

## Supplementary Materials

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BtVg1: GKNGNLKKEVNGRTLTALNOVADQAGLFRNLLVQFSDRLSAYIQNAEFAQVHAEISGYESHIPSSHNNKNMPLQEFEBNLKKVWSSRNQNVSDWEENIKAVVSI 120
BtVg2: GWQNGNVKMDVNGRTLTALNOVADQAGLFRNFIQVQLSSRLSAYIQNAEIAQVHTELAGYESHIPSSQNNKNMPLQEFEBNLKKVWSSRNQNVSDWEENIKAVVSI 120
AaVg : SMMPNYEYVNVTSKTMALAELEDDQIGFTRYLVRKSRVYVAYVKQPEYAVFNERLHGVAKFYHDMFKQPMPEFKGRYHKSAKGYEETIPNNEINILKAWISL 120
AgVg : AMEPNKEVNVNVTKTMTALPDLEDDQIGFTHGYLVRKDHVYVAYVDRPTYAAFNEYLRGYRELSRFNKQPMPEFKGRYHKSAKGYEETIPNNEINILKAWISL 120
NvVg : GWKDGKPYTKIRSRTLALFNRQSKQIGVMEIRLTQVNGDLIRAKISLPRYTQIHTRLENGHDEIPQSQNMQTFELGKFEFKTKNGVVRDINDLVPTWENVLKSIWISL 120
BmVg : PQVQKQPMVEVTSRTLAHQEGPS--SGSAFKQFTLRVKSPPGRQAKLENPOHGNFNEQLD---PRELPVDKQFTENIDKVEEIEIDGSRVSDFTSVVPVGENLIKGLISN 115

BmVN1
BtVg1: QVDTQCONKKSHQLKVKVPYGVYKIMEDSVIGECETIYVSPLEITLTKPWLVEFPNFR--EGQFDIVKTTNYSKCEERSAYHFGITCLTNKK--FASNCMQFISRNINRV 237
BtVg2: QVDTQCONKKSHQLKVKVPYGVYKIMEDSVIGECETIYVSPLEITLTKPWLVEFPNFR--EGQFDIVKTTNYSKCEERSAYHFGITCLTNKK--FASNCMQFISRNINRV 237
AaVg : QVDTQCONKKSHQLKVKVPYGVYKIMEDSVIGECETIYVSPLEITLTKPWLVEFPNFR--EGQFDIVKTTNYSKCEERSAYHFGITCLTNKK--FASNCMQFISRNINRV 237
AgVg : QVDTQCONKKSHQLKVKVPYGVYKIMEDSVIGECETIYVSPLEITLTKPWLVEFPNFR--EGQFDIVKTTNYSKCEERSAYHFGITCLTNKK--FASNCMQFISRNINRV 238
NvVg : QVDTQCONKKSHQLKVKVPYGVYKIMEDSVIGECETIYVSPLEITLTKPWLVEFPNFR--EGQFDIVKTTNYSKCEERSAYHFGITCLTNKK--FASNCMQFISRNINRV 235
BmVg : QVDTQCONKKSHQLKVKVPYGVYKIMEDSVIGECETIYVSPLEITLTKPWLVEFPNFR--EGQFDIVKTTNYSKCEERSAYHFGITCLTNKK--FASNCMQFISRNINRV 227

BmVN2
BtVg1: VISGIVKYTIQSVSSTNKIVISEQYESQKGVVSVVNLILASFHQANGSPR-SVSRKINLVYDINAASP-----NAYAQHYNNNGASSSSSSSSSSSS 336
BtVg2: IISGIVKYTIQSVSSTNKIVISEQYESQKGVVSVVNLILASFHQANGSPR-MVSRKINLVYDINAASP-----NADAQHYNNNGASSSSSSSSSSSS 336
AaVg : YLTGIVWYNTIQSVSSTNKIVISEQYESQKGVVSVVNLILASFHQANGSPR-LKVFVVLVYSNMPSDK-----KNYVRPGNETSSSSSSSSSSSSSE 339
AgVg : YLTGIVWYNTIQSVSSTNKIVISEQYESQKGVVSVVNLILASFHQANGSPR-LKVFVVLVYSNMPSDK-----KNYVRPGNETSSSSSSSSSSSSSE 339
NvVg : IISGIVKYTIQSVSSTNKIVISEQYESQKGVVSVVNLILASFHQANGSPR-LKVFVVLVYSNMPSDK-----KNYVRPGNETSSSSSSSSSSSSSE 344
BmVg : LTG---KEGFYKAEITSTVHURFHVYKQKAEVYSHVHMLISVDQDSGAEWPRAGAMRPAQSILYSLSTKQMT-----KHYESSSSSSSSSSEHFN- 317

BmVN3

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**Figure S1. Identification of the BmVg ligand.** *Bemisia tabaci* predicted vitellogenin-A1-like (BtVg1, XP\_018912902.1), *B. tabaci* predicted vitellogenin (BtVg2, XP\_018897090.1), *Aedes aegypti* vitellogenin (AaVg, AAA99486.1), *Anopheles gambiae* vitellogenin (AgVg, AAF82131.1), *Nasonia vitripennis* vitellogenin (NvVg, XP\_001607388.1) and *Bombyx mori* vitellogenin (BmVg, NP\_001037309.1) were aligned using ClustalW in MEGA 8.0. The “KV” amino acids (red box), proven to deliver cargo into ovary of *B. tabaci*, were manually aligned to match the “QV” of the vitellogenin in *B. mori* (green box). The 317 aa N-terminal portion of silkworm BmVg (BmVg-N) was divided into three segments (BmVgN1, BmVgN2, and BmVgN3) and fused with mCherry to test the ability to deliver cargo into the oocyte of silkworm.

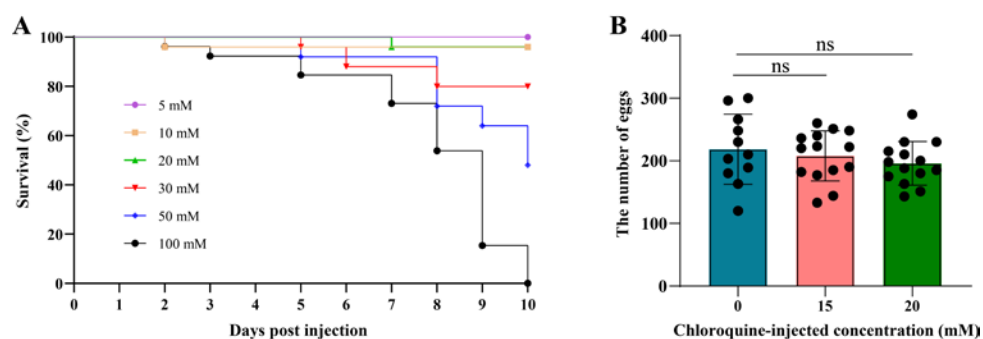
BmVg : MKLFLVLAAL-----AA-S-DRFSSQSQTGGQYTP-SFWQVCKYKYYEVRTLRLAHLOEGGSGSAKAQITLVKSPRLQKLENPHQGNFNQPDPREVLDLYCPTPN 112  
 TpVg : MMTFLVLAAL-----A-TAFCA-----SGDNWNHNDGQVWQVYVEEARTSALGDREWQVGLRRLVLAQSDRLRLRLA VRQRLQRLPEWNAAPAEPORP/PTDQR 109  
 CsVg : MKLFLVLAALAAAS--CANIKIKKEDKKGNSETYVTHSLDQCKVYIYVFNLSLEGGSSANTGHTLQLVRSQKLHKKLVVRHAAHKFNGERQAQDSLYKPEKSEH 118  
 SiVg : MKLFLVLAAL-----AV-SG-----NLS-EPQON-QWFWQTKCLYIYVFNHILARHOGCA-GTAR-GEIV-VKSP-RLQ-KLENPHQ-Q-H-Q-PNDMA-PKLYKETQNL 106  
 BmaVg : MKLFLVLAAL-----AA-S-DRFSSQSQTGGQYTP-SFWQVCKYKYYEVRTLRLAHLOEGGSGSAKAQITLVKSPRLQKLENPHQGNFNQPDPREVLDLYCPTPN 112  
 BaVg : MKLFLVLAAL-----LAALA--RSNND-QDNDEQSQWVKVGTLYIYVFNQITLALHOGCA-GTAR-GEIV-VKAP-RLQ-KLENPHQ-Q-H-Q-ORNEPVLKQKLPAPK 110  
 CmVg : MKLFLVLAAL-----AAV-TSH-----RSSQVDVNDQTYGWRVGTSYIYVFNFTVARLHOGCA-GTAR-KAH-VV-IHAD-RLQ-KLENPHQ-Q-H-Q-PGDRQVLDLYCPTPN 109  
 CcVg : MKLFLVLAAL-----AA-AAG-----QLDSTIEHQVQKVKGIYIYVFNHTLALHOGCA-GTAR-GEIV-VKSP-RLQ-KLENPHQ-Q-H-Q-LNNDKQFKE-NYCA-PKLD 105  
 LdVg : MKLFLVLAAL-----AV-S-PLTEPQPVHQSSWQVCKYKYYEVRTLRLAHLOEGGSGSAKAQITLVKSPRLQKLENPHQ-Q-H-Q-PNDMA-PKLYKETQNL 108  
 AyVg : MKLFLVLAAL-----AA-S-RRSDNNNPDSKN-SFWQVCKYKYYEVRTLRLAHLOEGGSGSAKAQITLVKSPRLQKLENPHQ-Q-H-Q-SYERD-PENLYCPTPN 108  
 AsVg : MKLFLVLAAL-----AA-S-RRSDNNNPDSKN-SFWQVCKYKYYEVRTLRLAHLOEGGSGSAKAQITLVKSPRLQKLENPHQ-Q-H-Q-SYERD-PENLYCPTPN 107  
 ApVg : MKLFLVLAAL-----AA-S-RRSDNNNPDSKN-SFWQVCKYKYYEVRTLRLAHLOEGGSGSAKAQITLVKSPRLQKLENPHQ-Q-H-Q-SYERD-PENLYCPTPN 108  
 SfVg : MKLFLVLAAL-----AV-SG-----NLS-EPQON-QWFWQTKCLYIYVFNHILARHOGCA-GTAR-GEIV-VKSP-RLQ-KLENPHQ-Q-H-Q-PNDMA-PKLYKETQNL 107  
 HaVg : MKLFLVLAAL-----AA-AAS-----PVVEN-AKWQVCKYKYYEVRTLRLAHLOEGGSGSAKAQITLVKSPRLQKLENPHQ-Q-H-Q-PNDMA-PKLYKETQNL 103  
 MaVg : MKLFLVLAAL-----AA-A-----ERLSGNQPEQSQWQVCKYKYYEVRTLRLAHLOEGGSGSAKAQITLVKSPRLQKLENPHQ-Q-H-Q-PNDMA-PKLYKETQNL 108  
 OfVg : MKLFLVLAAL-----AA-T-GR-----LSSSDVEALKQGWQVCKYKYYEVRTLRLAHLOEGGSGSAKAQITLVKSPRLQKLENPHQ-Q-H-Q-PNDMA-PKLYKETQNL 109  
 MvVg : MKLFLVLAAL-----AA-A-SH-----HKRHDVDQQTQGWQVCKYKYYEVRTLRLAHLOEGGSGSAKAQITLVKSPRLQKLENPHQ-Q-H-Q-PNDMA-PKLYKETQNL 109  
 DdpVg : MKLFLVLAAL-----VV-SG-----QLS-----DUVVESPWQVCKYKYYEVRTLRLAHLOEGGSGSAKAQITLVKSPRLQKLENPHQ-Q-H-Q-PNDMA-PKLYKETQNL 107  
 SeVg : MKLFLVLAAL-----AV-SG-----NLS-EPQON-QWFWQTKCLYIYVFNHILARHOGCA-GTAR-GEIV-VKSP-RLQ-KLENPHQ-Q-H-Q-PNDMA-PKLYKETQNL 107  
 PxVg : MKLFLVLAAL-----VA-SG-----RLSSDNQSQEQTQGWQVCKYKYYEVRTLRLAHLOEGGSGSAKAQITLVKSPRLQKLENPHQ-Q-H-Q-PNDMA-PKLYKETQNL 111  
 ObVg : MKLFLVLAAL-----S-T-----QLSDNQPEGLSQWQVCKYKYYEVRTLRLAHLOEGGSGSAKAQITLVKSPRLQKLENPHQ-Q-H-Q-PNDMA-PKLYKETQNL 105  
 GmVg : MKLFLVLAAL-----AL-A-G-----RHGLANHNNDQSQWQVCKYKYYEVRTLRLAHLOEGGSGSAKAQITLVKSPRLQKLENPHQ-Q-H-Q-PNDMA-PKLYKETQNL 108  
 LoVg : MKLFLVLAAL-----AAV-TSH-----RSSQVDVNDQTYGWRVGTSYIYVFNFTVARLHOGCA-GTAR-KAH-VV-IHAD-RLQ-KLENPHQ-Q-H-Q-PGDRQVLDLYCPTPN 109  
 CpVg : MKLFLVLAAL-----AAV-TSH-----RSSQVDVNDQTYGWRVGTSYIYVFNFTVARLHOGCA-GTAR-KAH-VV-IHAD-RLQ-KLENPHQ-Q-H-Q-PGDRQVLDLYCPTPN 114  
 EeVg : MKLFLVLAAL-----AA-ALGD-----PKVEVSTNWDQWQVCKYKYYEVRTLRLAHLOEGGSGSAKAQITLVKSPRLQKLENPHQ-Q-H-Q-PNDMA-PKLYKETQNL 110  
 PmVg : MKLFLVLAAL-----VA-SG-----RLSSDNQSQEQTQGWQVCKYKYYEVRTLRLAHLOEGGSGSAKAQITLVKSPRLQKLENPHQ-Q-H-Q-PNDMA-PKLYKETQNL 107  
 MseVg : MKLFLVLAAL-----AV-SG-----RLS-EQGLDNQWQWQVCKYKYYEVRTLRLAHLOEGGSGSAKAQITLVKSPRLQKLENPHQ-Q-H-Q-PNDMA-PKLYKETQNL 107  
 NiVg : MKLFLVLAAL-----VA-SG-----RLKLN-SEG-ETSQWQVCKYKYYEVRTLRLAHLOEGGSGSAKAQITLVKSPRLQKLENPHQ-Q-H-Q-PNDMA-PKLYKETQNL 109

BmVg : VEIEIDGGRVLSIDFETS-POENIKGLLSALQDLSAHVIHDSQNDORQO-GEFKKEIDVTGCTIYTS-VASEWRRELEK-AN-EQDEVEVVKTYGCHHRVAYHFG 231  
 TpVg : TQORTEGGRVLE-RVPAD-AHAHENIKGLLSALQDLSAHVIHDSQNDORQO-GEFKKEIDVTGCTIYTS-VASEWRRELEK-AN-EQDEVEVVKTYGCHHRVAYHFG 215  
 CsVg : PEIEIDGGRVLSIDFETS-POENIKGLLSALQDLSAHVIHDSQNDORQO-GEFKKEIDVTGCTIYTS-VASEWRRELEK-AN-EQDEVEVVKTYGCHHRVAYHFG 234  
 SiVg : IEIEIDGGRVLSIDFETS-POENIKGLLSALQDLSAHVIHDSQNDORQO-GEFKKEIDVTGCTIYTS-VASEWRRELEK-AN-EQDEVEVVKTYGCHHRVAYHFG 225  
 BmaVg : VEIEIDGGRVLSIDFETS-POENIKGLLSALQDLSAHVIHDSQNDORQO-GEFKKEIDVTGCTIYTS-VASEWRRELEK-AN-EQDEVEVVKTYGCHHRVAYHFG 231  
 BaVg : PEIEIDGGRVLSIDFETS-POENIKGLLSALQDLSAHVIHDSQNDORQO-GEFKKEIDVTGCTIYTS-VASEWRRELEK-AN-EQDEVEVVKTYGCHHRVAYHFG 229  
 CmVg : PEIEIDGGRVLSIDFETS-POENIKGLLSALQDLSAHVIHDSQNDORQO-GEFKKEIDVTGCTIYTS-VASEWRRELEK-AN-EQDEVEVVKTYGCHHRVAYHFG 228  
 CcVg : PEIEIDGGRVLSIDFETS-POENIKGLLSALQDLSAHVIHDSQNDORQO-GEFKKEIDVTGCTIYTS-VASEWRRELEK-AN-EQDEVEVVKTYGCHHRVAYHFG 224  
 LdVg : PEIEIDGGRVLSIDFETS-POENIKGLLSALQDLSAHVIHDSQNDORQO-GEFKKEIDVTGCTIYTS-VASEWRRELEK-AN-EQDEVEVVKTYGCHHRVAYHFG 227  
 AyVg : PEIEIDGGRVLSIDFETS-POENIKGLLSALQDLSAHVIHDSQNDORQO-GEFKKEIDVTGCTIYTS-VASEWRRELEK-AN-EQDEVEVVKTYGCHHRVAYHFG 227  
 AsVg : PEIEIDGGRVLSIDFETS-POENIKGLLSALQDLSAHVIHDSQNDORQO-GEFKKEIDVTGCTIYTS-VASEWRRELEK-AN-EQDEVEVVKTYGCHHRVAYHFG 226  
 ApVg : PEIEIDGGRVLSIDFETS-POENIKGLLSALQDLSAHVIHDSQNDORQO-GEFKKEIDVTGCTIYTS-VASEWRRELEK-AN-EQDEVEVVKTYGCHHRVAYHFG 227  
 SfVg : PEIEIDGGRVLSIDFETS-POENIKGLLSALQDLSAHVIHDSQNDORQO-GEFKKEIDVTGCTIYTS-VASEWRRELEK-AN-EQDEVEVVKTYGCHHRVAYHFG 226  
 HaVg : PEIEIDGGRVLSIDFETS-POENIKGLLSALQDLSAHVIHDSQNDORQO-GEFKKEIDVTGCTIYTS-VASEWRRELEK-AN-EQDEVEVVKTYGCHHRVAYHFG 222  
 MaVg : PEIEIDGGRVLSIDFETS-POENIKGLLSALQDLSAHVIHDSQNDORQO-GEFKKEIDVTGCTIYTS-VASEWRRELEK-AN-EQDEVEVVKTYGCHHRVAYHFG 227  
 OfVg : PEIEIDGGRVLSIDFETS-POENIKGLLSALQDLSAHVIHDSQNDORQO-GEFKKEIDVTGCTIYTS-VASEWRRELEK-AN-EQDEVEVVKTYGCHHRVAYHFG 228  
 MvVg : PEIEIDGGRVLSIDFETS-POENIKGLLSALQDLSAHVIHDSQNDORQO-GEFKKEIDVTGCTIYTS-VASEWRRELEK-AN-EQDEVEVVKTYGCHHRVAYHFG 228  
 DdpVg : PEIEIDGGRVLSIDFETS-POENIKGLLSALQDLSAHVIHDSQNDORQO-GEFKKEIDVTGCTIYTS-VASEWRRELEK-AN-EQDEVEVVKTYGCHHRVAYHFG 226  
 SeVg : PEIEIDGGRVLSIDFETS-POENIKGLLSALQDLSAHVIHDSQNDORQO-GEFKKEIDVTGCTIYTS-VASEWRRELEK-AN-EQDEVEVVKTYGCHHRVAYHFG 226  
 PxVg : PEIEIDGGRVLSIDFETS-POENIKGLLSALQDLSAHVIHDSQNDORQO-GEFKKEIDVTGCTIYTS-VASEWRRELEK-AN-EQDEVEVVKTYGCHHRVAYHFG 230  
 ObVg : PEIEIDGGRVLSIDFETS-POENIKGLLSALQDLSAHVIHDSQNDORQO-GEFKKEIDVTGCTIYTS-VASEWRRELEK-AN-EQDEVEVVKTYGCHHRVAYHFG 224  
 GmVg : PEIEIDGGRVLSIDFETS-POENIKGLLSALQDLSAHVIHDSQNDORQO-GEFKKEIDVTGCTIYTS-VASEWRRELEK-AN-EQDEVEVVKTYGCHHRVAYHFG 228  
 LoVg : PEIEIDGGRVLSIDFETS-POENIKGLLSALQDLSAHVIHDSQNDORQO-GEFKKEIDVTGCTIYTS-VASEWRRELEK-AN-EQDEVEVVKTYGCHHRVAYHFG 234  
 CpVg : PEIEIDGGRVLSIDFETS-POENIKGLLSALQDLSAHVIHDSQNDORQO-GEFKKEIDVTGCTIYTS-VASEWRRELEK-AN-EQDEVEVVKTYGCHHRVAYHFG 228  
 EeVg : PEIEIDGGRVLSIDFETS-POENIKGLLSALQDLSAHVIHDSQNDORQO-GEFKKEIDVTGCTIYTS-VASEWRRELEK-AN-EQDEVEVVKTYGCHHRVAYHFG 225  
 PmVg : PEIEIDGGRVLSIDFETS-POENIKGLLSALQDLSAHVIHDSQNDORQO-GEFKKEIDVTGCTIYTS-VASEWRRELEK-AN-EQDEVEVVKTYGCHHRVAYHFG 229  
 MseVg : PEIEIDGGRVLSIDFETS-POENIKGLLSALQDLSAHVIHDSQNDORQO-GEFKKEIDVTGCTIYTS-VASEWRRELEK-AN-EQDEVEVVKTYGCHHRVAYHFG 226  
 NiVg : PEIEIDGGRVLSIDFETS-POENIKGLLSALQDLSAHVIHDSQNDORQO-GEFKKEIDVTGCTIYTS-VASEWRRELEK-AN-EQDEVEVVKTYGCHHRVAYHFG 228

BmVg : VPVCAWTGTAHKTQQLIGRATYRRLTGKE-GLIYAETISVH-HEHLYGQKARVYHVE-ELI-VQDQ-SGA-PRAGAM-PAQS-LIS-ST-Q-TKHYE-SSSSSSS 342  
 TpVg : A-----YPRAWNRRHG-EDLVHOSHTFARYIIS-RNATVQSACA-KVVA-PAHVAHGARDGNVY-VEVR-OLVAVSP-SAP-EQLPSDA-DAGS-LT-TAR----- 307  
 CsVg : VPVCAWTGTAHKTQQLIGRATYRRLTGKE-GLIYAETISVH-HEHLYGQKARVYHVE-ELI-VQDQ-SGA-PRAGAM-PAQS-LIS-ST-Q-TKHYE-SSSSSSS 345  
 SiVg : VPVCAWTGTAHKTQQLIGRATYRRLTGKE-GLIYAETISVH-HEHLYGQKARVYHVE-ELI-VQDQ-SGA-PRAGAM-PAQS-LIS-ST-Q-TKHYE-SSSSSSS 336  
 BmaVg : VPVCAWTGTAHKTQQLIGRATYRRLTGKE-GLIYAETISVH-HEHLYGQKARVYHVE-ELI-VQDQ-SGA-PRAGAM-PAQS-LIS-ST-Q-TKHYE-SSSSSSS 342  
 BaVg : VPVCAWTGTAHKTQQLIGRATYRRLTGKE-GLIYAETISVH-HEHLYGQKARVYHVE-ELI-VQDQ-SGA-PRAGAM-PAQS-LIS-ST-Q-TKHYE-SSSSSSS 338  
 CmVg : VPVCAWTGTAHKTQQLIGRATYRRLTGKE-GLIYAETISVH-HEHLYGQKARVYHVE-ELI-VQDQ-SGA-PRAGAM-PAQS-LIS-ST-Q-TKHYE-SSSSSSS 339  
 CcVg : VPVCAWTGTAHKTQQLIGRATYRRLTGKE-GLIYAETISVH-HEHLYGQKARVYHVE-ELI-VQDQ-SGA-PRAGAM-PAQS-LIS-ST-Q-TKHYE-SSSSSSS 334  
 LdVg : VPVCAWTGTAHKTQQLIGRATYRRLTGKE-GLIYAETISVH-HEHLYGQKARVYHVE-ELI-VQDQ-SGA-PRAGAM-PAQS-LIS-ST-Q-TKHYE-SSSSSSS 337  
 AyVg : VPVCAWTGTAHKTQQLIGRATYRRLTGKE-GLIYAETISVH-HEHLYGQKARVYHVE-ELI-VQDQ-SGA-PRAGAM-PAQS-LIS-ST-Q-TKHYE-SSSSSSS 337  
 AsVg : VPVCAWTGTAHKTQQLIGRATYRRLTGKE-GLIYAETISVH-HEHLYGQKARVYHVE-ELI-VQDQ-SGA-PRAGAM-PAQS-LIS-ST-Q-TKHYE-SSSSSSS 335  
 ApVg : VPVCAWTGTAHKTQQLIGRATYRRLTGKE-GLIYAETISVH-HEHLYGQKARVYHVE-ELI-VQDQ-SGA-PRAGAM-PAQS-LIS-ST-Q-TKHYE-SSSSSSS 337  
 SfVg : VPVCAWTGTAHKTQQLIGRATYRRLTGKE-GLIYAETISVH-HEHLYGQKARVYHVE-ELI-VQDQ-SGA-PRAGAM-PAQS-LIS-ST-Q-TKHYE-SSSSSSS 337  
 HaVg : VPVCAWTGTAHKTQQLIGRATYRRLTGKE-GLIYAETISVH-HEHLYGQKARVYHVE-ELI-VQDQ-SGA-PRAGAM-PAQS-LIS-ST-Q-TKHYE-SSSSSSS 318  
 MaVg : VPVCAWTGTAHKTQQLIGRATYRRLTGKE-GLIYAETISVH-HEHLYGQKARVYHVE-ELI-VQDQ-SGA-PRAGAM-PAQS-LIS-ST-Q-TKHYE-SSSSSSS 338  
 OfVg : VPVCAWTGTAHKTQQLIGRATYRRLTGKE-GLIYAETISVH-HEHLYGQKARVYHVE-ELI-VQDQ-SGA-PRAGAM-PAQS-LIS-ST-Q-TKHYE-SSSSSSS 339  
 MvVg : VPVCAWTGTAHKTQQLIGRATYRRLTGKE-GLIYAETISVH-HEHLYGQKARVYHVE-ELI-VQDQ-SGA-PRAGAM-PAQS-LIS-ST-Q-TKHYE-SSSSSSS 339  
 DdpVg : VPVCAWTGTAHKTQQLIGRATYRRLTGKE-GLIYAETISVH-HEHLYGQKARVYHVE-ELI-VQDQ-SGA-PRAGAM-PAQS-LIS-ST-Q-TKHYE-SSSSSSS 337  
 SeVg : VPVCAWTGTAHKTQQLIGRATYRRLTGKE-GLIYAETISVH-HEHLYGQKARVYHVE-ELI-VQDQ-SGA-PRAGAM-PAQS-LIS-ST-Q-TKHYE-SSSSSSS 337  
 PxVg : VPVCAWTGTAHKTQQLIGRATYRRLTGKE-GLIYAETISVH-HEHLYGQKARVYHVE-ELI-VQDQ-SGA-PRAGAM-PAQS-LIS-ST-Q-TKHYE-SSSSSSS 341  
 ObVg : VPVCAWTGTAHKTQQLIGRATYRRLTGKE-GLIYAETISVH-HEHLYGQKARVYHVE-ELI-VQDQ-SGA-PRAGAM-PAQS-LIS-ST-Q-TKHYE-SSSSSSS 335  
 GmVg : VPVCAWTGTAHKTQQLIGRATYRRLTGKE-GLIYAETISVH-HEHLYGQKARVYHVE-ELI-VQDQ-SGA-PRAGAM-PAQS-LIS-ST-Q-TKHYE-SSSSSSS 338  
 LoVg : VPVCAWTGTAHKTQQLIGRATYRRLTGKE-GLIYAETISVH-HEHLYGQKARVYHVE-ELI-VQDQ-SGA-PRAGAM-PAQS-LIS-ST-Q-TKHYE-SSSSSSS 339  
 CpVg : VPVCAWTGTAHKTQQLIGRATYRRLTGKE-GLIYAETISVH-HEHLYGQKARVYHVE-ELI-VQDQ-SGA-PRAGAM-PAQS-LIS-ST-Q-TKHYE-SSSSSSS 344  
 EeVg : VPVCAWTGTAHKTQQLIGRATYRRLTGKE-GLIYAETISVH-HEHLYGQKARVYHVE-ELI-VQDQ-SGA-PRAGAM-PAQS-LIS-ST-Q-TKHYE-SSSSSSS 336  
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 MseVg : VPVCAWTGTAHKTQQLIGRATYRRLTGKE-GLIYAETISVH-HEHLYGQKARVYHVE-ELI-VQDQ-SGA-PRAGAM-PAQS-LIS-ST-Q-TKHYE-SSSSSSS 337  
 NiVg : VPVCAWTGTAHKTQQLIGRATYRRLTGKE-GLIYAETISVH-HEHLYGQKARVYHVE-ELI-VQDQ-SGA-PRAGAM-PAQS-LIS-ST-Q-TKHYE-SSSSSSS 339

**Figure S2.** Alignment of the amino acid sequences of vitellogenin N-terminal in Lepidoptera. Multiple alignment was performed by using ClustalW in MEGA 8.0 software. Amino acid sequence alignment between *B. mori* (BmVg, NP\_001037309.1), *Thitarodes pui* (TpVg, AWJ95280.1), *Conopomorpha sinensis* (CsVg, AXM43802.1), *Spodoptera litura* (SiVg, ABU68426.1), *Bombyx mandarina* (BmaVg, BAB32642.2), *Bicyclus*

*anyana* (BaVg, XP\_023941468.1), *Cnaphalocrocis medinalis* (CmVg, AEM75020.1), *Corcyra cephalonica* (CcVg, AHZ89334.1), *Lymantria dispar* (LdVg, AAC02818.1), *Antheraea yamamai* (AyVg, BAF45319.1), *Actias selene* (AsVg, ABP63663.1), *Antheraea pernyi* (ApVg, BAB16412.1), *Spodoptera frugiperda* (SfVg, UAJ21054.1 ), *Helicoverpa armigera* (HaVg, XP\_021195458.2), *Manduca sexta* (MsVg, XP\_030021772.1), *Eumeta japonica* (OfVg, GBP26713.1), *Ostrinia furnacalis* (OfVg, QIH04838.1), *Maruca vitrata* (MvVg, AXY55008.1), *Danaus plexippus plexippus* (DppVg, OWR44310.1 ), *Spodoptera exigua* (SeVg, AOH73254.1 ), *Papilio xuthus* (PxVg, KPJ04900.1), *Operophtera brumata* (ObVg, KOB78233.1), *Grapholita molesta* (GmVg, WGM49048.1), *Leucinodes orbonalis* (LoVg, WGJ61535.1), *Cydia pomonella* (CpVg, WES10828.1 ), *Ephestia elutella* (EeVg, WDY35013.1 ), *Papilio machaon* (PmVg, XP\_014366052.2 ), *Mythimna separata* (MseVg, AHG29547.1) and *Nymphalis io* (NiVg, XP\_050356948.1). Identical and similar residues are highlighted in black and grey, respectively. The amino acids of BmOTP, proven to deliver cargo into ovary into *B. mori*, were aligned to match the conserved region of vitellogenin in Lepidoptera (red box).



**Figure S3. The effect of chloroquine on silkworm.** A: The survival of chloroquine-injected females. At the 2<sup>nd</sup> day of pupal stage, different concentrations of chloroquine were injected into the hemolymph of females and the survival rate is calculated (n=30). B: The number of eggs was evaluated, after chloroquine-injected females pupae emerged and hybridized with wild-type male moths.

### Table S1. Oligonucleotide primers

Primers	Primer sequences (5'-3')
<b>For mCherry vector</b>	
>NLS-F	CCTGGT GCCGCGCGGCAGCCATATGCCAAAGAAGAAGCGGAAGGTCGGATCCGGTGGTG
>mCherry-F	AGGTCGGATCCGGTGGTGGAGGAAGCGGTGGAGGCGGGAGCATGGTGAGCAAGGGCGAG
>mCherry-R	CGTGGTCTTTATAGTCAAGCTTCTTGTACAGCTCGTCCATGCC
>FLAG-R1	GCTTGACTATAAGGACCACGACGGAGACTACAAGGATCATGATATTGATTACA AAGACG
>FLAG-R2	GCCGGCCTTTTTCTGTGGCCGCCGGCCTTTTCTTATCGTCATCGTCTTTGTAATCAATAT
>NLS-R	TGGTGGTGGTGGTGGTGCTCGAGCTTTTTCTTTTTTGCCCTGGCCGGCCTTTTTTCGTGGC
>DmP2C-F	AAGAAGAAGCGGAAGGTCGGATCGAATCTGCAGCAGCAGCGC
>DmP2C-R	ACCGCTTCCTCCACCACCGGATCCGTTCTTAACCTCCTCGCT
>BmQV-F	AAGAAGAAGCGGAAGGTCGGATCGCAGGGACTTTTCAGGAAAATGGAAACTGATGTG
>BmQV-R	ACCGCTTCCTCCACCACCGGATCCACATCAGTTTCCATTTTCCTGAAAAGTCCCTG
>BmVN1-F	AAGAAGAAGCGGAAGGTCGGATCGCCTTGGCAGGTTGGCAAAC
>BmVN1-R	ACCGCTTCCTCCACCACCGGATCCGTCGTAGTTGTTTTGAGAGT
>BmVN2-F	AAGAAGAAGCGGAAGGTCGGATCGTCAGTTCCTGTCCCCCAAG
>BmVN2-R	ACCGCTTCCTCCACCACCGGATCCTTCTGAAGCAACAGGAGAT
>BmVN3-F	AAGAAGAAGCGGAAGGTCGGATCGGGCGATTGTGAGACGCTGT
>BmVN3-R	ACCGCTTCCTCCACCACCGGATCCATTGAATTCTGTGAGATTCCG
>BmVN2.1-F	AAGAAGAAGCGGAAGGTCGGATCGAGCGCTCTGCAACTTGACAC
>BmVN2.1-R	ACCGCTTCCTCCACCACCGGATCCTTCTGAAGCAACAGGAGAT
>BmOTP-F	AAGAAGAAGCGGAAGGTCGGATCGGACAGAGAACAGCAACAGGG
>BmOTP-R	ACCGCTTCCTCCACCACCGGATCCAACAGGAGATACCGTGTAC
<b>For Cas9 vector</b>	
Linker-F	TACACGGTATCTCCTGTTGGATCCGGTGGTGGAGGAAGCGGTGGAGGCGGGAGCGACAA
>Cas9-F	CGGTGGAGGCGGGAGCGACAAGAAGTACAGCATCGGCCT
>Cas9-R	TCCGTCGTGGTCCTTATAGTCAAGCTTGTCGCCTCCCAGCTGAGACAG
<b>For generating sgRNA targeting <i>BmBLOS2</i></b>	
> T1-F	AAGTGGCTGAAATGGTTGCTGGAC
> T1-R	TGCTGGACGTTTTAGAGCTAGAAA
> T2-F	AAGTGGAGTAGGGGTTGGATCTGC
> T2-R	GGAGTAGGGGTTGGATCTGCGTTT
>T7- T1-F	TATCGTGCTCTACAAGTGGCTGAAATGGTTGCTGGAC
>T7 -T2-F	TATCGTGCTCTACAAGTGGAGTAGGGGTTGGATCTGC
>gRNA-R	AACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTTTTTTGCGGC

**For mutant analysis of *BmBLOS2***

>primer-F       GTAGGTAGTGTTTGAAGGGACA

>primer-R       CACGAGATAGCAGGGCACA

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**Supplementary Sequences 1.** DNA sequences for expression of mCherry using the pET28a vector. Color coding is as follows:

Magenta = His tag

Green = nuclear localization signal (NLS)

Orange = (G<sub>4</sub>S)<sub>2</sub> linker

Red = mCherry

Purple = 3×FLAG tag

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atgggcagcagccatcatcatcatcatcacagcagcggcctggtgccgcggcagccatatgccaagaagaagcgggaaggtcGGATCCggtggtggagg
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accaccaccaccaccactga
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**Supplementary Sequences 2.** DNA sequences for expression of fusion proteins (the ovary targeting ligands and mCherry) using the pET28a vector. Color coding is as follows:

Magenta = His tag

Green = nuclear localization signal (NLS)

Orange = (G<sub>4</sub>S)<sub>2</sub> linker

Blue = the ovary targeting ligands

Red = mCherry

Purple = 3×FLAG tag

BmOTP-mCherry:

atgggcagcagc**catcatcatcatcatcac**agcagcggcctggtgccgcggcgagccatatg**ccaaagaagaagcgggaagg**tcGGATCGGACAGAG  
AACAGCAACAGGGACTTTTCAGGAAAATGGAAACTGATGTGACTGGCGATTGTGAGACGCTGTACAC  
GGTATCTCCTGTTGGATCC**ggtggtggaggaagcgggtggaggcgggagc**ATGGTGAGCAAGGGCGAGGAGGATAACAT  
GGCCATCATCAAGGAGTTCATGCGCTTCAAGGTGCACATGGAGGGCTCCGTGAACGGCCACGAGTTCG  
AGATCGAGGGCGAGGGCGAGGGCCGCCCCCTACGAGGGCACCCAGACCGCCAAGCTGAAGGTGACCA  
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CGTGATGAACTTCGAGGACGGCGGCGTGTTGACCGTGACCCAGGACTCCTCCCTGCAGGACGGCGAG  
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GTACAAGAAGCTT**gactataaggaccacgacggagactacaaggatcatgatattgattacaaagacgatgacgataagaaaaggccggcgccacga**  
**aaaaggccggccaggc**aaaaaaagctcgag**accaccaccaccacc**actga

BmQV:

CAGGGACTTTTCAGGAAAATGGAAACTGATGTG

BmVgN1:

CCTTGGCAGGTTGGCAAACAATACCGGTATGAGGTCACTTCTCGCACTTTGGCGCACTTGCAGGAGGG  
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CGTAAGCCTCGATTTTCAAACCTTCAGTTCCCTGTCCCCCAAGAGAATTTAATAAAGGGTCTTATCAGCGC  
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BmVgN2:

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CACAGAGTCATTACGACTCTCAAAACAACACTACGACAGAGAACAGCAACAGGGACTTTTCAGGAAAA  
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BmVgN3:

GGCGATTGTGAGACGCTGTACACGGTATCTCCTGTTGCTTCAGAATGGCGGCGAGAGCTTCCGAAGTT  
CGCTAACGAACAGGACCCTGTTGAGGTTACAAAGAGCACAAATTACGGTCACTGTCACCACCGGGTC  
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BmVgN2.1:

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GGTATCTCCTGTTGCTTCAGAA

DmP2C:

AATCTGCAGCAGCAGCGCCAGCACGGCAAGAACGGCAACCAGGACTACCAGGATCAGAGCAACGAA  
CAGAGGAAGAACCAGAGGACCAGCAGCGAGGAGGACTACAGCGAGGAGGTTAAGAAC

**Supplementary Sequences 3.** DNA sequences for expression of fusion protein BmOTP-Cas9 using the pET28a vector. Color coding is as follows:

Magenta = His tag

Green = nuclear localization signal (NLS)

Blue = the ovary targeting ligand BmOTP

Orange = (G<sub>4</sub>S)<sub>2</sub> linker

Dark red = Cas9

Purple = 3×FLAG tag

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atgggcagcagccatcatcatcatcatcatcagcagcggcgctggtgccgcgcggcgagccatatgcaaagaagaagcggaaggtcGGATCGGACAGAG
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