Supplementary Table 1a. Complete list of OBP genes from *Anopheles gambiae* reported in this study. Alongside their identification and chromosomal locations, shown are their subfamilies, phylogenetic clusters and orthologues in *Aedes aegypti* and *Culex quinquefasciatus*. The four newly discoverd genes by us are AgamOBP65-68 and are denoted by an (*). The gene names used here do not completely coincide with the gene names in the were recently published work by Vieira & Rozas (2011). As an *addendum* to this Table, we are providing in supplementary Table 1b, a comparative analysis of the names between their study and ours. The last four genes were identified by Vieira & Rozas (2011) and were added to this Table at the last moment after renaming them AgamOBP69-72. †Two genes AgamOBP34 and AgamOBP37 share 100% sequence identity but are localized on distinct chromosome segments. We cannot resolve which of these two genes is the true orthologue of AaegOBP106. Two way (1:1) orthologues are indicated by a # sign. OBPs that did not clustered in a phylogenetic group were indicated as 'unclassified' in the 'Cluster' column.

n°	ID	Name	Length	Chromo-some	Start	End	Sub-family	Cluster	Ortholog in *Ae. aegyptii*	Ortholog in *Culex*
1	AGAP003309	AgamOBP1	144	2R	35643035	35644609	Classic	OS-E/OS-F	AaegOBP1	CquiOBP1
2	AGAP003306	AgamOBP2	157	2R	35434051	35434604	Classic	OS-E/OS-F	AaegOBP60	CquiOBP3
3	AGAP001409	AgamOBP3	153	2R	4210577	4212097	Classic	OS-E/OS-F	AaegOBP38	CquiOBP2
4	AGAP010489	AgamOBP4	150	3L	4997901	4998953	Classic	LUSH	AaegOBP39	CquiOBP6
5	AGAP009629	AgamOBP5	156	3R	37321107	37322204	Classic	LUSH		
6	AGAP003530	AgamOBP6	155	2R	39200905	39201673	Classic	OBP19a	AaegOBP27	CquiOBP13
7	AGAP001556	AgamOBP7	154	2R	6152013	6154470	Classic	Pbprp1	AaegOBP2	CquiOBP7
8	AGAP000279	AgamOBP8	176	X	5036744	5037431	Classic	*unclassified*		
9	AGAP000278	AgamOBP9	139	X	5035248	5036100	Classic	Obp99a	AaegOBP22	CquiOBP43
10	AGAP001189	AgamOBP10	131	2R	1034139	1169444	Classic	mclassic6	AaegOBP10	CquiOBP24
11	AGAP002025	AgamOBP11	192	2R	14069095	14069749	Classic	mclassic9		
12	AGAP002188	AgamOBP12	159	2R	17328044	17328912	Classic	*unclassified*		
13	AGAP002905	AgamOBP13	149	2R	29134157	29134861	Classic	Pbprp2/5	AaegOBP57	CquiOBP28
13	AGAP002189	AgamOBP14#	188	2R	17331871	17332553	Classic	mclassic9	AaegOBP18#	CquiOBP63#
15	AGAP003307	AgamOBP15	147	2R	35436449	35436969	Classic	OS-E/OS-F	AaegOBP36	CquiOBP5
16		AgamOBP16		Previously reported but same gene as AgamOBP15, hence not included in this analysis						
17		AgamOBP17		Previously reported but same gene as AgamOBP1, hence not included in this analysis						
18		AgamOBP18		Previously reported but same gene as AgamOBP6, hence not included in this analysis						
19	AGAP004433	AgamOBP19	137	2R	55987079	55987846	*Classic*	OBP19a	AaegOBP56	CquiOBP12
20	AGAP005208	AgamOBP20	142	2L	12288238	12289440	*Classic*	OBP19a	AaegOBP55	CquiOBP11
21	AGAP008398	AgamOBP21	131	3R	10317255	10317835	*Classic*	mclassic5	AaegOBP8	CquiOBP23
22	AGAP010409	AgamOBP22	144	3L	2853087	2853645	*Classic*	mclassic8	AaegOBP81	CquiOBP44
23	AGAP012318	AgamOBP23	131	3L	40168852	40169329	*Classic*	mclassic3	AaegOBP9	CquiOBP22
24	AGAP012319	AgamOBP24	176	3L	40171315	40172237	*Classic*	mclassic2	AaegOBP77	CquiOBP21

**Newly discovered genes in this study.*
 # Only a two way (1:1) orthology has been established for these genes and not a three way (1:1:1) orthology.
†Two genes AgamOBP34 and AgamOBP37 share 100% sequence identity but are localized on distinct chromosome segments. We cannot resolve which of these two genes is the true orthologue of AaegOBP106.
nd : not determined

Suppl. Table 1a

n°	ID	Name	Length	Chromo-some	Start	End	Sub-family	Cluster	Ortholog in *Ae. aegyptii*	Ortholog in *Culex*
25	AGAP012320	AgamOBP25	142	3L	40209434	40210326	*Classic*	mclassic3	AaegOBP11	CquiOBP19
26	AGAP012321	AgamOBP26	131	3L	40213816	40214477	*Classic*	mclassic3	AaegOBP35	CquiOBP20
27	AGAP012323	AgamOBP27	134	3L	40218226	40218764	*Classic*	mclassic1	AaegOBP65	CquiOBP16
28	AGAP012325	AgamOBP28	134	3L	40221011	40221620	*Classic*	mclassic3	AaegOBP12	CquiOBP18
29	AGAP012331	AgamOBP29	176	3L	40708383	40709402	*Classic*	Obp59a	AaegOBP83	CquiOBP55
30	AGAP011647	AgamOBP30	289	3L	30753689	30754558	*Two-domains*	matype4		
31	AGAP010649	AgamOBP31	313	3L	7968501	7969835	*Two-domains*	matype3	AaegOBP29	
32	AGAP000638	AgamOBP32	320	X	11413679	11414777	*Two-domains*	matype4	AaegOBP102	
33	AGAP000640	AgamOBP33	334	X	11416806	11417810	*Two-domains*	*unclassified*		
34	AGAP000644	AgamOBP34†	311	X	11428745	11429680	*Two-domains*	matype2	AaegOBP106	
35	AGAP000642	AgamOBP35	275	X	11422726	11423559	*Two-domains*	matype2		
36	AGAP000643	AgamOBP36	275	X	11426182	11427015	*Two-domains*	matype2		
37	AGAP000641	AgamOBP37†	311	X	11419447	11420382	*Two-domains*	matype2	AaegOBP106	
38	AGAP000580	AgamOBP38	336	X	10205844	10206981	*Two-domains*	*unclassified*		
39	AGAP002190	AgamOBP39	246	2R	17333035	17333892	*Two-domains*	matype1	AaegOBP40	CquiOBP84
40	AGAP002191	AgamOBP40	282	2R	17334179	17335132	*Two-domains*	matype1		
41	AGAP005182	AgamOBP41	279	2L	11685185	11686024	*Two-domains*	*unclassified*		
42	AGAP009065	AgamOBP42	288	3R	25310798	25311664	*Two-domains*	*unclassified*		
43	AGAP009402	AgamOBP43	333	3R	32225167	32226168	*Two-domains*	matype4		CquiOBP76
44	AGAP010648	AgamOBP44	327	3L	7964187	7965356	*Two-domains*	matype3		
45	AGAP010650	AgamOBP45	356	3L	7970287	7971357	*Two-domains*	matype3		
46	AGAP007289	AgamOBP46	202	2L	45014419	45015087	*PlusC*	mplus2	AaegOBP48	CquiOBP108
47	AGAP007287	AgamOBP47	228	2L	45011203	45012023	*PlusC*	mplus1		
48	AGAP007286	AgamOBP48	200	2L	45008928	45009814	*PlusC*	mplus1	AaegOBP42	CquiOBP106
49	AGAP006075	AgamOBP49	179	2L	26103215	26103894	*PlusC*	mplus9	AaegOBP73	CquiOBP112
50	AGAP006076	AgamOBP50	166	2L	26104148	26104931	*PlusC*	mplus9		

**Newly discovered genes in this study.*
 # Only a two way (1:1) orthology has been established for these genes and not a three way (1:1:1) orthology.
†Two genes AgamOBP34 and AgamOBP37 share 100% sequence identity but are localized on distinct chromosome segments. We cannot resolve which of these two genes is the true orthologue of AaegOBP106.
nd : not determined

n°	ID	Name	Length	Chromo-some	Start	End	Sub-family	Cluster	Ortholog in *Ae. aegyptii*	Ortholog in *Culex*
51	AGAP006077	AgamOBP51	203	2L	26129377	26130091	*PlusC*	mplus9		
52	AGAP006078	AgamOBP52	170	2L	26130285	26131425	*PlusC*	mplus9		
53	AGAP006079	AgamOBP53	171	2L	26131618	26132453	*PlusC*	mplus9		
54	AGAP006080	AgamOBP54#	181	2L	26133006	26133968	*PlusC*	mplus7	AaegOBP69#	CquiOBP111#
55	AGAP006081	AgamOBP55	156	2L	26134275	26135119	*PlusC*	mplus10		
56	AGAP011367	AgamOBP56	235	3L	22025830	22026752	*PlusC*	mplus11	AaegOBP26	CquiOBP102
57	AGAP011368	AgamOBP57	204	3L	22028532	22029250	*PlusC*	mplus11	AaegOBP25	CquiOBP104
58	AGAP006074	AgamObp58	286	2L	26101764	26135649	*PlusC*	mplus6	AaegOBP5	CquiOBP109
59	AGAP006760	AgamOBP59	155	2L	37923144	37923831	*PlusC*	*unclassified*		
60	AGAP007281	AgamOBP60#	198	2L	44998234	44999054	*PlusC*	mplus4	AaegOBP51#	CquiOBP110#
61	AGAP007282	AgamOBP61	204	2L	44999450	45000275	*PlusC*	mplus4		
62	AGAP002556	AgamOBP62	174	2R	22787889	22792798	*Classic*	Pbprp4	AaegOBP20	CquiOBP14
63	AGAP012322	AgamOBP63	135	3L	40217381	40217853	*Classic*	mclassic4	AaegOBP61	CquiOBP17
64	AGAP012324	AgamOBP64	142	3L	40219631	40220284	*Classic*	mclassic1	AaegOBP15	CquiOBP15
65	AGAP006759	AgamOBP65*	179	2L	37922005	37922885	*PlusC*	*unclassified*		
66	AGAP007283	AgamOBP66*	212	2L	45000529	45001413	*PlusC*	mplus10		
67	AGAP012659	AgamOBP67*	204	UNKN	22699010	22699835	*PlusC*	mplus4		
68	AGAP012658	AgamOBP68*	212	UNKN	22697816	22698745	*PlusC*	mplus10		
69	AGAP013182	AgamOBP69	229	2R	21343359	21344048	*PlusC*	*nd*		
70	AGAP006368	AgamOBP70	200	2L	30543243	30547869	*PlusC*	*nd*		CquiOBP114
71	AGAP012867	AgamOBP71	228	UNKN	35107623	35108585	*PlusC*	*nd*		
72	AGAP012714	AgamOBP72	121	UNKN	24728945	24729493	*Classic*	*nd*		

**Newly discovered genes in this study.*

 # Only a two way (1:1) orthology has been established for these genes and not a three way (1:1:1) orthology.

†Two genes AgamOBP34 and AgamOBP37 share 100% sequence identity but are localized on distinct chromosome segments. We cannot resolve which of these two genes is the true orthologue of AaegOBP106.

nd : not determined

Supplementary Table 1b. OBP gene names for *Anopheles gambiae.* Shown is the correspondence between the OBP gene names used in this study and the names used in the Vectorbase, Xu et al. 2003 and very recent work of Vieira & Rozas (2011).

n°	Gene identifier in Xu et al. (2003)	Corresponding vectorbase ID	Name in vectorbase	Name as defined in Xu et al. 2003	Name in (Vieira & Rozas. 2011)	Name in (Manoharan et al. 2012)	Comment
1	AY146721	AGAP003309	AgamOBP17	AgamOBP1	AgamOBP1	AgamOBP1	Gene name difference in vectorbase
2	AY146719	AGAP003306	AgamOBP2	AgamOBP2	AgamOBP2	AgamOBP2	
3	AY146745	AGAP001409	AgamOBP3	AgamOBP3	AgamOBP3	AgamOBP3	
4	AY146731	AGAP010489	AgamOBP4	AgamOBP4	AgamOBP4	AgamOBP4	
5	AY146729	AGAP009629	AgamOBP5	AgamOBP5	AgamOBP5	AgamOBP5	
6	AY146725	AGAP003530	AgamOBP6	AgamOBP6	AgamOBP6	AgamOBP6	
7	AY146742	AGAP001556	AgamOBP7	AgamOBP7	AgamOBP7	AgamOBP7	
8	AY146744	AGAP000279	AgamOBP8	AgamOBP8	AgamOBP8	AgamOBP8	
9	AY146740	AGAP000278	AgamOBP9	AgamOBP9	AgamOBP9	AgamOBP9	
10	AY146741	AGAP001189#	AgamOBP10	AgamOBP10	AgamOBP10	AgamOBP10	
11	AY146743	AGAP002025	AgamOBP11	AgamOBP11	AgamOBP11	AgamOBP11	
12	AY146716	AGAP002188	AgamOBP12	AgamOBP12	AgamOBP12	AgamOBP12	
13	AY146718	AGAP002905	AgamOBP14	AgamOBP13	AgamOBP13	AgamOBP13	Gene name difference in vectorbase
14	AY146717	AGAP002189	AgamOBP13	AgamOBP14	AgamOBP14	AgamOBP14	Gene name difference in vectorbase
15	AY146720	AGAP003307	AgamOBP15	AgamOBP15	AgamOBP15	AgamOBP15	
16	AY146722	Not available	Not available	AgamOBP16	AgamOBP16		Not included in this study
17	AY146723	Not available	Not available	AgamOBP17	AgamOBP17		Not included in this study
18	AY146724	Not available	Not available	AgamOBP18	AgamOBP18		Not included in this study
19	AY146726	AGAP004433	AgamOBP19	AgamOBP19	AgamOBP19	AgamOBP19	
20	AY146727	AGAP005208	AgamOBP20	AgamOBP20	AgamOBP20	AgamOBP20	
21	AY146728	AGAP008398	AgamOBP21	AgamOBP21	AgamOBP21	AgamOBP21	
22	AY146730	AGAP010409	AgamOBP22	AgamOBP22	AgamOBP22	AgamOBP22	
23	AY146733	AGAP012318	AgamOBP23	AgamOBP23	AgamOBP23	AgamOBP23	
24	AY146734	AGAP012319	AgamOBP18	AgamOBP24	AgamOBP24	AgamOBP24	Gene name difference in vectorbase
25	AY146735	AGAP012320	AgamOBP25	AgamOBP25	AgamOBP25	AgamOBP25	
26	AY146736	AGAP012321	AgamOBP26	AgamOBP26	AgamOBP26	AgamOBP26	
27	AY146737	AGAP012323	AgamOBP27	AgamOBP27	AgamOBP27	AgamOBP27	
28	AY146738	AGAP012325	AgamOBP28	AgamOBP28	AgamOBP28	AgamOBP28	
29	AY146739	AGAP012331	No name	AgamOBP29	AgamOBP29	AgamOBP29	

Vectorbase IDs specifically reported in Vieira & Rozas (2011).
† Newly identified OBP genes in Vieira & Rozas (2011) not included in this study.

Suppl. Table 1b

n°	Gene identifier in Xu et al. (2003)	Corresponding vectorbase ID	Name in vectorbase	Name as defined in Xu et al. 2003	Name in (Vieira & Rozas. 2011)	Name in (Manoharan et al. 2012)	Comment
30	AY146758	AGAP011647	No name	AgamOBP30	AgamOBP30	AgamOBP30	
31	AY146760	AGAP010649	No name	AgamOBP31	AgamOBP31	AgamOBP31	
32	AY146755	AGAP000638	AgamOBP32	AgamOBP32	AgamOBP32	AgamOBP32	
33	AY146754	AGAP000640	AgamOBP33	AgamOBP33	AgamOBP33	AgamOBP33	
34	AY146753	AGAP000641	AgamOBP34	AgamOBP34	AgamOBP34	AgamOBP34	
35	AY146752	AGAP000642	AgamOBP35	AgamOBP35	AgamOBP35	AgamOBP35	
36	AY146751	AGAP000643	AgamOBP36	AgamOBP36	AgamOBP36	AgamOBP36	
37	AY146750	AGAP000644	No name	AgamOBP37	AgamOBP37	AgamOBP37	
38	AY146749	AGAP000580	AgamOBP38	AgamOBP38	AgamOBP38	AgamOBP38	
39	AY146757	AGAP002190	AgamOBP39	AgamOBP39	AgamOBP39	AgamOBP39	
40	AY146756	AGAP002191#	AgamOBP40	AgamOBP40	AgamOBP40	AgamOBP40	
41	AY146748	AGAP005182	AgamOBP41	AgamOBP41	AgamOBP41	AgamOBP41	
42	AY146747	AGAP009065	AgamOBP42	AgamOBP42	AgamOBP42	AgamOBP42	
43	AY146746	AGAP009402	AgamOBP43	AgamOBP43	AgamOBP43	AgamOBP43	
44	AY146732	AGAP010648	AgamOBP44	AgamOBP44	AgamOBP44	AgamOBP44	
45	AY146759	AGAP010650	AgamOBP45	AgamOBP45	AgamOBP45	AgamOBP45	
46	AY330173	AGAP007289	AgamOBP46	AgamOBP46	AgamOBP46	AgamOBP46	
47	AY330174	AGAP007287	AgamOBP47	AgamOBP47	AgamOBP47	AgamOBP47	
48	AY330175	AGAP007286	No name	AgamOBP48	AgamOBP48	AgamOBP48	
49	AY330176	AGAP006075	AgamOBP49	AgamOBP49	AgamOBP49	AgamOBP49	
50	AY330177	AGAP006076	AgamOBP50	AgamOBP50	AgamOBP50	AgamOBP50	
51	AY330178	AGAP006077	AgamOBP51	AgamOBP51	AgamOBP51	AgamOBP51	
52	AY330172	AGAP006078	AgamOBP52	AgamOBP52	AgamOBP52	AgamOBP52	
53	AY330179	AGAP006079	AgamOBP53	AgamOBP53	AgamOBP53	AgamOBP53	
54	AY330180	AGAP006080	AgamOBP54	AgamOBP54	AgamOBP54	AgamOBP54	
55	AY330181	AGAP006081	AgamOBP55	AgamOBP55	AgamOBP55	AgamOBP55	
56	AY330182	AGAP011367	AgamOBP56	AgamOBP56	AgamOBP56	AgamOBP56	
57	AY330183	AGAP011368	AgamOBP57	AgamOBP57	AgamOBP57	AgamOBP57	
58		AGAP006074#	Not available	Not available	AgamOBP77	AgamOBP58	Gene name difference in between Vieira & Rozas (2011) and Manoharan et al (2011)
59		AGAP006760#	Not available	Not available	AgamOBP63	AgamOBP59	
60		AGAP007281#	Not available	Not available	AgamOBP64	AgamOBP60	
61		AGAP007282#	Not available	Not available	AgamOBP61	AgamOBP61	

Vectorbase IDs specifically reported in Vieira & Rozas (2011).
† Newly identified OBP genes in Vieira & Rozas (2011) not included in this study.

n°	Gene identifier in Xu et al. (2003)	Corresponding vectorbase ID	Name in vectorbase	Name as defined in Xu et al. 2003	Name in (Vieira & Rozas. 2011)	Name in (Manoharan et al. 2012)	Comment
62		AGAP002556#	Not available	Not available	AgamOBP60	AgamOBP62	Gene name difference in between Vieira & Rozas (2011) and Manoharan et al (2011)
63		AGAP012322#	Not available	Not available	AgamOBP58	AgamOBP63	
64		AGAP012324#	Not available	Not available	AgamOBP59	AgamOBP64	
65		AGAP006759#	Not available	Not available	AgamOBP66	AgamOBP65	Gene name difference in between Vieira & Rozas (2011) and Manoharan et al (2011)
66		AGAP007283#	Not available	Not available	AgamOBP62	AgamOBP66	
67		AGAP012659#	Not available	Not available	AgamOBP67	AgamOBP67	
68		AGAP012658#	Not available	Not available	AgamOBP68	AgamOBP68	
69		AGAP013182#	Not available	Not available	AgamOBP79	AgamOBP69†	New gene identified by Vieira & Rozas (2011). We suggest a new name following the naming in this study
70		AGAP006368#	Not available	Not available	AgamOBP80	AgamOBP70†	
71		AGAP012867#	Not available	Not available	AgamOBP82	AgamOBP71†	
72		AGAP012714#	Not available	Not available	AgamOBP83	AgamOBP72†	
73		Not available	Not available	Not available	AgamOBP65		No genomic data in VectorBase
74		AGAP008280#	Not available	Not available	AgamOBP69		D7 protein
75		AGAP008281#	Not available	Not available	AgamOBP70		D7 protein
76		AGAP008282#	Not available	Not available	AgamOBP71		D7 protein
77		AGAP008283#	Not available	Not available	AgamOBP72		D7 protein
78		AGAP008284#	Not available	Not available	AgamOBP73		D7 protein
79		AGAP008278#	Not available	Not available	AgamOBP74		D7 protein
80		AGAP008279#	Not available	Not available	AgamOBP75		D7 protein
81		AGAP008279#	Not available	Not available	AgamOBP76		D7 protein
82		AGAP006278#	Not available	Not available	AgamOBP78		D7 protein
83		Not available	Not available	Not available	AgamOBP81		No genomic data in VectorBase

Vectorbase IDs specifically reported in Vieira & Rozas (2011).
† Newly identified OBP genes in Vieira & Rozas (2011) not included in this study.

Supplementary Table 1c. Complete list of OBP genes from *Aedes aegypti* reported in this study. Alongside their identification and chromosomal locations, shown are their subfamilies, phylogenetic clusters and orthologues in *Anopheles gambiae* and *Culex quinquefasciatus*. The 47 OBPs newly identified in this study (AaegOBP67-AaegOBP114) are indicated by an (*). †Two genes AaegOBP42 and AaegOBP63 sahre 100% sequence identity but are localized on different chromosome segments. We cannot resolve which of these two genes is the true orthologue of AgamOBP48 and CquiOBP106. Two way (1:1) orthologues are indicated by a # sign. OBPs that did not clustered in a phylogenetic group were indicated as '*unclassified*' in the 'Cluster' column.

n°	**ID**	**Name**	**Full length**	**Super contig**	**Start**	**End**	**Sub-family**	**cluster**	**Ortholog in *An. gambiae***	**Ortholog in *Culex***
1	AAEL009449	AaegOBP1	143	1.397	1059780	1064175	Classic	OS-E/OS-F	AgamOBP1	CquiOBP1
2	AAEL006176	AaegOBP2	158	1.193	1418261	1435259	Classic	Pbprp1	AgamOBP7	CquiOBP7
3	AAEL013018	AaegOBP3	143	1.776	429862	431937	Classic	OS-E/OS-F		
4	AAEL000073	AaegOBP4	146	1.1	4140321	4154466	Classic	OBP19a		CquiOBP8
5	AAEL000139	AaegOBP5	269	1.2	651524	652909	PlusC	mplus6	AgamObp59a	CquiOBP109
6	AAEL000821	AaegOBP6	255	1.17	3417930	3418697	Two-domains	matype4		
7	AAEL000833	AaegOBP7	279	1.17	3935676	3936843	Two-domains	matype4		
8	AAEL001826	AaegOBP8	133	1.43	1541221	1541846	Classic	mclassic5	AgamOBP21	CquiOBP23
9	AAEL002596	AaegOBP9	132	1.61	1448858	1449413	Classic	mclassic3	AgamOBP23	CquiOBP22
10	AAEL007603	AaegOBP10	140	1.266	1269968	1270519	Classic	mclassic6	AgamOBP10	CquiOBP24
11	AAEL002587	AaegOBP11	137	1.61	1518773	1519546	Classic	mclassic3	AgamOBP25	CquiOBP19
12	AAEL002617	AaegOBP12	132	1.61	1525746	1526203	Classic	mclassic3	AgamOBP28	CquiOBP18
13	AAEL002591	AaegOBP13	132	1.61	1541151	1541767	Classic	mclassic4		
14	AAEL002605	AaegOBP14	133	1.61	1560540	1560999	Classic	mclassic4		
15	AAEL002598	AaegOBP15	136	1.61	1605563	1618454	Classic	mclassic1	AgamOBP64	CquiOBP15
16	AAEL003315	AaegOBP16	269	1.83	2455477	2456452	Two-domains	matype4		
17	AAEL004339	AaegOBP17	138	1.115	975305	1055633	Classic	mclassic7		CquiOBP53
18	AAEL004342	AaegOBP18	140	1.115	1056506	1057069	Classic	mclassic9	AgamOBP14	
19	AAEL004343	AaegOBP19	145	1.115	1059658	1060207	Classic	mclassic9		CquiOBP51
20	AAEL005778	AaegOBP20	166	1.174	827019	827663	Classic	Pbprp4	AgamOBP62	CquiOBP14
21	AAEL005770	AaegOBP21	146	1.174	1511030	1512166	Classic	Obp99a		
22	AAEL005772	AaegOBP22	138	1.174	1532891	1533675	Classic	Obp99a	AgamOBP9	CquiOBP43
23	AAEL006109	AaegOBP23	242	1.189	217057	217969	PlusC	mplus11		
24	AAEL006108	AaegOBP24	200	1.189	234195	245248	PlusC	mplus11		
25	AAEL006103	AaegOBP25	200	1.189	2037030	2054778	PlusC	mplus11	AgamOBP57	CquiOBP104
26	AAEL006106	AaegOBP26	352	1.189	2063847	2065664	PlusC	mplus11	AgamOBP56	CquiOBP102

**Newly discovered genes in this study.*
 # Only a two way (1:1) orthology has been established for these genes and not a three way (1:1:1) orthology.
†Two genes AaegOBP42 and AaegOBP63 share 100% sequence identity but are localized on different chromosome segments. We cannot resolve for these two genes which is the true orthologue of AgamOBP48 and CquiOBP106.

Suppl. Table 1c

n°	ID	Name	Full length	Super contig	Start	End	Sub-family	cluster	Ortholog in *An. gambiae*	Ortholog in *Culex*
27	AAEL000071	AaegOBP27	141	1.1	4056982	4057610	Classic	OBP19a	AgamOBP6	CquiOBP13
28	AAEL006393	AaegOBP28	322	1.203	1485149	1497912	Two-domains	matype3		
29	AAEL006387	AaegOBP29	286	1.203	1497040	1521142	Two-domains	matype3	AgamOBP31	
30		AaegOBP30		Previously reported, this gene is not available in VectorBase						
31	AAEL006396	AaegOBP31	331	1.203	1526927	1527922	Two-domains	matype3		
32	AAEL006398	AaegOBP32	336	1.203	1537009	1538019	Two-domains	matype3		CquiOBP86
33	AAEL006385	AaegOBP33	313	1.203	1538561	1539571	Two-domains	matype3		
34	AAEL014082	AaegOBP34	149	1.1002	187323	188351	Classic	LUSH		
35	AAEL002606	AaegOBP35	131	1.61	1497852	1498861	Classic	mclassic3	AgamOBP26	CquiOBP20
36	AAEL008011	AaegOBP36	152	1.294	802739	803197	Classic	OS-E/OS-F	AgamOBP15	CquiOBP5
37	AAEL008009	AaegOBP37	148	1.294	823671	828548	Classic	OS-E/OS-F		CquiOBP4
38	AAEL008013	AaegOBP38	140	1.294	1185169	1186628	Classic	OS-E/OS-F	AgamOBP3	CquiOBP2
39	AAEL006454	AaegOBP39	146	ig1.206	50736	67086	Classic	LUSH	AgamOBP4	CquiOBP6
40	AAEL009597	AaegOBP40	291	1.411	257365	258240	Two-domains	matype1	AgamOBP39	CquiOBP84
41	AAEL009599	AaegOBP41	297	1.411	258377	259352	Two-domains	matype1		CquiOBP85
42	AAEL010666	AaegOBP42†	157	1.495	848252	848790	PlusC	mplus1	†AgamOBP48	†CquiOBP106
43	AAEL010662	AaegOBP43	193	1.495	849614	850509	PlusC	mplus1		
44	AAEL010718	AaegOBP44	219	1.500	470519	471178	Two-domains	matype4		CquiOBP78
45	AAEL010714	AaegOBP45	260	1.500	485823	486827	Two-domains	matype4		
46	AAEL010872	AaegOBP46	298	1.514	549927	550986	Two-domains	matype4		
47	AAEL011499	AaegOBP47	191	1.584	253363	254080	PlusC	mplus1		
48	AAEL011494	AaegOBP48	214	1.584	270443	271204	PlusC	mplus2	AgamOBP46	CquiOBP108
49	AAEL011484	AaegOBP49	187	1.584	357678	358469	PlusC	mplus4		
50	AAEL011490	AaegOBP50	199	1.584	358749	359468	PlusC	mplus4		
51	AAEL011487	AaegOBP51	195	1.584	391587	398988	PlusC	mplus4	AgamOBP60	
52	AAEL011491	AaegOBP52	184	1.584	422989	423783	PlusC	mplus4		
53	AAEL011482	AaegOBP53	182	1.584	423953	424743	PlusC	mplus4		CquiOBP110
54	AAEL011481	AaegOBP54	181	1.584	434945	435608	PlusC	mplus4		
55	AAEL012377	AaegOBP55	151	1.685	122245	142217	Classic	OBP19a	AgamOBP20	CquiOBP11
56	AAEL000051	AaegOBP56	115	1.1	4124658	4140143	Classic	OBP19a	AgamOBP19	CquiOBP12

**Newly discovered genes in this study.*

 # Only a two way (1:1) orthology has been established for these genes and not a three way (1:1:1) orthology.

†Two genes AaegOBP42 and AaegOBP63 share 100% sequence identity but are localized on different chromosome segments. We cannot resolve for these two genes which is the true orthologue of AgamOBP48 and CquiOBP106.

Suppl. Table 1c

n°	ID	Name	Full length	Super contig	Start	End	Sub-family	cluster	Ortholog in *An. gambiae*	Ortholog in *Culex*
57	AAEL000035	AaegOBP57	151	1.1	3668288	3668784	Classic	Pbprp2/5	AgamOBP13	CquiOBP28
58	AAEL014430	AaegObp58	285	1.1115	141516	149446	Two-domains	*unclassified*		
59	AAEL015313	AaegOBP59	166	1.1784	37928	38729	Classic	Pbprp4		
60	AAEL015499	AaegOBP60	150	1.2733	6977	7459	Classic	OS-E/OS-F	AgamOBP2	CquiOBP3
61	AAEL015554	AaegOBP61	132	1.3221	5993	6448	Classic	mclassic4	AgamOBP63	CquiOBP17
62	AAEL015566	AaegOBP62	193	1.3337	1317	2221	PlusC	mplus1		
63	AAEL015567	AaegOBP63†	157	1.3337	2936	3570	PlusC	mplus1	†AgamOBP48	†CquiOBP106
64		AaegOBP64		Previously reported, this gene is not available in VectorBase						
65	AAEL002618	AaegOBP65	98	1.61	1577860	1578251	Classic	mclassic1	AgamOBP27	CquiOBP16
66		AaegOBP66		Previously reported but same gene as AaegOBP35						
67	AAEL011497	AaegOBP67*	158	1.584	380693	381721	PlusC	mplus4		
68	AAEL011489	AaegOBP68*	189	1.584	360426	380332	PlusC	mplus4		
69	AAEL000124	AaegOBP69*	180	1.2	673060	674073	PlusC	mplus7	AgamOBP54	
70	AAEL006105	AaegOBP70*	227	1.189	2070866	2071667	PlusC	mplus11		CquiOBP103
71	AAEL006094	AaegOBP71*	227	1.189	205937	206741	PlusC	mplus11		
72	AAEL004729	AaegOBP72*	178	1.128	259634	260619	PlusC	mplus8		CquiOBP111
73	AAEL004730	AaegOBP73*	168	1.128	267328	268254	PlusC	mplus8	AgamOBP49	CquiOBP112
74	AAEL011486	AaegOBP74*	193	1.584	304385	305157	PlusC	mplus5		
75	AAEL011483	AaegOBP75*	193	1.584	321689	322507	PlusC	mplus5		CquiOBP107
76	AAEL007604	AaegOBP76*	134	1.266	1288889	1290609	Classic	mclassic6		
77	AAEL002626	AaegOBP77*	138	1.61	1455363	1456069	Classic	mclassic2	AgamOBP24	CquiOBP21
78	AAEL001836	AaegOBP78*	135	1.43	1535067	1535644	Classic	minus C		CquiOBP70
79	AAEL007014	AaegOBP79*	154	1.132	2272455	2273324	Classic	*unclassified*		
80	AAEL007003	AaegOBP80*	152	1.231	1719941	1720462	Classic	*unclassified*		
81	AAEL011730	AaegOBP81*	151	1.606	650035	650560	Classic	mclassic8	AgamOBP22	CquiOBP44
82	AAEL014593	AaegOBP82*	145	1.1181	11402	11955	PlusC	mplus3		CquiOBP101
83	AAEL011416	AaegOBP83*	304	1.579	450825	451739	Classic	Obp59a	AgamOBP29	CquiOBP55
84	AAEL000827	AaegOBP84*	287	1.17	3989260	3990220	Two-domains	matype4		
85	AAEL000831	AaegOBP85*	253	1.17	3976929	3977690	Two-domains	matype4		
86	AAEL004856	AaegOBP86*	255	1.132	2272456	2273324	Two-domains	matype4		
87	AAEL003511	AaegOBP87*	265	1.89	1577417	1578335	Two-domains	matype4		CquiOBP76

**Newly discovered genes in this study.*
 # Only a two way (1:1) orthology has been established for these genes and not a three way (1:1:1) orthology.
†Two genes AaegOBP42 and AaegOBP63 share 100% sequence identity but are localized on different chromosome segments. We cannot resolve for these two genes which is the true orthologue of AgamOBP48 and CquiOBP106.

Suppl. Table 1c

n°	**ID**	**Name**	**Full length**	**Super contig**	**Start**	**End**	**Sub-family**	**cluster**	**Ortholog in *An. gambiae***	**Ortholog in *Culex***
88	AAEL010874	AaegOBP88*	299	1.514	517957	519061	Two-domains	matype4		
89	AAEL000377	AaegOBP89*	315	1.6	3059016	3060090	Two-domains	matype2		
90	AAEL013719	AaegOBP90*	202	1.902	36629	37757	Two-domains	matype2		
91	AAEL013720	AaegOBP91*	273	1.902	26444	29202	Two-domains	matype2		CquiOBP87
92	AAEL000318	AaegOBP92*	294	1.6	3110479	3111363	Two-domains	matype2		
93	AAEL000319	AaegOBP93*	287	1.6	3087173	3088138	Two-domains	matype2		
94	AAEL000344	AaegOBP94*	312	1.6	3052765	3053725	Two-domains	matype2		
95	AAEL000350	AaegOBP95*	294	1.6	3114188	3116137	Two-domains	matype2		
96	AAEL000796	AaegOBP96*	305	1.17	3920770	3922193	Two-domains	matype4		
97	AAEL000835	AaegOBP97*	260	1.17	3900849	3901700	Two-domains	matype4		
98	AAEL001174	AaegOBP98*	586	1.24	2847433	2850832	Two-domains	matype2		CquiOBP95
99	AAEL001179	AaegOBP99*	332	1.24	2705024	2711778	Two-domains	matype2		
100	AAEL003513	AaegOBP100*	278	1.89	1529116	1529952	Two-domains	matype4		CquiOBP77
101	AAEL003525	AaegOBP101*	370	1.89	1489315	1498788	Two-domains	matype4		
102	AAEL003538	AaegOBP102*	291	1.89	1554285	1555425	Two-domains	matype4	AgamOBP32	
103	AAEL010875	AaegOBP103*	299	1.514	538264	539163	Two-domains	matype4		
104	AAEL004516	AaegOBP104*	295	1.122	2397633	2398520	Two-domains	matype2		
105	AAEL001189	AaegOBP105*	309	1.24	2833159	2834187	Two-domains	matype2		
106	AAEL001153	AaegOBP106*#	302	1.24	2825960	2826974	Two-domains	matype2	AgamOBP34/37#	CquiOBP97#
107	AAEL014876	AaegOBP107*	299	1.1319	90885	91826	Atypical	matype2		CquiOBP94
108	AAEL014874	AaegOBP108*	278	1.1319	77202	78116	Two-domains	matype2		
109	AAEL009433	AaegOBP109*	278	1.396	502699	503646	Two-domains	matype2		
110	AAEL014431	AaegOBP110*	268	1.1115	149798	150604	Two-domains	*unclassified*		
111	AAEL003311	AaegOBP111*	347	1.83	658245	668798	Two-domains	matype4		

**Newly discovered genes in this study.*

 # Only a two way (1:1) orthology has been established for these genes and not a three way (1:1:1) orthology.

†Two genes AaegOBP42 and AaegOBP63 share 100% sequence identity but are localized on different chromosome segments. We cannot resolve for these two genes which is the true orthologue of AgamOBP48 and CquiOBP106.

n°	ID	Name	Full length	Super contig	Start	End	Sub-family	cluster	Ortholog in *An. gambiae*	Ortholog in *Culex*
112	AAEL000837	AaegOBP112*	306	1.17	3960390	3961459	Two-domains	matype4		
113	AAEL008640	AaegOBP113*	274	1.338	484248	485189	Two-domains	*unclassified*		
114	AAEL001487	AaegOBP114*	305	1.34	1695923	1698069	Two-domains	*unclassified*		

**Newly discovered genes in this study.*

 # Only a two way (1:1) orthology has been established for these genes and not a three way (1:1:1) orthology.

†Two genes AaegOBP42 and AaegOBP63 share 100% sequence identity but are localized on different chromosome segments. We cannot resolve for these two genes which is the true orthologue of AgamOBP48 and CquiOBP106.

Supplementary Table 1d. OBP gene names for *Culex quinquefasciatus PlusC* OBPs. Shown is the correspondence between the OBP gene names used in this study and the names used in (Pelletier and Leal. 2011).

n°	Gene identifier in Pelletier and Leal (2011)	Corresponding vectorbase ID	Name in(Pelletier and Leal. 2011)	Name used in this study
1	HQ845073	CPIJ002105	CquiOBP+C1	CquiOBP106
2	HQ845074	CPIJ002106	CquiOBP+C2	CquiOBP105
3	EDS32239	CPIJ002108	CquiOBP+C3	CquiOBP108
4	EDS32240	CPIJ002109	CquiOBP+C4	CquiOBP107
5	EDS32241	CPIJ002110	CquiOBP+C5	**New gene identified by Pelletier and Leal (2011)**
6	EDS32242	CPIJ002111	CquiOBP+C6	CquiOBP110
7	EDS42861	CPIJ004630	CquiOBP+C7	CquiOBP104
8	EDS42865	CPIJ004634	CquiOBP+C8	CquiOBP102
9	EDS42866	CPIJ004635	CquiOBP+C9	CquiOBP103
10	EDS32591	CPIJ008867	CquiOBP+C10	CquiOBP111
11	EDS32592	CPIJ008868	CquiOBP+C11	CquiOBP112
12	EDS28215	CPIJ006608	CquiOBP+C12	CquiOBP109
13	EDS32360	CPIJ008979	CquiOBP+C13	CquiOBP101

Supplementary Table 1e. Complete list of OBP genes from *Culex quinquefasciatus* Reported in this study. Alongside their identification and chromosomal locations, shown are their subfamilies, phylogenetic clusters and orthologues in *Anopheles gambiae* and *Aedes aegypti*. †The last two genes were identified by Vieira & Rozas (2011) and were added to this Table at the last moment after renaming them CquiOBP113 and CquiOBP114. Two way (1:1) orthologues are indicated by a # sign. OBPs that did not clustered in a phylogenetic group were indicated as 'unclassified' in the 'Cluster' column.

n°	**ID**	**Name**	**Full length**	**Super contig**	**Start**	**End**	**Sub-family**	**Cluster**	**Ortholog in *An. gambiae***	**Ortholog in *Ae. aegyptii***
1	CPIJ007604	CquiOBP1	149	3.150	170719	174721	Classic	OS-E/OS-F	AgamOBP1	AaegOBP1
2	CPIJ007617	CquiOBP2	146	3.150	672931	673546	Classic	OS-E/OS-F	AgamOBP3	AaegOBP38
3	CPIJ007611	CquiOBP3	147	3.150	540281	542064	Classic	OS-E/OS-F	AgamOBP2	AaegOBP60
4	CPIJ001730	CquiOBP4	150	3.25	734060	734572	Classic	OS-E/OS-F		AaegOBP37
5	CPIJ007608	CquiOBP5	143	3.150	516885	517412	Classic	OS-E/OS-F	AgamOBP15	AaegOBP36
6	CPIJ008793	CquiOBP6	89	3.206	489697	490937	Classic	LUSH	AgamOBP4	AaegOBP39
7	CPIJ001365	CquiOBP7	136	3.18	1720262	1721216	Classic	Pbprp1	AgamOBP7	AaegOBP2
8	CPIJ009568	CquiOBP8	144	3.240	122626	123234	Classic	OBP19a		AaegOBP4
9	CPIJ016948	CquiOBP9	139	3.865	41129	46297	Classic	OBP19a		
10	CPIJ013976	CquiOBP10	132	3.550	256165	256681	Classic	OBP19a		
11	CPIJ006551	CquiOBP11	144	3.121	270272	277928	Classic	OBP19a	AgamOBP20	AaegOBP55
12	CPIJ016949	CquiOBP12	121	3.865	46518	47165	Classic	OBP19a	AgamOBP19	AaegOBP56
13	CPIJ016952	CquiOBP13	143	3.865	54944	61815	Classic	OBP19a	AgamOBP6	AaegOBP27
14	CPIJ009586	CquiOBP14	170	3.240	569948	574407	Classic	Pbprp4	AgamOBP62	AaegOBP20
15	CPIJ012714	CquiOBP15	141	3.424	103588	109982	Classic	mclassic1	AgamOBP64	AaegOBP15
16	CPIJ012715	CquiOBP16	134	3.424	112183	112979	Classic	mclassic1	AgamOBP27	AaegOBP65
17	CPIJ012716	CquiOBP17	132	3.424	113896	114578	Classic	mclassic4	AgamOBP63	AaegOBP61
18	CPIJ012717	CquiOBP18	132	3.424	122946	123411	Classic	mclassic3	AgamOBP28	AaegOBP12
19	CPIJ012718	CquiOBP19	139	3.424	131078	131864	Classic	mclassic3	AgamOBP25	AaegOBP11
20	CPIJ012719	CquiOBP20	131	3.424	135879	136509	Classic	mclassic3	AgamOBP26	AaegOBP35
21	CPIJ012720	CquiOBP21	139	3.424	171439	171968	Classic	mclassic2	AgamOBP24	AaegOBP77
22	CPIJ012721	CquiOBP22	131	3.424	172603	173060	Classic	mclassic3	AgamOBP23	AaegOBP9
23	CPIJ001876	CquiOBP23	136	3.26	255589	259525	Classic	mclassic5	AgamOBP21	AaegOBP8
24	CPIJ014525	CquiOBP24	137	3.561	24869	25524	Classic	mclassic6	AgamOBP10	AaegOBP10
25	CPIJ010723	CquiOBP25	121	3.286	224289	224718	Classic	Pbprp2/5		
26	CPIJ010724	CquiOBP26	119	3.286	228005	228420	Classic	Pbprp2/5		
27	CPIJ010728	CquiOBP27	126	3.286	489935	490384	Classic	Pbprp2/5		
28	CPIJ016965	CquiOBP28	150	3.865	148161	148975	Classic	Pbprp2/5	AgamOBP13	AaegOBP57
29	CPIJ016966	CquiOBP29	130	3.865	149508	150489	Classic	Pbprp2/5		

**Newly discovered genes in this study.*
 # Only a two way (1:1) orthology has been established for these genes and not a three way (1:1:1) orthology.
nd : not determined
† New genes recently reported by Vieira & Rozas (2011)

Suppl. Table 1e

n°	ID	Name	Full length	Super contig	Start	End	Sub-family	Cluster	Ortholog in *An. gambiae*	Ortholog in *Ae. aegyptii*
30	CPIJ016967	CquiOBP30	143	3.865	154625	155111	Classic	Pbprp2/5		
31	CPIJ008285	CquiOBP31	124	3.167	404302	404732	Classic	Pbprp2/5		
32	CPIJ016479	CquiOBP32	126	3.770	2731	3167	Classic	Pbprp2/5		
33	CPIJ019607	CquiOBP33	124	3.1894	15149	15587	Classic	Pbprp2/5		
34	CPIJ019608	CquiOBP34	116	3.1894	29115	29465	Classic	Pbprp2/5		
35	CPIJ019609	CquiOBP35	126	3.1894	31188	31622	Classic	Pbprp2/5		
36	CPIJ019610	CquiOBP36	146	3.1894	41408	41883	Classic	Pbprp2/5		
37	CPIJ007931	CquiOBP37	135	3.181	460064	466993	Classic	Pbprp2/5		
38	CPIJ007932	CquiOBP38	137	3.181	467058	467528	Classic	Pbprp2/5		
39	CPIJ007933	CquiOBP39	126	3.181	481658	482092	Classic	Pbprp2/5		
40	CPIJ007934	CquiOBP40	107	3.181	487383	487920	Classic	Pbprp2/5		
41	CPIJ007935	CquiOBP41	98	3.181	488157	488453	Classic	Pbprp2/5		
42	CPIJ007936	CquiOBP42	111	3.181	492753	493384	Classic	Pbprp2/5		
43	CPIJ017326	CquiOBP43	138	3.984	153967	154634	Classic	Obp99a	AgamOBP9	AaegOBP22
44	CPIJ009937	CquiOBP44	147	3.265	418539	421106	Classic	mclassic8	AgamOBP22	AaegOBP81
45		CquiOBP45		Reported in previous paper, not available in VectorBase						
46	CPIJ010782	CquiOBP46	150	3.315	176953	177463	Classic	mclassic9		
47		CquiOBP47		Reported in previous paper, not available in VectorBase						
48		CquiOBP48		Reported in previous paper, not available in VectorBase						
49		CquiOBP49		Reported in previous paper, not available in VectorBase						
50		CquiOBP50		Reported in previous paper, not available in VectorBase						
51	CPIJ010787	CquiOBP51	144	3.315	189941	190471	Classic	mclassic9		AaegOBP19
52	CPIJ010788	CquiOBP52	143	3.315	190549	191091	Classic	mclassic9		
53	CPIJ010789	CquiOBP53	145	3.315	191345	193026	Classic	mclassic7		AaegOBP17
54	CPIJ007937	CquiOBP54*	170	3.181	496322	497393	Classic	Pbprp2/5		
55	CPIJ010367	CquiOBP55*	235	3.273	146471	147364	Classic	Obp59a	AgamOBP29	AaegOBP83
56	CPIJ010729	CquiOBP56*	214	3.286	493370	501823	Classic	Pbprp2/5		
57	CPIJ016951	CquiOBP57*	126	3.865	50440	50879	Classic	OBP19a		
58	CPIJ007609	CquiObp58*	141	3.150	526150	526551	Classic	OS-E/OS-F		
59	CPIJ001871	CquiOBP59*	113	3.26	242975	243783	Classic	minus C		
60	CPIJ012786	CquiOBP60*	138	3.443	357791	358353	Classic	minus C		
61	CPIJ015943	CquiOBP61*	138	3.727	98658	99154	Classic	minus C		
62	CPIJ015944	CquiOBP62*	120	3.727	99851	104141	Classic	minus C		
63	CPIJ016343	CquiOBP63*	181	3.758	25841	28252	Classic	mclassic9	AgamOBP14	

**Newly discovered genes in this study.*
 # Only a two way (1:1) orthology has been established for these genes and not a three way (1:1:1) orthology.
nd : not determined
† New genes recently reported by Vieira & Rozas (2011)

n°	ID	Name	Full length	Super contig	Start	End	Sub-family	Cluster	Ortholog in *An. gambiae*	Ortholog in *Ae. aegyptii*
64	CPIJ004145	CquiOBP64*	206	3.64	238526	238997	Classic	minus C		
65	CPIJ001875	CquiOBP65*	136	3.26	253862	254332	Classic	minus C		
66	CPIJ001865	CquiOBP66*	136	3.26	220863	221383	Classic	minus C		
67	CPIJ017432	CquiOBP67*	130	3.930	38452	43014	Classic	minus C		
68	CPIJ001873	CquiOBP68*	119	3.26	248382	249594	Classic	minus C		
69	CPIJ001874	CquiOBP69*	137	3.26	249635	250213	Classic	minus C		
70	CPIJ001872	CquiOBP70*	122	3.26	247521	248064	Classic	minus C		AaegOBP78
71	CPIJ001870	CquiOBP71*	136	3.26	234093	234614	Classic	minus C		
72	CPIJ001867	CquiOBP72*	134	3.26	226275	226723	Classic	minus C		
73	CPIJ001869	CquiOBP73*	98	3.26	232747	233357	Classic	minus C		
74	CPIJ001868	CquiOBP74*	132	3.26	226902	227400	Classic	minus C		
75	CPIJ008157	CquiOBP75*	128	3.183	230895	231773	Two-domains	matype4		
76	CPIJ008158	CquiOBP76#*	292	3.183	231998	233839	Two-domains	matype4	AgamOBP43#	AaegOBP87#
77	CPIJ008159	CquiOBP77*	521	3.183	234041	234919	Two-domains	matype4		AaegOBP100
78	CPIJ008155	CquiOBP78*	292	3.183	226602	227315	Two-domains	matype4		AaegOBP44
79	CPIJ008156	CquiOBP79*	237	3.183	227485	230705	Two-domains	matype4		
80	CPIJ008160	CquiOBP80*	250	3.183	235156	236019	Two-domains	matype4		
81	CPIJ008161	CquiOBP81*	287	3.183	237704	238659	Two-domains	matype4		
82	CPIJ008154	CquiOBP82*	309	3.183	225309	225992	Two-domains	matype4		
83	CPIJ000653	CquiOBP83*	227	3.7	1883021	1884070	Two-domains	matype4		
84	CPIJ015732	CquiOBP84*	349	3.670	26079	26960	Two-domains	matype1	AgamOBP39	AaegOBP40
85	CPIJ015733	CquiOBP85*	293	3.670	27043	27906	Two-domains	matype1		AaegOBP41
86	CPIJ009038	CquiOBP86*	287	3.216	624714	626149	Two-domains	matype3		AaegOBP32
87	CPIJ003865	CquiOBP87*	313	3.54	1105231	1106267	Two-domains	matype2		AaegOBP91
88	CPIJ003863	CquiOBP88*	307	3.54	1100660	1101583	Two-domains	matype2		
89	CPIJ003866	CquiOBP89*	307	3.54	1107587	1108531	Two-domains	matype2		
90	CPIJ003867	CquiOBP90*	314	3.54	1112050	1113000	Two-domains	matype2		

**Newly discovered genes in this study.*
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nd : not determined
† New genes recently reported by Vieira & Rozas (2011)

n°	ID	Name	Full length	Super contig	Start	End	Sub-family	Cluster	Ortholog in *An. gambiae*	Ortholog in *Ae. aegyptii*
91	CPIJ001690	CquiOBP91*	316	3.19	1064263	1065189	Two-domains	matype2		
92	CPIJ017342	CquiOBP92*	308	3.908	23349	24732	Two-domains	matype3		
93	CPIJ017170	CquiOBP93*	353	3.874	68127	69047	Two-domains	matype2		
94	CPIJ017166	CquiOBP94*	306	3.874	53265	54562	Two-domains	matype2		AaegOBP107
95	CPIJ017167	CquiOBP95*	303	3.874	54671	57028	Two-domains	matype2		AaegOBP98
96	CPIJ017164	CquiOBP96*	506	3.874	42543	45345	Two-domains	matype2		
97	CPIJ017165	CquiOBP97*	333	3.874	45828	48052	Two-domains	matype2		AaegOBP106
98	CPIJ017163	CquiOBP98*	309	3.874	40347	41997	Two-domains	matype2		
99	CPIJ017169	CquiOBP99*	400	3.874	66534	67385	Two-domains	matype2		
100	CPIJ017168	CquiOBP100*	274	3.874	59822	60630	Two-domains	matype2		
101	CPIJ008979	CquiOBP101*	251	3.212	2741	3415	PlusC	mplus3		AaegOBP82
102	CPIJ004634	CquiOBP102*	242	3.70	262125	262974	PlusC	mplus11	AgamOBP56	AaegOBP26
103	CPIJ004635	CquiOBP103*	228	3.70	268367	269111	PlusC	mplus11		AaegOBP70
104	CPIJ004630	CquiOBP104*	204	3.70	243833	244540	PlusC	mplus11	AgamOBP57	AaegOBP25
105	CPIJ002106	CquiOBP105*	127	3.21	701497	701945	PlusC	mplus1		
106	CPIJ002105	CquiOBP106*	194	3.21	699415	700558	PlusC	mplus1	AgamOBP48	AaegOBP42
107	CPIJ002109	CquiOBP107*	195	3.21	708381	709996	PlusC	mplus5		AaegOBP75
108	CPIJ002108	CquiOBP108*	205	3.21	705497	706243	PlusC	mplus2	AgamOBP46	AaegOBP48
109	CPIJ006608	CquiOBP109*	218	3.130	754816	760061	PlusC	mplus6	AgamOBP58	AaegOBP5
110	CPIJ002111	CquiOBP110#*	191	3.21	713441	714192	PlusC	mplus4	AgamOBP60#	AaegOBP53#
111	CPIJ008867	CquiOBP111#*	172	3.219	551750	552504	PlusC	mplus8	AgamOBP54#	AaegOBP72#
112	CPIJ008868	CquiOBP112*	175	3.219	554916	555746	PlusC	mplus8	AgamOBP49	AaegOBP73
113	CPIJ017524	CquiOBP113†	178	3.978	126190	127209	PlusC	nd		
114	CPIJ007337	CquiOBP114†	194	3.157	294891	306059	PlusC	nd	AgamOBP70	

**Newly discovered genes in this study.*
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nd : not determined
† New genes recently reported by Vieira & Rozas (2011)

Supplementary Table 2. Syntheny between chromosomes between the four dipterian species *Drosophila melanogaster, Anopheles gambiae, Aedes aegypti* and *Culex quinquefasciatus* (Arensburger *et al*, 2010).

Drosophila	**Anopheles**	**Aedes**	**Culex**
X	X	1p	1p
		1q	1q
2L	3R	2q	2p
2R	3L	3q	2q
3L	2L	2p	3p & 2q
3R	2R	3p	3q & 1q

Reference : Peter Arensburger, *et al*. Sequencing of *Culex quinquefasciatus* Establishes a Platform for Mosquito Comparative Genomics. *Science* **330**:86-88, (2010).

Supplementary Table 3a. Signal P prediction results for all the *Anopheles gambiae* OBP sequences.

# name	Signal peptide	D value
AGAP003309_AgamOBP1	1-19	0.868
AGAP003306_AgamOBP2	1-25	0.853
AGAP001409_AgamOBP3	1-29	0.83
AGAP010489_AgamOBP4	1-25	0.678
AGAP009629_AgamOBP5_	not detected	0.397
AGAP003530_AgamOBP6	not detected	0.309
AGAP001556_AgamOBP7	not detected	0.48
AGAP000279_AgamOBP8_	1-29	0.653
AGAP000278_AgamOBP9	1-17	0.924
AGAP001189_AgamOBP10	1-19	0.74
AGAP002025_AgamOBP11_	1-18	0.637
AGAP002188_AgamOBP12	1-27	0.841
AGAP002905_AgamOBP13_	1-22	0.845
AGAP002189_AgamOBP14_	1-26	0.756
AGAP003307_AgamOBP15	1-18	0.674
AGAP004433_AgamOBP19	not detected	0.112
AGAP005208_AgamOBP20_	not detected	0.242
AGAP008398_AgamOBP21_	1-20	0.646
AGAP010409_AgamOBP22_	1-21	0.876
AGAP012318_AgamOBP23_	1-19	0.909
AGAP012319_AgamOBP24	not detected	0.146
AGAP012320_AgamOBP25_	1-23	0.704
AGAP012321_AgamOBP26	1-18	0.864
AGAP012323_AgamOBP27_	1-25	0.539
AGAP012325_AgamOBP28_	1-16	0.812
AGAP012331_AgamOBP29_	not detected	0.446
AGAP011647_AgamOBP30_	not detected	0.377
AGAP010649_AgamOBP31_	1-21	0.822
AGAP000638_AgamOBP32_	1-25	0.6
AGAP000640_AgamOBP33_	1-25	0.725
AGAP000644_AgamOBP34_	not detected	0.404
AGAP000642_AgamOBP35	1-20	0.757
AGAP000643_AgamOBP36	1-20	0.757
AGAP000641_AgamOBP37	not detected	0.404
AGAP000580_AgamOBP38_	1-22	0.877
AGAP002190_AgamOBP39_	1-24	0.847
AGAP002191_AgamOBP40_	1-30	0.722
AGAP005182_AgamOBP41_	1-28	0.795
AGAP009065_AgamOBP42_	1-22	0.808
AGAP009402_AgamOBP43_	1-26	0.87
AGAP010648_AgamOBP44_	1-20	0.765
AGAP010650_AgamOBP45_	1-28	0.794
AGAP007289_AgamOBP46_	1-20	0.763
AGAP007287_AgamOBP47_	not detected	0.177
AGAP007286_AgamOBP48_	1-28	0.814

# name	Signal peptide	D value
AGAP006075_AgamOBP49_	1-25	0.855
AGAP006076_AgamOBP50_	not detected	0.385
AGAP006077_AgamOBP51_	1-24	0.817
AGAP006078_AgamOBP52_	not detected	0.218
AGAP006079_AgamOBP53	not detected	0.25
AGAP006080_AgamOBP54_	1-23	0.803
AGAP006081_AgamOBP55_	1-27	0.733
AGAP011367_AgamOBP56_	1-16	0.854
AGAP011368_AgamOBP57_	1-19	0.836
AGAP006074_AgamOBP58	1-35	0.561
AGAP006760_AgamOBP59_	not detected	0.119
AGAP007281_AgamOBP60_	1-17	0.892
AGAP007282_AgamOBP61_	1-22	0.869
AGAP002556_AgamOBP62_	1-29	0.715
AGAP012322_AgamOBP63_	1-19	0.809
AGAP012324_AgamOBP64_	1-29	0.836
AGAP006759_AgamOBP65	not detected	0.311
AGAP007283_AgamOBP66	1-28	0.926
AGAP012659_AgamOBP67_	1-22	0.806
AGAP012658_AgamOBP68_	1-28	0.935
AGAP013182_AgamOBP69	1-20	0.828
AGAP006368_AgamOBP70	1-29	0.704
AGAP012867_AgamOBP71	1-20	0.769
AGAP012714_AgamOBP72	not detected	0.102

Supplementary Table 3b. Signal P prediction results for all the *Aedes aegypti* OBP sequences.

# name	Signal peptide	D value
AAEL009449_AaegOBP1	1-18	0.776
AAEL006176_AaegOBP2	1-24	0.879
AAEL013018_AaegOBP3	1-18	0.783
AAEL000073_AaegOBP4	1-25	0.797
AAEL000139_AaegOBP5	1-17	0.8
AAEL000821_AaegOBP6	1-16	0.859
AAEL000833_AaegOBP7	1-20	0.782
AAEL001826_AaegOBP8	1-16	0.792
AAEL002596_AaegOBP9	1-20	0.675
AAEL007603_AaegOBP10	1-25	0.921
AAEL002587_AaegOBP11	1-18	0.824
AAEL002617_AaegOBP12	1-18	0.838
AAEL002591_AaegOBP13	1-18	0.826
AAEL002605_AaegOBP14	1-18	0.742
AAEL002598_AaegOBP15	1-23	0.795
AAEL003315_AaegOBP16	1-16	0.786
AAEL004339_AaegOBP17	1-19	0.893
AAEL004342_AaegOBP18	1-22	0.945
AAEL004343_AaegOBP19	1-26	0.818
AAEL005778_AaegOBP20	1-24	0.864
AAEL005770_AaegOBP21	1-18	0.659
AAEL005772_AaegOBP22	1-16	0.858
AAEL006109_AaegOBP23	1-16	0.805
AAEL006108_AaegOBP24	1-20	0.734
AAEL006103_AaegOBP25	1-20	0.653
AAEL006106_AaegOBP26	not detected	0.103
AAEL000071_AaegOBP27	1-21	0.727
AAEL006393_AaegOBP28	1-18	0.823
AAEL006387_AaegOBP29	not detected	0.183
AAEL006396_AaegOBP31	1-18	0.775
AAEL006398_AaegOBP32	1-18	0.862
AAEL006385_AaegOBP33	1-18	0.822
AAEL014082_AaegOBP34	1-24	0.873
AAEL002606_AaegOBP35	1-18	0.904
AAEL008011_AaegOBP36	1-21	0.825
AAEL008009_AaegOBP37	1-20	0.905
AAEL008013_AaegOBP38	1-16	0.871
AAEL006454_AaegOBP39	1-21	0.84
AAEL009597_AaegOBP40	1-21	0.813
AAEL009599_AaegOBP41	1-19	0.839
AAEL010666_AaegOBP42	not detected	0.101
AAEL010662_AaegOBP43	1-20	0.828
AAEL010718_AaegOBP44	1-22	0.78
AAEL010714_AaegOBP45	1-22	0.771
AAEL010872_AaegOBP46	1-21	0.851

# name	Signal peptide	D value
AAEL011499_AaegOBP47	1-20	0.847
AAEL011494_AaegOBP48	1-20	0.887
AAEL011484_AaegOBP49	not detected	0.104
AAEL011490_AaegOBP50	not detected	0.139
AAEL011487_AaegOBP51	1-21	0.914
AAEL011491_AaegOBP52	1-20	0.843
AAEL011482_AaegOBP53	1-17	0.639
AAEL011481_AaegOBP54	not detected	0.119
AAEL012377_AaegOBP55	1-24	0.726
AAEL000051_AaegOBP56	not detected	0.1
AAEL000035_AaegOBP57	1-26	0.529
AAEL014430_AaegOBP58	not detected	0.108
AAEL015313_AaegOBP59	1-24	0.864
AAEL015499_AaegOBP60	1-18	0.873
AAEL015554_AaegOBP61	1-18	0.795
AAEL015566_AaegOBP62	1-20	0.832
AAEL015567_AaegOBP63	not detected	0.101
AAEL002618_AaegOBP65	not detected	0.122
AAEL002606_AaegOBP66	1-18	0.904
AAEL011497_AaegOBP67	not detected	0.143
AAEL011489_AaegOBP68	1-16	0.788
AAEL000124_AaegOBP69	1-24	0.819
AAEL006105_AaegOBP70	1-17	0.825
AAEL006094_AaegOBP71	1-17	0.757
AAEL004729_AaegOBP72	1-23	0.693
AAEL004730_AaegOBP73	1-22	0.91
AAEL011486_AaegOBP74	1-19	0.83
AAEL011483_AaegOBP75	1-19	0.795
AAEL007604_AaegOBP76	not detected	0.103
AAEL002626_AaegOBP77	1-20	0.86
AAEL001836_AaegOBP78	1-18	0.756
AAEL007014_AaegOBP79	1-20	0.748
AAEL007003_AaegOBP80	1-20	0.712
AAEL011730_AaegOBP81	1-23	0.804
AAEL014593_AaegOBP82	not detected	0.097
AAEL011416_AaegOBP83	1-29	0.9
AAEL000827_AaegOBP84	1-20	0.696
AAEL000831_AaegOBP85	1-20	0.758
AAEL004856_AaegOBP86	1-20	0.86
AAEL003511_AaegOBP87	1-24	0.641
AAEL010874_AaegOBP88	1-24	0.614
AAEL000377_AaegOBP89	1-19	0.545
AAEL013719_AaegOBP90	not detected	0.112
AAEL013720_AaegOBP91	1-20	0.565
AAEL000318_AaegOBP92	1-19	0.915
AAEL000319_AaegOBP93	1-20	0.603
AAEL000344_AaegOBP94	1-20	0.888

# name	Signal peptide	D value
AAEL000350_AaegOBP95	1-19	0.884
AAEL000796_AaegOBP96	1-18	0.674
AAEL000835_AaegOBP97	1-18	0.599
AAEL001174_AaegOBP98	1-22	0.681
AAEL001179_AaegOBP99	not detected	0.219
AAEL003513_AaegOBP100	1-22	0.861
AAEL003525_AaegOBP101	not detected	0.111
AAEL003538_AaegOBP102	1-22	0.861
AAEL010875_AaegOBP103	1-24	0.609
AAEL004516_AaegOBP104	1-18	0.896
AAEL001189_AaegOBP105	1-22	0.782
AAEL001153_AaegOBP106	not detected	0.141
AAEL014876_AaegOBP107	1-31	0.833
AAEL014874_AaegOBP108	1-21	0.786
AAEL009433_AaegOBP109	1-21	0.786

Supplementary Table 3c. Signal P prediction results for all the *Culex quinquefasciatus* OBP sequences.

# name	Signal peptide	D value
CPIJ007604_CquiOBP1	1-24	0.872
CPIJ007617_CquiOBP2	1-22	0.889
CPIJ007611_CQUIOBP3	1-18	0.857
CPIJ001730_CquiOBP4	1-21	0.699
CPIJ007608_CquiOBP5	not detected	0.354
CPIJ008793_CquiOBP6	1-21	0.838
CPIJ001365_CquiOBP7	not detected	0.107
CPIJ009568_CquiOBP8	1-23	0.733
CPIJ016948_CquiOBP9	1-20	0.597
CPIJ013976_CquiOBP10	not detected	0.235
CPIJ006551_CquiOBP11	1-23	0.728
CPIJ016949_CquiOBP12	1-20	0.597
CPIJ016952_CquiOBP13	1-20	0.597
CPIJ009586_CquiOBP14	1-20	0.807
CPIJ012714_CquiOBP15	1-28	0.748
CPIJ012715_CquiOBP16	1-20	0.844
CPIJ012716_CquiOBP17	1-18	0.788
CPIJ012717_CquiOBP18	1-18	0.857
CPIJ012718_CquiOBP19	1-17	0.795
CPIJ012719_CquiOBP20	1-18	0.806
CPIJ012720_CquiOBP21	1-21	0.819
CPIJ012721_CquiOBP22	1-19	0.565
CPIJ001876_CquiOBP23	1-17	0.842
CPIJ014525_CquiOBP24	1-23	0.525
CPIJ010723_CquiOBP25	1-16	0.73
CPIJ010724_CquiOBP26	1-15	0.838
CPIJ010728_CquiOBP27	1-21	0.866
CPIJ016965_CquiOBP28	1-20	0.844
CPIJ016966_CquiOBP29	not detected	0.128
CPIJ016967_CquiOBP30	1-20	0.881
CPIJ008285_CquiOBP31	1-16	0.865
CPIJ016479_CquiOBP32	1-18	0.754
CPIJ019607_CquiOBP33	1-19	0.771
CPIJ019608_CquiOBP34	not detected	0.117
CPIJ019609_CquiOBP35	1-18	0.728
CPIJ019610_CquiOBP36	1-18	0.803
CPIJ007931_CquiOBP37	not detected	0.161
CPIJ007932_CquiOBP38	1-20	0.862
CPIJ007933_CquiOBP39	1-18	0.715
CPIJ007934_CquiOBP40	not detected	0.114
CPIJ007935_CquiOBP41	not detected	0.109
CPIJ007936_CquiOBP42	not detected	0.107
CPIJ017326_CquiOBP43	1-16	0.863
CPIJ009937_CquiOBP44	not detected	0.237

# name	Signal peptide	D value
CPIJ010782_CquiOBP46	1-22	0.629
CPIJ010787_CquiOBP51	1-22	0.787
CPIJ010788_CquiOBP52	1-19	0.817
CPIJ010789_CquiOBP53	1-19	0.828
CPIJ007937_CquiOBP54	not detected	0.102
CPIJ010367_CquiOBP55	1-25	0.936
CPIJ010729_CquiOBP56	not detected	0.1
CPIJ016951_CquiOBP57	1-20	0.597
CPIJ008979_CquiOBP58	not detected	0.121
CPIJ007609_CquiOBP59	not detected	0.119
CPIJ001871_CquiOBP60	1-18	0.877
CPIJ012786_CquiOBP61	1-17	0.794
CPIJ015943_CquiOBP62	not detected	0.204
CPIJ015944_CquiOBP63	not detected	0.117
CPIJ016343_CquiOBP64	1-40	0.766
CPIJ004145_CquiOBP65	1-20	0.861
CPIJ001875_CquiOBP66	1-17	0.872
CPIJ001865_CquiOBP67	1-15	0.742
CPIJ017432_CquiOBP68	not detected	0.101
CPIJ001873_CquiOBP69	1-20	0.82
CPIJ001874_CquiOBP70	not detected	0.097
CPIJ001872_CquiOBP71	1-19	0.883
CPIJ001870_CquiOBP72	1-17	0.781
CPIJ001867_CquiOBP73	not detected	0.108
CPIJ001869_CquiOBP74	1-17	0.777
CPIJ001868_CquiOBP75	1-20	0.697
CPIJ008157_CquiOBP76	1-21	0.621
CPIJ008158_CquiOBP77	1-16	0.621
CPIJ008159_CquiOBP78	1-19	0.807
CPIJ008155_CquiOBP79	1-20	0.727
CPIJ008156_CquiOBP80	1-19	0.608
CPIJ008160_CquiOBP81	1-19	0.725
CPIJ008161_CquiOBP82	not detected	0.218
CPIJ008154_CquiOBP83	1-15	0.718
CPIJ000653_CquiOBP84	1-15	0.823
CPIJ015732_CquiOBP85	1-20	0.893
CPIJ015733_CquiOBP86	1-19	0.741
CPIJ009038_CquiOBP87	not detected	0.109
CPIJ003865_CquiOBP88	1-20	0.796
CPIJ003863_CquiOBP89	1-20	0.748
CPIJ003866_CquiOBP90	1-20	0.863
CPIJ003867_CquiOBP91	1-20	0.838
CPIJ001690_CquiOBP92	1-24	0.744
CPIJ017342_CquiOBP93	1-18	0.851
CPIJ017170_CquiOBP94	1-18	0.582
CPIJ017166_CquiOBP95	1-28	0.76
CPIJ017167_CquiOBP96	1-20	0.832

# name	Signal peptide	D value
CPIJ017164_CquiOBP97	not detected	0.496
CPIJ017165_CquiOBP98	not detected	0.462
CPIJ017163_CquiOBP99	not detected	0.14
CPIJ017169_CquiOBP100	not detected	0.35
CPIJ017168_CquiOBP101	1-23	0.64
CPIJ004634_CquiOBP102	1-16	0.886
CPIJ004635_CquiOBP103	1-17	0.863
CPIJ004630_CquiOBP104	1-19	0.823
CPIJ002106_CquiOBP105	not detected	0.158
CPIJ002105_CquiOBP106	1-23	0.855
CPIJ002109_CquiOBP107	not detected	0.121
CPIJ002108_CquiOBP108	1-20	0.921
CPIJ006608_CquiOBP109	1-19	0.703
CPIJ002111_CquiOBP110	1-18	0.82
CPIJ008867_CquiOBP111	1-21	0.776
CPIJ008868_CquiOBP112	1-22	0.903

Supplementary Table 4a. CDD domain predictions for *Classic* OBPs from *Anopheles gambiae*.

#Batch CD-search tool		NIH/NLM/NCBI									
#cdsid		QM3-qcdsearch-7123E804E85D394-1EB89D7375F149F6									
#datatype		hits Concise data									
#status		0									
#Start time		2012-10-03T08:42:46	Run time	0:00:00:48							
#status		success									
Query		Hit type	PSSM-ID	From	To	E-Value	Bitscore	Accession	Short name	Incomplete	Superfamily
Q#1 - >AGAP003309/Aga	AgamOBP1	specific	201769	42	138	1.78E-18	76.4527	pfam01395	PBP_GOBP	-	cl11600
Q#1 - >AGAP003309/Aga	AgamOBP1	superfamily	209365	42	138	1.78E-18	76.4527	cl11600	PBP_GOBP superfamily	-	-
Q#1 - >AGAP003309/Aga	AgamOBP2	specific	201769	43	151	9.83E-22	85.3123	pfam01395	PBP_GOBP	-	cl11600
Q#2 - >AGAP003306/Aga	AgamOBP2	superfamily	209365	43	151	9.83E-22	85.3123	cl11600	PBP_GOBP superfamily	-	-
Q#3 - >AGAP001409/Aga	AgamOBP3	specific	201769	34	147	2.89E-21	84.1567	pfam01395	PBP_GOBP	-	cl11600
Q#3 - >AGAP001409/Aga	AgamOBP3	superfamily	209365	34	147	2.89E-21	84.1567	cl11600	PBP_GOBP superfamily	-	-
Q#4 - >AGAP010489/Aga	AgamOBP4	specific	201769	18	138	8.72E-18	74.5267	pfam01395	PBP_GOBP	-	cl11600
Q#4 - >AGAP010489/Aga	AgamOBP4	superfamily	209365	18	138	8.72E-18	74.5267	cl11600	PBP_GOBP superfamily	-	-
Q#5 - >AGAP009629/Aga	AgamOBP5	specific	201769	28	149	2.58E-21	84.1567	pfam01395	PBP_GOBP	-	cl11600
Q#5 - >AGAP009629/Aga	AgamOBP5	superfamily	209365	28	149	2.58E-21	84.1567	cl11600	PBP_GOBP superfamily	-	-
Q#6 - >AGAP003530/Aga	AgamOBP6	specific	201769	29	150	7.16E-19	77.6083	pfam01395	PBP_GOBP	-	cl11600
Q#6 - >AGAP003530/Aga	AgamOBP6	superfamily	209365	29	150	7.16E-19	77.6083	cl11600	PBP_GOBP superfamily	-	-
Q#7 - >AGAP001556/Aga	AgamOBP7	specific	201769	23	141	4.16E-18	75.6823	pfam01395	PBP_GOBP	-	cl11600
Q#7 - >AGAP001556/Aga	AgamOBP7	superfamily	209365	23	141	4.16E-18	75.6823	cl11600	PBP_GOBP superfamily	-	-
Q#8 - >AGAP000279/Aga	AgamOBP8	specific	201769	44	172	2.14E-13	62.9707	pfam01395	PBP_GOBP	-	cl11600
Q#8 - >AGAP000279/Aga	AgamOBP8	superfamily	209365	44	172	2.14E-13	62.9707	cl11600	PBP_GOBP superfamily	-	-
Q#9 - >AGAP000278/Aga	AgamOBP9	specific	201769	18	129	2.43E-29	104.572	pfam01395	PBP_GOBP	-	cl11600
Q#9 - >AGAP000278/Aga	AgamOBP9	superfamily	209365	18	129	2.43E-29	104.572	cl11600	PBP_GOBP superfamily	-	-
Q#10 - >AGAP001189/Aga	AgamOBP10	specific	201769	58	127	5.33E-16	69.1339	pfam01395	PBP_GOBP	N	cl11600
Q#10 - >AGAP001189/Aga	AgamOBP10	superfamily	209365	58	127	5.33E-16	69.1339	cl11600	PBP_GOBP superfamily	N	-
Q#11 - >AGAP002025/Aga	AgamOBP11	specific	201769	51	161	1.57E-14	66.4375	pfam01395	PBP_GOBP	-	cl11600
Q#11 - >AGAP002025/Aga	AgamOBP11	superfamily	209365	51	161	1.57E-14	66.4375	cl11600	PBP_GOBP superfamily	-	-
Q#12 - >AGAP002188/Aga	AgamOBP12	specific	201769	20	140	6.98E-17	72.6007	pfam01395	PBP_GOBP	-	cl11600
Q#12 - >AGAP002188/Aga	AgamOBP12	superfamily	209365	20	140	6.98E-17	72.6007	cl11600	PBP_GOBP superfamily	-	-
Q#13 - >AGAP002905/Aga	AgamOBP13	specific	201769	37	155	4.33E-19	79.1491	pfam01395	PBP_GOBP	-	cl11600
Q#13 - >AGAP002905/Aga	AgamOBP13	superfamily	209365	37	155	4.33E-19	79.1491	cl11600	PBP_GOBP superfamily	-	-
Q#14 - >AGAP002189/Aga	AgamOBP14	specific	201769	21	141	2.18E-14	65.2819	pfam01395	PBP_GOBP	-	cl11600
Q#14 - >AGAP002189/Aga	AgamOBP14	superfamily	209365	21	141	2.18E-14	65.2819	cl11600	PBP_GOBP superfamily	-	-
Q#15 - >AGAP003307/Aga	AgamOBP15	specific	201769	14	135	4.58E-20	80.6899	pfam01395	PBP_GOBP	-	cl11600
Q#15 - >AGAP003307/Aga	AgamOBP15	superfamily	209365	14	135	4.58E-20	80.6899	cl11600	PBP_GOBP superfamily	-	-
Q#16 - >AGAP004433/Aga	AgamOBP19	specific	201769	17	132	4.75E-18	74.9119	pfam01395	PBP_GOBP	-	cl11600

Supplementary Table 4a. CDD domain predictions for *Classic* OBPs from *Anopheles gambiae*.

Q#16 - >AGAP004433/Aga	AgamOBP19	superfamily	209365	17	132	4.75E-18	74.9119	cl11600	PBP_GOBP superfamily	-	-
Q#17 - >AGAP005208/Aga	AgamOBP20	specific	201769	23	137	1.22E-19	79.5343	pfam01395	PBP_GOBP	-	cl11600
Q#17 - >AGAP005208/Aga	AgamOBP20	superfamily	209365	23	137	1.22E-19	79.5343	cl11600	PBP_GOBP superfamily	-	-
Q#18 - >AGAP008398/Aga	AgamOBP21	specific	201769	6	127	1.33E-18	76.4527	pfam01395	PBP_GOBP	-	cl11600
Q#18 - >AGAP008398/Aga	AgamOBP21	superfamily	209365	6	127	1.33E-18	76.4527	cl11600	PBP_GOBP superfamily	-	-
Q#19 - >AGAP010409/Aga	AgamOBP22	specific	201769	19	133	4.96E-16	69.9043	pfam01395	PBP_GOBP	-	cl11600
Q#19 - >AGAP010409/Aga	AgamOBP22	superfamily	209365	19	133	4.96E-16	69.9043	cl11600	PBP_GOBP superfamily	-	-
Q#20 - >AGAP012318/Aga	AgamOBP23	specific	201769	10	128	2.19E-23	88.7791	pfam01395	PBP_GOBP	-	cl11600
Q#20 - >AGAP012318/Aga	AgamOBP23	superfamily	209365	10	128	2.19E-23	88.7791	cl11600	PBP_GOBP superfamily	-	-
Q#21 - >AGAP012319/Aga	AgamOBP24	specific	201769	56	157	2.66E-18	76.8379	pfam01395	PBP_GOBP	-	cl11600
Q#21 - >AGAP012319/Aga	AgamOBP24	superfamily	209365	56	157	2.66E-18	76.8379	cl11600	PBP_GOBP superfamily	-	-
Q#22 - >AGAP012320/Aga	AgamOBP25	specific	201769	70	138	1.09E-17	74.1415	pfam01395	PBP_GOBP	N	cl11600
Q#22 - >AGAP012320/Aga	AgamOBP25	superfamily	209365	70	138	1.09E-17	74.1415	cl11600	PBP_GOBP superfamily	N	-
Q#23 - >AGAP012321/Aga	AgamOBP26	specific	201769	9	128	6.24E-26	95.7127	pfam01395	PBP_GOBP	-	cl11600
Q#23 - >AGAP012321/Aga	AgamOBP26	superfamily	209365	9	128	6.24E-26	95.7127	cl11600	PBP_GOBP superfamily	-	-
Q#24 - >AGAP012323/Aga	AgamOBP27	specific	201769	60	125	4.22E-14	64.1263	pfam01395	PBP_GOBP	N	cl11600
Q#24 - >AGAP012323/Aga	AgamOBP27	superfamily	209365	60	125	4.22E-14	64.1263	cl11600	PBP_GOBP superfamily	N	-
Q#25 - >AGAP012325/Aga	AgamOBP28	specific	201769	9	130	1.10E-22	87.2383	pfam01395	PBP_GOBP	-	cl11600
Q#25 - >AGAP012325/Aga	AgamOBP28	superfamily	209365	9	130	1.10E-22	87.2383	cl11600	PBP_GOBP superfamily	-	-
Q#26 - >AGAP012331/Aga	AgamOBP29	superfamily	209365	81	157	0.00234741	35.2364	cl11600	PBP_GOBP superfamily	N	-
Q#59 - >AGAP002556/Aga	AgamOBP62	specific	201769	49	161	5.18E-10	53.3407	pfam01395	PBP_GOBP	-	cl11600
Q#59 - >AGAP002556/Aga	AgamOBP62	superfamily	209365	49	161	5.18E-10	53.3407	cl11600	PBP_GOBP superfamily	-	-
Q#60 - >AGAP012322/Aga	AgamOBP63	specific	201769	11	130	9.57E-28	100.335	pfam01395	PBP_GOBP	-	cl11600
Q#60 - >AGAP012322/Aga	AgamOBP63	superfamily	209365	11	130	9.57E-28	100.335	cl11600	PBP_GOBP superfamily	-	-
Q#61 - >AGAP012324/Aga	AgamOBP64	specific	201769	30	133	3.91E-16	69.9043	pfam01395	PBP_GOBP	-	cl11600
Q#61 - >AGAP012324/Aga	AgamOBP64	superfamily	209365	30	133	3.91E-16	69.9043	cl11600	PBP_GOBP superfamily	-	-
Q#69 - >AGAP012714/Aga	AgamOBP72	specific	201769	1	116	8.23E-18	73.7563	pfam01395	PBP_GOBP	-	cl11600
Q#69 - >AGAP012714/Aga	AgamOBP72	superfamily	209365	1	116	8.23E-18	73.7563	cl11600	PBP_GOBP superfamily	-	-

Supplementary Table 4b. CDD domain predictions for *Classic* OBPs from *Aedes aegypti*.

#Batch CD-search tool		NIH/NLM/NCBI									
#cdsid		QM3-qcdsearch-1D7EE3C6BCF9E4C3-94BF4515A2BFB89									
#datatype		hits Concise data									
#status		0									
#Start time		2012-10-03T09:09:54	Run time	0:00:01:28							
#status		success									
Query		Hit type	PSSM-ID	From	To	E-Value	Bitscore	Accession	Short name	Incomplete	Superfamily
Q#1 - >AAEL009449/Aae	AaegOBP1	specific	201769	17	140	2.11E-17	73.3711	pfam01395	PBP_GOBP	-	cl11600
Q#1 - >AAEL009449/Aae	AaegOBP1	superfamily	209365	17	140	2.11E-17	73.3711	cl11600	PBP_GOBP superfamily	-	-
Q#2 - >AAEL006176/Aae	AaegOBP2	specific	201769	21	136	4.49E-19	77.9935	pfam01395	PBP_GOBP	-	cl11600
Q#2 - >AAEL006176/Aae	AaegOBP2	superfamily	209365	21	136	4.49E-19	77.9935	cl11600	PBP_GOBP superfamily	-	-
Q#3 - >AAEL013018/Aae	AaegOBP3	specific	201769	1	110	2.25E-17	72.6007	pfam01395	PBP_GOBP	-	cl11600
Q#3 - >AAEL013018/Aae	AaegOBP3	superfamily	209365	1	110	2.25E-17	72.6007	cl11600	PBP_GOBP superfamily	-	-
Q#4 - >AAEL000073/Aae	AaegOBP4	specific	201769	22	141	2.28E-16	70.6747	pfam01395	PBP_GOBP	-	cl11600
Q#4 - >AAEL000073/Aae	AaegOBP4	superfamily	209365	22	141	2.28E-16	70.6747	cl11600	PBP_GOBP superfamily	-	-
Q#8 - >AAEL001826/Aae	AaegOBP8	specific	201769	8	130	3.55E-21	83.0011	pfam01395	PBP_GOBP	-	cl11600
Q#8 - >AAEL001826/Aae	AaegOBP8	superfamily	209365	8	130	3.55E-21	83.0011	cl11600	PBP_GOBP superfamily	-	-
Q#9 - >AAEL002596/Aae	AaegOBP9	specific	201769	11	130	2.71E-26	96.4831	pfam01395	PBP_GOBP	-	cl11600
Q#9 - >AAEL002596/Aae	AaegOBP9	superfamily	209365	11	130	2.71E-26	96.4831	cl11600	PBP_GOBP superfamily	-	-
Q#10 - >AAEL007603/Aae	AaegOBP10	specific	201769	34	136	2.90E-23	88.7791	pfam01395	PBP_GOBP	-	cl11600
Q#10 - >AAEL007603/Aae	AaegOBP10	superfamily	209365	34	136	2.90E-23	88.7791	cl11600	PBP_GOBP superfamily	-	-
Q#11 - >AAEL002587/Aae	AaegOBP11	specific	201769	10	133	5.18E-25	93.4015	pfam01395	PBP_GOBP	-	cl11600
Q#11 - >AAEL002587/Aae	AaegOBP11	superfamily	209365	10	133	5.18E-25	93.4015	cl11600	PBP_GOBP superfamily	-	-
Q#12 - >AAEL002617/Aae	AaegOBP12	specific	201769	9	128	2.09E-21	83.7715	pfam01395	PBP_GOBP	-	cl11600
Q#12 - >AAEL002617/Aae	AaegOBP12	superfamily	209365	9	128	2.09E-21	83.7715	cl11600	PBP_GOBP superfamily	-	-
Q#13 - >AAEL002591/Aae	AaegOBP13	specific	201769	9	128	2.67E-26	96.4831	pfam01395	PBP_GOBP	-	cl11600
Q#13 - >AAEL002591/Aae	AaegOBP13	superfamily	209365	9	128	2.67E-26	96.4831	cl11600	PBP_GOBP superfamily	-	-
Q#14 - >AAEL002605/Aae	AaegOBP14	specific	201769	9	128	6.32E-27	98.4091	pfam01395	PBP_GOBP	-	cl11600
Q#14 - >AAEL002605/Aae	AaegOBP14	superfamily	209365	9	128	6.32E-27	98.4091	cl11600	PBP_GOBP superfamily	-	-
Q#15 - >AAEL002598/Aae	AaegOBP15	specific	201769	9	127	3.76E-19	77.9935	pfam01395	PBP_GOBP	-	cl11600
Q#15 - >AAEL002598/Aae	AaegOBP15	superfamily	209365	9	127	3.76E-19	77.9935	cl11600	PBP_GOBP superfamily	-	-
Q#17 - >AAEL004339/Aae	AaegOBP17	specific	201769	4	127	1.24E-12	60.2743	pfam01395	PBP_GOBP	-	cl11600
Q#17 - >AAEL004339/Aae	AaegOBP17	superfamily	209365	4	127	1.24E-12	60.2743	cl11600	PBP_GOBP superfamily	-	-
Q#18 - >AAEL004342/Aae	AaegOBP18	specific	201769	27	135	5.17E-15	66.8227	pfam01395	PBP_GOBP	-	cl11600
Q#18 - >AAEL004342/Aae	AaegOBP18	superfamily	209365	27	135	5.17E-15	66.8227	cl11600	PBP_GOBP superfamily	-	-
Q#19 - >AAEL004343/Aae	AaegOBP19	specific	201769	32	140	9.75E-16	69.1339	pfam01395	PBP_GOBP	-	cl11600
Q#19 - >AAEL004343/Aae	AaegOBP19	superfamily	209365	32	140	9.75E-16	69.1339	cl11600	PBP_GOBP superfamily	-	-
Q#20 - >AAEL005778/Aae	AaegOBP20	specific	201769	55	150	1.19E-12	60.6595	pfam01395	PBP_GOBP	-	cl11600
Q#20 - >AAEL005778/Aae	AaegOBP20	superfamily	209365	55	150	1.19E-12	60.6595	cl11600	PBP_GOBP superfamily	-	-

Supplementary Table 4b. CDD domain predictions for *Classic* OBPs from *Aedes aegypti*.

Q#21 - >AAEL005770/Aae	AaegOBP21	specific	201769	12	135	1.66E-19	79.1491	pfam01395	PBP_GOBP	-	cl11600
Q#21 - >AAEL005770/Aae	AaegOBP21	superfamily	209365	12	135	1.66E-19	79.1491	cl11600	PBP_GOBP superfamily	-	-
Q#22 - >AAEL005772/Aae	AaegOBP22	specific	201769	17	128	1.66E-25	94.5571	pfam01395	PBP_GOBP	-	cl11600
Q#22 - >AAEL005772/Aae	AaegOBP22	superfamily	209365	17	128	1.66E-25	94.5571	cl11600	PBP_GOBP superfamily	-	-
Q#27 - >AAEL000071/Aae	AaegOBP27	specific	201769	32	142	1.47E-14	66.0523	pfam01395	PBP_GOBP	-	cl11600
Q#27 - >AAEL000071/Aae	AaegOBP27	superfamily	209365	32	142	1.47E-14	66.0523	cl11600	PBP_GOBP superfamily	-	-
Q#33 - >AAEL014082/Aae	AaegOBP34	specific	201769	22	137	1.05E-13	63.3559	pfam01395	PBP_GOBP	-	cl11600
Q#33 - >AAEL014082/Aae	AaegOBP34	superfamily	209365	22	137	1.05E-13	63.3559	cl11600	PBP_GOBP superfamily	-	-
Q#34 - >AAEL002606/Aae	AaegOBP35	specific	201769	23	127	2.70E-20	80.6899	pfam01395	PBP_GOBP	-	cl11600
Q#34 - >AAEL002606/Aae	AaegOBP35	superfamily	209365	23	127	2.70E-20	80.6899	cl11600	PBP_GOBP superfamily	-	-
Q#35 - >AAEL008011/Aae	AaegOBP36	specific	201769	49	145	2.52E-20	81.4603	pfam01395	PBP_GOBP	-	cl11600
Q#35 - >AAEL008011/Aae	AaegOBP36	superfamily	209365	49	145	2.52E-20	81.4603	cl11600	PBP_GOBP superfamily	-	-
Q#36 - >AAEL008009/Aae	AaegOBP37	specific	201769	24	143	1.33E-13	62.9707	pfam01395	PBP_GOBP	-	cl11600
Q#36 - >AAEL008009/Aae	AaegOBP37	superfamily	209365	24	143	1.33E-13	62.9707	cl11600	PBP_GOBP superfamily	-	-
Q#37 - >AAEL008013/Aae	AaegOBP38	specific	201769	21	134	5.36E-22	85.6975	pfam01395	PBP_GOBP	-	cl11600
Q#37 - >AAEL008013/Aae	AaegOBP38	superfamily	209365	21	134	5.36E-22	85.6975	cl11600	PBP_GOBP superfamily	-	-
Q#38 - >AAEL006454/Aae	AaegOBP39	specific	201769	20	137	8.19E-24	90.3199	pfam01395	PBP_GOBP	-	cl11600
Q#38 - >AAEL006454/Aae	AaegOBP49	superfamily	209365	20	137	8.19E-24	90.3199	cl11600	PBP_GOBP superfamily	-	-
Q#54 - >AAEL012377/Aae	AaegOBP55	specific	201769	26	146	5.16E-20	80.6899	pfam01395	PBP_GOBP	-	cl11600
Q#54 - >AAEL012377/Aae	AaegOBP55	superfamily	209365	26	146	5.16E-20	80.6899	cl11600	PBP_GOBP superfamily	-	-
Q#55 - >AAEL000051/Aae	AaegOBP56	specific	201769	20	137	5.21E-23	88.3939	pfam01395	PBP_GOBP	-	cl11600
Q#55 - >AAEL000051/Aae	AaegOBP56	superfamily	209365	20	137	5.21E-23	88.3939	cl11600	PBP_GOBP superfamily	-	-
Q#56 - >AAEL000035/Aae	AaegOBP57	specific	201769	23	142	9.89E-13	60.6595	pfam01395	PBP_GOBP	-	cl11600
Q#56 - >AAEL000035/Aae	AaegOBP57	superfamily	209365	23	142	9.89E-13	60.6595	cl11600	PBP_GOBP superfamily	-	-
Q#58 - >AAEL015313/Aae	AaegOBP59	specific	201769	55	150	1.09E-12	60.6595	pfam01395	PBP_GOBP	-	cl11600
Q#58 - >AAEL015313/Aae	AaegOBP59	superfamily	209365	55	150	1.09E-12	60.6595	cl11600	PBP_GOBP superfamily	-	-
Q#59 - >AAEL015499/Aae	AaegOBP60	specific	201769	23	140	5.96E-20	80.3047	pfam01395	PBP_GOBP	-	cl11600
Q#59 - >AAEL015499/Aae	AaegOBP60	superfamily	209365	23	140	5.96E-20	80.3047	cl11600	PBP_GOBP superfamily	-	-
Q#60 - >AAEL015554/Aae	AaegOBP61	specific	201769	9	128	1.62E-26	97.2535	pfam01395	PBP_GOBP	-	cl11600
Q#60 - >AAEL015554/Aae	AaegOBP61	superfamily	209365	9	128	1.62E-26	97.2535	cl11600	PBP_GOBP superfamily	-	-
Q#63 - >AAEL002618/Aae	AaegOBP65	specific	201769	2	88	8.06E-18	72.9859	pfam01395	PBP_GOBP	N	cl11600
Q#63 - >AAEL002618/Aae	AaegOBP65	superfamily	209365	2	88	8.06E-18	72.9859	cl11600	PBP_GOBP superfamily	N	-
Q#74 - >AAEL007604/Aae	AaegOBP76	specific	201769	17	133	1.60E-19	78.7639	pfam01395	PBP_GOBP	-	cl11600
Q#74 - >AAEL007604/Aae	AaegOBP76	superfamily	209365	17	133	1.60E-19	78.7639	cl11600	PBP_GOBP superfamily	-	-
Q#75 - >AAEL002626/Aae	AaegOBP77	specific	201769	20	129	2.16E-19	78.7639	pfam01395	PBP_GOBP	-	cl11600
Q#75 - >AAEL002626/Aae	AaegOBP77	superfamily	209365	20	129	2.16E-19	78.7639	cl11600	PBP_GOBP superfamily	-	-
Q#76 - >AAEL001836/Aae	AaegOBP78	specific	201769	10	131	7.82E-13	60.6595	pfam01395	PBP_GOBP	-	cl11600
Q#76 - >AAEL001836/Aae	AaegOBP78	superfamily	209365	10	131	7.82E-13	60.6595	cl11600	PBP_GOBP superfamily	-	-
Q#77 - >AAEL007014/Aae	AaegOBP79	specific	201769	16	136	1.06E-15	69.1339	pfam01395	PBP_GOBP	-	cl11600
Q#77 - >AAEL007014/Aae	AaegOBP79	superfamily	209365	16	136	1.06E-15	69.1339	cl11600	PBP_GOBP superfamily	-	-

Supplementary Table 4b. CDD domain predictions for *Classic* OBPs from *Aedes aegypti*.

Q#78 - >AAEL007003/Aae	AaegOBP80	specific	201769	15	139	2.28E-17	73.7563	pfam01395	PBP_GOBP	-	cl11600
Q#78 - >AAEL007003/Aae	AaegOBP80	superfamily	209365	15	139	2.28E-17	73.7563	cl11600	PBP_GOBP superfamily	-	-
Q#79 - >AAEL011730/Aae	AaegOBP81	specific	201769	9	136	2.65E-21	84.1567	pfam01395	PBP_GOBP	-	cl11600
Q#79 - >AAEL011730/Aae	AaegOBP82	superfamily	209365	9	136	2.65E-21	84.1567	cl11600	PBP_GOBP superfamily	-	-
Q#81 - >AAEL011416/Aae	AaegOBP83	specific	201769	210	286	3.97E-05	41.0143	pfam01395	PBP_GOBP	N	cl11600
Q#81 - >AAEL011416/Aae	AaegOBP83	superfamily	209365	210	286	3.97E-05	41.0143	cl11600	PBP_GOBP superfamily	N	-

Supplementary Table 4c. CDD domain predictions for *Classic* OBPs from *Culex quinquefasciatus*.

#Batch CD-search tool		NIH/NLM/NCBI									
#cdsid		QM3-qcdsearch-17F5D46C7CDF52FF-31922A2D6D85A9EB									
#datatype		hits Concise data									
#status		0									
#Start time		2012-09-27T06:55:	Run time	0:00:01:10							
#status		success									
Query		Hit type	PSSM-ID	From	To	E-Value	Bitscore	Accession	Short name	Incomplete	Superfamily
Q#1 - >CPIJ007604/Cqu	CquiOBP1	specific	201769	47	143	3.09E-20	81.0751	pfam01395	PBP_GOBP	-	cl11600
Q#1 - >CPIJ007604/Cqu	CquiOBP1	superfamily	209365	47	143	3.09E-20	81.0751	cl11600	PBP_GOBP superfamily	-	-
Q#2 - >CPIJ007617/Cqu	CquiOBP2	specific	201769	27	140	4.51E-21	83.3863	pfam01395	PBP_GOBP	-	cl11600
Q#2 - >CPIJ007617/Cqu	CquiOBP2	superfamily	209365	27	140	4.51E-21	83.3863	cl11600	PBP_GOBP superfamily	-	-
Q#3 - >CPIJ007611/CQU	CquiOBP3	specific	201769	39	136	3.06E-20	81.0751	pfam01395	PBP_GOBP	-	cl11600
Q#3 - >CPIJ007611/CQU	CquiOBP3	superfamily	209365	39	136	3.06E-20	81.0751	cl11600	PBP_GOBP superfamily	-	-
Q#4 - >CPIJ001730/Cqu	CquiOBP4	specific	201769	28	144	4.83E-15	67.2079	pfam01395	PBP_GOBP	-	cl11600
Q#4 - >CPIJ001730/Cqu	CquiOBP4	superfamily	209365	28	144	4.83E-15	67.2079	cl11600	PBP_GOBP superfamily	-	-
Q#5 - >CPIJ007608/Cqu	CquiOBP5	specific	201769	37	137	2.47E-19	78.7639	pfam01395	PBP_GOBP	-	cl11600
Q#5 - >CPIJ007608/Cqu	CquiOBP5	superfamily	209365	37	137	2.47E-19	78.7639	cl11600	PBP_GOBP superfamily	-	-
Q#7 - >CPIJ001365/Cqu	CquiOBP7	specific	201769	5	122	5.01E-17	72.2155	pfam01395	PBP_GOBP	-	cl11600
Q#7 - >CPIJ001365/Cqu	CquiOBP7	superfamily	209365	5	122	5.01E-17	72.2155	cl11600	PBP_GOBP superfamily	-	-
Q#8 - >CPIJ009568/Cqu	CquiOBP8	specific	201769	20	139	4.93E-19	77.9935	pfam01395	PBP_GOBP	-	cl11600
Q#8 - >CPIJ009568/Cqu	CquiOBP8	superfamily	209365	20	139	4.93E-19	77.9935	cl11600	PBP_GOBP superfamily	-	-
Q#9 - >CPIJ016948/Cqu	CquiOBP9	specific	201769	12	134	2.70E-14	64.8967	pfam01395	PBP_GOBP	-	cl11600
Q#9 - >CPIJ016948/Cqu	CquiOBP9	superfamily	209365	12	134	2.70E-14	64.8967	cl11600	PBP_GOBP superfamily	-	-
Q#10 - >CPIJ013976/Cqu	CquiOBP10	specific	201769	8	127	1.00E-15	68.7487	pfam01395	PBP_GOBP	-	cl11600
Q#10 - >CPIJ013976/Cqu	CquiOBP10	superfamily	209365	8	127	1.00E-15	68.7487	cl11600	PBP_GOBP superfamily	-	-
Q#11 - >CPIJ006551/Cqu	CquiOBP11	specific	201769	25	139	8.70E-20	79.9195	pfam01395	PBP_GOBP	-	cl11600
Q#11 - >CPIJ006551/Cqu	CquiOBP11	superfamily	209365	25	139	8.70E-20	79.9195	cl11600	PBP_GOBP superfamily	-	-
Q#12 - >CPIJ016949/Cqu	CquiOBP12	specific	201769	12	134	2.70E-14	64.8967	pfam01395	PBP_GOBP	-	cl11600
Q#12 - >CPIJ016949/Cqu	CquiOBP12	superfamily	209365	12	134	2.70E-14	64.8967	cl11600	PBP_GOBP superfamily	-	-
Q#13 - >CPIJ016952/Cqu	CquiOBP13	specific	201769	12	134	2.70E-14	64.8967	pfam01395	PBP_GOBP	-	cl11600
Q#13 - >CPIJ016952/Cqu	CquiOBP13	superfamily	209365	12	134	2.70E-14	64.8967	cl11600	PBP_GOBP superfamily	-	-
Q#14 - >CPIJ009586/Cqu	CquiOBP14	specific	201769	59	154	3.89E-12	59.1187	pfam01395	PBP_GOBP	-	cl11600
Q#14 - >CPIJ009586/Cqu	CquiOBP14	superfamily	209365	59	154	3.89E-12	59.1187	cl11600	PBP_GOBP superfamily	-	-
Q#15 - >CPIJ012714/Cqu	CquiOBP15	specific	201769	29	132	6.26E-17	72.2155	pfam01395	PBP_GOBP	-	cl11600
Q#15 - >CPIJ012714/Cqu	CquiOBP15	superfamily	209365	29	132	6.26E-17	72.2155	cl11600	PBP_GOBP superfamily	-	-

Supplementary Table 4c. CDD domain predictions for *Classic* OBPs from *Culex quinquefasciatus*.

Q#16 - >CPIJ012715/Cqu	CquiOBP16	specific	201769	21	124	2.38E-17	72.9859	pfam01395	PBP_GOBP	-	cl11600
Q#16 - >CPIJ012715/Cqu	CquiOBP16	superfamily	209365	21	124	2.38E-17	72.9859	cl11600	PBP_GOBP superfamily	-	-
Q#17 - >CPIJ012716/Cqu	CquiOBP17	specific	201769	9	128	9.63E-29	103.031	pfam01395	PBP_GOBP	-	cl11600
Q#17 - >CPIJ012716/Cqu	CquiOBP17	superfamily	209365	9	128	9.63E-29	103.031	cl11600	PBP_GOBP superfamily	-	-
Q#18 - >CPIJ012717/Cqu	CquiOBP18	specific	201769	20	128	2.42E-20	81.0751	pfam01395	PBP_GOBP	-	cl11600
Q#18 - >CPIJ012717/Cqu	CquiOBP18	superfamily	209365	20	128	2.42E-20	81.0751	cl11600	PBP_GOBP superfamily	-	-
Q#19 - >CPIJ012718/Cqu	CquiOBP19	specific	201769	36	135	1.46E-20	81.8455	pfam01395	PBP_GOBP	-	cl11600
Q#19 - >CPIJ012718/Cqu	CquiOBP19	superfamily	209365	36	135	1.46E-20	81.8455	cl11600	PBP_GOBP superfamily	-	-
Q#20 - >CPIJ012719/Cqu	CquiOBP20	specific	201769	22	127	5.54E-24	90.3199	pfam01395	PBP_GOBP	-	cl11600
Q#20 - >CPIJ012719/Cqu	CquiOBP20	superfamily	209365	22	127	5.54E-24	90.3199	cl11600	PBP_GOBP superfamily	-	-
Q#21 - >CPIJ012720/Cqu	CquiOBP21	specific	201769	23	131	5.35E-08	46.7923	pfam01395	PBP_GOBP	-	cl11600
Q#21 - >CPIJ012720/Cqu	CquiOBP21	superfamily	209365	23	131	5.35E-08	46.7923	cl11600	PBP_GOBP superfamily	-	-
Q#22 - >CPIJ012721/Cqu	CquiOBP22	specific	201769	10	129	1.72E-19	78.7639	pfam01395	PBP_GOBP	-	cl11600
Q#22 - >CPIJ012721/Cqu	CquiOBP22	superfamily	209365	10	129	1.72E-19	78.7639	cl11600	PBP_GOBP superfamily	-	-
Q#23 - >CPIJ001876/Cqu	CquiOBP23	specific	201769	9	131	1.62E-15	67.9783	pfam01395	PBP_GOBP	-	cl11600
Q#23 - >CPIJ001876/Cqu	CquiOBP23	superfamily	209365	9	131	1.62E-15	67.9783	cl11600	PBP_GOBP superfamily	-	-
Q#24 - >CPIJ014525/Cqu	CquiOBP24	specific	201769	31	133	5.80E-21	82.6159	pfam01395	PBP_GOBP	-	cl11600
Q#24 - >CPIJ014525/Cqu	CquiOBP24	superfamily	209365	31	133	5.80E-21	82.6159	cl11600	PBP_GOBP superfamily	-	-
Q#25 - >CPIJ010723/Cqu	CquiOBP25	specific	201769	13	120	4.52E-07	43.7107	pfam01395	PBP_GOBP	-	cl11600
Q#25 - >CPIJ010723/Cqu	CquiOBP25	superfamily	209365	13	120	4.52E-07	43.7107	cl11600	PBP_GOBP superfamily	-	-
Q#26 - >CPIJ010724/Cqu	CquiOBP26	specific	201769	23	118	2.36E-11	56.0371	pfam01395	PBP_GOBP	-	cl11600
Q#26 - >CPIJ010724/Cqu	CquiOBP26	superfamily	209365	23	118	2.36E-11	56.0371	cl11600	PBP_GOBP superfamily	-	-
Q#27 - >CPIJ010728/Cqu	CquiOBP27	specific	201769	24	123	7.00E-09	49.1035	pfam01395	PBP_GOBP	-	cl11600
Q#27 - >CPIJ010728/Cqu	CquiOBP27	superfamily	209365	24	123	7.00E-09	49.1035	cl11600	PBP_GOBP superfamily	-	-
Q#28 - >CPIJ016965/Cqu	CquiOBP28	specific	201769	31	139	1.94E-11	56.8075	pfam01395	PBP_GOBP	-	cl11600
Q#28 - >CPIJ016965/Cqu	CquiOBP28	superfamily	209365	31	139	1.94E-11	56.8075	cl11600	PBP_GOBP superfamily	-	-
Q#29 - >CPIJ016966/Cqu	CquiOBP29	specific	201769	20	118	2.82E-11	56.0371	pfam01395	PBP_GOBP	-	cl11600
Q#29 - >CPIJ016966/Cqu	CquiOBP29	superfamily	209365	20	118	2.82E-11	56.0371	cl11600	PBP_GOBP superfamily	-	-
Q#30 - >CPIJ016967/Cqu	CquiOBP30	specific	201769	24	132	3.26E-07	44.8663	pfam01395	PBP_GOBP	-	cl11600
Q#30 - >CPIJ016967/Cqu	CquiOBP30	superfamily	209365	24	132	3.26E-07	44.8663	cl11600	PBP_GOBP superfamily	-	-
Q#31 - >CPIJ008285/Cqu	CquiOBP31	specific	201769	5	118	6.29E-14	63.3559	pfam01395	PBP_GOBP	-	cl11600
Q#31 - >CPIJ008285/Cqu	CquiOBP31	superfamily	209365	5	118	6.29E-14	63.3559	cl11600	PBP_GOBP superfamily	-	-
Q#32 - >CPIJ016479/Cqu	CquiOBP32	specific	201769	25	124	5.42E-13	61.0447	pfam01395	PBP_GOBP	-	cl11600
Q#32 - >CPIJ016479/Cqu	CquiOBP32	superfamily	209365	25	124	5.42E-13	61.0447	cl11600	PBP_GOBP superfamily	-	-
Q#33 - >CPIJ019607/Cqu	CquiOBP33	specific	201769	20	122	3.30E-11	55.6519	pfam01395	PBP_GOBP	-	cl11600
Q#33 - >CPIJ019607/Cqu	CquiOBP33	superfamily	209365	20	122	3.30E-11	55.6519	cl11600	PBP_GOBP superfamily	-	-

Supplementary Table 4c. CDD domain predictions for *Classic* OBPs from *Culex quinquefasciatus*.

Q#34 - >CPIJ019608/Cqu	CquiOBP34	specific	201769	6	110	4.11E-11	55.2667	pfam01395	PBP_GOBP	-	cl11600
Q#34 - >CPIJ019608/Cqu	CquiOBP34	superfamily	209365	6	110	4.11E-11	55.2667	cl11600	PBP_GOBP superfamily	-	-
Q#35 - >CPIJ019609/Cqu	CquiOBP35	specific	201769	13	122	4.90E-09	49.4887	pfam01395	PBP_GOBP	-	cl11600
Q#35 - >CPIJ019609/Cqu	CquiOBP35	superfamily	209365	13	122	4.90E-09	49.4887	cl11600	PBP_GOBP superfamily	-	-
Q#36 - >CPIJ019610/Cqu	CquiOBP36	specific	201769	23	136	5.49E-07	44.0959	pfam01395	PBP_GOBP	-	cl11600
Q#36 - >CPIJ019610/Cqu	CquiOBP36	superfamily	209365	23	136	5.49E-07	44.0959	cl11600	PBP_GOBP superfamily	-	-
Q#37 - >CPIJ007931/Cqu	CquiOBP37	specific	201769	11	119	1.10E-08	48.7183	pfam01395	PBP_GOBP	-	cl11600
Q#37 - >CPIJ007931/Cqu	CquiOBP37	superfamily	209365	11	119	1.10E-08	48.7183	cl11600	PBP_GOBP superfamily	-	-
Q#38 - >CPIJ007932/Cqu	CquiOBP38	specific	201769	16	127	1.91E-07	45.2515	pfam01395	PBP_GOBP	-	cl11600
Q#38 - >CPIJ007932/Cqu	CquiOBP38	superfamily	209365	16	127	1.91E-07	45.2515	cl11600	PBP_GOBP superfamily	-	-
Q#39 - >CPIJ007933/Cqu	CquiOBP39	specific	201769	3	122	2.15E-09	50.6443	pfam01395	PBP_GOBP	-	cl11600
Q#39 - >CPIJ007933/Cqu	CquiOBP39	superfamily	209365	3	122	2.15E-09	50.6443	cl11600	PBP_GOBP superfamily	-	-
Q#40 - >CPIJ007934/Cqu	CquiOBP40	specific	201769	3	101	4.95E-10	52.1851	pfam01395	PBP_GOBP	-	cl11600
Q#40 - >CPIJ007934/Cqu	CquiOBP40	superfamily	209365	3	101	4.95E-10	52.1851	cl11600	PBP_GOBP superfamily	-	-
Q#41 - >CPIJ007935/Cqu	CquiOBP41	specific	201769	1	97	4.92E-10	51.7999	pfam01395	PBP_GOBP	N	cl11600
Q#41 - >CPIJ007935/Cqu	CquiOBP41	superfamily	209365	1	97	4.92E-10	51.7999	cl11600	PBP_GOBP superfamily	N	-
Q#42 - >CPIJ007936/Cqu	CquiOBP42	specific	201769	8	111	1.94E-10	53.3407	pfam01395	PBP_GOBP	-	cl11600
Q#42 - >CPIJ007936/Cqu	CquiOBP42	superfamily	209365	8	111	1.94E-10	53.3407	cl11600	PBP_GOBP superfamily	-	-
Q#43 - >CPIJ017326/Cqu	CquiOBP43	specific	201769	13	128	8.80E-27	98.0239	pfam01395	PBP_GOBP	-	cl11600
Q#43 - >CPIJ017326/Cqu	CquiOBP43	superfamily	209365	13	128	8.80E-27	98.0239	cl11600	PBP_GOBP superfamily	-	-
Q#44 - >CPIJ009937/Cqu	CquiOBP44	specific	201769	23	135	5.57E-18	74.9119	pfam01395	PBP_GOBP	-	cl11600
Q#44 - >CPIJ009937/Cqu	CquiOBP44	superfamily	209365	23	135	5.57E-18	74.9119	cl11600	PBP_GOBP superfamily	-	-
Q#45 - >CPIJ010782/Cqu	CquiOBP46	specific	201769	20	139	1.33E-16	71.4451	pfam01395	PBP_GOBP	-	cl11600
Q#45 - >CPIJ010782/Cqu	CquiOBP46	superfamily	209365	20	139	1.33E-16	71.4451	cl11600	PBP_GOBP superfamily	-	-
Q#46 - >CPIJ010787/Cqu	CquiOBP51	specific	201769	25	131	4.34E-14	64.5115	pfam01395	PBP_GOBP	-	cl11600
Q#46 - >CPIJ010787/Cqu	CquiOBP51	superfamily	209365	25	131	4.34E-14	64.5115	cl11600	PBP_GOBP superfamily	-	-
Q#47 - >CPIJ010788/Cqu	CquiOBP52	specific	201769	11	129	9.32E-16	69.1339	pfam01395	PBP_GOBP	-	cl11600
Q#47 - >CPIJ010788/Cqu	CquiOBP52	superfamily	209365	11	129	9.32E-16	69.1339	cl11600	PBP_GOBP superfamily	-	-
Q#48 - >CPIJ010789/Cqu	CquiOBP53	specific	201769	18	127	1.09E-11	57.5779	pfam01395	PBP_GOBP	-	cl11600
Q#48 - >CPIJ010789/Cqu	CquiOBP53	superfamily	209365	18	127	1.09E-11	57.5779	cl11600	PBP_GOBP superfamily	-	-
Q#49 - >CPIJ007937/Cqu	CquiOBP54	specific	201769	65	168	4.27E-12	59.1187	pfam01395	PBP_GOBP	-	cl11600
Q#49 - >CPIJ007937/Cqu	CquiOBP54	superfamily	209365	65	168	4.27E-12	59.1187	cl11600	PBP_GOBP superfamily	-	-
Q#50 - >CPIJ010367/Cqu	CquiOBP55	specific	201769	146	217	0.0001834	38.7031	pfam01395	PBP_GOBP	N	cl11600
Q#50 - >CPIJ010367/Cqu	CquiOBP55	superfamily	209365	146	217	0.0001834	38.7031	cl11600	PBP_GOBP superfamily	N	-
Q#51 - >CPIJ010729/Cqu	CquiOBP56	specific	201769	6	100	7.79E-07	45.2515	pfam01395	PBP_GOBP	-	cl11600
Q#51 - >CPIJ010729/Cqu	CquiOBP56	superfamily	209365	6	100	7.79E-07	45.2515	cl11600	PBP_GOBP superfamily	-	-

Supplementary Table 4c. CDD domain predictions for *Classic* OBPs from *Culex quinquefasciatus*.

Q#52 - >CPIJ016951/Cqu	CquiOBP57	specific	201769	12	134	2.70E-14	64.8967	pfam01395	PBP_GOBP	-	cl11600
Q#52 - >CPIJ016951/Cqu	CquiOBP57	superfamily	209365	12	134	2.70E-14	64.8967	cl11600	PBP_GOBP superfamily	-	-
Q#54 - >CPIJ007609/Cqu	CquiOBP58	specific	201769	12	107	3.12E-14	64.1263	pfam01395	PBP_GOBP	N	cl11600
Q#54 - >CPIJ007609/Cqu	CquiOBP58	superfamily	209365	12	107	3.12E-14	64.1263	cl11600	PBP_GOBP superfamily	N	-
Q#55 - >CPIJ001871/Cqu	CquiOBP59	specific	197837	31	133	9.15E-08	45.8828	smart00708	PhBP	-	cl11600
Q#55 - >CPIJ001871/Cqu	CquiOBP59	superfamily	209365	31	133	9.15E-08	45.8828	cl11600	PBP_GOBP superfamily	-	-
Q#56 - >CPIJ012786/Cqu	CquiOBP60	specific	201769	10	134	4.20E-07	44.4811	pfam01395	PBP_GOBP	-	cl11600
Q#56 - >CPIJ012786/Cqu	CquiOBP60	superfamily	209365	10	134	4.20E-07	44.4811	cl11600	PBP_GOBP superfamily	-	-
Q#57 - >CPIJ015943/Cqu	CquiOBP61	specific	201769	3	117	3.90E-08	46.7923	pfam01395	PBP_GOBP	-	cl11600
Q#57 - >CPIJ015943/Cqu	CquiOBP61	superfamily	209365	3	117	3.90E-08	46.7923	cl11600	PBP_GOBP superfamily	-	-
Q#58 - >CPIJ015944/Cqu	CquiOBP62	specific	201769	55	177	7.59E-11	55.6519	pfam01395	PBP_GOBP	-	cl11600
Q#58 - >CPIJ015944/Cqu	CquiOBP62	superfamily	209365	55	177	7.59E-11	55.6519	cl11600	PBP_GOBP superfamily	-	-
Q#59 - >CPIJ016343/Cqu	CquiOBP63	specific	201769	31	155	9.46E-12	58.7335	pfam01395	PBP_GOBP	-	cl11600
Q#59 - >CPIJ016343/Cqu	CquiOBP63	superfamily	209365	31	155	9.46E-12	58.7335	cl11600	PBP_GOBP superfamily	-	-
Q#60 - >CPIJ004145/Cqu	CquiOBP64	specific	201769	12	132	3.65E-09	50.2591	pfam01395	PBP_GOBP	-	cl11600
Q#60 - >CPIJ004145/Cqu	CquiOBP64	superfamily	209365	12	132	3.65E-09	50.2591	cl11600	PBP_GOBP superfamily	-	-
Q#61 - >CPIJ001875/Cqu	CquiOBP65	specific	201769	16	133	2.76E-12	59.1187	pfam01395	PBP_GOBP	-	cl11600
Q#61 - >CPIJ001875/Cqu	CquiOBP65	superfamily	209365	16	133	2.76E-12	59.1187	cl11600	PBP_GOBP superfamily	-	-
Q#62 - >CPIJ001865/Cqu	CquiOBP66	specific	201769	9	127	2.80E-11	56.0371	pfam01395	PBP_GOBP	-	cl11600
Q#62 - >CPIJ001865/Cqu	CquiOBP66	superfamily	209365	9	127	2.80E-11	56.0371	cl11600	PBP_GOBP superfamily	-	-
Q#63 - >CPIJ017432/Cqu	CquiOBP67	specific	201769	1	117	1.96E-10	53.3407	pfam01395	PBP_GOBP	-	cl11600
Q#63 - >CPIJ017432/Cqu	CquiOBP67	superfamily	209365	1	117	1.96E-10	53.3407	cl11600	PBP_GOBP superfamily	-	-
Q#64 - >CPIJ001873/Cqu	CquiOBP68	specific	201769	20	133	2.01E-12	59.5039	pfam01395	PBP_GOBP	-	cl11600
Q#64 - >CPIJ001873/Cqu	CquiOBP68	superfamily	209365	20	133	2.01E-12	59.5039	cl11600	PBP_GOBP superfamily	-	-
Q#65 - >CPIJ001874/Cqu	CquiOBP69	specific	201769	2	118	1.98E-13	61.8151	pfam01395	PBP_GOBP	-	cl11600
Q#65 - >CPIJ001874/Cqu	CquiOBP69	superfamily	209365	2	118	1.98E-13	61.8151	cl11600	PBP_GOBP superfamily	-	-
Q#66 - >CPIJ001872/Cqu	CquiOBP70	specific	201769	11	129	4.21E-14	64.1263	pfam01395	PBP_GOBP	-	cl11600
Q#66 - >CPIJ001872/Cqu	CquiOBP70	superfamily	209365	11	129	4.21E-14	64.1263	cl11600	PBP_GOBP superfamily	-	-
Q#67 - >CPIJ001870/Cqu	CquiOBP71	specific	201769	9	125	5.56E-11	55.2667	pfam01395	PBP_GOBP	-	cl11600
Q#67 - >CPIJ001870/Cqu	CquiOBP71	superfamily	209365	9	125	5.56E-11	55.2667	cl11600	PBP_GOBP superfamily	-	-
Q#68 - >CPIJ001867/Cqu	CquiOBP72	specific	201769	18	90	5.69E-09	48.7183	pfam01395	PBP_GOBP	N	cl11600
Q#68 - >CPIJ001867/Cqu	CquiOBP72	superfamily	209365	18	90	5.69E-09	48.7183	cl11600	PBP_GOBP superfamily	N	-
Q#69 - >CPIJ001869/Cqu	CquiOBP73	specific	201769	9	128	2.55E-11	56.4223	pfam01395	PBP_GOBP	-	cl11600
Q#69 - >CPIJ001869/Cqu	CquiOBP73	superfamily	209365	9	128	2.55E-11	56.4223	cl11600	PBP_GOBP superfamily	-	-
Q#70 - >CPIJ001868/Cqu	CquiOBP74	specific	201769	12	122	5.45E-09	49.4887	pfam01395	PBP_GOBP	-	cl11600
Q#70 - >CPIJ001868/Cqu	CquiOBP74	superfamily	209365	12	122	5.45E-09	49.4887	cl11600	PBP_GOBP superfamily	-	-