119	SSINR <b>G</b> Y-QGHFLCQLFGVAGAFSGGLA <b>S</b> ATNAAIAYDRFSTIAKPF <b>DG</b> -RMTY <b>G</b> R <b>A</b> LFLIVICIWYTYLPWGILPLTEKNWRFV	200	
Mper_UV-anc	119	SSINR <b>G</b> Y-QGHFLCQLFGVAGAFSGGLA <b>S</b> ATNAAIAYDRFSTIAKPF <b>DG</b> -RMTY <b>G</b> R <b>A</b> FFLIICIWYTYLPWGLLPLTEKNWRYV	200	
Sfla_UV-anc	119	GSVQR <b>T</b> Y-QGHFLCQAFALAG <b>T</b> ISGLGA <b>S</b> ITNAAIAYDRYSTIAKPF <b>EG</b> -RMTY <b>G</b> R <b>A</b> FFIMILIWAYVFPWCFLPATEKNWRYV	200	
Cced_UV-anc	118	NSIQR <b>G</b> Y-QGHLNCQIFAMAC <b>S</b> ISGIGA <b>S</b> ATNAAIAYDRFSTIAKPF <b>DG</b> -RMTF <b>G</b> K <b>A</b> FLIICIWYTVLPWCFLPLTEKNWRFV	199	
Apis_UV-der	114	DSIDH <b>K</b> Y-PGHLQCQIFALCG <b>S</b> ISGIGA <b>G</b> ATNAAIAYDRYSTIAKPF <b>EG</b> -RMTY <b>G</b> K <b>A</b> LILIIICIWIYVLPWCLLPLTEKNWRFV	195	
Rmai_UV-der	114	DSINH <b>K</b> Y-PGHLQCQIFALCG <b>S</b> ISGIGA <b>G</b> ATNAAIAYDRYSTIAKPF <b>EG</b> -RMTY <b>G</b> K <b>A</b> LILIIICIWIYVLPWCILPLTEKNWRFV	195	
Mper_UV-der	114	DSIDH <b>K</b> Y-PGHLQCQIFALCG <b>S</b> ISGIGA <b>G</b> ATNAAIAYDRYSTIAKPF <b>EG</b> -RMTY <b>G</b> K <b>A</b> LILIIICIWIYVLPWCLLPLTEKNWRYV	195	
Sfla_UV-der	112	DSINH <b>K</b> Y-PGHLQCQIFALCG <b>S</b> ISGIGA <b>G</b> ATNAAIAYDRYSTIAKPF <b>EG</b> -RMTY <b>G</b> K <b>A</b> LILIIICIWMYVFPWCFLPLTEKNWRYV	193	
Cced_UV-der	112	DSIDH <b>K</b> Y-PGHLQCQIFALCG <b>S</b> ISGIGA <b>G</b> ATNAAIAYDRYSTIAKPF <b>EG</b> -RMTY <b>G</b> K <b>A</b> LILIVICIWIWVPWCYLPLSEKNWRYV	193	
Ncin_UV	116	NSFNLGFALGQTGCQCVFSIMGSLSGIGAAATNAAIAYDRYSTIARPLDG-KMSRGKAFLFILCIWAYVSPWVFLPATQTWGRYA	198	
Evit_UV	119	NSFKLGFALGQFWCQVFAIAGSLSGIGAAATNAVIAIDRYSTIARPLDG-KMSKGKAFLFLLCIWIYTPPWVFLPATQTWGRYA	201	
Monu_UV	119	NSFKLGFALGQFWCQVFAIAGSLSGIGAAATNAVIAIDRYSTIARPLDG-KMSKGKAFLFLLCIWIYTPPWVFLPATQTWGRYA	201	
Nlug_UV-anc	115	NSFNLGFATGHLGCQIFATI GSFGSIGASATNAAIAYDRYNVI AKPLDG-RMSKGKAFLILLIWAYVTPWSLMPLYGVWSRFV	197	
Lstr_UV-anc	115	NSFNLGFASGHLGCQIFGTIGSFSGIGASATNAAIAYDRYNVIAKPFDG-KMSKGKAFLILLIWAYVTPWSLMPLYGYWSRFV	197	
Sfur_UV-anc	115	NSFNLGFASGHLGCQIFGTIGSFSGIGASATNAAIAYDRYNVIAKPFDG-KMSKGKAFLILLIWAYVTPWSLMPLYGYWSRFV	197	
Nlug_UV-der	115	NSFNLGFAAGHLGCQIFGTIGSFSGIGASATNAAIAYDRYNVIAKPFDG-KMSRGKAFLILLIWAYVTPWSIMPLLEVWSRFV	197	
Lstr_UV-der	115	NSFNLGFAAGHVGCQIFGTIGSFSGIGASATNAAIAYDRYNVIAKPFDG-KMSRGKAFLILLIWAYVTPWSIIPLEVWSRFV	197	
Sfur_UV-der	115	NSFNLGFAAGHLGCQIFGTIGSFSGIGASATNAAIAYDRYNVIAKPFDG-KMSRGKAFLILLIWAYVTPWSIMPLFEVWSRFV	197	

[illegible]

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	333333334444	44	444	
	34567890123	45	678	
Btau_rhodopsin	333	-ASTTVSKTETS-QV-APA-----	348	
Craj_UV2-anc	356	-SDTQSTATESS-TN-K---P-----	370	
Adif_UV2-anc	374	-SDAQSVTTETA-SK-----G-----	387	
Craj_UV1-der	361	-TDTASAVTEAS-NP-ATR-T-----	377	
Adif_UV1-der	359	-SDSASVATESA-AP-NTGKI-----	376	
Focc_UV	370	ASETASTTTEAT-SA-NPD-----	386	
Dcit_UV	389	-KETASAQTEAT-T---P-----H	402	
Pcel_UV	310	-KETASANTEAT-T---P-----H	323	
Apis_UV-anc	367	AS <b>E</b> TQSTTTA-----A	377	
Rmai_UV-anc	367	AS <b>E</b> TQSTTTTT-----A	378	
Mper_UV-anc	366	PS <b>E</b> TQSTTTTT-----A	377	
Sfla_UV-anc	367	AS <b>E</b> TQSTTTTT-----A	378	
Cced_UV-anc	366	VS <b>E</b> TQSATTT-----A	376	
Apis_UV-der	361	TS <b>D</b> TQSITTA-----A	371	
Rmai_UV-der	361	TS <b>D</b> TQSITTA-----A	371	
Mper_UV-der	361	TS <b>D</b> TQSITTA-----A	371	
Sfla_UV-der	359	SP <b>D</b> TQSTTTT-----A	369	
Cced_UV-der	359	LA <b>E</b> TQSTTTS-----A	369	
Ncin_UV	363	SE-TVSTTTETTAA-TTPA-----E	380	
Evit_UV	367	HDNVSTTTTEAT-A-TTPA-----E	384	
Monu_UV	367	HDNVSTTTTEAT-A-TTPA-----E	384	
Nlug_UV-anc	363	-SETQS <b>A</b> VTETT-AS-TPAES-----	380	
Lstr_UV-anc	363	-SETQS <b>A</b> VTETT-AT-TPAE-----	379	
Sfur_UV-anc	363	-SETQS <b>A</b> VTETT-AT-TPAE-----	379	
Nlug_UV-der	363	-SETQS <b>T</b> VTEST-VTATPAE-----	380	
Lstr_UV-der	363	-SETQS <b>T</b> VTEST-VTAPPAE-----	380	
Sfur_UV-der	363	-SETQS <b>T</b> VTEST-VSATPAVTATECN	386	