Table S5-11. Genome coordinates of the *Ae.albopictus* ABC transporter gene family

Scaffold	Start	End	Strand	ID	Protein length	Incl. in phyl. analysis?	ABC Subfamily*
53	270857	274610	+	CCG019768.1	623	YES	H
66	196264	238222	-	CCG022692.1	728	YES	H
82	392918	427185	+	CCG025850.1	1401	YES	C
82	429863	469378	+	CCG025851.1	1575	YES	C
82	474687	488345	-	AalbABC008	1365	YES	C
82	512460	522164	-	AalbABC009	1504	YES	C
110	129776	163443	+	CCG001378.1	1401	YES	C
123	42950	75993	-	CCG003003.1	692	YES	G
218	241206	266983	+	CCG009768.1	742	YES	B_HT
230	285457	308054	-	CCG010258.1	678	YES	G
400	415066	463337	-	CCG016086.2	521	YES, included because partial SUR	C
429	333287	342293	-	CCG016930.1	1641	YES	A
429	371552	389383	-	CCG016931.2	1547	YES	A
429	397928	407132	-	CCG016932.1	1626	YES	A
429	426324	431779	-	AalbABC007	1637	YES	A
429	437895	451203	-	CCG016933.1	1637	YES	A
481	1156	33879	+	CCG018349.1	576	YES	G
481	33880	43958	-	AalbABC011	522	YES	G
481	61300	72857	+	CCG018350.1	587	YES	G
481	82076	127043	+	CCG018351.1	616	YES	G
551	240810	267403	-	CCG020313.2	1524	YES	C
672	379932	394110	-	CCG022957.1	1961	YES	A
680	34823	73197	-	CCG023127.1	569	YES	G
684	190732	205935	+	CCG023213.1	690	YES	B_HT
782	14877	16679	-	CCG025183.1	518	YES	G
858	60196	75892	-	CCG026446.1	891	YES	G
892	23308	40148	+	CCG026987.1	713	YES	F
982	217483	227261	-	CCG028396.1	580	YES	G
982	240303	247916	-	CCG028397.2	595	YES	G
982	281439	291309	-	AalbABC010	607	YES	G
1027	183223	191969	-	CCG000392.1	1274	YES	B_FT
1243	217501	261645	-	CCG003172.1	659	YES	D
1266	20301	74003	+	CCG003415.1	676	YES	G
1266	135970	247363	+	CCG003416.1	732	YES	G
1299	95247	154632	-	CCG003816.1	676	YES	G
1340	13541	50522	-	CCG004226.1	604	YES	G

1579	203126	205809	+	CCG006376.1	728	YES	B_HT
1666	231530	242183	+	CCG007028.1	1503	YES	C
1666	257611	271004	+	AalbABC003	1370	YES	C
1666	271218	276098	-	AalbABC004	1517	YES	C
1994	7868	23216	-	AalbABC005	783	YES	H
2235	123822	154000	-	CCG010006.1	621	YES	G
2404	207949	215282	-	CCG010651.1	1689	YES	A
2408	162989	177025	-	CCG010663.1	847	YES	B_HT
3175	27877	30113	-	CCG013515.1	624	YES	E
3375	157323	176897	-	CCG014205.1	1861	YES	A
3472	31665	66056	+	CCG014561.1	1098	YES	C
3490	25963	41943	-	AalbABC006	868	YES	G
3525	128772	163152	-	CCG014705.1	1673	YES	A
3668	26024	58408	-	CCG015143.1	727	YES	H
4013	42293	67705	-	CCG016142.2	1422	YES	C
4013	78622	116281	-	CCG016143.1	1389	YES	C
4554	13472	32971	+	CCG017683.1	1190	YES	C
4631	111061	122448	-	CCG017876.1	713	YES	F
4957	13572	30451	-	CCG018772.1	656	YES	D
5068	126482	136630	+	CCG019098.1	605	YES	F
5433	102742	112033	-	CCG020100.1	1648	YES	A
6029	15874	73665	-	CCG021530.1	598	YES	G
6527	84062	97020	-	CCG022541.1	1291	YES	C
6739	10685	26620	-	CCG022988.1	2576	YES	A
6872	39928	42687	-	CCG023304.1	882	YES	F
7113	18816	23022	+	CCG023783.1	1334	YES	C
7113	28498	32980	+	CCG023784.1	1341	YES	C
7946	4985	7324	+	CCG025406.1	738	YES	G
8966	27806	64302	+	CCG027071.1	1181	YES	C
9335	16004	59328	-	CCG027679.1	1637	YES	A
10705	20884	45521	+	CCG000985.1	410	YES, combined with CCG007754.1	G
11258	11367	23818	+	CCG001707.1	560	YES	D
15461	1487	10833	-	CCG006139.1	601	YES	G
17709	1000	5140	+	CCG007754.1	436	YES	G
23893	777	4583	-	CCG010570.1	1196	YES	C
1022_0	118842	125575	+	AalbABC001	618	YES	G
110	198447	201750	+	CCG001379.1	1012	NO	C
15489	1896	14480	-	AalbABC002	976	NO	C
174929	58	762	-	AalbABC012	235	NO	C

14964	26989	27591	+	AalbABC013	201	NO	D
3472	258	1312	+	AalbABC014	330	NO	C
3232	618	1588	-	AalbABC015	304	NO	G
1845	32159	34088	-	AalbABC016	623	NO	C
1322	296398	297982	-	CCG004072.1	207	NO	G
142	616323	617175	-	CCG005047.1	245	NO	C
14258	8223	25179	+	CCG005085.1	985	NO	C
15461	19309	20304	-	CCG006142.1	193	NO	G
4851	3009	50982	+	CCG018484.1	833	NO	C
5103	96830	97828	-	CCG019201.1	267	NO	G
5464	103961	110667	+	CCG020167.1	602	NO	C
6516	85156	99466	+	CCG022510.1	939	NO	C
6516	102411	107423	-	CCG022511.1	233	NO	C
66	184104	184845	-	CCG022691.1	197	NO	H
7492	87057	88594	-	CCG024536.1	257	NO	C
82	469682	473131	-	CCG025852.1	1091	NO	C

* based on BLASTp search against *D. melanogaster* ABC proteins; B-FT = ABCB full transporter; B_HT=ABCB half-transporter