Table S1. Homologs of *fatty acid desaturase* genes in 12 *Drosophila* genomes[a]

Ortholog	Species	Symbol (Synonym)	Flybase ID	Genomic location
desat1	*D. melanogaster*	*CG5887* (*dmel_desat1*)	FBgn0086687	3R:8270531..8272663 [+]
	D. simulans	*GD18837* (*dsim_GLEANR_2646*)	FBgn0027803	3R:13116857..13118963 [-]
	D. sechellia	*GM24036* (*dsec_GLEANR_7049*)[b]	FBgn0178901	scaffold_0:13674699..13676859 [-]
	D. yakuba	*GE26198* (*dyak_GLEANR_9761*)	FBgn0067988	3R:12593935..12595999 [+]
	D. erecta	*GG18949* (*dere_GLEANR_374*)	FBgn0111155	scaffold_4770:13348445..13350478 [-]
	D. ananassae	*GF17961* (*dana_GLEANR_19223*)	FBgn0094979	scaffold_13340:7652350..7654184 [+]
	D. persimilis	*GL27316* (*dper_GLEANR_9932*)	FBgn0164897	scaffold_19:1215069..1216653 [+]
	D. pseudoobscura	*GA19204* (*dpse_GLEANR_5093*)	FBgn0079201	2:5,498,572..5,500,156 [+]
	D. willistoni	*GK14407* (*dwil_GLEANR_14726*)	FBgn0216413	scf2_1100000004943:14785806..14787424 [-
	D. mojavensis	*GI10485* (*dmoj_GLEANR_10408*)	FBgn0133249	scaffold_6540:27937726..27939979 [+]
	D. virilis	*GJ23166* (*dvir_GLEANR_8526*)	FBgn0210268	scaffold_13047:8252067..8254552 [-]
	D. grimshawi	*GH21229* (*dgri_GLEANR_541*)	FBgn0128691	scaffold_15074:1355903..1358096 [+]
desat2	*D. melanogaster*	*CG5925* (*dmel_desat2*)	FBgn0043043	3R:8262143..8263481 [+]
	D. simulans	*GD18836* (*dsim_GLEANR_2645*)	FBgn0190352	3R:13126012..13127348 [-]
	D. sechellia	*GM24035* (*dsec_GLEANR_7048*)	FBgn0178900	scaffold_0:13683759..13685095 [-]
	D. yakuba	*GE26197* (*dyak_GLEANR_9760*)	FBgn0243231	3R:12585391..12586717 [+]
	D. erecta	NA		
	D. ananassae	*GF17959* (*dana_GLEANR_19221*)	FBgn0094977	scaffold_13340:7642863..7644162 [+]
	D. persimilis	*GL27314* (*dper_GLEANR_9930*)	FBgn0164895	scaffold_19:1204796..1206118 [+]
	D. pseudoobscura	*GA19234* (*dpse_GA19234*)	FBgn0079231	2:5488491..5489718 [+]
	D. willistoni	*GK14406* (*dwil_GLEANR_14725*)	FBgn0216412	scf2_1100000004943:14779457..14780725 [-
	D. mojavensis	*GI10484* (*dmoj_GLEANR_10407*)	FBgn0133248	scaffold_6540:27929644..27930945 [+]
	D. virilis	*GJ23165* (*dvir_GLEANR_8525*)	FBgn0210267	scaffold_13047:8261264..8262614 [-]
	D. grimshawi	*GH21218* (*dgri_GLEANR_540*)	FBgn0128680	scaffold_15074:1348964..1350306 [+]
Fad2 (*desatF*)	*D. melanogaster*	*CG7923* (*dmel_Fad2*, *desatF-α*)	FBgn0029172	3L:11016639..11017706 [+]
	D. simulans	*GD14271* (*dsim_GLEANR_14282*, *desatF-α*)	FBgn0185956	3L:10413484..10414551 [+]
	D. sechellia	*GM25238* (*dsec_GLEANR_8211*, *desatF-α*)	FBgn0180098	scaffold_0:3239851..3240915 [+]

Table S1. (Continued)

Ortholog	Species	Symbol (Synonym)	Flybase ID	Genomic location
	D. yakuba	*GE21776* (*dyak_GLEANR_5510*, *desatF-α*)[c]	FBgn0239021	3L:11044102..11045156 [+]
	D. erecta	*GG15465* (*dere_GLEANR_15537*, *desatF-α*)	FBgn0107716	scaffold_4784:11026003..11027067 [+]
	D. ananassae	*GF24026* (*dana_GLEANR_8783*, *desatF-α'*)[d]	FBgn0101020	scaffold_13337:12461680..12462747 [-]
		GF16174 (*dana_GLEANR_17446*, *desatF-δ*)[d]	FBgn0093196	scaffold_13340:21312697..21313764 [-]
		GF18504 (*dana_GLEANR_19760*, *desatF-ε*)[d]	FBgn0095522	scaffold_13340:15668648..15669706 [+]
	D. persimilis	*GL15669* (*dper_GLEANR_17057*, *desatF-α*)	FBgn0153273	scaffold_47:509015..510076 [-]
		GL23117 (*dper_GLEANR_5476*, *desatF-β*)[d]	FBgn0160707	scaffold_0:9749674..9750762 [-]
		GL22317 (*dper_GLEANR_4392*, *desatF-γ*)[d]	FBgn0159909	scaffold_3:6548217..6549302 [+]
	D. pseudoobscura	*GA20691* (*dpse_GLEANR_1238*, *desatF-α*)	FBgn0080685	XR_group6:6011391..6012452 [-]
		GA27148 (*dpse_GLEANR_5384*, *desatF-β*)[d]	FBgn0248519	2:10728335..10729423 [+]
		GA27452 (*dpse_GLEANR_6152*, *desatF-γ*)[d]	FBgn0248819	2:23774445..23775530 [+]
	D. willistoni	*GK17186* (*dwil_GLEANR_17505*, *desatF-ζ*)[d]	FBgn0219185	scf2_1100000004511:2193764..2194855 [+]
		GK11373 (*dwil_GLEANR_1159*, *desatF-η*)[d]	FBgn0213384	scf2_1100000004762:97180..98253 [+]
	D. mojavensis	NA[e]		
	D. virilis	NA[e]		
	D. grimshawi	NA[e]		
CG8630	*D. melanogaster*	*CG8630*	FBgn0038130	3R:9108124..9109675 [+]
	D. simulans	*GD18893* (*dsim_GLEANR_2702*)	FBgn0190404	3R:12316156..12317679 [-]
	D. sechellia	*GM24094* (*dsec_GLEANR_7103*)	FBgn0178958	scaffold_0:12894947..12896458 [-]
	D. yakuba	*GE26257* (*dyak_GLEANR_9814*)	FBgn0243288	3R:13412487..13414053 [+]
	D. erecta	*GG19533* (*dere_GLEANR_427*)	FBgn0111735	scaffold_4770:12539421..12541069 [-]
	D. ananassae	*GF17588* (*dana_GLEANR_18851*)	FBgn0094606	scaffold_13340:1662762..1664203 [+]
	D. persimilis	*GL24461* (*dper_GLEANR_6749*)	FBgn0162050	scaffold_0:10476768..10488896 [+]
	D. pseudoobscura	*GA21221* (*dpse_GLEANR_4085*)	FBgn0081209	2:9994113..9995561 [-]
	D. willistoni	*GK13932* (*dwil_GLEANR_14252*)	FBgn0215938	scf2_1100000004943:6191658..6193093 [+]
	D. mojavensis	*GI24327* (*dmoj_GLEANR_9484*)	FBgn0147050	scaffold_6540:10145793..10147297 [+]
	D. virilis	*GJ10413* (*dvir_GLEANR_10340*)	FBgn0197694	scaffold_12855:3052346..3053856 [-]

Table S1. (Continued)

Ortholog	Species	Symbol (Synonym)	Flybase ID	Genomic location
	D. grimshawi	*GH18426* (*dgri_GLEANR_2804*)	FBgn0125894	scaffold_14906:5753675..5755127 [-]
CG9743	*D. melanogaster*	*CG9743*	FBgn0039756	3R:26022359..26024615 [-]
	D. simulans	*GD17212* (*dsim_GLEANR_1736*)	FBgn0188775	3R:25690152..25692391 [-]
	D. sechellia	*GM12168* (*dsec_GLEANR_12599*)	FBgn0167108	scaffold_4:4874849..4877078 [-]
	D. yakuba	*GE23401* (*dyak_GLEANR_7191*)	FBgn0240592	3R:26956123..26958286 [-]
	D. erecta	*GG11952* (*dere_GLEANR_12006*)	FBgn0104247	scaffold_4820:1973564..1975704 [+]
	D. ananassae	*GF16192* (*dana_GLEANR_17463*)	FBgn0093214	scaffold_13340:21056664..21059300 [-]
	D. persimilis	*GL14059* (*dper_GLEANR_14504*)	FBgn0151664	scaffold_7:4285074..4287260 [+]
	D. pseudoobscura	*GA22002* (*dpse_GLEANR_4847*)	FBgn0081987	2:1482261..1484415 [+]
	D. willistoni	*GK13141* (*dwil_GLEANR_13473*)	FBgn0215150	scf2_1100000004943:9484681..9487579 [-]
	D. mojavensis	*GI24323* (*dmoj_GLEANR_9480*)	FBgn0147046	scaffold_6540:10097851..10101121 [+]
	D. virilis	*GJ10408* (*dvir_GLEANR_10336*)	FBgn0197690	scaffold_12855:3095571..3099015 [-]
	D. grimshawi	*GH18422* (*dgri_GLEANR_2800*)	FBgn0125890	scaffold_14906:5797460..5801093 [-]
CG9747	*D. melanogaster*	*CG9747*	FBgn0039754	3R:26011566..26016463 [-]
	D. simulans	*GD17234* (*dsim_GLEANR_1738*)	FBgn0188797	3R:25679027..25683922 [-]
	D. sechellia	*GM12172* (*dsec_GLEANR_12601*)	FBgn0167112	scaffold_4:4864314..4869213 [-]
	D. yakuba	*GE23403* (*dyak_GLEANR_7193*)	FBgn0240594	3R:26945103..26950087 [-]
	D. erecta	*GG11954* (*dere_GLEANR_12008*)	FBgn0104249	scaffold_4820:1981496..1986547 [+]
	D. ananassae	*GF16194* (*dana_GLEANR_17465*)	FBgn0093216	scaffold_13340:21045994..21051062 [-]
	D. persimilis	*GL14061* (*dper_GLEANR_14506*)	FBgn0151666	scaffold_7:4293137..4297511 [+]
	D. pseudoobscura	*GA22005* (*dpse_GLEANR_4849*)	FBgn0081990	2:1490305..1494712 [+]
	D. willistoni	*GK13143* (*dwil_GLEANR_13475*)	FBgn0215152	scf2_1100000004943:9472854..9477605 [-]
	D. mojavensis	*GI24325* (*dmoj_GLEANR_9482*)	FBgn0147048	scaffold_6540:10111520..10118082 [+]
	D. virilis	*GJ10410* (*dvir_GLEANR_10338*)	FBgn0197692	scaffold_12855:3079765..3086153 [-]
	D. grimshawi	*GH18424* (*dgri_GLEANR_2802*)	FBgn0125892	scaffold_14906:5783728..5789396 [-]

Table S1. (Continued)

Ortholog	Species	Symbol (Synonym)	Flybase ID	Genomic location
CG15531	*D. melanogaster*	*CG15531*	FBgn0039755	3R:26020605..26021890 [-]
	D. simulans	*GD17223 (dsim_GLEANR_1737)*	FBgn0188786	3R:25688409..25689688 [-]
	D. sechellia	*GM12171 (dsec_GLEANR_12600)*	FBgn0167111	scaffold_4:4873106..4874385 [-]
	D. yakuba	*GE23402 (dyak_GLEANR_7192)*	FBgn0240593	3R:26954354..26955635 [-]
	D. erecta	*GG11953 (dere_GLEANR_12007)*	FBgn0104248	scaffold_4820:1976171..1977465 [+]
	D. ananassae	*GF16193 (dana_GLEANR_17464)*	FBgn0093215	scaffold_13340:21054974..21056242 [-]
	D. persimilis	*GL14060 (dper_GLEANR_14505)*	FBgn0151665	scaffold_7:4287668..4288986 [+]
	D. pseudoobscura	*GA26941 (dpse_GLEANR_4848)*	FBgn0248312	2:1484823..1486141 [+]
	D. willistoni	*GK13142 (dwil_GLEANR_13474)*	FBgn0215151	scf2_1100000004943:9482984..9484270 [-]
	D. mojavensis	*GI24324 (dmoj_GLEANR_9481)*	FBgn0147047	scaffold_6540:10102110..10103733 [+]
	D. virilis	*GJ10409 (dvir_GLEANR_10337)*	FBgn0197691	scaffold_12855:3093065..3095092 [-]
	D. grimshawi	*GH18423 (dgri_GLEANR_2801)*	FBgn0125891	scaffold_14906:5795284..5796956 [-]

[a] Symbols and genomic locations of each gene are based on the genome release of *D. melanogaster* (R5.2), *D. pseudoobscura* (R2), and Comparative Assembly Freeze 1 (CAF1) of all the other 10 *Drosophila* genomes.

[b] *desat1* homolog in *D. sechellia* was excluded for all the analyses due to low coverage in the current CAF1 release.

[c] *GE21776* is the only *desatF* homolog with annotated intron. This gene was not analyzed in codon based analyses.

[d] homologs are not located in the syntenic region.

[e] NA, homologs are not available in current genome assembling.

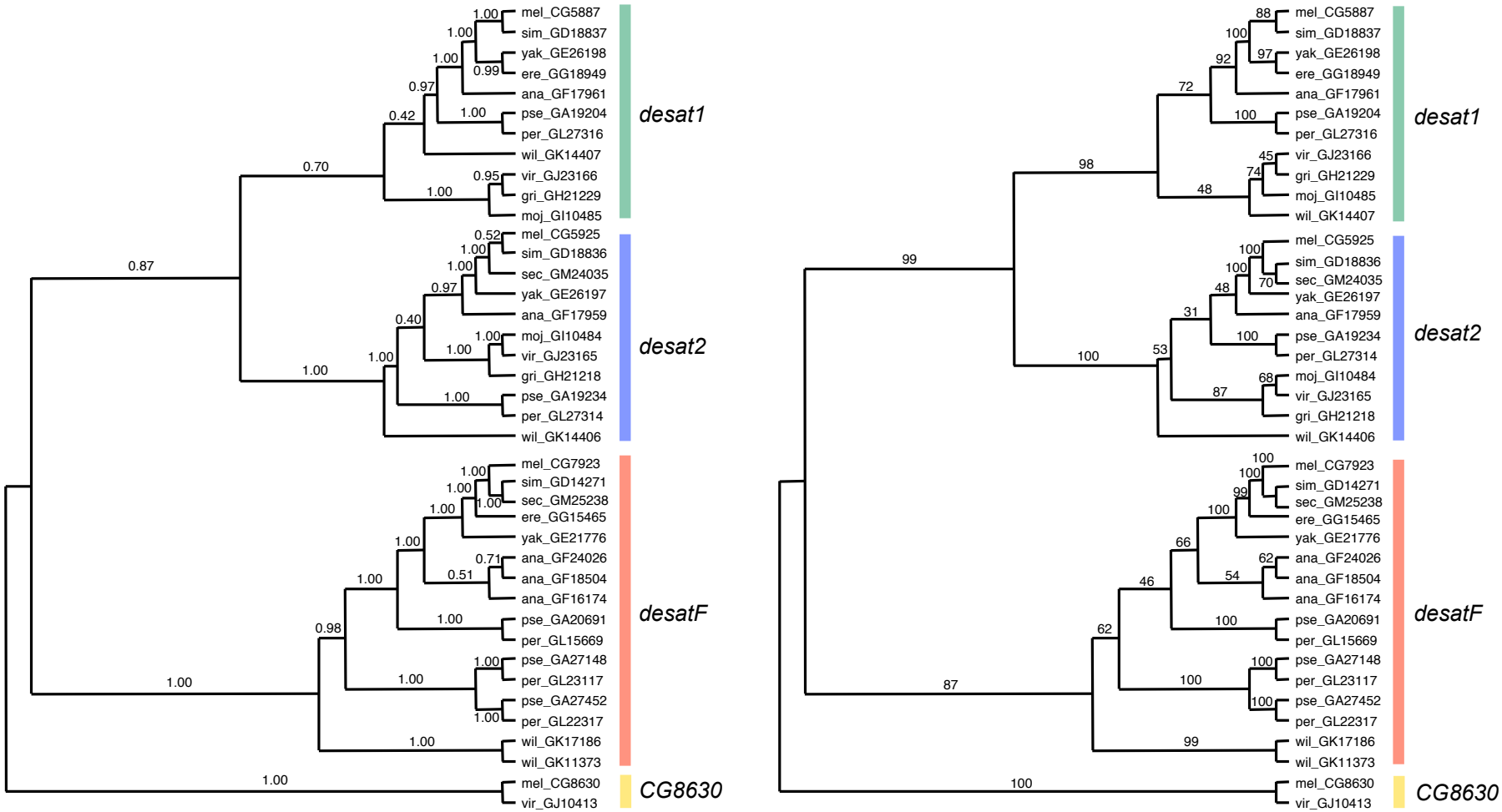

Figure S2. Phylogeny of *desat1*, *desat2*, and *desatF* homologs in *Drosophila*, showing the relationship among the three clades. Both trees obtained by Bayesian inference and maximum parsimony method are shown, and corresponding posterior probabilities and bootstrap values are listed. Bayesian inference used GTR model with gamma distribution, and two runs, each with two million generations, were performed. Trees were sampled per one thousand generations, and 500 of the sampled trees were described as burn-in while summarizing the result. Maximum parsimony method used all sites in the three codon positions without weighting, and branch support was obtained from one thousand bootstrap replicates.

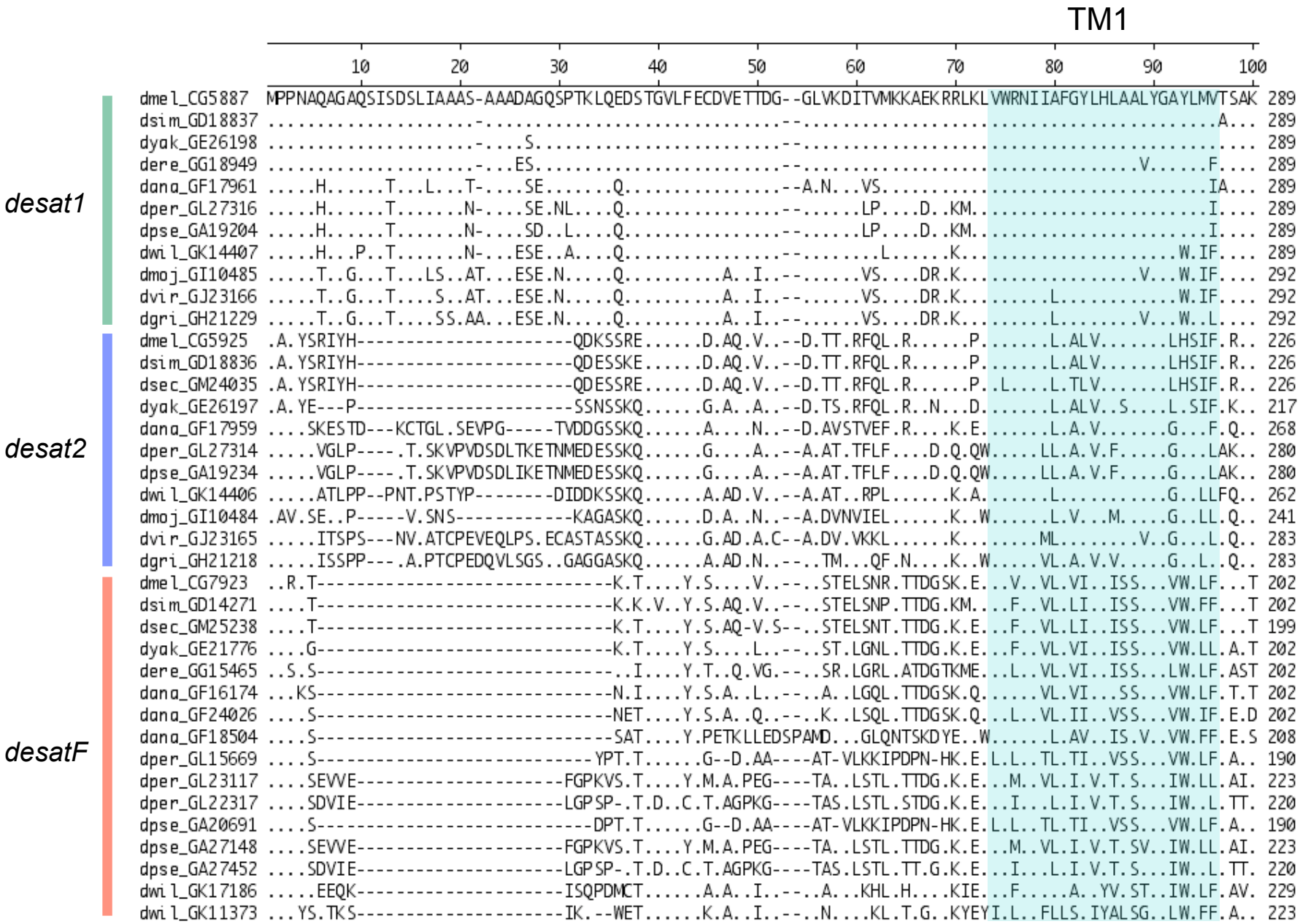

Fig. S3. Amino acid alignment of Desat1, Desat2, and DesatF. The hypothetical transmembrane domains (TM1-4), and 3 histidine boxes (H1-3) are highlighted based on Knipple et al. (2002).

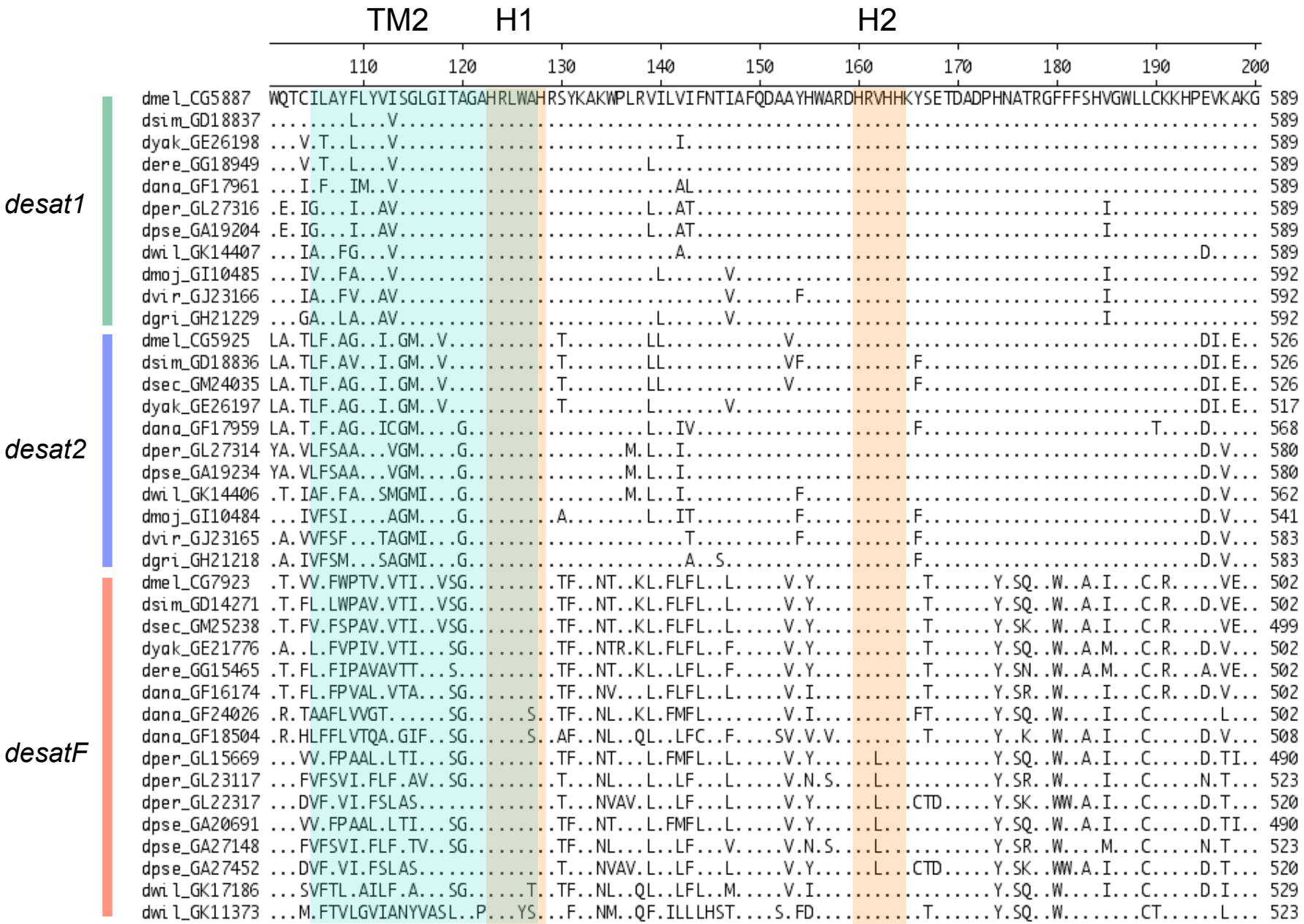
TM2
H1
H2
110
120
130
140
150
160
170
180
190
200
desat1
desat2
desatF
dmel_CG5887 WQTCILAYFLYVISGLGITAGAHRLWAHRSYKAKWPLRVILVIFNTIAFQDAAYHWARDHRVHHKYSETDADPHNATRGFFFSHVGWLLCKKHPEVKAKG 589
dsim_GD18837 .....L...V..... 589
dyak_GE26198 ...V.T..L...V.....I..... 589
dere_GG18949 ...V.T..L...V.....L..... 589
dana_GF17961 ...I.F..IM..V.....AL..... 589
dper_GL27316 .E.IG...I..AV.....L..AT.....I..... 589
dpse_GA19204 .E.IG...I..AV.....L..AT.....I..... 589
dwil_GK14407 ...IA..FG...V.....A.....D..... 589
dmoj_GI10485 ...IV..FA...V.....L.....V.....I..... 592
dvir_GJ23166 ...IA..FV..AV.....V.....F.....I..... 592
dgri_GH21229 ...GA..LA..AV.....L.....V.....I..... 592
dmel_CG5925 LA.TLF.AG..I.GM..V.....T.....LL.....V.....DI.E.. 526
dsim_GD18836 LA.TLF.AV..I.GM..V.....T.....LL.....VF.....F.....DI.E.. 526
dsec_GM24035 LA.TLF.AG..I.GM..V.....T.....LL.....V.....F.....DI.E.. 526
dyak_GE26197 LA.TLF.AG..I.GM..V.....T.....L.....V.....DI.E.. 517
dana_GF17959 LA.T.F.AG..ICGM....G.....L..IV.....F.....T....D..... 568
dper_GL27314 YA.VLFSAA...VGM....G.....M.L..I.....D.V... 580
dpse_GA19234 YA.VLFSAA...VGM....G.....M.L..I.....D.V... 580
dwil_GK14406 .T.IAF.FA..SMGMI...G.....M.L..I.....F.....D.V... 562
dmoj_GI10484 ...IVFSI....AGM....G.....A.....L..IT.....F.....F.....D.V... 541
dvir_GJ23165 .A.VVFSF...TAGMI...G.....T.....F.....F.....D.V... 583
dgri_GH21218 .A.IVFSM...SAGMI...G.....A..S.....F.....D.V... 583
dmel_CG7923 .T.VV.FWPTV.VTI..VSG.....TF..NT..KL.FLFL..L.....V.Y.....T.....Y.SQ..W..A.I...C.R.....VE.. 502
dsim_GD14271 .T.FL.LWPAV.VTI..VSG.....TF..NT..KL.FLFL..L.....V.Y.....T.....Y.SQ..W..A.I...C.R...D.VE.. 502
dsec_GM25238 .T.FV.FSPAV.VTI..VSG.....TF..NT..KL.FLFL..L.....V.Y.....T.....Y.SK..W..A.I...C.R.....VE.. 499
dyak_GE21776 .A..L.FVPIV.VTI...SG.....TF..NTR.KL.FLFL..F.....V.Y.....T.....Y.SQ..W..A.M...C.R...D.V... 502
dere_GG15465 .T.FL.FIPAVAVTT...S.....TF..NT..KL..LFL..F.....V.Y.....T.....Y.SN..W..A.M...C.R...A.VE.. 502
dana_GF16174 .T.FL.FPVAL.VTA...SG.....TF..NV...L.FLFL..L.....V.I.....T.....Y.SR..W....I...C.R...D.V... 502
dana_GF24026 .R.TAAFLVVGT......SG.....S..TF..NL..KL.FMFL.....V.I.....FT.....Y.SQ..W....I...C.....L... 502
dana_GF18504 .R.HLFFLVTQA.GIF..SG.....S..AF..NL..QL..LFC..F....SV.V.V.....T.....Y..K..W..A.I...C.....D.V... 508
dper_GL15669 ...VV.FPAAL.LTI...SG.....TF..NT...L.FMFL..L.....V.Y.....L.....Y.SQ..W..A.I...C.....D.TI.. 490
dper_GL23117 ...FVFSVI.FLF.AV..SG.....T...NL...L..LF...L.....V.N.S....L.....Y.SR..W....I...C.....N.T... 523
dper_GL22317 ...DVF.VI.FSLAS.....T...NVAV.L..LF...L.....V.Y.....L...CTD.....Y.SK..WW.A.I...C.....D.T... 520
dpse_GA20691 ...VV.FPAAL.LTI...SG.....TF..NT...L.FMFL..L.....V.Y.....L.....Y.SQ..W..A.I...C.....D.TI.. 490
dpse_GA27148 ...FVFSVI.FLF.TV..SG.....TF..NL...L..LF...V.....V.N.S....L.....Y.SR..W....M...C.....N.T... 523
dpse_GA27452 ...DVF.VI.FSLAS.....T...NVAV.L..LF...L.....V.Y.....L...CTD.....Y.SK..WW.A.I...C.....D.T... 520
dwil_GK17186 ...SVFTL.AILF.A...SG.....T..TF..NL..QL..LFL..M.....V.I.....Y.SQ..W....I...C.....D.I... 529
dwil_GK11373 ...M.FTVLGVIANYVASL..P...YS..F..NM..QF.ILLLHST....S.FD.....T.....Y.SQ..W.....CT.....L... 523

Fig. S2-2

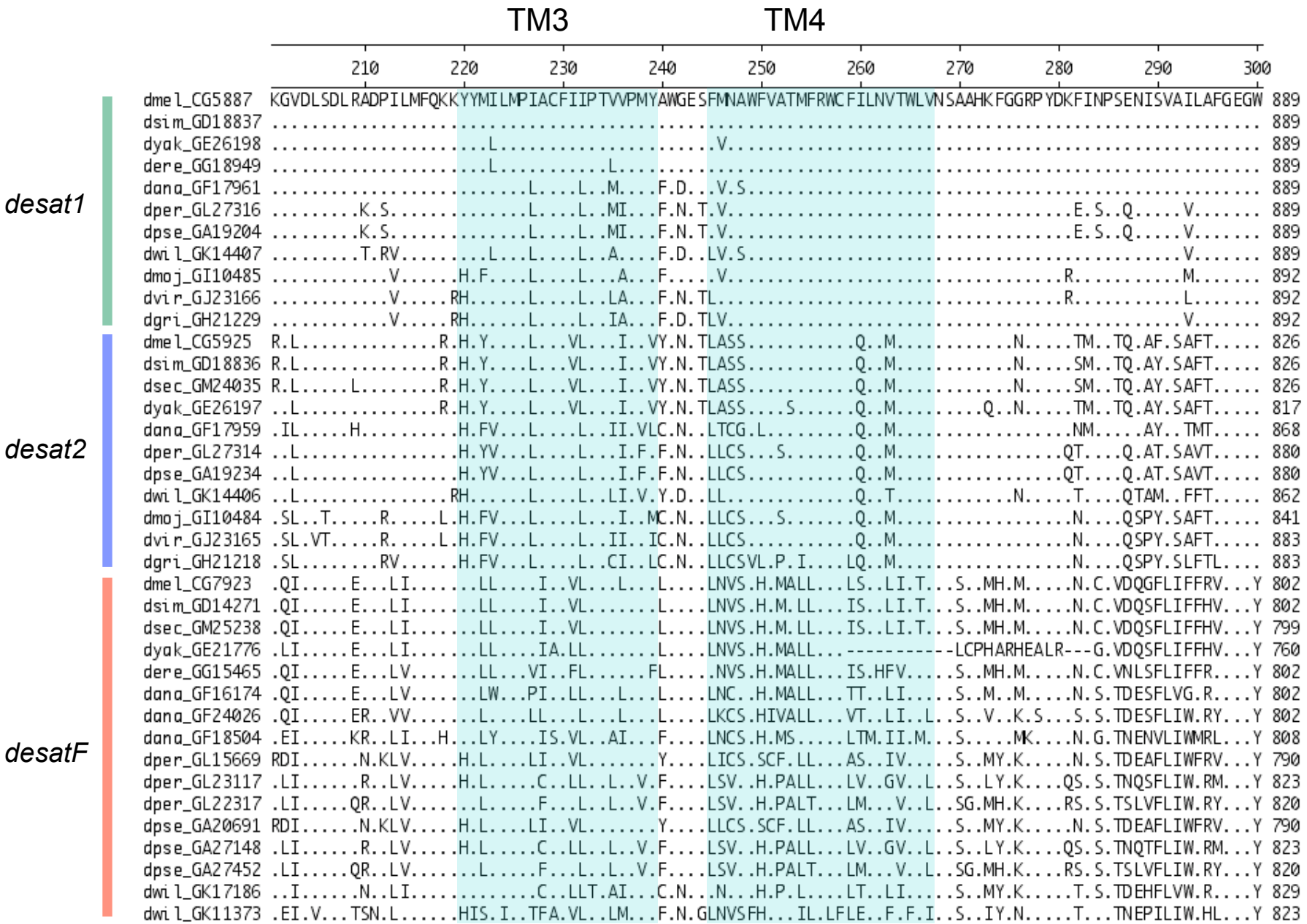
TM3
TM4
210
220
230
240
250
260
270
280
290
300
desat1
desat2
desatF
dmel_CG5887 KGVDLSDLRADPILMFQKKYYMILMPIACFIIPTVVPMYAWGESFMNAWFVATMFRWCFILNVTWLVNSAAHKFGGRPYDKFINPSENISVAILAFGEGW 889
dsim_GD18837 889
dyak_GE26198 ...L.....V..... 889
dere_GG18949 ...L.....L..... 889
dana_GF17961 .....L....L..M....F.D...V.S..... 889
dper_GL27316 .....K.S.....L....L..MI...F.N.T.V.....E.S..Q.....V..... 889
dpse_GA19204 .....K.S.....L....L..MI...F.N.T.V.....E.S..Q.....V..... 889
dwil_GK14407 .....T.RV.....L...L....L..A....F.D..LV.S.....V..... 889
dmoj_GI10485 .....V.....H.F....L....L...A...F.....V.....R.....M..... 892
dvir_GJ23166 .....V.....RH.....L....L..LA...F.N.TL.....R.....L..... 892
dgri_GH21229 .....V.....RH.....L....L..IA...F.D.TLV.....V..... 892
dmel_CG5925 R.L.....R.H.Y....L...VL...I..VY.N.TLASS.....Q..M.....N.....TM..TQ.AF.SAFT..... 826
dsim_GD18836 R.L.....R.H.Y....L...VL...I..VY.N.TLASS.....Q..M.....N.....SM..TQ.AY.SAFT..... 826
dsec_GM24035 R.L.....L.....R.H.Y....L...VL...I..VY.N.TLASS.....Q..M.....N.....SM..TQ.AY.SAFT..... 826
dyak_GE26197 ..L.....R.H.Y....L...VL...I..VY.N.TLASS....S.....Q..M.....Q..N.....TM..TQ.AY.SAFT..... 817
dana_GF17959 .IL.....H.....H.FV...L....L..II.VLC.N..LTCG.L.....Q..M.....NM.....AY..TMT..... 868
dper_GL27314 ..L.....H.YV...L....L...I.F.F.N..LLCS...S.....Q..M.....QT....Q.AT.SAVT..... 880
dpse_GA19234 ..L.....H.YV...L....L...I.F.F.N..LLCS.....Q..M.....QT....Q.AT.SAVT..... 880
dwil_GK14406 ..L.....RH.....L....L..LI.V.Y.D..LL.....Q..T.....N.....T....QTAM..FFT..... 862
dmoj_GI10484 .SL..T.....R.....L.H.FV...L....L...I..MC.N..LLCS...S.....Q..M.....N....QSPY.SAFT..... 841
dvir_GJ23165 .SL.VT.....R.....L.H.FV...L....L..II..IC.N..LLCS.....Q..M.....N....QSPY.SAFT..... 883
dgri_GH21218 .SL.....RV.....H.FV...L....L..CI..LC.N..LLCSVL.P.I....LQ..M.....N....QSPY.SLFTL.... 883
dmel_CG7923 .QI.....E...LI.....LL....I..VL...L...L....LNVS.H.MALL...LS..LI.T...S..MH.M.....N.C.VDQGFLIFFRV...Y 802
dsim_GD14271 .QI.....E...LI.....LL....I..VL.....L....LNVS.H.M.LL...IS..LI.T...S..MH.M.....N.C.VDQSFLIFFHV...Y 802
dsec_GM25238 .QI.....E...LI.....LL....I..VL.....L....LNVS.H.M.LL...IS..LI.T...S..MH.M.....N.C.VDQSFLIFFHV...Y 799
dyak_GE21776 .LI.....E...LI.....LL....IA.LL.....L....LNVS.H.MALL...----------LCPHARHEALR---G.VDQSFLIFFHV...Y 760
dere_GG15465 .QI.....E...LV.....LL...VI..FL.....FL.....NVS.H.MALL...IS.HFV.....S..MH.M.....N.C.VNLSFLIFFR....Y 802
dana_GF16174 .QI.....E...LV.....LW...PI..LL...L...L....LNC..H.MALL...TT..LI.....S..M..M.....N.S.TDESFLVG.R....Y 802
dana_GF24026 .QI.....ER..VV.....L....LL...L...L...L....LKCS.HIVALL...VT..LI..L..S..V..K.S...S.S.TDESFLIW.RY...Y 802
dana_GF18504 .EI.....KR..LI...H...LY....IS.VL..AI...F....LNCS.H.MS.....LTM.II.M...S.....MK....N.G.TNENVLIWMRL...Y 808
dper_GL15669 RDI.....N.KLV.....H.L....LI..VL.....Y....LICS.SCF.LL...AS..IV.....S..MY.K.....N.S.TDEAFLIWFRV...Y 790
dper_GL23117 .LI.....R..LV.....H.L.....C..LL..L..V.F....LSV..H.PALL...LV..GV..L..S..LY.K....QS.S.TNQSFLIW.RM...Y 823
dper_GL22317 .LI.....QR..LV.....L.....F...L..L..V.F....LSV..H.PALT...LM...V..L..SG.MH.K....RS.S.TSLVFLIW.RY...Y 820
dpse_GA20691 RDI.....N.KLV.....H.L....LI..VL.....Y....LLCS.SCF.LL...AS..IV.....S..MY.K.....N.S.TDEAFLIWFRV...Y 790
dpse_GA27148 .LI.....R..LV.....H.L.....C..LL..L..V.F....LSV..H.PALL...LV..GV..L..S..LY.K....QS.S.TNQTFLIW.RM...Y 823
dpse_GA27452 .LI.....QR..LV.....L.....F...L..L..V.F....LSV..H.PALT...LM...V..L..SG.MH.K....RS.S.TSLVFLIW.RY...Y 820
dwil_GK17186 ..I.....N..LI.....C..LLT.AI...C.N...N...H.P.L....LT..LI.....S..MY.K.....T.S.TDEHFLVW.R....Y 829
dwil_GK11373 .EI.V...TSN.L.....HIS.I..TFA.VL..LM...F.N.GLNVSFH...IL.LFLE..F.F.I..S..IY.N.....T...TNEPILIW.HL...Y 823

Fig. S2-3

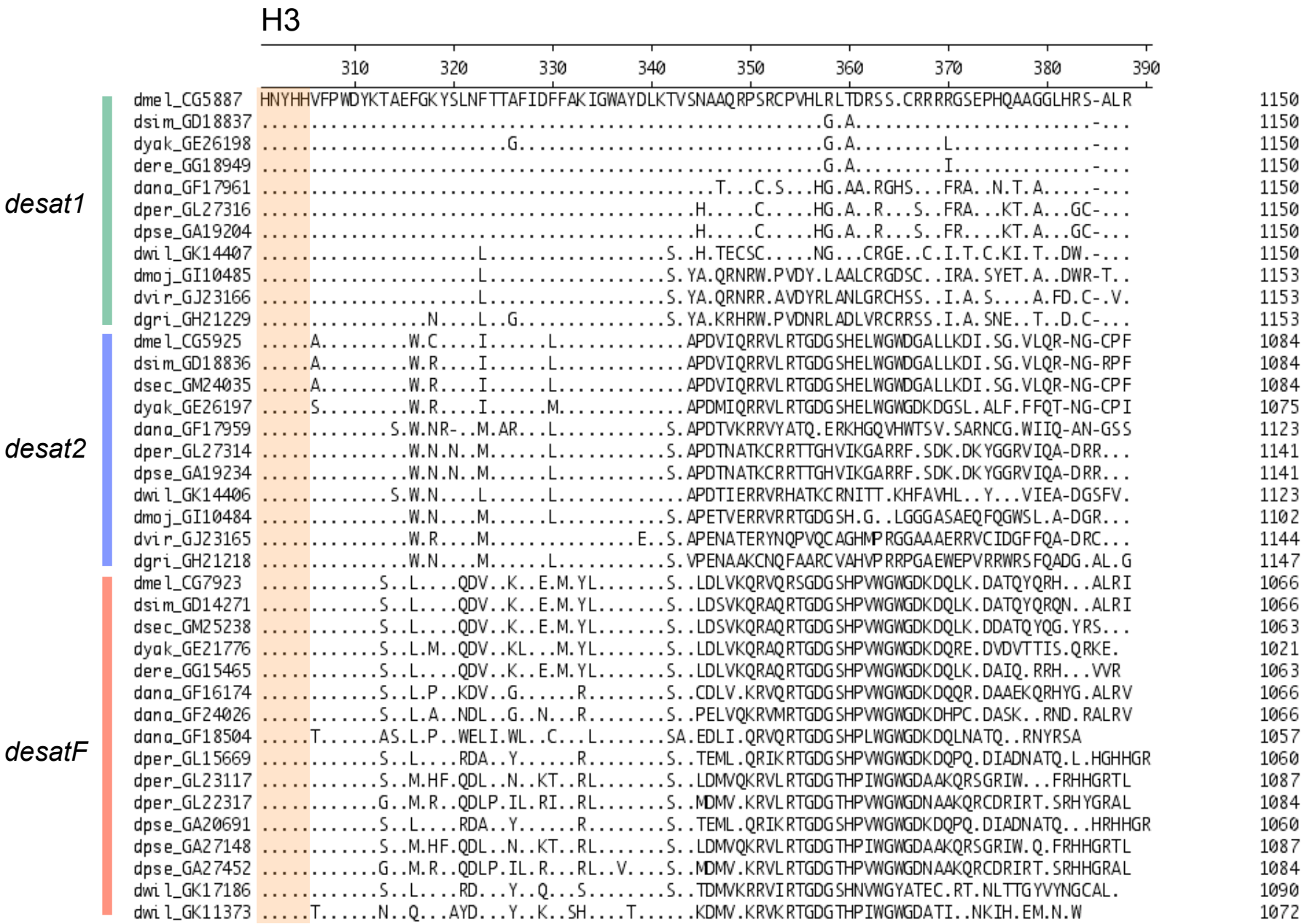
H3
310
320
330
340
350
360
370
380
390
desat1
desat2
desatF
dmel_CG5887 HNYHHVFPWDYKTAEFGKYSLNFTTAFIDFFAKIGWAYDLKTVSNAAQRPSRCPVHLRLTDRSS.CRRRGSEPHQAAGGLHRS-ALR 1150
dsim_GD18837 .....G.A.....-... 1150
dyak_GE26198 .....G.....G.A.....L.....-... 1150
dere_GG18949 .....G.A.....I.....-... 1150
dana_GF17961 .....T...C.S...HG.AA.RGHS...FRA..N.T.A.....-... 1150
dper_GL27316 .....H.....C.....HG.A..R...S..FRA...KT.A...GC-... 1150
dpse_GA19204 .....H.....C.....HG.A..R...S..FR....KT.A...GC-... 1150
dwil_GK14407 .....L.....S..H.TECSC.....NG...CRGE..C.I.T.C.KI.T..DW.-... 1150
dmoj_GI10485 .....L.....S.YA.QRNRW.PVDY.LAALCRGDSC..IRA.SYET.A..DWR-T.. 1153
dvir_GJ23166 .....L.....S.YA.QRNRR.AVDYRLANLGRCHSS..I.A.S....A.FD.C-.V. 1153
dgri_GH21229 .....N....L..G.....S.YA.KRHRW.PVDNRLADLVRCRRSS.I.A.SNE..T..D.C-... 1153
dmel_CG5925 .....A.....W.C....I.....L.....APDVIQRRVLRTGDGSHELWGWDGALLKDI.SG.VLQR-NG-CPF 1084
dsim_GD18836 .....A.....W.R....I.....L.....APDVIQRRVLRTGDGSHELWGWDGALLKDI.SG.VLQR-NG-RPF 1084
dsec_GM24035 .....A.....W.R....I.....L.....APDVIQRRVLRTGDGSHELWGWDGALLKDI.SG.VLQR-NG-CPF 1084
dyak_GE26197 .....S.....W.R....I.....M.....APDMIQRRVLRTGDGSHELWGWGDKDGSL.ALF.FFQT-NG-CPI 1075
dana_GF17959 .....S.W.NR-..M.AR...L.....S.APDTVKRRVYATQ.ERKHGQVHWTSV.SARNCG.WIIQ-AN-GSS 1123
dper_GL27314 .....W.N.N..M.....L.....S.APDTNATKCRRTTGHVIKGARRF.SDK.DKYGGRVIQA-DRR... 1141
dpse_GA19234 .....W.N.N..M.....L.....S.APDTNATKCRRTTGHVIKGARRF.SDK.DKYGGRVIQA-DRR... 1141
dwil_GK14406 .....S.W.N....L.....L.....APDTIERRVRHATKCRNITT.KHFAVHL..Y...VIEA-DGSFV. 1123
dmoj_GI10484 .....W.N....M.....L.....S.APETVERRVRRTGDGSH.G..LGGGASAEQFQGWSL.A-DGR... 1102
dvir_GJ23165 .....W.R....M.....E..S.APENATERYNQPVQCAGHMPRGGAAAERRVCIDGFFQA-DRC... 1144
dgri_GH21218 .....W.N....M.....L.....S.VPENAAKCNQFAARCVAHVPRRPGAEWEPVRRWRSFQADG.AL.G 1147
dmel_CG7923 .....S..L....QDV..K..E.M.YL.....S..LDLVKQRVQRSGDGSHPVWGWGDKDQLK.DATQYQRH...ALRI 1066
dsim_GD14271 .....S..L....QDV..K..E.M.YL.....S..LDSVKQRAQRTGDGSHPVWGWGDKDQLK.DATQYQRQN..ALRI 1066
dsec_GM25238 .....S..L....QDV..K..E.M.YL.....S..LDSVKQRAQRTGDGSHPVWGWGDKDQLK.DDATQYQG.YRS... 1063
dyak_GE21776 .....S..L.M..QDV..KL...M.YL.....S..LDLVKQRAQRTGDGSHPVWGWGDKDQRE.DVDVTTIS.QRKE. 1021
dere_GG15465 .....S..L....QDV..K..E.M.YL.....S..LDLVKQRAQRTGDGSHPVWGWGDKDQLK.DAIQ.RRH...VVR 1063
dana_GF16174 .....S..L.P..KDV..G.....R.....S..CDLV.KRVQRTGDGSHPVWGWGDKDQQR.DAAEKQRHYG.ALRV 1066
dana_GF24026 .....S..L.A..NDL..G..N...R.....S..PELVQKRVMRTGDGSHPVWGWGDKDHPC.DASK..RND.RALRV 1066
dana_GF18504 .....T.....AS.L.P..WELI.WL..C...L.....SA.EDLI.QRVQRTGDGSHPLWGWGDKDQLNATQ..RNYRSA 1057
dper_GL15669 .....S..L....RDA..Y.....R.....S..TEML.QRIKRTGDGSHPVWGWGDKDQPQ.DIADNATQ.L.HGHHGR 1060
dper_GL23117 .....S..M.HF.QDL..N..KT..RL.....S..LDMVQKRVLRTGDGTHPIWGWGDAAKQRSGRIW...FRHHGRTL 1087
dper_GL22317 .....G..M.R..QDLP.IL.RI..RL.....S..MDMV.KRVLRTGDGTHPVWGWGDNAAKQRCDRIRT.SRHYGRAL 1084
dpse_GA20691 .....S..L....RDA..Y.....R.....S..TEML.QRIKRTGDGSHPVWGWGDKDQPQ.DIADNATQ...HRHHGR 1060
dpse_GA27148 .....S..M.HF.QDL..N..KT..RL.....S..LDMVQKRVLRTGDGTHPIWGWGDAAKQRSGRIW.Q.FRHHGRTL 1087
dpse_GA27452 .....G..M.R..QDLP.IL.R...RL..V....S..MDMV.KRVLRTGDGTHPVWGWGDNAAKQRCDRIRT.SRHHGRAL 1084
dwil_GK17186 .....S..L....RD...Y..Q...S.....S..TDMVKRRVIRTGDGSHNVWGYATEC.RT.NLTTGYVYNGCAL. 1090
dwil_GK11373 .....T.....N..Q...AYD...Y..K..SH....T.....KDMV.KRVKRTGDGTHPIWGWGDATI..NKIH.EM.N.W 1072

Fig. S2-4