

SUPPLEMENTAL DATA

Table S1. The fibrinogen-related proteins in *Anopheles gambiae*.

FBN#	FREP#	New Ensembl Transcript ID	Old Ensembl Transcript ID	Old Ensembl Gene ID	VectorBase ID	Chr. Location	Truncated	Size (a.a)
FBN1	FREP3	T15012	T15012	G12523	AGAP011307	3L/42B	3'-T	175
FBN2		T11265	T11265	G08776	AGAP011228	3L/42A	T	198
FBN3	FREP18	G08773	T11262	G08773		3L/42A	3'-T	347
FBN4	FREP29	T15683	T08256	G06227	AGAP011276	3L/42B	3'-T	230
FBN5	FREP5	T08288	T08288	G06254	AGAP011226	3L/42A	5'-T	199
FBN6	FREP59	T15644	T15644	G13155	AGAP011231	3L/42A	3'-T	274
FBN7	FREP60	T08282	T08282	G06248	AGAP011239	3L/42A	3'-T	267
FBN8	FREP57	T11296	T11252	G08763	AGAP011223	3L/42A	3'-T	214
FBN9	FREP13	T11248	T11248	G08759	AGAP011197	3L/42A	3'-T	282
FBN10	FREP58	T15680	T15680	G13191	AGAP011230	3L/42A	T	176
FBN11	FREP28	T26109	T11293	G08804	AGAP011225	3L/42A	3'-T	255
FBN12	FREP2	T20573	T20573	G18084	AGAP010531	3L/39A	full	283
FBN13	FREP23	G19285	T21774	G19285		3L/40A	3'-T	204
FBN14	FREP19	T21297	T21297	G18808	AGAP010811	3L/40A	full	291
FBN15	FREP15	T12794	T12794	G10305	AGAP012539	UNKN	full	372
FBN16	FREP54	T29613	T19675	G17186		3L/39C	3'-T	212
FBN17	FREP22	T30368	T19654	G17165	AGAP010773	3L/39C	3'-T	142
FBN18	FREP55	T20281	T20281	G17792	AGAP010772	3L/39C	3'-T	320
FBN19	FREP27	T19678	T19684	G17195	AGAP010774	3L/39C	3'-T	231
FBN20	FREP21	T27497	T20238	G17749	AGAP010763	3L/39C	3'-T	267
FBN21	FREP51	T19647	T19678	G17189		3L/39C	3'-T	214
FBN22	FREP26	T20282	T20282	G17793	AGAP010775	3L/39C	T	199
FBN23	FREP30	T18192	T18192	G15703	AGAP010869	3L/40B	3'-T	268
FBN24	FREP10	T02335	T02335	G01963		2L/20D	full	287
FBN25	FREP63	T21318	T21318	G18829	AGAP004918	2L/20D	full	305
FBN26	FREP62	T16439	T11448	G08959	AGAP012651	UNKN	full	284
FBN27	FREP43	T10854	T10854	G08365	AGAP004996	2L/21A	full	423
FBN28	FREP64	T11478	T11478	G08989	AGAP004997	2L/21A	full	436
FBN29	FREP14	T32176	T11521	G09032	AGAP012650	UNKN	3'-T	261
FBN30	FREP8	T21698	T21698	G19209	AGAP006914	2L/26B	full	280
FBN31	FREP34	T20268	T20268	G17779	AGAP006790	2L/26A	full	272
FBN32	FREP39	T07635	T07635	G05762	AGAP007041	2L/26D	full	370
FBN33	FREP65	T20316	T20316	G17827	AGAP006743	2L/25D	full	330
FBN34	FREP16	T11564	T11564	G09075	AGAP001554	2R/8B	full	548
FBN35	FREP48	T11308	T11308	G08819	AGAP002005	2R/10A	5'-T	246
FBN36	FREP46	T16460	T13811	G11322	AGAP012000	3L/45A	full	322
FBN37	FREP9	T19563	T19563	G17074	AGAP009042	3R/33B	full	653
FBN38	FREP42	T10235	T10235	G07746	AGAP009728	3R/35C	3'-T	233
FBN39	FREP40	T21380	T21380	G18891	AGAP000806	X/5A	full	326
FBN50	FREP44	T22867			AGAP005848	2L/23B	full	299

FBN51	FREP50	T29396			AGAP009556	3R/34C	3'-T	190
	FREP1	T26193			AGAP007031	2L/26C	full	738
	FREP4	T32282			AGAP010762	3L/39C	3'-T	279
	FREP6				AGAP011277	3L/42B	T	194
	FREP7	T22610			AGAP009184	3R/33C	3'-T	314
	FREP11				AGAP004916	2L/20D	full	309
	FREP12	T30878			AGAP004917	2L/20D	full	298
	FREP17				AGAP010760	3L/39C	3'-T	220
	FREP20					3L/39C	full	323
	FREP25	T29579				3L/39C	3'-T	306
	FREP31					UNKN	T	209
	FREP32	T30831			AGAP010759	3L/39C	3'-T	241
	FREP36	T30748			AGAP004999	2L/21A	full	284
	FREP37	T30361				3L/42A	full	290
	FREP38	T30362				3L/42A	full	293
	FREP41					3L/42A	T	235
	FREP47					UNKN	T	156
	FREP49	T16440			AGAP004998	2L/21A	full	294
					AGAP011224	3L/42A	3'-T	167

FBN#: IDs from [40] ; FREP#: FREP IDs from the CEGG database [37]; the corresponding new Ensembl transcript ID #; the old designations (with abbreviations), with only the last 5 digits shown (ENSANGT#); the new VectorBase ID (AGAP#); chromosomal locations (Chr. location), FBG domain truncated (T denotes truncated), UNKN denotes unknown location.

Table S2. Primers used for semi-quantitative RT-PCR analysis, *dsRNA* synthesis, and RNAi gene silencing verification primers together with silencing efficiency.

FBN#	Forward Primer	Reverse Primer	PCR length (bp)	RNAi Verification Primer Forward	KD% (\pm SE)
FBN1	ATCGCTGAAGCCATGTTGAT	GCGTGCTTCATTCTGTGTGT	361	AAGAGAATATTGAACTA	78 (\pm 12)
FBN2	AGTTTCGGAGGAGGTTGGTT	CATCCTCCACGATCAGGTCT	386		
FBN3	GCAGACCACCTACCAGTCGT	TGCCAATCTCGAAGTGTCTG	359	TCGAGTAGAATGCTTGCC	62 (\pm 16)
FBN4	GGACTTTTACCGCAACTGGA	TTGTGCACAGTTTCCACCAT	322	GGCTTGTGTCCAGTACC	69 (\pm 8)
FBN5	AGGATGGCTTGTGTTCCAGT	CATCATTTTCCCGATCCTTG	335	GACCAGACTACATTCCGG	70 (\pm 18)
FBN6	GGACTTTTACCGCAATTGGA	GTACCACCATGCTCCCTCAT	346	GTGTTCCAGCATCGTTACG	58 (\pm 13)
FBN7	GCCATTCTGGGATACTGTG	CAATGAGTTTCCCTGCCGTTT	325	CCTGCTGAAAAATGAAGAGCC	75 (\pm 18)
FBN8	TTCAAGGGCAATTTTGGTTC	ATATTGTTCCGCCTCACTGC	387	CCACGAACAAATGCGGAACG	71 (\pm 6)
FBN9	CCAAGATGTCGGGCAAGTAT	TTGTGGTACGTCAGCGAGTC	402	CGCTCCCTGTTTCGAGCTGCA	56 (\pm 18)
FBN10	TGTCTGGAGCCATCAGTCAG	TAAATCGGTGCTGGAACACA	339	GTGGGCCATCGATCAAAAAGC	78 (\pm 14)
FBN11	ACACGTTTTGGAGGAGGTTG	CCACCATGCTCCCTGTACT	396	TCATTACCCGTTTCGTGGGAC	67 (\pm 9)
FBN12	GGAAGCAGCCACGACATTAT	TCGAGGCCTAACCAATGTTC	378	GCAGTTATCTGTGCTCTG	56 (\pm 17)
FBN13	AGGAACCATCAAAGCAATCG	TGGTAGTTCAACCCGCTCTCC	388	CGAAACTTCTCGTTCG	67 (\pm 18)
FBN14	CAATCAGCAAAGCCAGACAA	CAGAACTCCCATCAATGCT	396	GACGCAAGGCTTATTAAC	56 (\pm 17)
FBN15	GGTGGAGCTGAAAGACTTCG	TTTGGTTTACGGATCATCA	355		
FBN16	CGCACGGTATGATGAATTTG	AGTTTCGGAATGGATGCTTG	374	CGGCTCAAAAGCACGAGC	40 (\pm 7)
FBN17	GCAAGGAAGAGCCATCAAAG	TGCTAACGGAAATGCTCCT	347	GCTCGGTTTAAAGCCAG	82 (\pm 12)

FBN18	ACAACCAACGGAGAAGGATG	AACTTCATGCCCTTGTGGAC	369		
FBN19	GGACTTTTACCGCAACTGGA	GTGCCACCATGCTCCTTAT	346	GGAGGTTGGTTAGTGTCC	63 (±15)
FBN20	AACAGACTGCTTTCGGAGGA	CACCTCCTTGACACTGGTT	397	GATGAGCCATTCCTGGG	70 (±17)
FBN21	TGCACGATTGTGACCATT	GCGGATATTGGTCTCCTCA	398	GCGTCAAAGAAAGATCTTGC	66 (±18)
FBN22	TTTCCTGGGATATTGCGAAC	CCACCGAACAGCTATCATT	384	CCTAATAAAGCCTAACAA	78 (±17)
FBN23	AGCGTATCGGAATGGTTTTG	GCCATTTTTGTAGCGTCCAT	358		
FBN24	TGCACCATTGCTTCTTCTG	CCGAATACTTTTGGCCTTCA	338	GAAAGAAAACGAAATAAACG	75 (±12)
FBN25	GATTGCTTGCGAAAATGTA	TCCGTCAAACGATGCTGTA	371	GGGATTGTTTTGCTGATT	74 (±16)
FBN26	GGACGCAATTGCCTACCTTA	ACTGTGCCAGCGAGGTTATC	359	GTGTGCCGGGTATTCAGGT	65 (±8)
FBN27	CGCCAAGGAGAGTACAGACC	CAGCAGATGAACAACCTCGT	321	CCGAATCTATTCTGGATCTGG	80 (±15)
FBN28	TCAAGAAAACGGGCACCTAC	GAAGCCCTTCAGCTCAAGA	344	GGATCTACTTCTTGTGAGG	75 (±12)
FBN29	TCCTCAGTCGCTGTGTTTTG	CCGAAGCCGTTCTGATAGTC	369		
FBN30	TTGCCGCTAGTGTGATCTG	TCAAACCAAGCCAATGTCA	363	GTGCAAATTACCCACCGTC	65 (±17)
FBN31	CCAGGGTCAGTGGCATATTT	ATGTATCCATCGTCCGCATT	328	GCTCGTGCCGCGAGGTCCC	77 (±7)
FBN32	CGATGGTACGGTCGATTTCT	CCGTGATAGTACGACGGACA	333	GGCTTGTCTCCAGCAGCGG	67 (±8)
FBN33	TACCAGATACGGCCCGAGTA	GTACCGCTGTATCCGTCGAT	341	CCCGTTCGCAGCGTCCGGCG	52 (±12)
FBN34	GCTACGACGACAATGTGGAG	CTGCCAAACGTAAGAGCACA	241		
FBN35	CGAGGGAAAATCTCATCGAA	CGTCAAAGTCCTCCAGCAGT	372		
FBN36	TTCGGTGGTAATTGGATCGT	TATCTTGATCGTGCGTGGA	337		
FBN37	ACGAGGACTGAACGACTGT	GATCATCATGGTCGCCTTCT	187	GGCGGCTGGTGGTGAAG	75 (±17)
FBN38	AGAAAAGCCGCGTGAGATAG	GTATTGCGTCGTTGGACCTT	307		
FBN39	CGCTACACCCTGTTGAGAT	TACTTGCGGCGCTTCTTAT	332	GGCCGAATCGTTCAAGGGCG	58 (±10)

KD% (± SE): denotes the gene silencing efficiency with standard errors from three replicates

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10      20      30      40      50      60      70      80
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Structure
Tachylectin5A GYRIWPKSWMT-VGTLN-----V*CDME---TDGG-GWIVIQRRGNPSDY-FYKPTKNYKLGFCGNIE-K
FREP3/FBN1      -----MLSDVYTIKPPAS-SVAEPFV*CECG-----YRKG-GWIVLSRRFDGSLN-FDRDWIDYRIGFCSPB-G
FREP24/FBN2     -----KQSGKYLQIPT--ENGELFLG*CEC-----VSFCGGWLVQHRMGMED-FDRNWTDYRN GFCSIG-G
FREP18/FBN3     TSYRACKKEEPSKVGKYLQIPT--ANDEPFLG*CEC-----TRFCGGWLVQHRFNGSVD-FYRNWTEYRN GFCGSD-G
FREP29/FBN4     VSFRSCKENPSKRSKYLQILT--ENDQEPFLG*CEC-----TAYCGGWLVQHRMDGSVD-FYRNWTEYRN GFCGSD-G
FREP5/FBN5      -----VFQY-----RFDGGSVD-FYRNWTEYRN GFCGSD-G
FREP59/FBN6     VSFRSCKKTPSKRSKYLQIPT--ENDEPFLG*CEC-----TSFCGGWLVQHRFNGSVD-FYRDWTEYRN GFCGSD-G
FREP60/FBN7     SPISSCKG---VTKKHLIQPT--ANDEPFLAI*CEE-----TSFCGGWLVQHRFNGSVD-FYRNWTEYRN GFCGSD-G
FREP57/FBN8     TPVRSCKEEPSKQSGKYLQIPT--ENDEPFG*CDQ-----TTFCGGWLVQHRFNGSLN-FYRNWTEYRN RFGSVD-G
FREP13/FBN9     GPFESCRDEPSKMSGKYLIRAS--NDVEPFLAI*CEC-----TKFCGGWLVQHRFNGSVD-FYRNWTEYRN GFCGSD-G
FREP58/FBN10    -----TRFCGGWLVQHRFNGSVD-FYRNWTEYRN GFCGSD-G
FREP28/FBN11    TSIRSCKAEPKSLSGKYLQIPT--ENHYEPFV*GCEC-----TRFCGGWLVQHRFNGSVD-FYRNWTEYRN GFCGSD-G
FREP2/FBN12     LKQDFEOKLAHQDQSGVYLQIRF-SNESPEV*FDGS--NNHGYGNNIVQRRFDGSLN-FYRNWTEYRN GFCNLD-G
FREP23/FBN13    M---CFTHGVRPLINTIDPHFIHP--YHTY--CTSSF-----CGGWLVQHRMDGALD-FYRDWTEYRN GFCGSD-G
FREP19/FBN14    VTFRSCKENPSQLSGKYLQIST--EADEPFLG*CEC-----TAFAGGWLVQHRMDGSVD-FYRNWTEYRN GFCGSD-G
FREP15/FBN15    ISFESCKENLSKRSKYLQIPT--ENDEPFLG*CAQ-----TAFCGGWLVQHRMDGSVD-FYRNWTEYRN GFCGSD-G
FREP54/FBN16    IAFESCKEILSKRSKYLKIPN--KNDEPFLG*CEC-----TAFCGGWLVQHRMDGSVD-FYRNWTEYRN GFCGSD-G
FREP22/FBN17    -----MY-R
FREP55/FBN18    ISFESCKEILSKRSKYLQIPS--KIDKPEFV*VCEC-----TAFCGGWLVQHRMDGSVD-FYRNWTEYRN GFCGSD-G
FREP27/FBN19    ISSRSCKNEVPSNKSGLKYLQIPS--KTNEPFLV*GCEC-----TAFCGGWLVQHRMDGSVD-FYRNWTEYRN GFCGSD-G
FREP21/FBN20    ISSGSCKEEPSKESGKYLQIST--EKDEPFLG*CEC-----TAFCGGWLVQHRMDGSVD-FYRNWTEYRN GFCGSD-G
FREP51/FBN21    ISFESCKEILSKRSKYLQIRS--KIDKPEFV*VCEC-----TAFCGGWLVQHRMDGSVD-FYRNWTEYRN GFCGSD-G
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FREP63/FBN25    VYSS--CRKTP--AGGVYIQPEKP-FKEPITV*ICQE-----YESG-GWIVIQHRFDGSLN-FYRNWTEYRN GFCGSD-G
FREP62/FBN26    IYQS--CDDVTGP--PGLYRVRDGN--DVETHY*ICQE-----LLGG-GWIVIQRRTSGRIN-FYRNWTEYRN GFCGSD-G
FREP43/FBN27    IFTS--CDDSRITQIGTYLQVDAF--SEP-TKV*VCLD----FVSG-RWIVIQRRDGSVD-FYRNWTEYRN GFCGSD-G
FREP64/FBN28    IYSS--CEDPNIKKIGTYWIKANF--YKP-VKV*ICMLD----YGG--RWIVIQRRDGSVD-FYRNWTEYRN GFCGSD-G
FREP14/FBN29    SYKS--CSDVPPNSPSGVYKLRGE--FGSQKAI*CNMS----YAGG-GWIVIQRRFNGSVD-FYRNWTEYRN GFCGSD-G
FREP8/FBN30     LG---ELRPFPGADKLPAAGRS-NYRLEKIAELT--GGQNLAGDWLVQHRFNGSLN-FYRNWTEYRN GFCGSD-G
FREP34/FBN31    IYSS--CREVPSRVSGIFLKIISD--DARDMNL*ICDAH----ANDV-GWIVIQRRFNGSES-FYRNWTEYRN GFCGSD-G
FREP39/FBN32    LEHQIR--AAAHGSEEHENPDGR-ENGSPFV*SVSA--NNRLYCDGWLVQHRFDGSLN-FYRNWTEYRN GFCGSD-G
FREP65/FBN33    VYRS--CGKVPFAASGVYQIRPEYP-FKEPITV*ICQE-----YESG-GWIVIQRRFDGSLN-FYRNWTEYRN GFCGSD-G
FREP16/FBN34    GCHQILKRFSG-VITFAEVELNEA-RDFNRRI*CEFA---TCGP-ATTVVQRRDLOEN-FYRNWTEYRN GFCGSD-G
FREP48/FBN35    IYSS--CDDRIIKIGTYLQVDAF--TNS-MYV*ICSLD----FGQN-ATTVVQRRDGSVD-FYRNWTEYRN GFCGSD-G
FREP46/FBN36    LEHRLDQLPEQ--SGVYFMQPDPA-KNASFEV*IRDWT--NNHGFSGWLVQHRFNGSVD-FYRNWTEYRN GFCGSD-G
FREP9/FBN37     SCVDILMAGMR-QSGVYVYLRGT-TWFLKVI*CEQE-----IADG-GWIVIQRRFDGSLN-FYRNWTEYRN GFCGSD-G
FREP42/FBN38    ---S--CSEAPK--IGIVSLKLPN--NVS-TEVI*ICDAE----YDKG-GWIVIQRRFNGSVD-FYRNWTEYRN GFCGSD-G
FREP40/FBN39    RSCREIPDGMSGEELIYPSAGPAGGE-ELEV*ICDQFED----G-GWIVIQRRF-DGFVNFYRNWTEYRN GFCGSD-G
FREP44/FBN50    --AS--CRDVPKRVSGITRIDPDHP-FNEPMTV*ICDQ-----YEGG-GWIVIQRRFDGSLN-FYRNWTEYRN GFCGSD-G
FREP1/FBN**     KLPRICSQIERMRTAGTANQPGD--GGLYLIAEAEHHP*ICDQ-----YEGG-GWIVIQRRFDGSLN-FYRNWTEYRN GFCGSD-G
FREP11/FBN**    VYRS--CKETP--TIGVYMIQPEKP-FKEPITV*ICQE-----YESG-GWIVIQRRFDGSLN-FYRNWTEYRN GFCGSD-G
FREP12/FBN**    VYKS--CNAAPFASCGVHKIQPEKP-FKEPITV*ICQE-----YESG-GWIVIQRRFDGSLN-FYRNWTEYRN GFCGSD-G
FREP49/FBN**    SYKS--CSDVPPNSPSGVYKLRGE--FGSQKAI*CNMS----YAGG-GWIVIQRRFNGSVD-FYRNWTEYRN GFCGSD-G
FREP36/FBN**    IYQS--CDDVTGP--PGLYRVRDGN--DVETHY*ICQE-----LLGG-GWIVIQRRTSGRIN-FYRNWTEYRN GFCGSD-G
FREP32/FBN**    ISTRSCKEEPSNRIGELIQPT--QNDEPFLG*CEC-----TAFCGGWLVQHRMDGSVD-FYRNWTEYRN RFGSVD-G
FREP25/FBN**    IAARSCKQVQSERPKWFIQPA--ADSEPF*LGCAQ-----TAFCGGWLVQHRMDGSVD-FYRNWTEYRN GFCGSD-G
FREP20/FBN**    ISFRSCKENPSKRSKYLQIPS--KNDEPFLG*CEC-----TAFCGGWLVQHRMDGSVD-FYRNWTEYRN GFCGSD-G
FREP7/FBN**     VSFRSCKGNPSKRSKYLQIPA--ETDEPFLG*CEC-----TAYCGGWLVQHRMDGSVD-FYRNWTEYRN GFCGSD-G
FREP6/FBN**     -----MILQILT--ENDQEPFLG*CEC-----TAYCGGWLVQHRMDGSVD-FYRNWTEYRN GFCGSD-G
FREP41/FBN**    -----EEPSKQSGKYLQIPT--ENDEPFG*CDQ-----TTFCGGWLVQHRFNGSLN-FYRNWTEYRN RFGSVD-G
FREP47/FBN**    -VAPIGRSRLCFLAPTDLSGR---PELAAPSC*TEP---TVT-----REDNSL-HQR-----SID-G
FREP31/FBN**    MRKGRFQKSVFQISMMMMMT---PGSFAWKRI*STS---TTTAFCGGWLVQHRMDGSVD-FYRNWTEYRN GFCGSD-G
FREP37/FBN**    ISSRSCKAAGQEQSGKFLIQPT--EHDEPFLG*CVQ-----YSGGNLIIQHRNRRLEVDYRNWTEYRN GFCNVE-E
FREP38/FBN**    ISSRSCKAAGQEQSGKFLIQPT--EHDEPFLG*CVQ-----TNGCGWLVQHRNRRWLD-FYRNWTEYRN GFCGSD-E
FREP17/FBN**    ISTRSCKEEPSNRIGELIQPT--QNDEPFLG*CEC-----TAFCGGWLVQHRMDGSVD-FYRNWTEYRN GFCGSD-G
FREP4/FBN**     ISSRSCKEEPSKESGKYLQIPT--EKDEPFLG*CEC-----TAFCGGWLVQHRMDGSVD-FYRNWTEYRN GFCGSD-G
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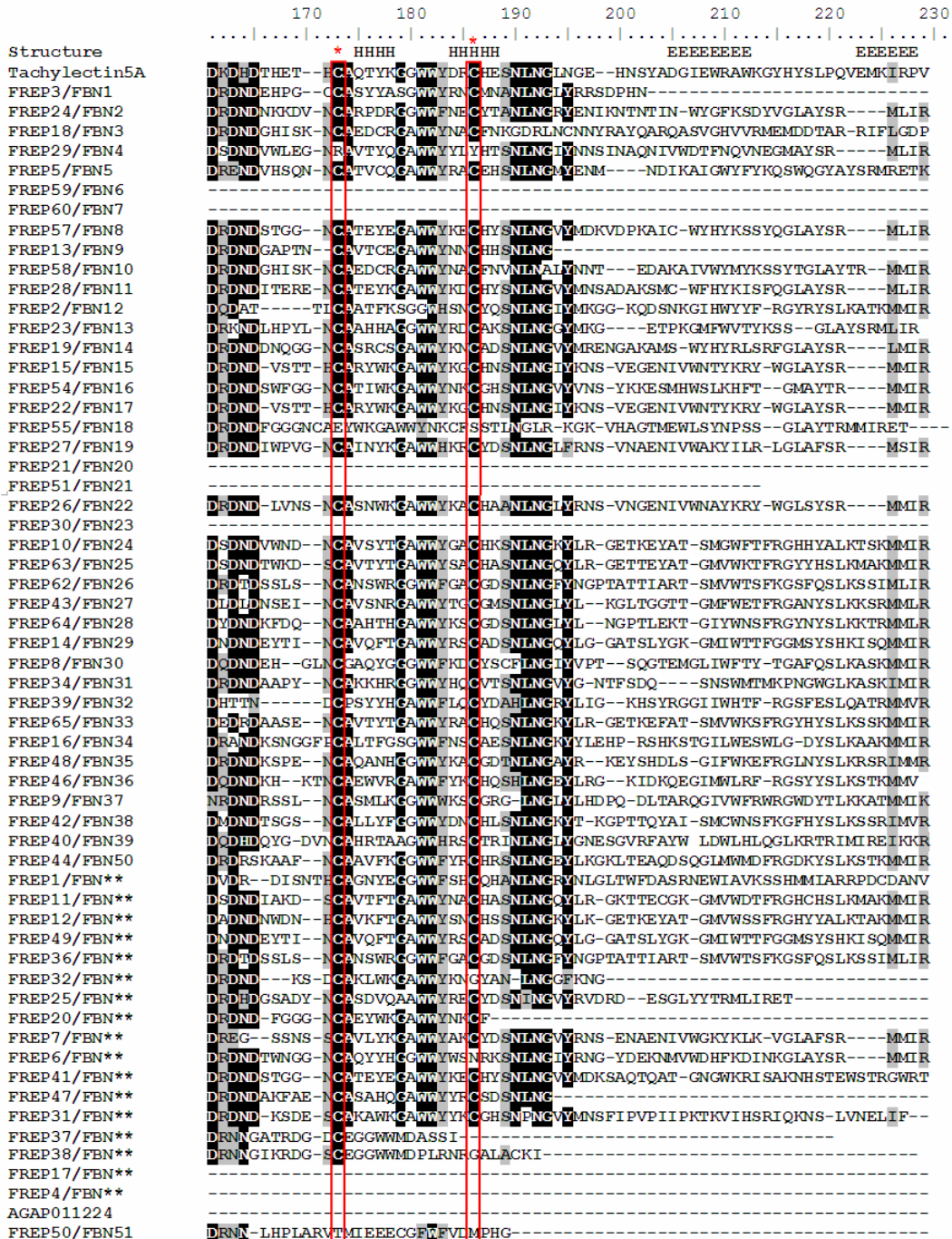



Fig. S1. Multiple sequence alignment of FBG domains of total 59 members of *FREP* gene family in *A. gambiae*. ClustalX program was used to construct the multiple sequence alignment. Sequences with over 60% identity were shaded with black box, and the PHD secondary structure is shown above with H indicating an α -helix and E representing a β sheet. The four red boxes with asterisks are indicating the four conserved cysteine residues.

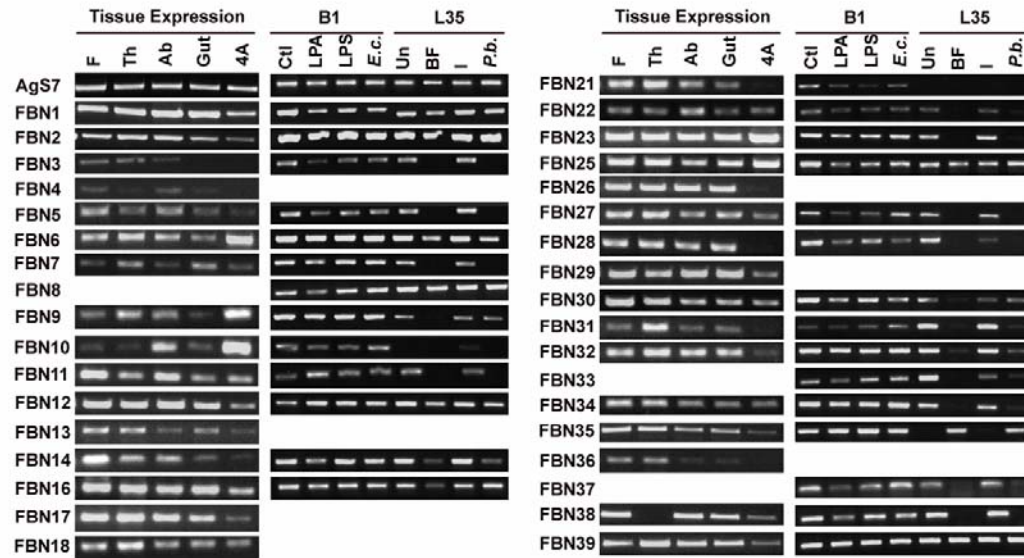


Fig. S2. RT-PCR analysis of *FREP* tissue specific expression in adult female *A. gambiae* Keele mosquitoes, and expression in cell line (B1) and *A. gambiae* L35 strain mosquitoes challenged with different elicitors. Agrose gels here were stained with ethidium bromide for visual presentation and with SYBR green for PCR product quantification were not shown here. F: total female mosquitoes; Th: Thorax; Ab: abdomen; 4A: *A. gambiae* cell line Sua4A; Ctl: PBS treated control; LPA: Alpha-lipoic acid; LPS: Lipopolysaccharide; *E.c.*: *E. coli* infected cells; Un: uninfected control mosquitoes; BF: non-infected human blood fed mosquitoes; I: control mosquitoes fed with human blood; *P.b.*: *P. berghei* infected mosquitoes. This figure represents one of three biological replicates.

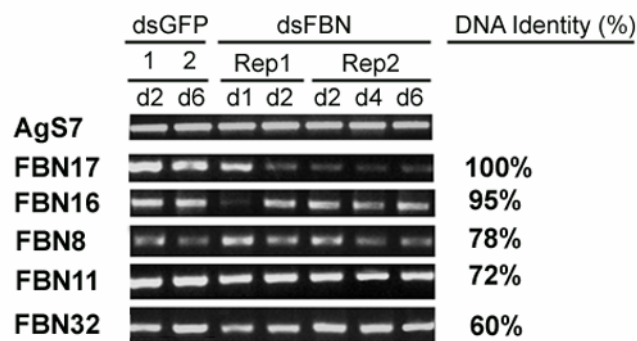


Fig. S3. Verification of RNAi gene-silencing efficiency with RT-PCR. *FREP* genes with high homology with targeted gene could be partially silenced, but the effect of gene silencing for non-targeted genes was not significant. dsGFP: control mosquitoes treated with *dsGFP* injection; dsFBN: gene silenced mosquitoes treated with *FBN17dsRNA* injection; d1-d6: days after *dsRNA* injection; Rep1 and Rep2 denotes for the biological replicate 1 and 2, respectively.