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ScalObp71 -----MNK-----CAFIILLWAFS-LCQVYAEILDGKRPSWYPDDSP EI--- 40
Hirr_10749 -----MKK-----FAYIILLCWSCVMIREVYAEILDGKRPSWYPDDGPEI--- 41
ScalObp70 -----MNRMTLEQGFIIVIGI-----VLLTASNAQRPDWFPENRAEI--- 39
Hirr_23522 -----MKI-----FFYVFA-----MLIAVSMFAKRPDWYKNGIEI--- 31
ScalObp68 -----MKR-----LTIFA-----FIVSASAVFERPDWYPENGVEI--- 31
ScalObp69 -----MRNMKQ-----LLVICA-----IILSASAAFERPDWYPENGSI--- 34
Hirr_18958 -----0-----
ScalObp67 -----MLISKMFN-----TIFAFL-----MLFGLGILAEERPEWYPKNAEI--- 36
Hirr_22727 -----MNK-----IVFVLI-----VLSSSMIFAERPSWYPENSAEL--- 31
ScalObp64 -----MTK-----LIIGLV-----LLALTMALAEERPSWYPENAAEL--- 31
Hirr_15556 -----MSK-----IIGVFL-----LLSITAILAEERPSWYPENAAEL--- 31
Hirr_18389 LQINLQTLNSKMTK-----FIVVLL-----VLSMTMIFAERPEWYPENAAEL--- 42
Hirr_5709 -----0-----HRPEWYPENSLDI--- 13
ScalObp65 -----MHK-----FTVLL-----IPVLSLVIAQRPDWLPENSP EI--- 30
ScalObp66 -----MLK-----LTVLL-----IPVLSLVIAQRPDWYPENSLDI--- 30
ScalObp74 -----M-----FYILVL-----ILTARTILAQRPDWYPENPAKI--- 29
ScalObp72 -----MNR-----LLVVFL-----ILFLSKTFAERPDWYPENAAEI--- 31
ScalObp73 -----MIK-----LLIGCI-----MISITLILGERPEWYPENASLF--- 31
ScalObp10 -----MK-----FAAVVL-----FALFAVASAEYKLRNQEDLMKA 30
DmelObp99c -----MLK-----YLIVAL-----ALCAVAHADDTWPKTGEEIRNI 31
ScalObp62 -----MK-----FMVILL-----AIFACVSADDTWPKKSREIREI 30
ScalObp61 -----MK-----YFVALL-----VIVACVSAEEWPKTAD EIKTL 30
ScalObp63 -----MFEAIK-----YLIILL-----AVVVCISADDTWPKVKNELKSI 34

C1 C2 C3
EAECEMEDFTISEESLKQIR-NLQIANTPAVRAYLLCFLKETNVYRPDKGPEIKRIAWSLK 99
Hirr_10749 EAECEVEDHSISKETLDDIK-MLHIDNTPTVRAYLLCYLKETNVYRPEKGP ELRRIASLK 100
ScalObp70 EANCLMENSIDDETLTNIR-QLKLDDTPQIRSLIMCSLINTNAYRPDREPADRLVVAQ 98
Hirr_23522 ENACKAKICPNEDILNKLKRLKQIEDNDKTRQLIMCCLKNTNVYRPGNGPEADRI GVAFE 90
ScalObp68 EALCSAKLADDDIILNKLRLKLEIEDNEKTRLELILCCLKNTNVYREDHGPEADRI AVAFE 90
ScalObp69 EADCMKSIAGDDIILNKLRLKQIDNNEKTRDLILCCLRNNTVYRPGQVPEADRI AVAFQ 93
Hirr_18958 ---DCMAKISVSDSILQNLRLRKIDNNEETRLILCCLRNNTVYRPGYGYGPEADRI AVAFQ 57
ScalObp67 DAECMKKHVLSAEIMEKLNDFLTEDPTMRSLVFCSALGKQVFRPNVGF EA VRVVEGLQ 96
Hirr_22727 DAECMKKHVPVSAEIEKVR-SFHLEDTPNMRALVYCGATSKNVYIPGEGFNSERFVEGMK 90
ScalObp64 EVCKMKEHAVSPETVANMR-AFNLDEAPAIVAVLFCSGKAKKIYTP ELGFPVPERFAYAMK 90
Hirr_15556 EVNCKMKEHSVSPETVSKMR-GFHLEEAPAIVSVLFCSGKAKNIYTD LGFVPERFAYGMK 90
Hirr_18389 EVNCKMDHNVTPEIVAKIR-SFHLDTP EIRDVVYCSAKAKNIYRPGVGFEPE RFLVGR 101
Hirr_5709 EAECLRKNGLDYETMNDIL-SLRVEDTPALRSFLYCSAVGNVYRPDI GFEMDRFELGLK 72
ScalObp65 EAECLAKNCLSP EIMNDIL-NLHVEDTPAMRAFLFCAAVRN NVYRPEIGFEIDRFDMGLK 89
ScalObp66 EAECCMAINCLSP EIMYDIL-NLHVEDTPAMRAFLFCAAVGN NVYRPEIGFEIDRFDMGLK 89
ScalObp74 EEQCMREHSITPEIWS TIR-SFHLDTPNVGSFFLCCLNTKKGVFRPEKGFEPERLAIGIR 88
ScalObp72 EADCKKENGITPEIWSQML-SLDLEDTPPVRSVLLCLVKKRTVYRPENGFEAERLQVGLQ 90
ScalObp73 EKACLVENDLRPDQWARMR-TMHLEDTPAERAFLLCLVKTKNVFRPEKGF EAERLRLGLQ 90
ScalObp10 RKECMEAKKVTPELIEKYK-KFDFPDDETTRCYIECVFEKFELF DAKEGFKNDNLVAQLG 89
DmelObp99c RVECLKENPLSNDQISQLK-NLIFPNPEPDVRQYLTCSATKLGI FCDQGGYHADRLAKQFK 90
ScalObp62 RQACMETISLTESQKKIE-NFDFPNDEAVRKYIVCTLEKMEICCTSHGFHVNRLIKQTN 89
ScalObp61 RAACLQEHPLEEQMNRMK-VFDFPDEEAVRKYIMCTSEKMDVYCPHEGYHADRIAKQFK 89
ScalObp63 RDECLNEVPVTEDQQRKMN-ALDFPNEEAVRN FILCAVQKLGIYSTE HGYADRLTKQFN 93

* C4 : : C5 . C6 ..
QNYHLNKCDDADMIRDCIEEQGDQ-DLKDYAFFNIICKVFHKNRIYGTNKLSP IYL----- 153
EYLKLNKCDDADMIRDCIEEHGAQ-DLKDYAYFHIIICKAYEKAPDRCLAKVKDN*----- 152
QNLKRD-CDIDMVESSCIDQYKHL-QPDDYKYFTIICKIFNEAPTCKTCLIK----- 146
Hirr_23522 QSLRLH-CEADLIAGCIQTFKDT-TNEYEQFFNVIKCIYDVAPEKCKPE*----- 137
ScalObp68 QSLKLH-CEPELIQEC SQKFKEE-KPESYEFFRIICKIYDEAPQKCKP----- 136
ScalObp69 QSLKLN-CEEDLINGCIPKYKDE-KPENYQFFRIICKIYDEAPARCKP----- 139
Hirr_18958 QSLKLN-CDIDLIGQCIKPKFIHE-MPEKYQFFRTIKCIYDEAPQRCLP*----- 103
ScalObp67 ENAKLN-CSLEAVQHCA DQFRNA-NSNEAMFFSTMKCLFDDISENCSKMKETE----- 147
Hirr_22727 ESSKMN-CNMDSVRNCADKHKNA-ESDEAIFFNVLKCVFDDINGICNKVV*----- 138
ScalObp64 TNVKMD-CNVDYIRNCAEQHKDV-QPVD TMYFKVVKCFVDNREGHCTKV----- 137
Hirr_15556 QNVKLD-CDVDFIRNCAETHKEV-QPAETMYFRVVKCFVDNREGHCKKVE*----- 138
Hirr_18389 ESVKMD-CNINYIRSCGEHKYV-QPE----- 126
Hirr_5709 YKIKLD-CNKEFLNSCGELYKEE-ISPESLYFHIVKCFVDNSEDNCIRTH*----- 120
ScalObp65 YKIKID-CSKEFLNYCVELYQSE-ENPESLYFYIVKYVSNTTTEVP----- 133
ScalObp66 YKIKID-CSKEFLNYCVELYQSE-ENPESLYFYIVKYVSNTTTEVP----- 133
ScalObp74 MTTKVD-CDVNMIRNCGDRYKEL-KPHDHMILNIICKIFENKEGNCRKIQ----- 136
ScalObp72 QVAKRK-CDLNHIKDCGEKFCDL-EPEDFKIFSIKCTLDDRHEKCEKVE----- 138
ScalObp73 QSIKAD-CDIEHIEHCKQMYGHL-KPDDVMVFQIAKVCDDVKDEKCRKLIKNEL----- 142
ScalObp10 QGKDNKDAVKT DVEKCADKNEQK-SDSCSWAFRGFKCFIKSNLPLVMDSLKKN----- 141
DmelObp99c MDLSEE-EALQIAQSCVDDNAQK-SPTDVWAFRGHQCMMASKIGDKVRAVFKAKAEAKK 148
ScalObp62 KDLGSE-QGKDVVEECLRNPNKGDNEIEIYAHDVYTC LIDEVTKIIES----- 136
ScalObp61 MDMVED-DVKKLAEDCISSNPKGDKANDVHVYEVHKLMASEVGQVKSYIKSRQEQ LAK 148
ScalObp63 SELHGD-DGKEPVDNCLNNPNQGYKENDVYVYEMHLC LIEARKEHAKRHK-----EQ--- 144

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Figure S1A. Amino acid sequence alignment of horn fly candidate Minus-C OBPs with a Minus-C OBP from *Drosophila* (DmelObp99c) and *Stomoxys calcitrans* (Scal). ScalOBP10, a classical OBP, is included in the alignment for reference to location of conserved cysteine residues. Conserved cysteine residues shared between sequences are shaded in blue. The C₂ and C₅ cysteines that are missing from the Minus-C OBPs are shaded in orange and within these the cysteine in ScalOBP10 is in bold text. The cysteine shaded in pink reflects the alternate cysteine residue located seven residues upstream of C₄.

		C1	
ScalObp10	-MKFAAVVLF-----LFAVAS-----AEYKLRNQEDLMKARKE C MEAKKVTPELIEKYKKF	51	
DmelObp99a	-MK-VFVAICV-----LIGLAS-----ADYVVKNRHDMVFRDE C VKELAVPVDLVEKYQKW	50	
DmelObp99d	-----MIHLRLAII C ---WSCLLIVMATTT E AASVW----- C ---KLPTAEMVYEDLEKC	43	
DmelObp8a	MMRRSQIWLLRLLLLLVEMTPPAIPVPMRSSQSLALLRARD C CGRELTA AQ RL--QLDRM	58	
MdomObp58	-MKSRTFVAL---LLCNIL---ILVTGQNTISDNFYDKSEK C FDQLHVPQRYKATFQAF	52	
Hirr_326	-MKSFAFCG-----LFLNIW---LSVHGQNTISDRFFDVSEK C FEQLHVPQRYKSEFQQF	51	
ScalObp58	-MKLVAFIL-----LFLS-L---PAVFGQNTISDQFFSKSEI C FELLHVPNRYRSEFGNF	50	
	.	.	.
	C2 C3	C4	
ScalObp10	DFPDDETR C YIE C VFEKFE L DAKEGFKNDNLVAQL-GQGKDNKDAVKT D VEK C ADKNE	110	
DmelObp99a	EYPNDAKT C YIK C VFTKWGLFDVQSGFNVENIHQQLVGNHADHNEAFHASLAA C VDKNE	110	
DmelObp99d	RQESQEEDA A TLR C LVKKLGLWTDESGYNARRIAKIFAGH--NQMEELMLVVEH C NRKEQ	101	
DmelObp8a	QFEDA A HVRH Y LH C FWSRLQLWLDE T GFQAQRIVQSF G GERRLNVEQALPAING C NAKTS	118	
MdomObp58	RYPDEEIVH K YVH C LAMKLEIWTNRSGFNIEKIYNQYRN--RVNDEIMLPTIS C NRSAQ	110	
Hirr_326	RYADTEMVH K YI H CVSTELHIWNNRSGFDIEKIYNEYHA--RANDEVMLPIIS C NRRTTQ	109	
ScalObp58	SYADEEVH K YI H CVTELDIWNRSGFNIEKIYHQRN--RANDEVMLPIIS C NRSSQ	108	
	.	:.*. . :: . *:. .:	: : : *
	C5 C6		
ScalObp10	Q----KSD S CSWAFRGFK C FIKSNLPLVMDSLKKN-----	141	
DmelObp99a	Q----GSN A CEWAYRGAT C LLKENLAQIQKSLAPKA-----	142	
DmelObp99d	D----TSH L DDWAFLAYRCATSGQFGHWKDFMSQKD V DQ-----	137	
DmelObp8a	SRGSGTQT V VD C FR A FV C VLATPVGEWYKRHMSDVINGNA-----	159	
MdomObp58	N-----SNKELW C YRAFL C ILNTDVGKWFKEDVQ R SRQANNVPNGHH-	152	
Hirr_326	N-----SNKELW C YRAF V ILNTDVGKWFKEDVQ R SRQAG-IPNGYH*	150	
ScalObp58	N-----NNKELW C YRAF V ILNTDVGQWFKEDVQ R KRQAN-ISNGHH-	149	

Figure S1B. Amino acid sequence alignment of horn fly candidate Minus-C OBP, *Hirr_326*, with Minus-C OBPs from *Drosophila* (DmelObp99a, 99d) and *Stomoxys calcitrans* (Scal). ScalOBP10, a classical OBP, is included in the alignment for reference to location of conserved cysteine residues. Conserved cysteine residues shared between sequences are shaded in blue. The C₂ and C₅ cysteines that are missing from *Hirr_326* are shaded in orange and within these the cysteine in ScalOBP10 is in bold text. The cysteine shaded in pink reflects the alternate cysteine residue located three residues downstream of C₅.