Supplementary Information

Interaction between *Borrelia miyamotoi* variable major proteins Vlp15/16 and Vlp18 with plasminogen and complement

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Supplementary Figure 1

Vlp15/16 protein of *B. miyamotoi* LB-2001 (WP_025444482.1)

HHHHHHGSGSGSGIEGRPYNGTGSNNGGGEDPQKVFLTSIANLGKGFLDVFVTFGDMVTGAFGIKAET
KKSDVGQYFTSIAETMESVKKKLQDEVAANGNYEKVKTVVEQFITGTLDKIAAGAKEAAKGATTDAAIGN
ATSTGHGATPANKESVVSLVKGMKTIVDVVLKDKGDASATKTGDDKKDIGKLFTDDAGKADAKEENIAK
AAASIGAVTGADVLQAIVQSNENPTADSTNGIEKAKDAAEIAIAPAVNNKKEIKEVSAKKDAIIAAGIALRA
MAKGGKFAANNDAKDADAVNGAAASAVGKTLSTLIIAVRNTVDSGLKKINEVLATVKQEDKSVEATKTA
EVTTSAQK

The deduced protein sequence of the pQE-30 Xa vector including the hexahistidine tag, the factor Xa splicing site, and the multiple cloning site is highlighted in light blue and the lysine residues in Vlp15/16 are indicated in green. The Vlp15/16 protein consists of 42 lysine residues. The *vlp15/16* gene lacks the N-terminal nucleotides encoding for 20 amino acid residues (MSKRKTLSAIIMTLFLIIGC).

Supplementary Figure 2

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                     * * *                               *         *                    *     **                   ***
                                        20                                40                                60                                80
Vlp15_16          MKKRKTLSAI IMTLFLIIGC NNGGGE-DPQ KVFLTSIANL GKGFLDVFVT FGDMVTGAFG IKAETKKSDV GQYFTSIAET MESVKKKLQD 89
WP_070401544.1|   MKKRKTLSAI IMTLFLIIGC NNGGGE-DPQ KVFLTSIANL GKGFLDVFVT FGDMVTGAFG IKAETKKSDV GQYFTSIAET MESVKKKLQD 89
gb|ALN43423.1|    -SKTKKVRQI KMTLFLIIGC NNGGGE-DPQ KVFLTSIANL GKGFLDVFVT FGDMVTGAFG IKAETKKSEV GQYFTSIAET MESVKKKLQD 88
WP_152305643.1|   MSKRKTLSAI IMTLFLIIGC NNGGGE-DPQ KVFLTSIANL GKGFLDVFVT FGDMVTGAFG IKAETKKSEV GQYFTSIAET MESVKKKLQD 89
WP_099528510.1|   MSKRKTLSAI IMTLFLIIGC NNGGGE-DPQ KVFLTSIANL GKGFLDVFVT FGDMVTGAFG IKAETKKSEV GQYFTSIAET MEFVKKKLQS 89
WP_025444482.1|   MSKRKTLSAI IMTLFLIIGC NNGGGE-DPQ KVFLTSIANL GKGFLDVFVT FGDMVTGAFG IKAETKKSEV GQYFTSIAET MESVKKKLQS 89
WP_152301127.1|   MSKRKTLSAI IMTLFLIIGC NNGGGE-DPQ KVFLTSIANL GKGFLDVFVT FGDMVTGAFG IKAETKKSDV GKYFTDIAET MESVKKKLQA 89
WP_132987283.1|   MSKRKKVSAI IMTLFLIIGC NNGGGE-DPQ KVFLTSIANL GKGFLDVFVT FGDMVTGAFG IKAETKKSDV GKYFTDIAET MESVKKKLQA 89
WP_152305642.1|   MSKRKKVSAI IMTLFLIIGC NNGGGE-DPQ KVFLTSIANL GKGFLDVFVT FGDMVTGAFG IKAETKKSDV GKYFTDIETT MKTVKDKLNN 89
WP_152305607.1|   MSKRKKVSAI IMTLFLIIGC NNGGGE-DPQ KVFLTSIANL GKGFLDVFVT FGDMVTGAFG IKAETKKSDV GKYFTDIETT MKAVKDKLNT 89
WP_099528608.1|   MSKRKKVSAI IMTLFLIIGC NNGGGEIEKR NEFLTSIANL GKGFLDVFVT FGDMVTGAFG IKAETKKSEI GQYFIDIEKT MISVKNKLNN 90
WP_025444452.1|   MKKRKTLSAI IMTLFLIIGC NNGGGE-DPQ KVFLTSIANL GKGFLDVFVT FGDMVTGAFG IKAETKKSDI GQYFIDIERT MTSVKNKLNT 89
WP_099591073.1|   MSKRKTLSAI IMTLFLIIGC NNGGGE-DPQ KVFLTSIANL GKGFLDVFVT FGDMVTGAFG IKAETKKSDV GKYFADIETT MKTVKDKLNT 89
WP_025444236.1|   MSKRKTLSAI IMTLFLIIGC NNGGGE-DPQ KVFLTSIANL GKGFLDVFVT FGDMVTGAFG IKAETKKSDV GKYFTDIETT MKAVKDKLNT 89
WP_099497170.1|   MKKRKTLSAI IMTLFLIIGC NNGGGE-DPQ KVFLTSIANL GKGFLDVFVT FGDMVTGAFG IKAETKKSDV GKYFTDIETT MKAVKDKLNT 89
WP_099591077.1|   MSKRKTLSAI IMTLFLIIGC NNGGGE-DPQ KVFLTSIANL GKGFLDVFVT FGDMVTGAFG IKAETKKSDV GKYFTDIEKT MTSVKNKLNT 89
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WP_070401545.1|   MKKRKTLSAI IMTLFLIIGC NNGGGE-DPQ KVFLTSIANL GKGFLDVFVT FGDMVTGAFG IKAETKKEDI GKYFADIEKT MTLVKEKLQA 89
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WP_099528607.1|   MSKRKTLSAI IMTLFLIIGC NNGGGE-DPQ KVFLTSIANL GKGFLDVFVT FGDMVTGAFG IKAETKKSDV GKYFTDIEKT MTSVKEKLQA 89
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WP_070401529.1|   MKKRKTLSAI IMTLFLIIGC NNGGGE-DPQ KVFLTSIANL GKGFLDVFVT FGDMISGAFG IKAETKKSDV GKYFADIEKT MTSVKNKLNT 89
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WP_152305643.1| EVAKNGNYLK IKEVVDKFIT ETLDKIAEGA KEAAKGATGD AAIGNAVK-G EDAAPA-EVS SVNALVRGIK EIVGVVLK-G KGDATATKTA 176
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WP_025444452.1| VVTENGNYPK VKEVVDQFIT GTLDKIAKGA KTAASGATDG ASIGEVVK-S NA-GTSVDAT SVNALVKGIK EIVDLVIKDG NGQTDKTKPV 177
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WP_133017146.1| EVVKNGNYEK VKTVVDQFIT GTLDKIAAGA KEAAKGATGE -AIGNATSAG HGASPA-DKD SVISLVKGIK TIVGVVLKDN EGNATATKTA 177
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WP_070401560.1| EVAANGNYEK VKTVVDQFIT GTLDKIAAGA KEASKGATTD IAIGNAVK-G EDAAPA-EVA SVNALVKGIK EIVGVVLKDA EGDAGATKTA 177
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WP_099568461.1| EVAANGNYEK VKTVVDKFIT ETLDKIASGA KEAAKGATTD VAIGNAKK-E EAAVAA-DTS SVNSLVKGIK AIVAVVLR-- EGKADATKTA 175
WP_070401529.1| VVAENSNYPK VQEVVNQFIT GTLDKIVAGA KKAASGATDG AVISGVVK-S DAAGNGPEAD SVKNLVVGIK EIVDLVIKEG DGQADKTKPV 178
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                 *  *    *         *  200    *     *                220                        240   *  *                       260 *    *     **
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WP_152301127.1|  ESEQKSIGKL FSSKK-DDD- -GTEAQAAAA SASIGAVSGA DILQAIAKSG E--A-TSEAK IETAKDAASI AAAK-VE-ES KSL--DVAKQ 255
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WP_099528608.1|  EAEKKSVGKL LGK---KDD- -ATEAVAAAA SASIGAVSGA DILQAIAKSG E--AANNDVE IEKAKNAAEI AAAKK-E-DT KEL--TAVQK 255
WP_025444452.1|  DDDKKNIGKL FGGKNSDANG GAEEKHVASA SASIGAVSGA DILKAIAAAN AD--AKKDGK VNEATDASSL ALAKGTSTDN EDQLGDSAKK 265
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WP_025444236.1|  DDDKKNIGKL FGAKN-EASK GAEDKHVAAA SASIGAVTGA DILKAIAAAN AD--AKKDGK VSEATDAAAL ALAKGTSTDN EDQLGDSAKK 265
WP_099497170.1|  DDDKKNIGKL FGAKN-EASK GAEDKHVAAA SASIGAVTGA DILKAIAAAN AD--AKKDGK VSEATDAAAL ALAKGTSTDN EDQLGDSAKK 265
WP_099591077.1|  DDSKKDIGKL FTATTDANR- -ADNAAAQAA AASIGAVSGA DILQAITKSK ENPNADGTEG IEKAEDAAEI AVAPAKD-NK KEIKD-GAKR 260
WP_133017146.1|  EEQQKSIGNL FADSAGKTD- -AKEENIAKA SASIGAVSGA DILQAIAQSK ENPAVDSTDG IEKAKDAADI AIAPAVA-GK KEIKEDSAKK 264
WP_152301126.1|  EEQQKSIGNL FADSAGKTD- -AKEENIAKA SASIGAVSGA DILQAIAQSK ENPAVDSTDG IEKAKDAADI AIAPAVA-GK KEIKEDSAKK 264
WP_070401517.1|  DDK-KDIGAL FIDNTGKAD- -AKEENIAKA AASIGAVTGA DILQAIAQSK ENPTANSTEG IEKATDAAEI AIAPAVA-NK KEIKEDSAKK 262
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WP_025444399.1|  DAEQKSIGKL LGKK---DD- -GTEAHAAAA SASIGAVSGA DILQAIAKSG E--AANNDVG IEQAKNAAEI AAAKK-E-DD KEFGIASAKK 258
WP_133017147.1|  EDDKKDIGKL FEK---KDS- -GTEAEAAKA NASIGAVTGA DILKAISKSG E--TADNSKN IEEAKDAASI ASAKKED-NK KEIKDE-AKK 259
WP_132987284.1|  EDDKKDIGKL FEK---KDS- -GTEAEAAKA NASIGAVTGA DILKAISKSG E--TADNSKN IEEAKDAASI ASAKKED-NK KEIKDE-AKK 259
WP_070401545.1|  EDDKKDIGKL FEK---KDS- -GTETEAAKA SASIGAVTGA DILQAIAKSG E--TADDSKN IEEAKDAASI ASAKKED-DK KEIKDE-AKK 259
WP_152301325.1|  DDQQKSIGKL FEK---KES- -GTEAEAAAA SASIGAVSGA DILQAIAKSS E--TADNNKN IEEASNAAEI AAVKKED-NK KEIKNAGAKK 259
WP_099528607.1|  DDQQKTIGKL FEK---KES- -GTEAEAAAA SATIGAVSGA DILQAIAKSS E--TADNNKN IEEASNAAEI AAVKKED-NK KEIKNAGAKK 259
WP_099528537.1|  EDDKKNIGKL FGAKNSDANG GAEDKHVAAA SASIGAVSGA DILQAIAAAN AD--AKKDGK VSEATDAAAL ALAKGTSTDN EDQLGDSAKK 266
WP_025444405.1|  DDQQKTIGKL FEK---KES- -GTEAEAAAA SATIGAVTGA DILQAIAKSS E--TADNNKN IEEASNAAEI AAVKKED-NK KEIKNAGAKK 259
WP_099528574.1|  DDDKKNIGKL FGGKNSDANG GAEEKHVASA SASIGAVSGA DILKAIAAAN AD--AKKDGK VNEATDASSL ALAKGTSTDN EDQLGDSAKK 265
WP_099498354.1|  DDQQKTIGKL FEK---KES- -GTEAEAAAA SATIGAVTGA DILQAIAKSS E--TADNNKN IEEASNAAEI AAVKKED-NK KEIKNAGAKK 259
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WP_099528606.1|  DEQQKSIGNL FADSAGKDD- -AKEENIAKA SASIGAVSGA DILQAIAQSK ENPAVDSTDG IEKAKDAAEI AIAPAVA-NK KEIKEASAKK 264
WP_025444237.1|  DEQQKSIGNL FADSAGKDD- -AKEENIAKA SASIGAVSGA DILQAIAQSK ENPAVDSTDG IEKAKDAAEI AIAPAVA-NK KEIKEASAKK 264
WP_070401543.1|  EEQQKTIGKL FAKKD-DDR- -AQEAEAAAA NASIGAVSGV DILQAIAKSG E--ISDNNKN IEEAKDAASI AAAKQTD-DK KEIKDEAAKK 261
WP_099528535.1|  DAEKKSVGKL LG-GK-DNG- -GTETQAAAA SASIGAITGA DILQAIASSE K--AAG-EPT IEQAKNAAEI AIAKKED-NK E--LNTA-KK 255
WP_157773731.1|  EDDKKDIGKL FEK---KDS- -GTEAEAAKA NASIGAVTGA DILKAISKSG E--TADNSKN IEEAKDAASI ASAKKED-NK KEIKDE-AKK 259
WP_025444401.1|  EDDKKDIGKL FEK---KDS- -GTEAEAAKA NASIGAVTGA DILKAISKSG E--TADNSKN IEEAKDAASI ASAKKED-NK KEIKDE-AKK 259
WP_099591080.1|  DDK-KDIGAL FIDNTGKDD- -AKEENIAKA VASIGAVTGA DVLRAIVQSN ENPTANSTDG IEKAKDAAEI AIAPAVA-NK KEIKEASAKK 263
WP_099528514.1|  DDK-KDIGAL FIDNTGKDD- -AKEENIAKA VASIGAVTGA DVLRAIVQSN ENPTANSTDG IEKAKDAAEI AIAPAVA-NK KEIKEASAKK 263
gb|ALU64349.1|   NTEQKSIGKL LGKKD--D-- -GTEAHAAAA NASIGAVTGV DILQAIAKSG E--AGTSEIK IEEAKNVAEI AAAKK-D-DD KEFGDTLKDK 258
WP_070401560.1|  EAEKKSIGKL FGTNA-AD-- -GTEAHGAAA SASIGAVSGA DILQAIAKTG E--AGSGEIE IAKAKNAAEI AVAKK-E-AA KELEVAEVQK 259
WP_070401542.1|  NTEQKSIGKL LGKKD--D-- -GTEAHAAAA NASIGAVTGV DILQAIAKSG E--AGTSEIK IEEAKNVAEI AAAKK-D-DD KEFGDTLKDK 258
WP_152305604.1|  DAEQKSIGKL FGKGA-QND- -GTEAEAAAA SASIGAVTGA DVLQAIASSD K--ADGNEVE IAKAKNAAEI AVAKVEQ-GK T--LDAVVKK 258
WP_099528616.1|  DTEKKSIGKL LGTNA-AD-- -GTEAQAAAA SASIGAVTGA DILQAIAKSD E--AANNDVG IDQAKNAAEI AAAKK-E-A- KEFKAD--QK 255
WP_025444483.1|  DDK-KDIGNL FADDAGKAE- -AKEENIAKA VASIGAVTGA DVLQAIVQSN ENPTANSTDG IEKAKDAAEI AIAPAVS-NK KEIKEASAKK 264
WP_133017188.1|  ESEQKSIGKL FSSKK-DDD- -GTEAQAAAA SASIGAVSGA DILQAIAKSG E--A-TSEAK IETAKDAASI AAAK-VE-ES KSL--DVAKQ 255
WP_025444400.1|  ESEQKSIGKL FSSKK-DDD- -GTEAQAAAA SASIGAVSGA DILQAIAKSG E--A-TSEAK IETAKDAASI AAAK-VE-ES KSL--DVAKQ 255
WP_099568461.1|  ESEQKSIGKL FSSKK-DDD- -GTEAQAAAA SASIGAVSGA DILQAIAKSG E--A-TSEAK IETAKDAASI AAAK-VE-ES KSL--DVAKQ 255
WP_070401529.1|  EDDKKKIGKL FGAKNS-ADS GAEDKHVAAA SASIGAVTGA DILKAIAAAN AD--AKKDGK VSEAQDAAAL ALAKGTSTDN EDQLGDLARK 265
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                              280     *  *        *  300               *    320              **    340 *   *      *       360 *
Vlp15_16         DAIIAAGIAL RAMAKGGKFA AN-NDAK--D ADAVNGAAAS AVGKTLSTLI IAVRNTVDSG LKKINEVLAT VKQEDKSVEA TKTAEVTASAQK--- 352
WP_070401544.1|  DAIIAAGIAL RAMAKGGKFA AN-NDAK--D ADAVNGAAAS AVGKTLSTLI IAVRNTVDSG LKKINEVLAT VKQEDKSVEA TKTAEVTASAQN--- 352
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WP_152305643.1|  DAVIAAGIAL RAMAKDGKFT AKNNEDK--S AHAVNGAAAS AVGKTLSPLV VAIRNTVDSG LRIVNEALAK VKQEDKSAEA TNTTESTTSAQN--- 345
WP_099528510.1|  DAVIAGGIAL RAMAKNGKFA AKNNEDK--S AHSVNGVAAS AVGKTLSTLI IAIRNTVDSG LKAINEVLAT VKQEDKSGES TNAAEVTTSAQK--- 348
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WP_152301127.1|  DAVIAAGIAL RAMAKDGKFT AKKDEEK--S AHAVNGAAAS AVGKTLSTLI IAIRDTVDSG LKTINETLAT VKQEDKSAEA TKTAESTASVKN--- 345
WP_132987283.1|  DAVIAAGIAL RAMAKDGKFT AKKDEEK--S AHAVNGAAAS AVGKTLSTLI IAIRDTVDSG LKTINETLAT VKQEDKSAEA TKTAESTASVKN--- 345
WP_152305642.1|  DAVIAAGIAL RAIAKDGKFA AN-NDAK--Y ANAVNGAAAN AVGKTLSTLI IAIRNTVDSG LKTINAALAT VKQEDKSSAA AGAIKTEKN-NNKEV 345
WP_152305607.1|  DAIIAAGIAL RAMAKDGKFI VKDTAEKKTE AESAKGVAAS AVGKTLSTLI IAIRDTVDSG LKKINEALAT VKQEDKSAEA TNTAESTAS---AQQ 357
WP_099528608.1|  DAVIAAGIAL RAIAKDGKFA AN-NDAK--Y ANAVNGAAAN AVGKTLSTLI IAIRNTVDSG LKTINAALAT VKQEDKSSAA AGAIKTEKN-NNKEV 346
WP_025444452.1|  DAIIAAGISL RAMAKDGKFV VKDTAENKTE AESAKGVAAS AVGKTLSTLI IAIRNTVDDG LKKINEVLAT VKQEDKSAEV TNTSEATAS--SVSN 358
WP_099591073.1|  DAIIAAGIAL RAMAKDGKFI VKDTAANKTE AESAKGVAAS EVGKTLSTLI IAIRNTVDSG LKTINEVLAT VKQEDRSAET ANTTELTAS---VQK 357
WP_025444236.1|  DAIIAAGIAL RAMAKDGKFI VKDTAEKKTE AESAKGVAAS AVGKTLSTLI IAIRDTVDSG LKKINEALAT VKQEDKSAEA TKTAESTAS---AQQ 357
WP_099497170.1|  DAIIAAGIAL RAMAKDGKFI VKDTAEKKTE AESAKGVAAS AVGKTLSTLI IAIRDTVDSG LKKINEALAT VKQEDKSAEA TKTAESTAS---AQQ 357
WP_099591077.1|  DAIIAAGIAL RAMSKNGKFS IKNNENE--A VTTINSAAAS AVNKTLSTLI IAIRNTVDSG LKKINEALAT VKQGDKSAEA TKTAESTASAQQ--- 350
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WP_152301126.1|  DAIIAAGIAL RAMAKGGKFA AN-NNAK--D ADAVNGVAAS AVGKILSTLI IAVRNTVDSG LKTINAALAT VNQEDKSAEV TNAAEVTASVKN--- 353
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WP_070401566.1|  DVVIAAGIAL RAMAKDGKFA AKSNEEK--S AHAVNGVAAS AVGKTLSTLI IAIRNTVDSG LKTINASLAT VKQEDKSSEA AGSIET-----EKKK 346
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WP_133017147.1|  DAVIAAGIAL RAMAKDGKFA AKSNEEK--S AHAVNGVAAS AVGKTLSTLI IAIRNTVDSG LRTINAALAT VKQEDKSSEV TKTEEVRTNVKS--- 349
WP_132987284.1|  DAVIAAGIAL RAMAKDGKFA AKSNEEK--S AHAVNGVAAS AVGKTLSTLI IAIRNTVDSG LRTINAALAT VKQEDKSSEV TKTEEVRTNVKS--- 349
WP_070401545.1|  DAVIAAGIAL RAMAKGGKFA AKSNEEK--S AHAVNGMAAS AVGKTLSTLI IAIRNTVDSG LKTINEVLAT VKQEDKSVEV TKTAEAT----S--- 345
WP_152301325.1|  DAVIAGGIAL RAMAKYGKFA AK-NEDK--S ADSVNGVAAS AVGKTLSTLI IAIRNTVDSG LRTINAALAT VKQEDKTSEA TNTAESTASVKN--- 348
WP_099528607.1|  DAVIAGGIAL RAMAKDGKFA AK-NEDK--S ADSVNGVAAS AVGKTLSTLI IAIRNTVDSG LKTINAALAT VKQEDKTSEA TNTAESTASVKN--- 348
WP_099528537.1|  DAIIAAGIAL RAMAKDGKFI VKDTAEKKTE AESAKGVAAS AVGKTLSTLI IAIRNTVDSG LKTINEVLAT VKQEDRSAET ANTTESTAS---VEK 358
WP_025444405.1|  DAVIAGGIAL RAMAKDGKFA AK-NEDK--S ADSVNGVAAS AVGKTLSTLI IAIRNTVDSG LKTINAALAT VKQEDKTSEA TNTAESTASVKN--- 348
WP_099528574.1|  DAIIAAGISL RAMAKDGKFV VKDTAENKTE AESAKGVAAS AVGKTLSTLI IAIRNTVDDG LKKINEVLAT VKQEDKSAEV TNTSEATAS--SVSN 358
WP_099498354.1|  DAVIAGGIAL RAMAKDGKFA AK-NEDK--S ADSVNGVAAS AVGKTLSTLI IAIRNTVDSG LKTINAALAT VKQEDKTSEA TNTAESTASVKN--- 348
WP_025444448.1|  DAIIAAGIAL RAMAKGGKFA AN-NNAK--D ADAVNGVAAS AVGKTLSTLI IAVRNTVDSG LKTINAALAT IKQEDKSAEV TNTAEVTASVQK--- 352
WP_099528606.1|  DAVIAAGIAL RAMAKDGKFA AK-NEEK--S AHAVNGAAAS AVGKTLSTLI IAIRNTVDSG LKKINEALAT VKQEDKSAEV INATESTS------- 349
WP_025444237.1|  DAVIAAGIAL RAMAKDGKFA AK-NEEK--S AHAVNGAAAS AVGKTLSTLI IAIRNTVDSG LKTINETLAT VKQEDKSAEA TNTAESTASVKK--- 353
WP_070401543.1|  DAVIAAGIAL RAMAKDGKFT AKNNEEK--S AHAVNGAAAS AVGKTLSTLI IAIRNTVDSG LKKINEALAT VKQEDKSARA TKTAEVTASVQN--- 351
WP_099528535.1|  DAVIAAGIAL RAMAKDGKFA AKSNEEK--S AHAVNGVAAS AVGKTLSTLI IAIRNTVDSG LRTINEALAT VKQEDKSSEV TKTEEVKTNVKS--- 345
WP_157773731.1|  DAVIAAGIAL RAMAKDGKFA VKSNEEK--S AHAVNGVAAS AVGKTLSTLI IAIRNTVDSG LRTINEALAT VKQEDKSSEV TKTEEVRTNVKS--- 349
WP_025444401.1|  DAVIAAGIAL RAMAKDGKFA VKSNEEK--S AHAVNGVAAS AVGKTLSTLI IAIRNTVDSG LRTINEALAT VKQEDKSSEV TKTEEVRTNVKS--- 349
WP_099591080.1|  DAVIAAGIAL RAMAKDGKFA AK-NEEK--S AHAVNGAAAS AVGKTLSTLI IAIRDTVDSG LRTINAALAT VKQEDKSAEV INATESTS------- 348
WP_099528514.1|  DAVIAAGIAL RAMAKDGKFA AK-NEEK--S AHAVNGAAAS AVGKTLSTLI IAIRDTVDSG LRTINAALAT VKQEDKSAEV INATESTS------- 348
gb|ALU64349.1|   DAVIAGGIAL RAMAKDGKFA AKN-DDK--S ANAVNGAAAS AVNKTLSSLI IAIRNTVDSG LKKINEALAT VKQEDKSAEA TKTAEATTSVQN--- 347
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WP_152305604.1|  DAVIAAGIAL RAMAKDGKLT AKTGEDK--S AHAVNGAAAS AVGKTLSTLI IAIRDTVDSG LRTINAALAT VKQEDKSAEV INA----TESTS--- 344
WP_099528616.1|  DAVIAAGVAL RAMAKDGKFT AKTGEEK--S AHAVNGAAAS AVGKTLSTLI IAIRDTVDSG LKTINEVLAT VKQEDKSEEV TKTAEATASVKK--- 345
WP_025444483.1|  DAVIAAGIAL RAMAKGGKFA AN-NNAK--D ADAVNGVAAS VVGKTLSTLI IAVRNTVDSG LKTINEVLST LKQEDKSAEV TKTAESTASVKNKEL 356
WP_133017188.1|  DAVIAAGIAL RAMAKDGKFT AKKDEEK--S AHAVNGAAAS AVGKTLSTLI IAIRDTVDSG LKKINEALAT VKQEDKSVEA TKTAESTASAQQ--- 345
WP_025444400.1|  DAVIAAGIAL RAMAKDGKFT AKKDEEK--S AHAVNGAAAS AVGKTLSTLI IAIRDTVDSG LKKINEALAT VKQEDKSAEA TKTAESTASAQQ--- 345
WP_099568461.1|  DAVIAAGIAL RAMAKDGKFT AKKDEEK--S AHAVNGAAAS AVGKTLSTLI IAIRDTVDSG LKKINEALAT VKQEDKSAEA TKTAESTASAQQ--- 345
WP_070401529.1|  DAIIAAGIAL RAMAKDGKFI VKDTAEKKTE AESAKGIAAS AVGKTLSTLI IAIRNTVDSG LKTINEALAT VKQEDRSAET ANTTEATAS---AQN 357
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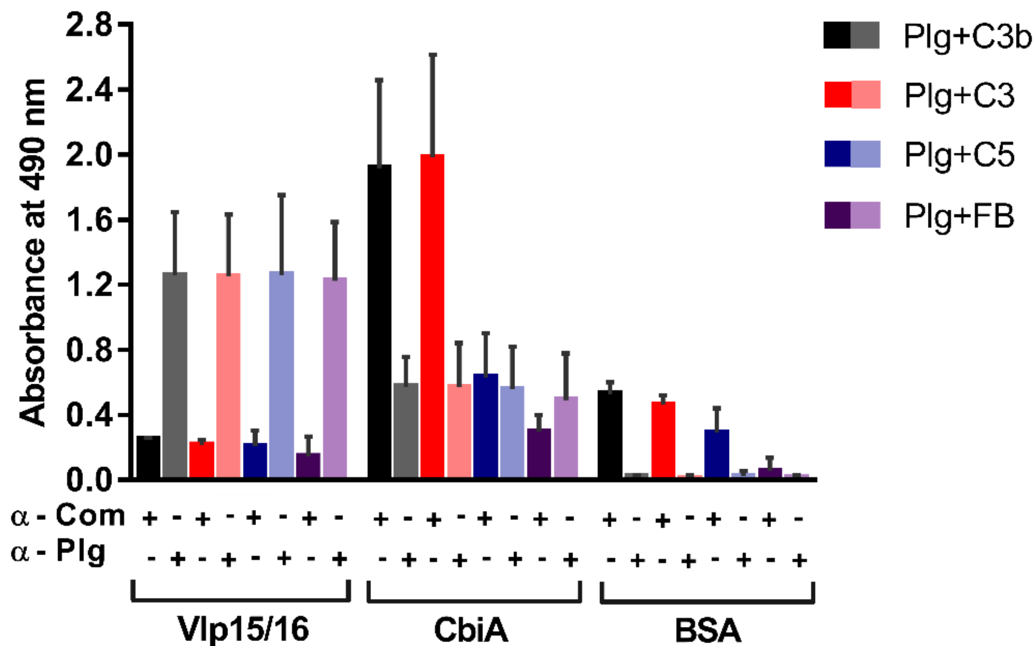
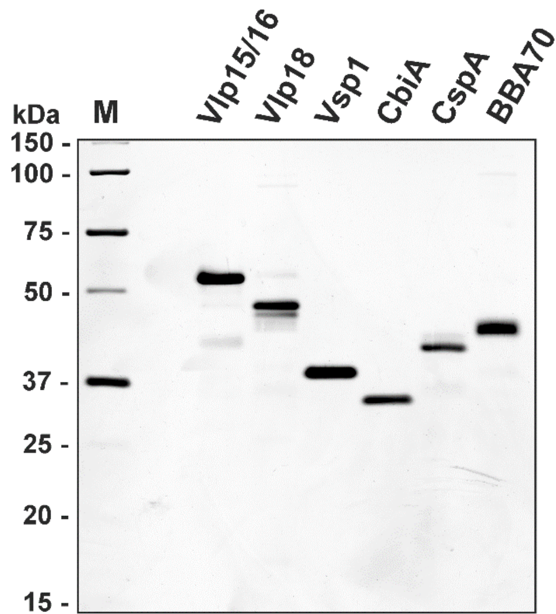
Deduced amino acid alignment of diverse Vlp orthologs (δ-subfamily) of *B. miyamotoi* (taxid:47466). Only full sequences have been used to created the alignment by employing the Constraint-based Multiple Alignment Tool of BLASTp (COBALT). Residues differing from the Vlp15/16 sequence of strain LB-2001 are boxed and the lysine residues are marked by an asterisk.

Supplementary Figure 3



Binding of complement components to plasminogen bound to Vlp15/16. To assess binding of complement components C3b, C3, C5 and Factor B (FB) to plasminogen bound to Vlp15/16, 96-well microtiter plates (MaxiSorp, Nunc) were coated with 0.1 µM of Vlp15/16, CbiA (additional control), and BSA (negative control), respectively, in 100 µl PBS at 4 °C overnight. Following blocking with 100 µl PBS containing 0.2% (w/v) gelatin. For each reaction mixtures, two duplicates were prepared to detect binding of plasminogen (Plg) or binding of complement components (Com) to plasminogen bound to Vlp15/16, CbiA, and BSA, respectively. In addition, four duplicates of each protein were coated to serve as primary antibody controls and where the ligands were omitted. The respective wells were subsequently washed and incubated with 0.1 µM plasminogen in 100 µl PBS for 1 h at room temperature. Afterwards, complement components C3b, C3, C5, and FB were added to the respective wells at a concentration of 0.1 µM in 100 µl PBS and incubated for 1 h at RT. The wells were then washed twice and binding of the ligands was detected by using a polyclonal antiserum (1:1,000) raised against human plasminogen or C3, C5, and FB, respectively. After incubation with a HRP-conjugated anti-goat antiserum (1:2,000), the plates were washed and developed with *o*-phenylenediamine (Sigma-Aldrich, Steinheim, Germany) for 8 min and the absorbance was measured at 490 nm (PowerWave HT, Bio-Tek Instruments, Winooski, VT, USA). Finally, the values of the antibody controls were subtracted from the values obtained from the reaction mixtures containing plasminogen and complement components. Data represent means and standard deviation of at least two independent experiments, each conducted in duplicate. For visualization of the data, GraphPad Prism 7 was conducted.

Supplementary Figure 4



Characterization of purified His_6-tagged proteins by silver staining. Purified Vlp15/16, Vlp18, Vsp1, CbiA, CspA, and BBA70 (1 µg each) were separated by a 10% Tris/Tricine-SDS-gel and stained with silver nitrate. The molecular weight markers (M) Precision Plus Protein Standards, Bio-Rad) are indicated on the left. The gel was scanned using a GS-900 Imaging Densitometer (Bio-Rad) and for image processing the Image Lab software, Version 6.1.0 (Bio-Rad) was applied. The figure shows the original version of the scanned gel. The general settings were as follows: Application: silver gel; Filter setting: Silver stain; Resolution: 63.5 * 63.5 microns.

Supplementary table 1. Oligonucleotides used in this study

Oligonucleotide	Sequence (5'-3')[a]	Use in this work
Vlp15/16_FP	GATATACATATGGCTGGATCCAATAATGGAGGAGGGGAAG	Recloning of *vlp15/16* into pQE-30Xa vector
Vlp15/16_RP	CTGCAGGTCGACTTATTACTTCTGTGCACTAGTTGTTAC	Recloning of *vlp15/16* into pQE-30Xa vector
Vlp18_FP	CAACAAACAGAGGATCCGTATCAGGAGGAGATAAACAAGGGGTTG	Recloning of *vlp18* into pQE-30Xa vector
Vlp18_RP	CTGCAGGTCGACTTATTACTCTGCTGTTTTTGAGTTTCTTG	Recloning of *vlp18* into pQE-30Xa vector
BmVsp1_Bam	CATATGGCTAGCTGTGGATCCGGGGGACCGGCACC	Recloning of *vsp1* into pQE-30Xa vector
BmVsp1_Sal	GTGGTGGTGGTGGTCGACCTATTATGAAGATTGACCAGCAG	Recloning of *vsp1* into pQE-30Xa vector

[a] Sequences of specific restriction endonuclease recognition sites are underlined