**Supporting information**

**Plasmids.** Features of pBAD30\_*kanR* and pYEYP2.2 are listed in Table S1 and S2. The DNA sequences of the plasmids are depicted below the corresponding tables.

**Table S1:** Features of pBAD30\_*kanR*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Name** | **Type** | **Start** | **Stop** | **Length (bp)** |
| **p15A** | Origin of Replication | 3,955 | 4,782 | 828 |
| ***kanR*** | Gene | 2,605 | 1,788 | 818 |
| **ara01** | Operator | 1,172 | 1,161 | 12 |
| **ara02** | Operator | 1,019 | 1,004 | 16 |
| ***araC*** | Gene | 974 | 96 | 879 |
| ***PBAD*** | Promoter | 1,248 | 1,276 | 29 |

pBAD30\_*kanR* DNA sequence

 1 10 20 30 40 50

 | | | | | |

 ATCGATGCATAATGTGCCTGTCAAATGGACGAAGCAGGGATTCTGCAAAC

 CCTATGCTACTCCGTCAAGCCGTCAATTGTCTGATTCGTTACCAATTATG

 ACAACTTGACGGCTACATCATTCACTTTTTCTTCACAACCGGCACGGAAC

 TCGCTCGGGCTGGCCCCGGTGCATTTTTTAAATACCCGCGAGAAATAGAG

 TTGATCGTCAAAACCAACATTGCGACCGACGGTGGCGATAGGCATCCGGG

 TGGTGCTCAAAAGCAGCTTCGCCTGGCTGATACGTTGGTCCTCGCGCCAG

 CTTAAGACGCTAATCCCTAACTGCTGGCGGAAAAGATGTGACAGACGCGA

 CGGCGACAAGCAAACATGCTGTGCGACGCTGGCGATATCAAAATTGCTGT

 CTGCCAGGTGATCGCTGATGTACTGACAAGCCTCGCGTACCCGATTATCC

 ATCGGTGGATGGAGCGACTCGTTAATCGCTTCCATGCGCCGCAGTAACAA

 TTGCTCAAGCAGATTTATCGCCAGCAGCTCCGAATAGCGCCCTTCCCCTT

 GCCCGGCGTTAATGATTTGCCCAAACAGGTCGCTGAAATGCGGCTGGTGC

 GCTTCATCCGGGCGAAAGAACCCCGTATTGGCAAATATTGACGGCCAGTT

 AAGCCATTCATGCCAGTAGGCGCGCGGACGAAAGTAAACCCACTGGTGAT

 ACCATTCGCGAGCCTCCGGATGACGACCGTAGTGATGAATCTCTCCTGGC

 GGGAACAGCAAAATATCACCCGGTCGGCAAACAAATTCTCGTCCCTGATT

 TTTCACCACCCCCTGACCGCGAATGGTGAGATTGAGAATATAACCTTTCA

 TTCCCAGCGGTCGGTCGATAAAAAAATCGAGATAACCGTTGGCCTCAATC

 GGCGTTAAACCCGCCACCAGATGGGCATTAAACGAGTATCCCGGCAGCAG

 GGGATCATTTTGCGCTTCAGCCATACTTTTCATACTCCCGCCATTCAGAG

 AAGAAACCAATTGTCCATATTGCATCAGACATTGCCGTCACTGCGTCTTT

 TACTGGCTCTTCTCGCTAACCAAACCGGTAACCCCGCTTATTAAAAGCAT

 TCTGTAACAAAGCGGGACCAAAGCCATGACAAAAACGCGTAACAAAAGTG

 TCTATAATCACGGCAGAAAAGTCCACATTGATTATTTGCACGGCGTCACA

 CTTTGCTATGCCATAGCATTTTTATCCATAAGATTAGCGGATCCTACCTG

 ACGCTTTTTATCGCAACTCTCTACTGTTTCTCCATACCCGTTTTTTTGGG

 CTAGCGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGTCGACCTGCAG

 GCATGCAAGCTTGGCTGTTTTGGCGGATGAGAGAAGATTTTCAGCCTGAT

 ACAGATTAAATCAGAACGCAGAAGCGGTCTGATAAAACAGAATTTGCCTG

 GCGGCAGTAGCGCGGTGGTCCCACCTGACCCCATGCCGAACTCAGAAGTG

 AAACGCCGTAGCGCCGATGGTAGTGTGGGGTCTCCCCATGCGAGAGTAGG

 GAACTGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCC

 TTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCCTGAGTAGGACAAA

 TCCGCCGGGAGCGGATTTGAACGTTGCGAAGCAACGGCCCGGAGGGTGGC

 GGGCAGGACGCCCGCCATAAACTGCCAGGCATCAAATTAAGCAGAACTCG

 AGCCATGGAACTTGGTCTGACAGTTACCAATGCTTAATCTTAGAAAAACT

 CATCGAGCATCAAATGAAACTGCAATTTATTCATATCAGGATTATCAATA

 CCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAG

 GCAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCCGACTC

 GTCCAACATCAATACAACCTATTAATTTCCCCTCGTCAAAAATAAGGTTA

 TCAAGTGAGAAATCACCATGAGTGACGACTGAATCCGGTGAGAATGGCAA

 AAGTTTATGCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTACGCT

 CGTCATCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGTGATTGC

 GCCTGAGCGAGACGAAATACGCGGTCGCTGTTAAAAGGACAATTACAAAC

 AGGAATCGAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATAT

 TTTCACCTGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCG

 GGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGATAAAATG

 CTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCA

 TCTCATCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAAC

 AACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGA

 TTGCCCGACATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCA

 TGTTGGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAATATGG

 CTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTG

 TCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG

 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACC

 ATTATTATCCTCGAGCCATGGCATATATACTTTAGATTGATTTACGCGCC

 CTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGA

 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCT

 TCCTTTCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGG

 GCTCCCTTTAGGGTTCCGATTTAGTGCTTTACGGCACCTCGACCCCAAAA

 AACTTGATTTGGGTGATGGTTCACGTAGTGGGCCATCGCCCTGATAGACG

 GTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGACTCTT

 GTTCCAAACTTGAACAACACTCAACCCTATCTCGGGCTATTCTTTTGATT

 TATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATT

 TAACAAAAATTTAACGCGAATTTTAACAAAATATTAACGTTTACAATTTA

 AAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCT

 TAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAA

 AGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAA

 CAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTA

 CCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAA

 TACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTG

 TAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTCAGGCAT

 TTGAGAAGCACACGGTCACACTGCTTCCGGTAGTCAATAAACCGGTAAAC

 CAGCAATAGACATAAGCGGCTATTTAACGACCCTGCCCTGAACCGACGAC

 CGGGTCGAATTTGCTTTCGAATTTCTGCCATTCATCCGCTTATTATCACT

 TATTCAGGCGTAGCACCAGGCGTTTAAGGGCACCAATAACTGCCTTAAAA

 AAATTACGCCCCGCCCTGCCACTCATCGCAGTACTGTTGTAATTCATTAA

 GCATTCTGCCGACATGGAAGCCATCACAGACGGCATGATGAACCTGAATC

 GCCAGCGGCATCAGCACCTTGTCGCCTTGCGTATAATATTTGCCGCTAGC

 GGAGTGTATACTGGCTTACTATGTTGGCACTGATGAGGGTGTCAGTGAAG

 TGCTTCATGTGGCAGGAGAAAAAAGGCTGCACCGGTGCGTCAGCAGAATA

 TGTGATACAGGATATATTCCGCTTCCTCGCTCACTGACTCGCTACGCTCG

 GTCGTTCGACTGCGGCGAGCGGAAATGGCTTACGAACGGGGCGGAGATTT

 CCTGGAAGATGCCAGGAAGATACTTAACAGGGAAGTGAGAGGGCCGCGGC

 AAAGCCGTTTTTCCATAGGCTCCGCCCCCCTGACAAGCATCACGAAATCT

 GACGCTCAAATCAGTGGTGGCGAAACCCGACAGGACTATAAAGATACCAG

 GCGTTTCCCCCTGGCGGCTCCCTCGTGCGCTCTCCTGTTCCTGCCTTTCG

 GTTTACCGGTGTCATTCCGCTGTTATGGCCGCGTTTGTCTCATTCCACGC

 CTGACACTCAGTTCCGGGTAGGCAGTTCGCTCCAAGCTGGACTGTATGCA

 CGAACCCCCCGTTCAGTCCGACCGCTGCGCCTTATCCGGTAACTATCGTC

 TTGAGTCCAACCCGGAAAGACATGCAAAAGCACCACTGGCAGCAGCCACT

 GGTAATTGATTTAGAGGAGTTAGTCTTGAAGTCATGCGCCGGTTAAGGCT

 AAACTGAAAGGACAAGTTTTGGTGACTGCGCTCCTCCAAGCCAGTTACCT

 CGGTTCAAAGAGTTGGTAGCTCAGAGAACCTTCGAAAAACCGCCCTGCAA

 GGCGGTTTTTTCGTTTTCAGAGCAAGAGATTACGCGCAGACCAAAACGAT

 CTCAAGAAGATCATCTTATTAATCAGATAAAATATTTGCTCATGAGCCCG

 AAGTGGCGAGCCCGATCTTCCCCATCGGTGATGTCGGCGATATAGGCGCC

 AGCAACCGCACCTGTGGCGCCGGTGATGCCGGCCACGATGCGTCCGGCGT

 AGAGGATCTGCTCATGTTTGACAGCTTATC

**Table S2:** Features of pYEYP2.2

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Name** | **Type** | **Start** | **Stop** | **Length (bp)** |
| ***kanR*** | Gene | 3,656 | 2,862 | 795 |
| **pSC101\*** | Origin of Replication | 1,028 | 2,723 | 1,696 |
| ***ypet*** | Gene | 50 | 766 | 717 |
| **SD** | Shine Dalgarno sequence | 36 | 41 | 6 |

pYEYP2.2 DNA sequence

 1 10 20 30 40 50

 | | | | | |

 CTCGAGGATCCCGGGTACCTGCAGCTAGCGTCGACAGGAGAAATTAAGCA

 TGAGCAAAGGTGAAGAACTGTTTACCGGTGTTGTTCCGATTCTGGTTGAA

 CTGGATGGTGATGTTAATGGCCACAAATTTTCAGTTAGCGGTGAAGGCGA

 AGGTGATGCAACCTATGGTAAACTGACCCTGAAACTGCTGTGTACCACCG

 GCAAACTGCCGGTTCCGTGGCCGACCCTGGTTACCACCCTGGGTTATGGT

 GTTCAGTGTTTTGCACGTTATCCGGATCATATGAAACAGCACGATTTTTT

 CAAAAGCGCAATGCCGGAAGGTTATGTTCAAGAACGTACCATCTTCTTCA

 AAGATGACGGCAACTATAAAACCCGTGCCGAAGTTAAATTTGAAGGTGAT

 ACCCTGGTGAATCGCATTGAACTGAAAGGCATCGATTTTAAAGAGGATGG

 TAATATCCTGGGCCACAAACTGGAATATAATTATAACAGCCACAACGTGT

 ATATCACCGCAGACAAACAGAAAAATGGCATCAAAGCCAACTTCAAAATC

 CGCCATAATATTGAAGATGGTGGTGTGCAGCTGGCAGATCATTATCAGCA

 GAATACCCCGATTGGTGATGGTCCGGTTCTGCTGCCGGATAATCATTATC

 TGAGCTATCAGAGCGCACTGTTTAAAGATCCGAATGAAAAACGTGATCAT

 ATGGTGCTGCTGGAATTTCTGACCGCAGCAGGTATTACCGAAGGTATGAA

 TGAACTGTATAAATGAGCGGCCGCTCTAGAGGCATCAAATAAAACGAAAG

 GCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTCGGTGAA

 CGCTCTCCTGAGTAGGACAAATCCGCCGCCCTAGACCTAGGCGTTCGGCT

 GCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAG

 AATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAG

 GCCAGGAACCGTAAAAAGGCCGCGTTGTCAGATCCTTCCGTATTTAGCCA

 GTATGTTCTCTAGTGTGGTTCGTTGTTTTTGCGTGAGCCATGAGAACGAA

 CCATTGAGATCATGCTTACTTTGCATGTCACTCAAAAATTTTGCCTCAAA

 ACTGGTGAGCTGAATTTTTGCAGTTAAAGCATCGTGTAGTGTTTTTCTTA

 GTCCGTTACGTAGGTAGGAATCTGATGTAATGGTTGTTGGTATTTTGTCA

 CCATTCATTTTTATCTGGTTGTTCTCAAGTTCGGTTACGAGATCCATTTG

 TCTATCTAGTTCAACTTGGAAAATCAACGTATCAGTCGGGCGGCCTCGCT

 TATCAACCACCAATTTCATATTGCTGTAAGTGTTTAAATCTTTACTTATT

 GGTTTCAAAACCCATTGGTTAAGCCTTTTAAACTCATGGTAGTTATTTTC

 AAGCATTAACATGAACTTAAATTCATCAAGGCTAATCTCTATATTTGCCT

 TGTGAGTTTTCTTTTGTGTTAGTTCTTTTAATAACCACTCATAAATCCTC

 ATAGAGTATTTGTTTTCAAAAGACTTAACATGTTCCAGATTATATTTTAT

 GAATTTTTTTAACTGGAAAAGATAAGGCAATATCTCTTCACTAAAAACTA

 ATTCTAATTTTTCGCTTGAGAACTTGGCATAGTTTGTCCACTGGAAAATC

 TCAAAGCCTTTAACCAAAGGATTCCTGATTTCCACAGTTCTCGTCATCAG

 CTCTCTGGTTGCTTTAGCTAATACACCATAAGCATTTTCCCTACTGATGT

 TCATCATCTGAGCGTATTGGTTATAAGTGAACGATACCGTCCGTTCTTTC

 CTTGTAGGGTTTTCAATCGTGGGGTTGAGTAGTGCCACACAGCATAAAAT

 TAGCTTGGTTTCATGCTCCGTTAAGTCATAGCGACTAATCGCTAGTTCAT

 TTGCTTTGAAAACAACTAATTCAGACATACATCTCAATTGGTCTAGGTGA

 TTTTAATCACTATACCAATTGAGATGGGCTAGTCAATGATAATTACTAGT

 CCTTTTCCCGGGAGATCTGGGTATCTGTAAATTCTGCTAGACCTTTGCTG

 GAAAACTTGTAAATTCTGCTAGACCCTCTGTAAATTCCGCTAGACCTTTG

 TGTGTTTTTTTTGTTTATATTCAAGTGGTTATAATTTATAGAATAAAGAA

 AGAATAAAAAAAGATAAAAAGAATAGATCCCAGCCCTGTGTATAACTCAC

 TACTTTAGTCAGTTCCGCAGTATTACAAAAGGATGTCGCAAACGCTGTTT

 GCTCCTCTACAAAACAGACCTTAAAACCCTAAAGGCTTAAGTAGCACCCT

 CGCAAGCTCGGGCAAATCGCTGAATATTCCTTTTGTCTCCGACCATCAGG

 CACCTGAGTCGCTGTCTTTTTCGTGACATTCAGTTCGCTGCGCTCACGGC

 TCTGGCAGTGAATGGGGGTAAATGGCACTACAGGCGCCTTTTATGGATTC

 ATGCAAGGAAACTACCCATAATACAAGAAAAGCCCGTCACGGGCTTCTCA

 GGGCGTTTTATGGCGGGTCTGCTATGTGGTGCTATCTGACTTTTTGCTGT

 TCAGCAGTTCCTGCCCTCTGATTTTCCAGTCTGACCACTTCGGATTATCC

 CGTGACAGGTCATTCAGACTGGCTAATGCACCCAGTAAGGCAGCGGTATC

 ATCAACAGGCTTACCCGTCTTACGACTAGTGCTTGGATTCTCACCAATAA

 AAAACGCCCGGCGGCAACCGAGCGTTCTGAACAAATCCAGATGGAGTTCT

 GAGGTCATTACTGGATCTATCAACAGGAGTCCAAGCGAGCTCTCGAACCC

 CAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCG

 CTGCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCC

 ATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCC

 TGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAAAA

 GCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCA

 CGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGT

 TCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGAC

 AAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTT

 GGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATT

 GCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAG

 GAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTT

 CAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGC

 CACGATAGCCGCGCTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGACAG

 GTCGGTCTTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACA

 CGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAAT

 AGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGTTC

 AATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCC

 TGCGCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAG

 GGCTTCCCAACCTTACCAGAGGGCGCCCCAGCTGGCAATTCCGACGTCTA

 AGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGA

 GGCCCTTTCGTCTTCAC

**Rhabdopeptide fragmentation patterns:** Figure S1 shows a comparison of fragmentation patterns from two known *X. nematophila* rhabdopeptides and two putative rhabdopeptide derivatives from *X. szentirmaii*. The characteristic multiple losses of *m/z* Δ113 that correspond to leucine or N-methylated valine and *m/z* Δ99 that corresponds to a loss of valine (Reimer *et. al.* 2013) are also present in the putative derivatives. The putative rhabdopeptides do not show a loss of phenylethylamine *m/z* Δ121 but a loss of *m/z* Δ220 which has not been elucidated yet. The retention times of the known rhabdopeptides and the putative rhabdopeptides are also similar (Rt 8.6-9.4 min).



**Figure S1.** a) MS2 spectra of rhabdopeptide 1 from *X. nematophila* (Rt: 8.8 min). b) MS2 spectra of rhabdopeptide 2 from *X. nematophila* (Rt: 9.4 min). c) MS2 spectra of putative rhabdopeptide from *X. szentirmaii* *m/z* 659.3 [M+H]+ (Rt: 8.6 min). c) MS2 spectra of putative rhabdopeptide from *X. szentirmaii* *m/z* 772.3 [M+H]+ (Rt: 9.1 min).

**References**

Reimer, D., Cowles, K. N., Proschak, A., Nollmann, F. I., Dowling, A. J., Kaiser, M., *et al.* (2013). Rhabdopeptides as insect-specific virulence factors from entomopathogenic bacteria. *Chembiochem* 14, 1991–1997. doi: 10.1002/cbic.201300205