

**Supplementary Table 1.** Oligonucleotides used for RNAi and RT-qPCR analysis in *S. frugiperda*. T<sub>m</sub> = 60°C

| Gene  | Primer orientation | Primer sequence (5'-3')                         | Purpose         | PCR efficiency (%) | Standard curve R <sup>2</sup> |
|-------|--------------------|-------------------------------------------------|-----------------|--------------------|-------------------------------|
| CAD   | Sense              | <u>GAGCTC</u> GTGTTGAACGACGGTGACAA <sup>a</sup> | dsRNA synthesis | NA                 | NA                            |
|       | Antisense          | <u>AAGCTT</u> GACCCTGTACTGCTCCTGTT <sup>b</sup> |                 |                    |                               |
| ABCC2 | Sense              | <u>GAGCTC</u> TGCTGGCAAGTCATCTCTGA              | dsRNA synthesis | NA                 | NA                            |
|       | Antisense          | <u>AAGCTT</u> CTTTTGGATCAGAGCGTCGG              |                 |                    |                               |
| ALP1  | Sense              | <u>GAGCTC</u> GACTCGCTCATTGTGGTCAC              | dsRNA synthesis | NA                 | NA                            |
|       | Antisense          | <u>AAGCTT</u> ACAAGGAGAGAGAGCAGCAG              |                 |                    |                               |
| APN   | Sense              | <u>GAGCTC</u> CTTGCTACGATGAACCTGGC              | dsRNA synthesis | NA                 | NA                            |
|       | Antisense          | <u>AAGCTT</u> CCAGTTTTCCATAGCACCGG              |                 |                    |                               |
| GFP   | Sense              | <u>GAGCTC</u> GCAGAGCGAGGTATGTAGGC <sup>a</sup> | dsRNA synthesis | NA                 | NA                            |
|       | Antisense          | <u>AAGCTT</u> CTGCCTCGGTGAGTTTTCTC <sup>b</sup> |                 |                    |                               |
| CAD   | Sense              | GAGAGCTGAGGGTCACTTGG                            | RT-qPCR         | 104.8              | 0.952                         |
|       | Antisense          | ATATCGGCCAGTTGTCGTTC                            |                 |                    |                               |
| ABCC2 | Sense              | GTCAGGGCGAGTACTTCGAG                            | RT-qPCR         | 102.9              | 0.921                         |
|       | Antisense          | CACGCTCCAATAAGACAGCA                            |                 |                    |                               |
| ALP1  | Sense              | CAAGGAGAGCGTGAAGAAGG                            | RT-qPCR         | 100.6              | 0.905                         |
|       | Antisense          | TCTGAGCGTTCACGCAATAC                            |                 |                    |                               |
| APN   | Sense              | CTATACGCGAGCGTTGAACA                            | RT-qPCR         | 106.4              | 0.922                         |
|       | Antisense          | TGAGATGCATACGGAGCAAG                            |                 |                    |                               |
| RPS3  | Sense              | ACAGAGTGTGCTCGGAGAGA                            | RT-qPCR         | 107.0              | 0.904                         |
|       | Antisense          | GGCAAGACCTCCAATGAGTT                            |                 |                    |                               |

<sup>a</sup> underlined sequence indicates *Sac*I endonuclease site, <sup>b</sup> underlined sequence indicates *Hind*III endonuclease site, NA-not applicable.