Anatomy of a pest control failure: Introgression of cytochrome P450 337B3 alleles from invasive

old-world bollworm into native corn earworm (Lepidoptera: Noctuidae).

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Abstract

The establishment of invasive species populations can threaten the ecological balance in naïve

habitats and impact agricultural production practices. *Helicoverpa armigera* (old-world

bollworm, OWBW) and *H. zea* (corn earworm, CEW) were geographically separated prior to the

2013 report of OWBW invasion into South America. Introgression of OWBW-specific

cytochrome P450 337B3 (CYP337B3) gene into CEW was repeatedly detected across South

America and the Caribbean. Two hybrids were documented from Texas in 2019. In this study,

screening insects collected in Olathe, Colorado, USA, where a failure of pyrethroids to control

CEW damage to conventional sweetcorn in 2023 detected 28.6% of insects with the OWBW-

specific CYP337B3 marker. Nucleotide sequencing of the CYP337B3 gene identified 73.1 and

26.9% of insects carried CYP337B3v2 and CYP337B3v6 alleles, respectively and 0.15 overall

frequency of CYP337B3 alleles. Based on prior data for distinct phylogeographic origins of

CYP337B3v2 and v6 alleles, our results indicate Olathe samples were derived from two different

introductions; An uncertain source of the v6 allele that was initially reported in West Africa and

possibly South American or Caribbean origin of the globally distributed v2 allele. One of the

1618 individuals screened also carried a ribosomal RNA internal transcribed spacer 1 (ITS1)

derived from OWBW. Local selection pressures at the Olathe location imposed by repeated

pyrethroid exposures are likely attributed to the prevalence of CYP337B3, where control

practices hasten the accumulation of phenotypic resistance by adaptive introgression. Pyrethroid

and other resistance factors carried by invasive OWBW may continue to impact CEW

management tactics across the Americas.

Keywords: tomato fruit worm, Noctuid pest, insecticide, pest management, selective advantage

Introduction

Invasive insect species can disrupt naïve ecosystems, impact the health of native species, and

introduce challenges to agricultural production (Venette and Hutchison 2021). An invasive

species undergoes an initial establishment phase with varying levels of adaptation to new

ecosystems and environmental conditions (Colautti et al. 2017). Ironically, invasive populations

typically undergo a genetic bottleneck due to a small number of founders, where this reduced

genetic diversity would reduce adaptive potential. Bottleneck effects can be alleviated through

admixture following multiple introduction events from genetically distinct source populations,

where increased genetic diversity in admixed populations can lead to higher fitness (Jaspers et al.

2021). Establishment can also be facilitated by interspecific hybridization with native species,

which can transfer locally adapted alleles to invasive populations through a mechanism referred

to as adaptive introgression (Arnold and Martin 2009, Jin et al. 2023). Conversely, native

populations may also acquire alleles with a selective advantage from an invasive species

(Burgarella et al. 2019)

The sister species *Helicoverpa armigera* (Hübner) (Lepidoptera: Noctuidae) and *H. zea*

(Boddie) (Lepidoptera: Noctuidae) are morphologically similar but distinguishable via

differences in male genitalia (Pouge 2004). The endemic range of *H. zea* spans the Americas,

wherein larvae cause feeding damage to multiple high-value crops (Reay-Jones 2019).

Helicoverpa armigera feeds on a broader range of host plants (Fitt 1989) and is historically

distributed across Africa, Asia, Europe, and Oceania (Kitching and Rawlins 1998). Invasion and

establishment of *H. armigera* into the Americas were first reported in Bahia, Goiás, and Mato

Grosso states in Brazil in 2013 using morphological characters and the histology of male

genitalia (Czepak et al. 2013). The presence of *H. armigera* was confirmed through analysis of

mitochondrial DNA (Tay et al. 2013). Later, *H. armigera* was reported in other regions of Brazil

and additional South American countries including Argentina, Colombia, Paraguay, Uruguay,

and Venezuela (Specht et al. 2013, Arnemann et al. 2016, Arnemann et al. 2019, Riaz et al.

2021). Evidence suggests that these *H. armigera* populations resulted from multiple independent

introductions (Tay et al. 2017, Arnemann et al. 2019, Tembrock et al. 2019). Laboratory

experiments produced viable progeny from reciprocal crosses and backcrosses between *H.*

armigera and *H. zea* (Laster and Sheng 1995), demonstrating incomplete barriers to

reproduction. Genomic analyses of *Helicoverpa* populations detected evidence of hybridization

between *H. armigera* and *H. zea* among field collections, and the introgression of *H. armigera*

alleles into *H. zea* (Valencia-Montoya et al. 2020). These findings include the characterization of

introgression of the *H. armigera* locus for a cytochrome P450, CYP337B3, associated with

insecticide resistance into the *H. zea* genomic background (Walsh et al. 2018).

High mobility of migratory *Helicoverpa* and its modeling predict a high probability of *H.*

armigera spreading and establishing in North America (Kriticos et al. 2015). *Helicoverpa*

armigera was initially detected outside South America in Puerto Rico and Florida in 2014 and

2015, respectively (Smith 2014, Hayden and Brambila 2015, USDA-APHIS 2024). *Helicoverpa*

armigera genome introgression was also predicted using genomic DNA sequence data from prior

studies (Anderson et al. 2018) to characterize four *H. zea* samples collected from New York in

2017 as hybrids (Trujillo et al. 2024). The pest surveillance program of the USDA Animal and

Plant Health Inspection Service (USDA APHIS) later detected several *H. armigera* adults near

the Chicago O'Hare International Airport between 2019 and 2022, however, no individuals were

detected in surrounding agricultural areas (USDA-APHIS 2024). Introgression between these

two species was shown by the detection of the invasive *H. armigera*-specific CYP337B3 allele

in two *H. zea* collected from a Texas population in 2019 (North et al. 2024). Our current study

focuses on a collection of *Helicoverpa* moths from Olathe, Colorado, where a failure to control

damage to conventional sweetcorn was reported following repeated pyrethroid insecticide

applications in 2023. Noctuid pest management effort involved initial applications of fenvalerate

and mid-season applications of methomyl, chlorantraniliprole, nucleopolyhedroviruses, and

Spinetoram. Evaluations of increased carrier volumes for aerial applications, maximum labeled

rate use per spray, maximum allowable frequency on repeat applications, and daily and every-

other-day spraying regimes were all undertaken, using the aforementioned active ingredients.

An additional active ingredient, methoxyfenozide, labeled for sweet corn and lepidopteran pests,

was trialed under the direction of the product's manufacturer to evaluate the potential for that

material to be used via fixed-wing aircraft, with reduced carrier volume applications. However

those trials proved ineffective at adding to the suppression of larval populations in the sweetcorn

fields.

Currently a limited number of genetic markers are available to screen invasive *H.*

armigera. Regardless, our analyses of species-specific genetic markers at ITS1 (Perera et al.

2015) and CYP337B3 loci (Joußen et al. 2012) detected *H. armigera* alleles in the Olathe

samples. DNA from *H. zea* collected in 2006 from Mississippi and Texas was used as the

reference. Our work constitutes the second report of *H. zea* carrying genes introgressed from *H.*

armigera within the USA. Pyrethroid resistance conferred by the movement of the CYP337B3

allele into the *H. zea* population has implications for the continued efficacy of insecticidal

control tactics used to manage this crop pest.

Materials and Methods

Insects were collected using *Helicoverpa zea* pheromone lures in bucket traps (Trece, Adair,

OK) at 53 locations near Olathe, CO, USA, during the summer of 2023 (**Supp. Table S1 and**

Supp. Fig. S1). A sweetcorn grower near these traps reported that repeated applications of

pyrethroid insecticide failed to control insect damage to the crop, and local scouting provided

visual identification of surviving larval *H. zea*. Initial screening of insects was carried out by

pooling a single leg from each adult male from each trap collection (or all the detached legs in a

collection bag) and extracting DNA using a modified squish buffer containing 10 mM Tris-HCl,

0.25 mM EDTA, and 0.25 mM NaCl (Perera et al. 2015). Two 3-mm stainless steel beads were

added to the tubes containing insect legs and homogenized using a bead beater (Biospec

Products, Bartlesville, OK) for 1 min at the highest speed. Homogenates were centrifuged briefly

and heated for 5 min in a heating block set to 100 °C, followed by centrifugation at 12,500 x g

for 10 min. DNA was also extracted from *H. zea* collected in 2006 from ten counties in Texas (*n*

= 200) and five counties in Mississippi (*n* = 100), and included in this study. For these, a small

piece of thoracic tissue from five insects was pooled into one tube to extract DNA using 150 μl

of squish buffer as described above.

Several strategies were used to identify invasive *H. armigera* in the samples and confirm

the presence of introgressed genes. First, the legs of insects were pooled by collection date to

perform ITS1 melt curve analysis that identifies *H. armigera* in bulk samples (Perera et al.

2015). Second, the *H. armigera* ITS1 gene was identified in a pooled set of samples, and the

DNA of individual insects from that pool was PCR amplified and sequenced to confirm the

presence of *H. armigera* ITS1 gene. Next, DNA from individual insects was PCR amplified with

primers specific for the *H. armigera* CYP337B3 gene followed by verification of hemizygous or

homozygous state of the CYP337B3 gene by PCR amplification of CYP337B1 and CYP337B2

genes using gene gene-specific primers. Lastly, longer PCR amplicons for CYP337B3 were

generated and sequenced to obtain nucleotide sequences for the differentiation of alleles.

The supernatant from each extract was transferred to a new tube and used in the melt

curve analysis (Perera et al. 2015). Briefly, 1 µl of each DNA pool was used in a 20 µl reaction

containing final concentrations of 1X Fast SYBR Master mix (Life Technologies Corporation,

Carlsbad, CA) 0.4 µM common forward primer 3373Ha_Hz_ITS1F for internal transcribed

spacer 1 (ITS1) of ribosomal RNA gene, *H. armigera*-specific reverse primer 3374Ha_ITS1R,

and 0.2 µM of *H. zea*-specific reverse primer 3377Hz_ITS1R (**Table 1**). DNA amplification and

melt curve analysis were performed in an ABI7500 Fast real-time PCR instrument (Applied

Biosystems, Foster City) with 95 °C initial denaturation for 30 seconds followed by 40 cycles of

denaturation at 95 °C for 5 seconds and annealing and extension at 60 °C for 30 seconds. A melt

curve step was performed after the amplification cycles to determine the presence of species-

specific amplicons. Agarose gel electrophoresis was performed to visualize the amplicons as a

verification step.

Full-length ITS1 was amplified from individual DNA using the primers 310-18S-rDNA-

2F and 312-5.8S-rDNA-R (**Table 1**) in reactions containing 1X ThermoPol buffer (12.5 mM

tricine, 42.5 mM KCl, 1.5 mM MgCl$_2$, 6% dextran; New England BioLabs, Ipswich, MA), 0.32

mM dNTP mix, 0.4 µM of each primer, 1 unit of *Taq* polymerase, and 10–100 ng of genomic

DNA in a 25 ml reaction. Amplification was performed in a PTC-200 thermal cycler (MJ

Research, BioRad, Hercules, CA) with a 30 s initial denaturation step at 95 °C, 35 cycles of 15 s

denaturation at 95 °C, 10 s annealing at 52 °C followed by a final extension of 5 min at 72 °C

(Perera et al. 2015). Amplicons were purified using AmPure XP magnetic beads according to

manufacturer instructions (Beckman Coulter, Brea, CA). Approximately 2 ng of amplicon from

82 separate pools was used as input for the Oxford Nanopore library construction reagent set

SQK-LSK114 and the native DNA barcode kit SQK-NDB-96. The resulting 82 indexed libraries

were sequenced in a FLO-MIN114.001 flow cell following the manufacturer's instructions

(Oxford Nanopore Technologies, New York, NY). Purified ITS1 DNA from sample 61e was

also cloned into TA cloning vector (Invitrogen, Carlsbad, CA) and transformed into DH5α

competent cells. Plasmid DNA prepared from 24 colonies were screened for the presence of *H.*

armigera- and *H. zea*-specific amplicons as described previously. Nucleotide sequences of

clones positive for ITS1 specific for each species were obtained by Sanger sequencing. DNA

Sequences were analyzed using CLC Genome WorkBench v22.02 (Qiagen, Redwood City, CA).

Phylogenetic analysis was performed using Molecular Evolutionary Genetic Analysis

(MEGA) 11 (Tamura et al. 2021) based on a multiple sequence alignment of the ITS1 region

from *H. armigera*, *H. zea,* and *H. assulta* (Guenée) (KT342378.1, KT343380.1, and

KT343379.1, respectively), and our Sanger read data for Olathe, CO, individual 61e.

Relationships were estimated using the Maximum Likelihood (ML) method (Nei and Kumar

2000, Beerli and Felsenstein 2001) applying the Kimura-2-Parameter model of sequence

evolution (Kimura 1980), that implemented a discrete Gamma shape parameter and node support

inferred from 10,000 bootstrap pseudo replications (Felsenstein 1985) of the aligned data. The

tree was rooted by the *Chloridea* (*Heliothis*) *virescens* (Fabricius) ITS1 (GenBank accession

KT342279.1)

A short fragment of the cytochrome P450 337B3 (CYP337B3) gene was amplified from

Olathe, CO, Texas and Mississippi samples using gene-specific primers 3713CYP337B3F and

3714CYP337B3R (**Table 1**) following the protocol described in Joußen et al. (2012). Briefly, the

25µl amplification reactions contained 1x standard Taq polymerase buffer (10 mM Tris-HCl, 50

mM KCl, pH 8.3) (New England Biolabs, Ipswich, MA), 2.5 mM MgCl$_2$, 0.4 μM dNTP mix, 0.4

μM of each primer, and 0.025 units of Taq polymerase. A thermal cycling profile with a 15 s

initial denaturation step at 95 °C, 35 cycles of 10 s denaturation at 95 °C, 10 s annealing at 53

°C, an extension of 30 sec at 72 °C followed by a final extension of 5 min at 72 °C.

Amplicons were resolved by 1.0% agarose gel electrophoresis to identify insects positive

for the CYP337B3 gene. For each insect identified as positive for CYP337B3, the full-length

CYP337B3 gene was then amplified with primers 4268CYP337B3F and 4269CYP337B1_B3R.

PCR amplification reaction and thermal cycling parameters were the same as those used for

amplification of the short fragment of CYP337B3, except for an annealing temperature of 50 °C

and extension time increased to 2.75 min. Amplicons were purified using AmPure XP beads

(Beckman Coulter) prior to use in sequencing reactions. Barcoded Oxford Nanopore libraries

were constructed and sequenced as described above for full-length CYP337B3 gene sequences

from 143 insects. CYP337B3 allele versions v1 through v8 (JQ995292.1, KJ636466.1,

KM675665.1, KM675666.1, KX958388.1, KX958389.1, KX958390.1, and KX958391.1,

respectively), CYP337B1v1, and CYP337B2v2 (JQ995291) were used as references for

subsequent alignment of Oxford Nanopore amplicon sequences. Evolutionary relationships of

the CYP337B3 alleles from Olathe, CO population and previously published CYP337B genes

was inferred in an ML tree constructed using MEGA 11 as described above.

The CYP337B1 and CYP337B2 genes were subsequently PCR amplified from all

CYP337B3 positive DNA samples in reactions with the primers for CYP337B1 and CYP337B2

genes using the primer pairs 3709CYP337B1F/3710CYP337B1R and

3711CYP337B2F/3712CYP337B2R, respectively (Table 1). PCR conditions for amplification of

CYP337B1 and CYP337B2 were identical to those used to amplify the CYP337B3 gene, and

resulting amplicons were resolved by electrophoresis in 1.0% agarose gels.

Results

Initial screening of 1618 insects collected from Olathe, CO in 2023 occurred within 82 pools by

PCR with *H. armigera*-specific ITS1 primers, where an amplicon was generated from a single

pool, pool 61. This indicated at least one *H. armigera* or a hybrid insect in pool 61 carried an *H.*

armigera ITS1 region sequence. In contrast, none were detected in the Texas or Mississippi

samples collected in 2006. Analysis of Oxford Nanopore sequence data from pool 61 also

identified ITS1 sequences closely resembling *H. armigera* ITS1. Screening of DNA from

individual insects from pool 61 identified one insect (61e) from which both *H. armigera*- and *H.*

zea-specific ITS1 amplicons were produced. Subsequent alignment found that the ribosomal

RNA (rRNA) gene sequence of insect 61e contained both *H. zea* rRNA repeats and a variant of

H. armigera rRNA repeats. Specifically, this was shown from Oxford Nanopore sequencing and

Sanger sequencing of cloned full-length ITS1 PCR products from 61e (**Fig. 1**) where

insertion/deletion (indel) mutations were shown in the *H. armigera* compared to *H. zea* ITS1

references sequences at positions 138-167, 401-403, and 431-433. Sequence data from sample

61e showed two variants, with indels in each identical to respective *H. armigera*- and H. zea

ITS1 reference sequences. However, there were 23 single nucleotide polymorphisms in the *H.*

armigera-like ITS1 sequence from sample 61e that were identical to the *H. zea* ITS1 reference.

Phylogenetic reconstruction of ITS1 region showed clustering of the two ITS region variants

from Olathe, CO individual 61e with corresponding *H. armigera* (KT342378.1) and *H. zea*

references (KT343380.1; **Fig. 2**). ITS1 nucleotide sequences from the Olathe, CO sample 61e

were deposited in the GenBank database under accession numbers PP456864.1

(Olathe_61e_Ha_ITS1), and PP456865.1 (Olathe_61e_Hz_ITS1).

Ribosomal RNA units in eukaryotes are arranged as head-to-tail tandem repeats at one or

more loci (Nei and Rooney 2005, Naidoo et al. 2013). One study indicated that the rRNA gene

copy number in animals is highly variable, ranging from 39 in the mosquito *Sabethes cyaneus*

(Fabricius) to 19,300 in the salamander *Amphiuma means* Garden in Smith (Prokopowich et al.

2003). Although precise copy number estimates are not available for noctuid moths, the silk

moth *Bombyx mori* (L.) has approximately 240 copies of rRNA genes (Prokopowich et al. 2003).

In the reference *H. zea* genome assembly, ilHelZeax1.1 (RefSeq assembly GCF_022581195.2;

(Stahlke et al. 2023), BioProject: PRJNA818699), one complete set of rRNA repeats and one

18S rRNA subunit are annotated at one end of the chromosome 30 (Accession: NC_061481.1;

XR_006986104.1, XR_006986099.1, and XR_006986099.1). Similarly, one rRNA repeat unit is

annotated at one end of chromosome 30 in *H. armigera* (Accession: OZ005796.1; BioProject:

PRJEB72184). Collapse of identical rRNA repeat units during the assembly of the genome may

have reduced the number of repeats in the final assembly.

Tandem CYP337B genes (paralogs) are located in chromosome 2 of the *H.* zea reference

genome (Stahlke et al. 2023) and the orthologous chromosome 15 of the *H. armigera* genome

(Zhang et al. 2022). Different alleles of CYP337B3 resulted from independent recombination

events that joined exon 1 of the CYP337B2 gene with exon 2 of the CYP337B1 gene (Joußen et

al. 2012, Rasool et al. 2014, Walsh et al. 2018) (**Supp. Fig. S2a**). Therefore, wild-type tandem

genes CYP337B1 and CYP337B2 and recombinant CYP337B3 genes in *H. zea* can occur in five

different genotypic configurations: homozygous *H. zea* CYP337B1/CYP337B2 genes (**Supp.**

Fig. S2b), heterozygous *H. armigera* and *H. zea* CYP337B1/CYP337B2 genes (**Supp. Fig. S2c**),

hemizygous *H. armigera* CYP337B1/CYP337B2 and CYP337B3 genes (**Supp. Fig. S2d**),

hemizygous *H. zea* CYP337B1/CYP337B2 and CYP337B3 genes (**Supp. Fig. S2e**), and

homozygous CYP337B3 genes (**Supp. Fig. S2f**). Insects homozygous or hemizygous for

introgressed CYP337B3 gene can be identified using gene-specific primers (Joußen et al. 2012).

PCR screening of insects from the Olathe, CO, collection from 2023 with primers

3713CYP337B3F and 3714CYP337B3R identified 243 of 850 (28.6%) as PCR positive and

carrying at least one copy of a CYP337B3 gene. Screening all 243 samples positive for the

CYP337B3 gene with primers for CYP337B1 and CYP337B2 genes indicated that 12 samples

were negative for both wild-type genes and homozygous for the CYP337B3 gene. Remaining

insects were hemizygous with wild-type CYP337B1/CYP337B2 genes on one chromosome and

CYP337B3 gene on the other chromosome. Therefore, the overall allele frequency of CYP337B3

in Olathe, CO, population of *H. zea* estimated from 12 homozygous and 231 hemizygous insects

was 0.15 (255/1700). The estimated frequencies of CYP337B3 homozygotes, hemizygotes, and

wild-type homozygotes in the Olathe, CO, population were 0.0225, 0.2550, and 0.7225,

respectively. The observed frequency of CYP337B3 homozygotes (0.0141) was less than the

expectation under the Hardy-Weinberg equilibrium whereas the observed frequency of

hemizygotes was higher.

None of the samples in our study from Texas or Mississippi collected in 2006 generated

amplicons for the *H. armigera* CYP337B3 gene. Oxford Nanopore sequencing and mapping of

individual reads from 113 full-length amplicons and 28 short amplicons from 141 CYP337B3

positive insects from Olathe, CO, predicted 100 and 99.3% nucleotide identity to the reference

genomic sequences of CYP337B3 alleles v2 (KJ636466.1) and v6 (KX 958389.1), respectively.

The subsequent consensus built from mapped reads (coverage > 200-fold) indicated that

CYP337B3 alleles v2 (accession#: PP461124) and v6 (accession#: PP461125) were present

among individuals from Olathe, CO. Approximately 26.9% of the analyzed samples (38 out of

141) had CYP337B3v6 while the remaining were from the CYP337B3v2 allele.

Four of the samples identified with the CYP337B3v2 allele also contained 5.3 to 7.6%

Oxford Nanopore sequence reads that mapped to the CYP337B3v6 allele. The percentages of

CYP337B3v6 reads identified in these four samples were significantly lower than the 50% reads

expected from a heterozygous genotype with v2 and v6 alleles. Whether these reads resulted

from cross-contamination of samples during collection in traps and shipping in bags as bulk

samples, errors in base calling of barcodes during Nanopore sequencing, or PCR bias is

unknown.

Alignment of the mRNA and genomic sequences of CYP337B1v1, CYP337B2v2, and

CYP337B3 alleles v1-v8, including two consensus CYP337B3v2 and CYP337B3v6 alleles

sequences found in the Olathe, CO, showed Olathe CYP337B3v2 genomic and mRNA

nucleotide sequences were nearly 100% identical to the reference CYP337B3v2 (KJ636466.1)

sequence (**Supp. Figs. S3 and S4**). Specifically, there was one synonymous T to C substitution

in the coding regions between the reference CYP337B3v2 allele (KJ636466.1) and the

CYP337B3v2 gene variant present in the Olathe, CO population (**Supp. Fig. S5**). Alignments

also showed that CYP337B3v6 genomic DNA and mRNA sequences were 99.4% and 98.9%

identical to the reference CYP337B3v6 (KX 958389.1) allele, respectively. There were 16 SNPs

between the reference CYP337B3v6 allele from Uganda (KX958389.1) and the v6 allele variant

found in Olathe, CO (**Supp. Fig. S6**), but only a single mutation, an A to T transversion at the

nucleotide position 232, resulted in a conservative isoleucine to leucine substitution at the amino

acid position 78 (I78L). The consensus ML tree indicated that predicted CYP337B3v2 and v6

alleles from the Olathe, CO population clustered with corresponding reference alleles with node

support from ≥ 99% of the bootstrap iterations (**Fig. 3**).

Discussion

The chimeric CYP337B3 gene associated with the functional cause of pyrethroid resistance in *H.*

armigera evolved from an unequal crossover between paralogs CYP337B1 and CYP337B2 and

had not evolved natively in *H. armigera* (Joußen et al. 2012, Rasool et al. 2014). The *H.*

armigera CYP337B3 gene confers resistance to class II pyrethroid insecticides, including

cypermethrin, deltamethrin, and fenvalerate (Rasool et al. 2014, Durigan et al. 2017). Evidence

of hybridization between invasive *H. armigera* and native *H. zea* was previously reported in

South America (Tay et al. 2013, Anderson et al. 2018), wherein the introgression of CYP337B3

into sympatric populations was detected (Valencia-Montoya et al. 2020, Ivey and Hillier 2023).

The initial report of hybridization in North America detected CYP337B3 in two *H. zea* collected

in Texas in 2019 that had no described or documented history of pyrethroid exposures (North et

al. 2024). In this study, we found that approximately 28.6% of the adult *H. zea* collected in 2023

near Olathe, CO, where repeated pyrethroid applications by growers failed to control larval

feeding damage to sweetcorn during the same growing season, carried one of two different

alleles, CYP337B3v2 or CYP337B3v6, at the CYP337B3 locus. This CYP337B locus of *H.*

armigera exists in homozygous, heterozygous, and hemizygous states for the

CYP337B1/CYP337B2 pair and recombinant CYP337B3 (Walsh et al. 2018). Invasive *H.*

armigera populations in the Americas may have contributed recombinant CYP337B3 to *H. zea*

(Valencia-Montoya et al. 2020, North et al. 2024), which is detectable using a gene- and species-

specific marker (Joußen et al. 2012). However, *H. armigera*-derived CYP337B1/CYP337B2

cannot be detected in hybrid *H. zea* using the PCR screening methods in this or prior studies.

Evaluation remains limited to detecting alleles of hybrid *Helicoverpa* via the CYP337B3 gene

and thus possibly underestimates the proportion of introgression. Out of 243 insects identified to

be positive for the CYP337B3 gene, only 12 were homozygous, and the remaining insects were

hemizygous at the CYP337B locus with wild-type CYP337B1/CYP337B2 gene pair from *H. zea*

or *H. armigera*.

Reference *H. zea* populations from Texas and Mississippi collected in 2006 prior to the

documented *H. armigera* invasion of South America in 2013 or North America in 2019 (North et

al. 2024, USDA-APHIS 2024) did not contain the CYP337B3 gene. Our results thus suggest that

the *H. armigera* invasion into the United States occurred after 2006 or was previously

undetectable due to low frequency during its initial establishment. Regardless, a more

comprehensive spatial and temporal screening of archived samples would be needed to

approximate the time(s) and the location(s) of the introduction. Previous population genetic

studies postulated that the CYP337B3 locus may be under strong selection in Brazil due to the

association between the high frequency of this gene and failures of pyrethroid insecticides to

control damage among field populations (Durigan et al. 2017, Valencia-Montoya et al. 2020).

Pyrethroid resistance due to knock-down resistance (*kdr*) mutations in the voltage-gated sodium

channel (*vgsc*) and significantly increased expression of cytochrome P450 6B (*cyp6b*) genes was

previously reported in the *H. zea* populations in the USA (Pietrantonio et al. 2007, Hopkins and

Pietrantonio 2010, Hopkins et al. 2011). In contrast, *kdr* mutations were not reported among

pyrethroid-resistant *H. armigera* populations in China, whereas the CYP337B3 gene was fixed

among all samples tested (Ni et al. 2023).

The above lines of evidence, along with introgression of genome regions flanking

CYP337B (Durigan et al. 2017, Valencia-Montoya et al. 2020, North et al. 2023), support the

premise that the chimeric CYP337B3 detected in the Americas originated from invasive *H.*

armigera. Olathe is in western Colorado, where a discontinuous cropping landscape, punctuated

by expanses of non-arable land and high mountain elevations, exists. Thus, the detection of the

H. armigera CYP337B3 in *H. zea* from such remote and isolated fields may be considered not

surprising even given the known mobility (Westbrook and López 2010, Jones et al. 2019) and

high gene flow of *H. zea* within the continent (Seymour et al. 2016, Perera et al. 2020). Our

findings, along with that of two hybrid *H. zea* with the CYP337B3 gene found in samples

collected in 2019 from Texas (North et al. 2023) and the dispersal behavior of this species might

suggest hybrids exist in the regions of the southwestern United States. CYP337B3-positive

insects identified in samples collected in New York, Texas, and Virginia from 2016 to 2023

(Perera, unpublished) most likely indicate the presence of hybrid *H. zea* with genes introgressed

from *H. armigera* within the continent. Instance of continuous and repeated use of pyrethroid

insecticides in the United States could provide high selection pressures, as previously

hypothesized in South America, to facilitate adaptive introgression of the CYP337B3 gene

(Durigan et al. 2017, Valencia-Montoya et al. 2020). Such a scenario might lead to transient

increases in CYP337B3 frequency among local populations that could become homogenized due

to high gene flow in the *H. zea* population. This admixture of locally adapted phenotypes may

effectively remediate impacts on agricultural production practices through an overall reduction in

resistance allele frequency in a landscape if persistent and widespread selective pressure is

lacking or contributes to the spread and accumulation of resistance across the population. The

latter possible outcome would depend on the prevalence of pyrethroid use by growers, be

modulated by the implementation of integrated pest management (IPM) practices, and be

impacted by the interaction of ecological, genetic, and other factors. Furthermore, pyrethroid

resistance developed previously among *H. zea* in the United States (Abd-Elghafar et al. 1993,

Jacobson et al. 2009) prior to this recent introgression of CYP337B3. Thus, evaluating

phenotypic levels of pyrethroid resistance conferred by *H. zea kdr* and CYP6B mechanisms

compared to those by *H. armigera*-derived CYP337B3 alleles may provide an estimate of any

selective advantages attained by introgression. Regardless, in contrast to adaptive introgression

resulting in the transfer of locally adapted alleles from indigenous populations of genetically-

compatible species to invasive species (Edelman and Mallet 2021, Jin et al. 2023), our results

and prior evidence suggest the reverse scenario exists in *Helicoverpa* due to the influence of

selection by pyrethroid insecticide use.

It was postulated that all allelic variants of CYP337B3 formed independently in different

geographic regions (Walsh et al. 2018). In Olathe, CO, population, the CYP337B3v2 allele was

present in 73.1% of the hybrid insects, while the remaining hybrid insects had the CYP337B3 v6

allele. The high-throughput sequencing of CYP337B3 amplicons interestingly did not indicate

the presence of CYP337B3v2/CYP337B3v6 heterozygotes among all 141 samples sequenced.

Assuming the increase in metabolic capacity of homozygotes, the high prevalence of these

alleles may be anticipated at locations such as Olathe, CO, where selection pressure was imposed

following repeated exposures to pyrethroid applications. Regardless, mating between lineages

carrying different haplotypes at the CYP337B3 locus would predict the formation of

heterozygotes in the population unless admixture is suppressed due to recency of contact or yet

undescribed barriers to gene flow exist. Our data indicate that the frequency of observed

homozygotes is less than the estimated homozygote frequency. Additional research will be

necessary to understand the fitness of different configurations of CYP337B genotypes.

The CYP337B3v2 allele was first reported in Pakistan and associated with an

approximately 7-fold increase in resistance to cypermethrin (Rasool et al. 2014), and

subsequently in Australia, China, and the African and European continents (Han et al. 2015,

Walsh et al. 2018). In contrast, the CYP337v6 allele has only thus far been reported in Uganda

(Walsh et al. 2018), and further description of any pyrethroid resistance phenotype it confers is

currently lacking. In a previous study of *Helicoverpa*, almost all *H. armigera* analyzed from

Brazil (*n* = 92) were reported homozygous for the CYP337B3v2 allele. At the same time, one

insect was heterozygous for CYP337B3v2/ CYP337B3v5 alleles and found one of 59 *H. zea*

carried the CYP337B3v2 allele (Walsh et al. 2018). Thus, the source population(s) for the

introgressed CYP337B3v2 allele in Olathe, CO may be the South American *H. armigera* or

hybrid *H. zea-armigera* populations that migrated or were transported northward, but an

independent introduction source of CYP337B3 into North America cannot be ruled out.

Our study is the first to report the African-derived CYP337B3v6 allele in the Americas,

providing evidence that a proportion of individuals in the Olathe population may be derived

directly or indirectly from an African source population. It is possible that previous studies on

South American populations of *H. zea* did not detect this allele due to very low frequencies on

that continent. However, it should be noted that 26.9% of the CYP337B3 alleles observed in this

study were CYP337B3v6 alleles, but this higher frequency could have resulted from genetic drift

following a genetic bottleneck or selection upon introduction to North America. Therefore, it is

not possible to determine if this allele was introduced directly from an African or South

American population until additional genomic data are obtained. Although the point source(s) of

the CYP337B3 alleles detected in Olathe, CO remains uncertain, a comparison of CYP337B3

flanking genomic regions between Olathe, CO and prior introgressed hybrids detected in North

America (North et al. 2024) or *H. armigera* detected near O'Hare airport (USDA-APHIS 2024)

might provide for such prediction. The sixteen nucleotide substitutions present between the

CYP337B3v6 allele from Olathe, CO, and the v6 allele from Uganda may also point to an origin

other than the African continent for CYP337B3v6 allele found in Olathe, CO. Although

conserved amino acid substitutions such as I78L found in CYP337B3v6 allele from Olathe, CO,

generally do not affect the function of a protein, alteration of function have been observed in

some isoleucine to leucine substitutions (Sitbon et al. 1991, Brown et al. 2002, Christoffers et al.

2002). Therefore, the implications of this I78L substitution on resistance to pyrethroids remain

unknown and in need of future empirical assessments. Nevertheless, the origins of two

CYP337B3 alleles detected among *H. zea* from Olathe, CO, in this study indicate that at least

two different hybridization events occurred between *H. armigera* and *H. zea* in the Americas,

and the CYP337B3v6 allele could represent the signature of one or more new *H. armigera*

introductions into the Americas.

The *H. armigera* rRNA ITS1 sequence identified in one insect (61e) in the Olathe, CO

population further confirms introgression from *H. armigera* into *H. zea* through hybridization.

We inferred that orthologous rRNA genes are located only in chromosome 30, because rRNA

genes are not found on other chromosomes in the genome assemblies of either *Helicoverpa*

species. It is conceivable that the crossover of orthologous chromosome regions in a hybrid

progeny of *H. zea* and *H. armigera* could result in the introgression of some of the rRNA repeats

into the *H. zea* genome. Regardless, several repetitive gene families in prokaryotes and

eukaryotes are known to undergo concerted evolution, which functions to limit variation between

repeat units (Coen et al. 1982, Mullins and Fultz 1989, Benedict et al. 1996, Liao 2000,

Bettencourt and Feder 2002, Rooney and Ward 2005, Peel et al. 2006, Ganley and Kobayashi

2007, Naidoo et al. 2013). This insect 61e may have had rRNA gene repeats introgressed from

H. armigera during a crossover event between *H. zea* and *H. armigera* haplotypes and in the

process of gene conversion and repeated backcrossing to *H. zea.* However, it is not possible to

determine the structure of the rRNA repeats in this insect and the origin of the sequences

resembling ITS1 of both *H. armigera* and *H. zea* without haplotype phased sequence data from

the segment of chromosome 30 containing the rRNA repeats. Concerted evolution would predict

that the single nucleotide polymorphisms (SNP) specific to *H. armigera* ITS1 or the *H. zea* ITS1

would be converted over time, and unconverted variants may thus be indicative of how recent

that introgression of the rRNA genes occurred. It should be noted that sample 61e was not

positive for the CYP337B3 gene, indicating it may have originated from a hybridization event

independent of those that led to the introgression of CYP337B1v2 and v6 alleles or the loci

segregated independently in the population as expected for genes that have no known level of

linkage disequilibrium. Thus, due to the lack of linkage between the ITS region and CYP337B

loci, recombination in a backcross likely disentangled these two *H. armigera*-derived loci.

Invasive species are a threat to agricultural production in the United States and

worldwide (Coates et al. 2015). A scenario of adaptive introgression facilitated by the transfer of

a novel gene from an invasive to a native insect, as predicted for the *Helicoverpa* pest complex,

provides a unique opportunity to study evolution and selection in real-time. Specifically, our

evidence supports the admixture of previously geographically distinct introgressed CYP337B3v2

and CYP337B3V6 alleles into a single population. However, any hybrid vigor or advantageous

phenotypic effects conferred by a unique combination of two pyrethroid resistance alleles in the

North American population remains to be determined. The prevalence of these alleles across the

continent remains unknown, high gene flow between North American *H. zea* populations (Perera

et al. 2020) predicts these genes could spread rapidly across the continent. The CYP337B3 gene

is currently used as a genetic marker to indicate the extent of gene transfer between these two

species but likely underestimates actual introgression rates due to inability to detect *H. armigera*-

derived CYP337B1/CYP337B2 haplotypes. The transfer of other genes with selective advantage,

such as those conferring resistance to *Bacillus thuringiensis* insecticidal proteins, remains

undetermined. The overall impacts of genes derived from invasive *H. armigera* on grower

production practices remain uncertain, but continued selection for pest adaptions to practices that

rely on insecticidal agents may be predicted to drive introgression of associated resistance alleles

into *H. zea*. This may necessitate the development of alternative management strategies and the

adoption of IPM practices.

Declaration of interest

The authors declare that they have no known competing financial interests or personal

relationships that could have appeared to influence the work reported in this paper.

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Table 1. Primers used in PCR amplification and nucleotide sequencing of ribosomal RNA internal transcribed spacer 1 and cytochrome P450 337B, CYP337B3, from *Helicoverpa* samples collected from Olathe, Colorado, USA.

Primer Name	Sequence (5' to 3	Gene	Reference
3373Ha_Hz_ITS1F	GAGGAAGTAAAAGTCGTAACAAGGTTTCC	ITS1 (rRNA)	(Perera, OP et al. 2015)
3374Ha_ITS1R	CGTTCGACTCTGTGTCCTCTAGTGG	ITS1 (rRNA)	(Perera, OP et al. 2015)
3377Hz_ITS1R	TTGATTGTTAACGAACGCGCCG	ITS1 (rRNA)	(Perera, OP et al. 2015)
310-18S-rDNA-2F	ATCATTTAGAGGAAGTAAAAGTCGTAACAAGGT	ITS1 (rRNA)	(Perera, OP et al. 2015)
312-5.8S-rDNA-R	GAARTGTCGATGTTCAAATGTGTCCTGC	ITS1 (rRNA)	(Perera, OP et al. 2015)
3709CYP337B1F	AATAATAAGCAACGCCAATGACTTAC	CYP337B1	(Joußen, N et al. 2012)
3710CYP337B1R	TGCAATAACAACTATTACATTTTGAATAAA	CYP337B1	(Joußen, N et al. 2012)
3711CYP337B2F	AATAATAACCAGTCCAAACGATGTGT	CYP337B2	(Joußen, N et al. 2012)
3712CYP337B2R	CGCAATTATAGTCACTATGATTGCATATA	CYP337B2	(Joußen, N et al. 2012)
3713CYP337B3F	AATAATAACCAGTCCAAACGATGTGT	CYP337B3	(Joußen, N et al. 2012)
3714CYP337B3R	TGCAATAACAACTATTACATTTTGAATAAA	CYP337B3	(Joußen, N et al. 2012)
4268CYP337B3F	ATGTTGTTCGTRATATTACTCACGA	CYP337B3	This study
4269CYP337B1_B3R	TTATATGTCTCTTAACTTTAATTCATAACGAG	CYP337B3	This study

Figure 1. Alignment of reference ITS1 sequences of *Helicoverpa armigera* (Ha) and *H. zea* (Hz) with ITS1 sequences obtained from Olathe, CO sample 61e. Nucleotides identical in both *H. armigera* and *H. zea* ITS1 sequences are shown in black. Olathe_61e_Ha_ITS1 sequence was highly similar to *H. zea* ITS1 sequence except for the *H. armigera*-specific ITS1 sequences. Differences between ITS1 sequences from the two *Helicoverpa* species are shown by white text with black background. Alignment gaps are indicated by a hyphen (-).

Figure 2. The evolutionary history was inferred among internal transcribed spacer 1 (ITS1) regions using Maximum Likelihood based on the Kimura 2-parameter model of sequence evolution (Kimura, 1980). The phylogeny among ITS1 regions among Helicovera armigera (Harm), *H. zea* (Hzea) and *H. assulta* (Hass) was rooted by the *Chloridea (Heliothis) virescens* (Cvir) ITS1 (GenBank accession provided at branch tips), based on a 601 nucleotide-long consensus alignment of 11 nucleotide sequences. The bootstrap consensus at each node was inferred from 10,000 replicates (Felsenstein, 1985) and partitions with less than 50% bootstrap support are collapsed. Neighbor-Join and BioNJ algorithms were applied to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach and the topology with superior log likelihood value was selected to obtain the initial tree(s). A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.3073)). Evolutionary analyses were conducted in MEGA11 (Tamura et al. 2021).

Figure 3. The evolutionary history was inferred among cytochrome P450 337B orthologs, CYP3B1-3, from *Helicoverpa armigera* and *H. zea* by using Maximum Likelihood and based on the Kimura 2-parameter model of sequence evolution (Kimura, 1980) with 10,000 bootstrap replicates (Felsenstein, 1985) as implemented in Mega 11 (Tamura et al. 2021). Relationships of alleles from the Olathe, CO population are shown with respect to reference sequences for CYP337B1, CYP337B2 and CYP337B3 paralogs (GenBank accessions include at respective branch tips) and based on 3605 positions in a consensus sequence alignment. Neighbor-Join and BioNJ algorithms were applied to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach and the topology with superior log likelihood value was selected to obtain the initial tree(s). A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.3794) and the tree with the highest log likelihood (-9917.03) is shown.

Table S1. Trap numbers, GPS coordinates and the number of *Helicoverpa zea* samples used for screening CYP337B and ITS1 genes in this study.

Trap Number	GPS Coordinates	Number of *H. zea* analyzed	Trap Number	GPS Coordinates	Number of *H. zea* analyzed
132	-108.011098, 38.562165	1	169	-107.971621, 38.498372	13
134	-108.015825, 38.547827	4	211	-108.091077, 38.650081	12
135	-107.916943, 38.489266	6	212	-108.080870, 38.664141	14
136	-108.011098, 38.562165	1	213	-108.077449, 38.683565	17
137	-108.054434, 38.584557	6	214	-108.078346, 38.704736	12
138	-108.015825, 38.547827	8	215	-108.067737, 38.639066	29
141	-108.068547, 38.649694	16	216	-108.072320, 38.704661	24
142	-108.059322, 38.60264	5	217	-108.091077, 38.650081	25
145	-107.909639, 38.487477	6	218	-108.077434, 38.632005	74
146	-108.073293, 38.591758	11	219	-108.074783, 38.671722	62
149	-108.016373, 38.540598	8	220	-108.071173, 38.631818	46
150	-108.016991, 38.551457	24	221	-108.091077, 38.650081	60
151	-108.053704, 38.610456	11	222	-108.101899, 38.709269	105
152	-108.111687, 38.657228	13	311	-108.001276, 38.544657	2
153	-108.044431, 38.646102	73	312	-108.099386, 38.635561	28
154	-108.016991, 38.551457	14	313	-108.002041, 38.533634	7
155	-107.960479, 38.489219	21	314	-108.083571, 38.697376	12
156	-108.050124, 38.584472	13	315	-108.085612, 38.695765	15
157	-108.023570, 38.558725	25	317	-107.999232, 38.533403	9
158	-108.023570, 38.558725	20	318	-108.101954, 38.701580	22
159	-108.040675, 38.575491	35	319	-108.097406, 38.649842	2
160	-107.990482, 38.539044	23	320	-108.097406, 38.649842	4
161	-108.040675, 38.575491	34	321	-108.099386, 38.635561	14
162	-107.950764, 38.474691	25	322	-108.076984, 38.660800	30
163	-107.914918, 38.487321	66	323	-108.113262, 38.719266	66
164	-107.960479, 38.489219	16	324	-108.077128, 38.638438	81
165	-107.970694, 38.496597	75	325	-107.951346, 38.518697	37
166	-107.954929, 38.551128	8	326	-108.002959, 38.547599	92
167	-107.954929, 38.551128	15	CSU 1	-108.070247, 38.660805	64
168	-107.971621, 38.498372	20	CSU 2	-107.973397, 38.492867	37

Figure S1. Locations of pheromone-lured traps used for collection of *Helicoverpa zea* in Olathe, Colorado, USA. Number of insects analyzed from each trap is indicated in parenthesis next to the trap number. R version 4.3.1 and the packages cowplot v. 1.1.3 (Wilke 2024), ggrepel v. 0.9.5 (Slowikowski 2024), ggsflabel v. 0.0.1 (Yutani 2024), ggspatial v. 1.1.9 (Dunnington 2023), maps v. 3.4.2 (Richard A. Becker, Ray Brownrigg. Enhancements by Thomas P Minka, and Deckmyn. 2023), rnaturalearth v. 1.0.1 (Massicotte and South 2023), rnaturalearthdata v. 1.0.0 (South, Michael, and Massicotte 2024), sf v. 1.0.16 (Pebesma 2018; Pebesma and Bivand 2023), tidyverse v. 2.0.0 (Wickham et al. 2019) were used in generating the site map using the data provided in the Supp. Table S1.

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Figure S2. Schematic representation of CYP337B genes and potential genotypic configurations of CYP337B1/CYP337B2 genes and CYP337B3 genes in a population of *Helicoverpa zea* with CYP337B genes introgressed from *H. armigera.* a). unequal crossover between CYP337B1 and CYP337B2 genes to produce CYP337B3 gene. b). homozygous CYP337B1/CYP337B2 genes originated from wild type *H. zea.* c). heterozygotes of CYP337B1/CYP337B2 with each chromosome originating from *H. armigera* and *H. zea*. d). CYP337B3 hemizygotes with *H. armigera* CYP337B1/CYP337B2 genes. e). CYP337B3 hemizygotes with *H. zea* CYP337B1/CYP337B2 genes. f). CYP337B3 homozygotes. Allelic variants of different genes are not shown. B2E1: exon 1 of CYP337B2; B2E2: exon 2 of CYP337B2; B1E1: exon 1 of CYP337B1; B1E2: exon 2 of CYP337B1.

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                          1                                                                            80
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CYP337B2v2_JQ995291      ATGTTGTTCATAATATTACTCACGATATTAATAGTACTGTGCTCAATAGTGCTCCATTTCAAGTTCACAAACAGCAAATA
CYP337B3v1_JQ995292      ATGTTGTTCGTAATATTACTCACGATATTAATAGTACTGTGCTCAATAGTGCTCCATTTTAAGTTCACAAACAGCAAATA
CYP337B3v2_KM675664      ATGTTGTTCGTAATATTACTCACGATATTAATAGTACTGTGCTCAATAGTGCTCCATTTCAAGTTCACAAACAGCAAATA
CYP337B3v3_KM675665      ATGTTGTTCGTAATATTACTCACGATATTAATAGTACTGTGCTCAATAGTGCTCCATTTCAAGTTCACAAACAGCAAATA
CYP337B3v4_KM675666      ATGTTGTTCGTAATATTACTCACGATATTAATAGTACTGTGCTCAATAGTGCTCCATTTCAAGTTCACAAACAGCAAATA
CYP337B3v5_KX958388      ATGTTGTTCGTAATATTACTCACGATATTAATAGTACTGTGCTCAATAGTGCTCCATTTCAAGTTCACAAACAGCAAATA
CYP337B3v6_KX958389      ATGTTGTTCGTGATATTACTCACGATATTAATAGTACTGTGCTCAATAGTGCTCCATTTCAAGTTCACAAACAGCAAATA
CYP337B3v7_KX958390      ATGTTGTTCGTGATATTACTCACGATATTAATAGTACTGTGCTCAATAGTGCTCCATTTCAAGTTCACAAACAGCAAATA
CYP337B3v8_KX958391      ATGTTGTTCGTAATATTACTCACGATATTAATAGTACTGTGCTCAATAGTGCTCCATTTCAAGTTCACAAACAGCAAATA
   CYP337B3_Olathe-2     ATGTTGTTCGTAATATTACTCACGATATTAATAGTACTGTGCTCAATAGTGCTCCATTTCAAGTTCACAAACAGCAAATA
   CYP337B3_Olathe-6     ATGTTGTTCGTAATATTACTCACGATATTAATAGTACTGTGTTCAATAGTGCTCCATTTTAAGTTCACAAACAGCAAATA
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   CYP337B3_Olathe-6     CTGGAAAAAGAAGAATATAATACAGATAAAAGATTTGACATTCACCTTTCTGTTCAACAAGCAATCGATGCCAGAACTAA
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   CYP337B3_Olathe-6     TCAAATCGATTTACGATAAACATAATGAACCGTATATTGGAACGACGTCGGCGACAATACCAACGCTCATTTTAAAGAAC
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CYP337B3v8_KX958391   CTGCAAAAGGTTCCATTCAATCTGGTAAGCAGATACACCACAGCATCGATCAGTGCTGCTGTATTCGGTATAGATACTCA
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 CYP337B3_Olathe-6    CTGCGAAAGAAACCGTTCAAACTTATGACCAGATACACTACAGCGTCTATTAGTGCTGCAGTATTTGGTATAGATACTCA
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CYP337B2v2_JQ995291   AGTGAAGAATTCCATGGAGTCACCCCTTGTGGATATGGCATTCAAGGCATTAGAACCCTCAGTATATGCAATCA-TAGTG
CYP337B3v1_JQ995292   AGTAAAGAGTACCATGGAATCACCATTCGTTGAATTGGCATTTAGAGCTTTACGACCATC-GTTTATTCAAAATGTAATA
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CYP337B3v5_KX958388   AGTGAAGAGTACCATGGAATCACCATTCGTTGAATTGGCATTTAGAGCTTTGCGACCATC-GTTTATTCAAAATGTAATA
CYP337B3v6_KX958389   AGTAAAGAGTACCATGGAATCACCATTCGTTGAATTGGCATTTAGAGCTTTACGACCATC-GTTTATTCAAAATGTAATA
CYP337B3v7_KX958390   AGTAAAGAGTACCATGGAATCACCATTCGTTGAATTAGCATTTAGAGCTTTACGACCATC-GTTTATTCAAAATGTAATA
CYP337B3v8_KX958391   AGTAAAGAGTACCATGGAATCACCATTCGTTGAATTGGCATTTAGAGCTTTACGACCATC-GTTTATTCAAAATGTAATA
 CYP337B3_Olathe-2    AGTAAAGAGTACCATGGAATCACCATTCGTTGAATTGGCATTTAGAGCTTTACGACCATC-GTTTATTCAAAATGTAATA
 CYP337B3_Olathe-6    AGTAAAGAGTACCATGGAATCACCATTCGTTGAATTGGCATTTAGAGCTTTACGACCATC-GTTTATTCAAAATGTAATA
                      641                                                                  720
CYP337B1v1_JQ995291   GTTGTTATTGCAAATACTTTCCCTAGATTGTACAAACTCTTGCAGTTGAAACTTTTTGGTGAACATGAAGAATTTTTTGT
CYP337B2v2_JQ995291   ACTATAATTGCGAATACTTTCCCTAAAGTACACAAACTTTTGAAGCTCAAAACCTTCGGTGGACAAGAAGATTTTTTTGT
CYP337B3v1_JQ995292   GTTGTTATTGCAAATACTTTCCCTAGATTGTACAAACTCTTGCAGTTGAAACTTTTTGGTGAACATGAAGAATTTTTTGT
CYP337B3v2_KM675664   GTTGTTATTGCAAATACTTTCCCTAGATTGTACAAACTCTTGCAGTTGAAACTTTTTGGTGAACATGAAGAATTTTTTGT
CYP337B3v3_KM675665   GTTGTTATTGCAAATACTTTCCCTAGATTGTACAAACTCTTGCAGTTGAAACTTTTTGGTGAACATGAAGAATTTTTTGT
CYP337B3v4_KM675666   GTTGTTATTGCAAATACTTTCCCTAGATTGTACAAACTCTTGCAGTTAAAACTTTTTGGTGAACATGAAGAATTTTTTGT
CYP337B3v5_KX958388   GTTGTTATTGCAAATACTTTCCCTAGATTGTACAAACTCTTGCAGTTGAAACTTTTTGGTGAACATGAAGAATTTTTTGT
CYP337B3v6_KX958389   GTTGTTATTGCAAATACTTTCCCTAGATTGTACAAACTCTTGCAGTTGAAACTTTTTGGTGAACATGAAGAATTTTTTGT
CYP337B3v7_KX958390   GTTGTTATTGCAAATACTTTCCCTAGATTGTACAAACTCTTGCAGTTGAAACTTTTTGGTGAACATGAAGAATTTTTTGT
CYP337B3v8_KX958391   GTTGTTATTGCAAATACTTTCCCTAGATTGTACAAACTCTTGCAGTTGAAACTTTTTGGTGAACATGAAGAATTTTTTGT
 CYP337B3_Olathe-2    GTTGTTATTGCAAATACTTTCCCTAGATTGTACAAACTCTTGCAGTTGAAACTTTTTGGTGAACATGAAGAATTTTTTGT
 CYP337B3_Olathe-6    GTTGTTATTGCAAATACTTTCCCTAGATTGTACAAACTCTTGCAGTTGAAACTTTTTGGTGAACATGAAGAATTTTTTGT
                      721                                                                  800
CYP337B1v1_JQ995291   GGGTGCAGTGAAAACTGTTTTAGAAAGTAGGAGGCATGATACTACTAAAAGATATGATTTTATTGAGATTTGCTTGGAAC
CYP337B2v2_JQ995291   TGGTATGGTTAAAAAAGTTTTAGACAGTAGAAGGCATGACACGACTAAGAGACATGATTTTATTGAGATATGTTTGGAGT
CYP337B3v1_JQ995292   GGGTGCAGTGAAAACTGTTTTAGAAAGTAGGAGGCATGATACTACTAAAAGATATGATTTTATTGAGATTTGCTTGGAAC
CYP337B3v2_KM675664   GGGTGCAGTGAAAACTGTTTTAGAAAGTAGGAGGCATGATACTACTAAAAGATATGATTTTATTGAGATTTGCTTGGAAC
CYP337B3v3_KM675665   GGGTGCAGTGAAAACTGTTTTAGAAAGTAGGAGGCATGATACTACTAAAAGATATGATTTTATTGAGATTTGCTTGGAAC
CYP337B3v4_KM675666   GGGTGCAGTGAAAACTGTTTTAGAAAGTAGGAGGCATGATACTACTAAAAGATATGATTTTATTGAGATTTGCTTGGAAC
CYP337B3v5_KX958388   GGGTGCAGTGAAAACTGTTTTAGAAAGTAGGAGGCATGATACTACTAAAAGATATGATTTTATTGAGATTTGCTTGGAAC
CYP337B3v6_KX958389   GGGGGCAGTGAAAACTGTTTTAGAAAGTAGGAGGCATGATACTACTAAAAGATATGATTTTATTGAGATTTGCTTGGAAC
CYP337B3v7_KX958390   GGGTGCAGTGAAAACTGTTTTAGAAAGTAGGAGGCATGATACTACTAAAAGATATGATTTTATTGAGATTTGCTTGGAAC
CYP337B3v8_KX958391   GGGTGCAGTGAAAACTGTTTTAGAAAGTAGGAGGCATGATACTACTAAAAGATATGATTTTATTGAGATTTGCTTGGAAC
 CYP337B3_Olathe-2    GGGTGCAGTGAAAACTGTTTTAGAAAGTAGGAGGCATGATACTACTAAAAGATATGATTTTATTGAGATTTGCTTGGAAC
 CYP337B3_Olathe-6    GGGGGCAGTGAAAACTGTTTTAGAAAGTAGGAGGCATGATACTACTAAAAGATATGATTTTATTGAGATTTGCTTGGAAC
```

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                        801                                                                    880
CYP337B1v1_JQ995291     TACAGAAGAATGGAATAATGCAGGACTTTTCAACTGGATATAAATTGGAGCCGACCGACGAACTGATGGCTGCTCAAGCA
CYP337B2v2_JQ995291     TACAAAAACATGGAGTAATGCAAGACTTTACGACTGGATACGAGTTGGAGCCAACAGATGAACTAATGGCTGCACAGGCG
CYP337B3v1_JQ995292     TACAGAAGAATGGAATAATGCAGGACTTCTCAACTGGATATAAATTGGAGCCGACCGACGAACTGATGGCTGCTCAAGCA
CYP337B3v2_KM675664     TACAGAAGAATGGAATAATGCAGGACTTTTCAACTGGATATAAATTGGAGCCGACCGACGAACTGATGGCTGCTCAAGCA
CYP337B3v3_KM675665     TACAGAAGAATGGAATAATGCAGGACTTCTCAACTGGATATAAATTGGAGCCGACCGACGAACTGATGGCTGCTCAAGCA
CYP337B3v4_KM675666     TACAGAAGAATGGAATAATGCAGGACTTCTCAACTGGATATAAATTGGAGCCGACTGACGAACTGATGGCTGCTCAAGCA
CYP337B3v5_KX958388     TACAGAAGAATGGAATAATGCAGGACTTCTCAACTGGTTATAAATTGGAGCCAACCGACGAACTGATGGCTGCTCAAGCA
CYP337B3v6_KX958389     TACAGAAGAATGGAATAATGCAGGACTTTTCAACTGGATATAAATTGGAGCCGACCGACGAACTGATGGCTGCTCAAGCA
CYP337B3v7_KX958390     TACAGAAGAATGGAATAATGCAGGACTTCTCAACTGGATATAAGTTGGAGCCGACCGACGAACTGATGGCTGCTCAAGCA
CYP337B3v8_KX958391     TACAGAAGAATGGAATAATGCAGGACTTCTCAACTGGATATAAATTGGAGCCGACTGACGAACTGATGGCTGCTCAAGCA
 CYP337B3_Olathe-2      TACAGAAGAATGGAATAATGCAGGACTTTTCAACTGGATATAAATTGGAGCCGACCGACGAACTGATGGCTGCTCAAGCA
 CYP337B3_Olathe-6      TACAGAAGAATGGAATAATGCAGGACTTTTCAACTGGATATAAATTGGAGCCGACCGACGAACTGATGGCTGCTCAAGCA
                        881                                                                    960
CYP337B1v1_JQ995291     TTCTTCTTTTTTGTGGCTGGTGCAGACACCTCTGCTAACACAATGCATTATTCTTTGTTAGAGCTGTCAAACAATCCAAA
CYP337B2v2_JQ995291     TTTGCCTTCTATCTAGCTGGTACAGACACCTCTGCGAATACAATGAATTATACTTTATTGGAACTATCAAACAATCCAAA
CYP337B3v1_JQ995292     TTCTTCTTTTTTGTCGCTGGTGCAGACACCTCTGCTAACACAATGCATTATTCTTTGTTAGAGCTGTCAAACAATCCAAA
CYP337B3v2_KM675664     TTCTTCTTTTTTGTGGCTGGTGCAGACACCTCTGCTAACACAATGCATTATTCTTTGTTAGAGCTGTCAAACAATCCAAA
CYP337B3v3_KM675665     TTCTTCTTTTTTGTGGCTGGTGCAGACACCTCTGCTAACACAATGCATTATTCTTTGTTAGAGCTGTCAAACAATCCAAA
CYP337B3v4_KM675666     TTCTTCTTTTTTGTGGCTGGTGCAGACACCTCTGCTAACACAATGCATTATTCTTTGTTAGAGCTGTCAAACAATCCAAA
CYP337B3v5_KX958388     TTCTTCTTTTTTGTGGCTGGTGCAGACACCTCTGCTAACACAATGCATTATTCTTTGTTAGAGCTGTCAAACAATCCAAA
CYP337B3v6_KX958389     TTCTTCTTTTTTGTGGCTGGTGCAGACACCTCTGCTAACACAATGCATTATTCTTTGTTAGAGCTGTCAAACAATCCAAA
CYP337B3v7_KX958390     TTCTTCTTTTTTGTGGCTGGTGCAGACACCTCTGCTAACACAATGCATTATTCTTTGTTAGAGCTGTCAAACAATCCAAA
CYP337B3v8_KX958391     TTCTTCTTTTTTGTGGCTGGTGCAGACACCTCTGCTAACACAATGCATTATTCTTTGTTAGAGCTGTCAAACAATCCAAA
 CYP337B3_Olathe-2      TTCTTCTTTTTTGTGGCTGGTGCAGACACCTCTGCTAACACAATGCATTATTCTTTGTTAGAGCTGTCAAACAATCCAAA
 CYP337B3_Olathe-6      TTCTTCTTTTTTGTGGCTGGTGCAGACACCTCTGCTAACACAATGCATTATTCTTTGTTAGAGCTGTCAAACAATCCAAA
                        961                                                                   1040
CYP337B1v1_JQ995291     AATCTTGGCAAAACTACATGAGGAAATTGACAAAGTTTTCGAAGGCGGAGCTGGGGAACTAACTTATAATGACATTGATA
CYP337B2v2_JQ995291     AATCTTAAGGAAAGTACATGAAGAAATTGACAAAGTTTTCGAAGGCGGAGTTGAAGAATTAAGTTATAATGACATTGATA
CYP337B3v1_JQ995292     AATCTTGGCAAAACTACATGAGGAAATTGACAAAGTTTTCGAAGGCGGAGCTGGGGAACTAACTTATAATGACATTGATA
CYP337B3v2_KM675664     AATCTTGGCAAAACTACATGAGGAAATTGACAAAGTTTTCGAAGGCGGAGCTGGGGAACTAACTTATAATGACATTGATA
CYP337B3v3_KM675665     AATCTTGGCAAAACTACATGAGGAAATTGACAAAGTTTTCGAAGGCGGAGCTGGGGAACTAACTTATAATGACATTGATA
CYP337B3v4_KM675666     AATCTTGGCAAAACTACATGAGGAAATTGACAAAGTTTTCGAAGGCGGAGCTGGGGAACTAACTTATAATGACATTGATA
CYP337B3v5_KX958388     AATCCTGGCAAAACTACACGAGGAAATTGACAAAGTTTTCGAAGGCGGAGCTGGGGAACTAACTTATAATGACATTGATA
CYP337B3v6_KX958389     AATCTTGGCAAAACTACATGAGGAAATTGACAAAGTTTTCGCAGGTGGAGCTGGGGAACTAACTTATAATGACATTGATA
CYP337B3v7_KX958390     AATCTTGGCAAAACTACATGAGGAAATTGACAAAGTTTTCGAAGGCGGAGCTGGGGAACTAACTTATAATGACATTGATA
CYP337B3v8_KX958391     AATCTTGGCAAAACTACATGAGGAAATTGACAAAGTTTTCGAAGGCGGAGCTGGGGAACTAACTTATAATGACATTGATA
 CYP337B3_Olathe-2      AATCTTGGCAAAACTACATGAGGAAATTGACAAAGTTTTCGAAGGCGGAGCTGGGGAACTAACTTATAATGACATTGATA
 CYP337B3_Olathe-6      AATCTTGGCAAAACTACATGAGGAAATTGACAAAGTTTTCGCAGGTGGAGCTGGGGAACTAACTTATAATGACATTGATA
                        1041                                                                  1120
CYP337B1v1_JQ995291     AGTTACAATATTTAGATCAGGTTATAAATGAAGCAATAAGAAAGTATCCTCCCATAGGTGTCATGCAAAGATTGTGTACT
CYP337B2v2_JQ995291     AATTACAATATTTAGACGAAGTAGTTAATGAAGCACTGAGAAAGTATCCTCCAATAGGTTTTATGCAAAGAATGTGTACC
CYP337B3v1_JQ995292     AGTTACAATATTTAGATCAGGTTATAAATGAAGCAATGAGAAAGTATCCTCCCATAGGTGTCATGCAAAGATTGTGTACT
CYP337B3v2_KM675664     AGTTACAATATTTAGATCAGGTTATAAATGAAGCAATGAGAAAGTATCCTCCAGTAGGTGTCATGCAAAGATTGTGTACT
CYP337B3v3_KM675665     AGTTACAATATTTAGATCAGGTTATAAATGAAGCAATGAGAAAGTATCCTCCAGTAGGTGTCATGCAAAGATTGTGTACT
CYP337B3v4_KM675666     AGTTACAATATTTAGATCAGGTTATAAATGAAGCAATGAGAAAGTATCCTCCAGTAGGTGTCATGCAAAGATTGTGTACT
CYP337B3v5_KX958388     AGTTACAATATTTAGATCAGGTTATAAATGAAGCAATGAGAAAGTATCCTCCAGTAGGTGTCATGCAAAGATTGTGCACT
CYP337B3v6_KX958389     AGTTACAATATTTAGATCAGGTTATAAATGAAGCAATGAGAAAGTATCCTCCAGTAGGTGTCATGCAAAGATTGTGTACT
CYP337B3v7_KX958390     AGTTACAATATTTAGATCAGGTTATAAATGAAGCGATGAGAAAGTATCCTCCAGTAGGTGTCATGCAAAGATTGTGCACT
CYP337B3v8_KX958391     AGTTACAATATTTAGATCAGGTTATAAATGAAGCAATGAGAAAGTATCCTCCAGTAGGTGTCATGCAAAGATTGTGTACT
 CYP337B3_Olathe-2      AGTTACAATATTTAGATCAGGTTATAAATGAAGCAATGAGAAAGTATCCTCCAGTAGGTGTCATGCAAAGATTGTGTACT
 CYP337B3_Olathe-6      AGTTACAATATTTAGATCAGGTTATAAATGAAGCAATGAGAAAGTATCCTCCAGTAGGTGTCATGCAAAGATTGTGTACT
                        1121                                                                  1200
CYP337B1v1_JQ995291     AAAGATACAGTTTTACCGTCTGGTATACCCATAGCAAAGGGTAACACAATAATGATTCCAGTGTTCGGTCTTCACAGAGA
CYP337B2v2_JQ995291     AAGGACACAGTTTTGCCATCTGGTTTACCTGTATCAAAAGATGAAATTATCATTGTGCCCCTTTATGGAATCCACAAAGA
CYP337B3v1_JQ995292     AAAGATACAGTTTTACCGTCTGGTATACCCATAGCAAAGGGTAACACAATAATGATTCCAGTGTTCGGTCTTCACAGAGA
CYP337B3v2_KM675664     AAAGATACAGTTTTACCTTCTGGTATACCCATAGCAAAGGGTAACACAATAATGATACCAGTGTTCGGTCTTCACAGAGA
CYP337B3v3_KM675665     AAAGATACAGTTTTACCTTCTGGTATACCCATAGCAAAGGGTAACACAATAATGATTCCAGTGTTCGGTCTTCACAGAGA
CYP337B3v4_KM675666     AAAGATACAGTTTTACCTTCTGGTATACCCATAGCAAAGGGTAACACAATAATGATTCCAGTGTTCGGTCTTCACAGAGA
CYP337B3v5_KX958388     AAAGATACAGTTTTACCTTCTGGTATACCCATAGCAAAGGGTAACACAATAATGATTCCAGTGTTCGGTCTTCACAGAGA
CYP337B3v6_KX958389     AAAGATACGGTTTTACCTTCTGGTATACCCATAGCAAAGGGTAACACAATAATGATACCAGTGTTCGGTCTTCACAGAGC
CYP337B3v7_KX958390     AAAGATACAGTTTTACCTTCTGGTATACCCATAGCAAAAGGTAACACAATAATGATTCCAGTGTTCGGTCTTCACAGAGA
CYP337B3v8_KX958391     AAAGATACAGTTTTACCTTCTGGTATACCCATAGCAAAGGGTAACACAATAATGATTCCAGTGTTCGGTCTTCACAGAGA
 CYP337B3_Olathe-2      AAAGATACAGTTTTACCTTCTGGTATACCCATAGCAAAGGGTAACACAATAATGATACCAGTGTTCGGTCTTCACAGAGA
 CYP337B3_Olathe-6      AAAGATACAGTTTTACCTTCTGGTATACCCATAGCAAAGGGTAACACAATAATGATACCAGTGTTCGGTCTTCACAGAGA
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Figure S3. Alignment of the mRNA sequences of cytochrome P450 337B (CYP337B) genes CYP337B1v1, CYP337B2v2, and CYP337B3 alleles v1 through v8 with mRNA sequences extracted from CYP337B3 alleles identified from Olathe, CO population of *Helicoverpa zea*. Identical and conserved nucleotide positions are shown in black text and nucleotide polymorphisms, insertions, and deletions are shown with grey background. Alignment gaps are indicated with a hyphen (-).

```
                                    1                                                          60
CYP337B3v1_JQ995292    (1)   ATGTTGTTCGTGATATTACTCACGATATTAATAGTACTGTGCTCAATAGTGCTCCATTTT
CYP337B3v2_KJ636466    (1)   ATGTTGTTCGTAATATTACTCACGATATTAATAGTACTGTGCTCAATAGTGCTCCATTTC
CYP337B3v3_KM675665    (1)   ATGTTGTTCGTAATATTACTCACGATATTAATAGTACTGTGCTCAATAGTGCTCCATTTC
CYP337B3v4_KM675666    (1)   ATGTTGTTCGTAATATTACTCACGATATTAATAGTACTGTGCTCAATAGTGCTCCATTTC
CYP337B3v5_KX958388    (1)   ATGTTGTTCGTAATATTACTCACGATATTAATAGTACTGTGCTCAATAGTGCTCCATTTC
CYP337B3v6_KX958389    (1)   ATGTTGTTCGTGATATTACTCACGATATTAATAGTACTGTGCTCAATAGTGCTCCATTTC
CYP337B3v7_KX958390    (1)   ATGTTGTTCGTGATATTACTCACGATATTAATAGTACTGTGCTCAATAGTGCTCCATTTC
CYP337B3v8_KX958391    (1)   ATGTTGTTCGTAATATTACTCACGATATTAATAGTACTGTGCTCAATAGTGCTCCATTTC
 CYP337B3_Olathe-2     (1)   ATGTTGTTCGTAATATTACTCACGATATTAATAGTACTGTGCTCAATAGTGCTCCATTTC
 CYP337B3_Olathe-6     (1)   ATGTTGTTCGTAATATTACTCACGATATTAATAGTACTGTGTTCAATAGTGCTCCATTTT
                                    61                                                         120
CYP337B3v1_JQ995292    (61)  AAGTTCACAAACAGCAAATACTGGAAAAAGAAGAATATAATCCAGATAAAAGATTTGACA
CYP337B3v2_KJ636466    (61)  AAGTTCACAAACAGCAAATACTGGAAAAAGAAGAACATTATCCAGATAAAAGATTTGACA
CYP337B3v3_KM675665    (61)  AAGTTCACAAACAGCAAATACTGGAAAAAGAAGAACATTATCCAGATAAAAGATTTGACA
CYP337B3v4_KM675666    (61)  AAGTTCACAAACAGCAAATACTGGAAAAAGAAGAACATTATCCAGATAAAAGATTTGACA
CYP337B3v5_KX958388    (61)  AAGTTCACAAACAGCAAATACTGGAAAAAGAAGAACATTATCCAGATAAAAGATTTGACA
CYP337B3v6_KX958389    (61)  AAGTTCACAAACAGCAAATACTGGAAAAAGAAGAACATTATCCAGATAAAAGATTTGACA
CYP337B3v7_KX958390    (61)  AAGTTCACAAACAGCAAATACTGGAAAAAGAAGAACATAATCCAGATAAAAGATTTGACA
CYP337B3v8_KX958391    (61)  AAGTTCACAAACAGCAAATACTGGAAAAAGAAGAACATAATCCAGATAAAAGACTTGACA
 CYP337B3_Olathe-2     (61)  AAGTTCACAAACAGCAAATACTGGAAAAAGAAGAACATTATCCAGATAAAAGATTTGACA
 CYP337B3_Olathe-6     (61)  AAGTTCACAAACAGCAAATACTGGAAAAAGAAGAATATAACACAGATAAAAGATTTGACA
                                    121                                                        180
CYP337B3v1_JQ995292    (121) TTCACCTTTCTGTTCAACAAGCAATCGATGCCAGAACTAATCAAATCGATTTACGATAAA
CYP337B3v2_KJ636466    (121) TTCACCTTTCTGTTCAACAAGCAATCGATGCCAGAACTAATCAAATCGATTTACGATAAA
CYP337B3v3_KM675665    (121) TTCACCTTTCTGTTCAACAAGCAATCGATGCCAGAACTAATCAAATCGATTTACGATAAA
CYP337B3v4_KM675666    (121) TTCACCTTTCTGTTCAACAAGCAATCGATGCCAGAACTAATCAAATCGATTTACGATAAA
CYP337B3v5_KX958388    (121) TTCACCTTTCTGTTCAACAAGCAATCGATGCCAGAACTAATCAAATCGATTTACGATAAA
CYP337B3v6_KX958389    (121) TTCACCTTTCTGTTCAACAAGCAATCGATGCCAGAACTAATCAAATCGATTTACGATAAA
CYP337B3v7_KX958390    (121) TTCACCTTTCTGTTCAACAAGCAATCGATGCCAGAACTAATCAAGTCGATTTACGATAAA
CYP337B3v8_KX958391    (121) TTCACTTTTCTGTTCAACAAGCAATCGATGCCAGAACTAATCAAATCGATTTACGATAAA
 CYP337B3_Olathe-2     (121) TTCACCTTTCTGTTCAACAAGCAATCGATGCCAGAACTAATCAAATCGATTTACGATAAA
 CYP337B3_Olathe-6     (121) TTCACCTTTCTGTTCAACAAGCAATCGATGCCAGAACTAATCAAATCGATTTACGATAAA
                                    181                                                        240
CYP337B3v1_JQ995292    (181) CATGATGAACCGTATATTGGAACGACGTCGGCGACAATACCAACGCTCATTATAAAGAAC
CYP337B3v2_KJ636466    (181) CATGATGAACCGTATATTGGAACGACGTCGGCGACAATACCAACGCTCATTATAAAGAAC
CYP337B3v3_KM675665    (181) CATGATGAACCGTATATTGGAACGACGTCGGCGACAATACCAACGCTCATTATAAAGAAC
CYP337B3v4_KM675666    (181) CATGATGAACCGTATATTGGAACGACGTCGGCGACAATACCAACGCTCATTATAAAGAAC
CYP337B3v5_KX958388    (181) CATGATGAACCGTATATTGGAACGACGTCCGCGACAATACCAACGCTCATTATAAAGAAC
CYP337B3v6_KX958389    (181) CATGATGAACCGTATATTGGAACGACGTCCGCGACAATACCAACGCTCATTATAAAGAAC
CYP337B3v7_KX958390    (181) CATGATGAACCGTATATTGGGACGACGTCGGCGACAATACCAACGCTGATTATAAAGAAC
CYP337B3v8_KX958391    (181) CATGATGAACCGTATATTGGAACGACGTCCGCGACAATACCAACGCTGATTATAAAGAAC
 CYP337B3_Olathe-2     (181) CATGATGAACCGTATATTGGAACGACGTCGGCGACAATACCAACGCTCATTATAAAGAAC
 CYP337B3_Olathe-6     (181) CATAATGAACCGTATATTGGAACGACGTCGGCGACAATACCAACGCTCATTTTAAAGAAC
                                    241                                                        300
CYP337B3v1_JQ995292    (241) CTCGATGATATTCAAGCAGTGTTAGCTGGTGACTTCCAAAGTTTCTACAGTCGAGGAATA
CYP337B3v2_KJ636466    (241) CTCGATGATATTCAAGCAGTGTTAGCTGGTGACTTCCAAAGTTTCTACAGTCGAGGAATA
CYP337B3v3_KM675665    (241) CTCGATGATATTCAAGCAGTGTTAGCTGGTGACTTCCAAAGTTTCTACAGTCGAGGAATA
CYP337B3v4_KM675666    (241) CTCGATGATATTCAAGCAGTGTTAGCTGGTGACTTCCAAAGTTTCTACAGTCGAGGAATA
CYP337B3v5_KX958388    (241) CTCGATGATATTCAAGCAGTGTTAGCTGGTGACTTCCAAAGTTTCTACAGTCGAGGAATA
CYP337B3v6_KX958389    (241) CTCGATGATATTCAAGCAGTGTTAGCTGGTGACTTCCAAAGTTTCTACAGTCGAGGAATA
CYP337B3v7_KX958390    (241) CTCGATGATATTCAAGCAGTGTTAGCTGGTGACTTCCAAAGTTTCTACAGTCGAGGAATA
CYP337B3v8_KX958391    (241) CTCGATGATATTCAAGCGGTGTTAGCTGGTGACTTCCAAAGTTTCTACAGTCGAGGAATA
 CYP337B3_Olathe-2     (241) CTCGATGATATTCAAGCAGTGTTAGCTGGTGACTTCCAAAGTTTCTACAGTCGAGGAATA
 CYP337B3_Olathe-6     (241) CTCGATGATATTCAAGCAGTGTTAGCTGGTGACTTCCAAAGTTTCTACAGTCGAGGAATA
                                    301                                                        360
CYP337B3v1_JQ995292    (301) ATAACCAGTCCAAACGATGTGTTAGCTGATAATTTGTTATTAATGGACGACTTCAAAAAA
CYP337B3v2_KJ636466    (301) ATAACCAGTCCAAACGACGTGTTAGCTGATAATTTGTTATTAATGGACGACTTCAAAAAA
CYP337B3v3_KM675665    (301) ATAACCAGTCCAAACGATGTGTTAGCTGATAATTTGTTATTAATGGACGACTTCAAAAAA
CYP337B3v4_KM675666    (301) ATAACCAGTCCAAACGATGTGTTAGCTGATAATTTGTTATTAATGGACGACTTCAAAAAA
CYP337B3v5_KX958388    (301) ATAACCAGTCCAAACGATGTGTTAGCTGATAATTTGTTATTAATGGACGACTTCAAAAAA
CYP337B3v6_KX958389    (301) ATAACCAGTCCAAACGATGTGTTAGCTGATAATTTGTTATTAATGGACGACTTCAAAAAA
CYP337B3v7_KX958390    (301) ATAACCAGTCCAAATGATGTGTTAGCTGATAATTTGTTATTAATGGACGACTTCAAAAAG
CYP337B3v8_KX958391    (301) ATAACCAGTCCAAACGATGTGTTAGCTGATAATTTGTTATTAATGGACGACTTCAAAAAA
CYP337B3_Olathe-2      (301) ATAACCAGTCCAAACGACGTGTTAGCTGATAATTTGTTATTAATGGACGACTTCAAAAAA
CYP337B3_Olathe-6      (301) ATAACCAGTCCAAACGATGTGTTAGCTGATAATTTGTTATTAATGGACGACTTCAAAAAA
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                             361                                                    420
CYP337B3v1_JQ995292   (361) TGGAAACTCATACGACAAAAACTCACTCCAATTTTCACTAGTGCGAAACTCAAAAATATG
CYP337B3v2_KJ636466   (361) TGGAAACTCATACGACAAAAACTCACTCCAATTTTCACTAGTGCGAAACTCAAAAACATG
CYP337B3v3_KM675665   (361) TGGAAACTCATACGACAAAAACTCACTCCAATTTTCACTAGTGCGAAACTCAAAAACATG
CYP337B3v4_KM675666   (361) TGGAAACTCATACGACAAAAACTCACTCCAATTTTCACTAGTGCGAAACTCAAAAACATG
CYP337B3v5_KX958388   (361) TGGAAACTCATACGACAAAAACTCACTCCAATTTTCACTAGTGCGAAACTCAAAAACATG
CYP337B3v6_KX958389   (361) TGGAAACTCATACGACAAAAACTCACTCCAATTTTCACTAGTGCGAAACTCAAAAACATG
CYP337B3v7_KX958390   (361) TGGAAACTCATACGACAAAAACTCACTCCAATTTTCACTAGTGCGAAACTTAAAAACATG
CYP337B3v8_KX958391   (361) TGGAAACTCATACGACAAAAACTCACTCCAATTTTCACTAGTGCGAAACTCAAAAACATG
 CYP337B3_Olathe-2    (361) TGGAAACTCATACGACAAAAACTCACTCCAATTTTCACTAGTGCGAAACTCAAAAACATG
 CYP337B3_Olathe-6    (361) TGGAAACTCATACGACAAAAACTCACTCCAATTTTCACTAGTGCGAAACTCAAAAACATG
                             421                                                    480
CYP337B3v1_JQ995292   (421) TTTTACATCATAGAAAAAAGTGCCCGAGATTTTGTTGAGTTGGTTGAAGATAATGTTCAT
CYP337B3v2_KJ636466   (421) TTTTACATCATAGAAAAAAGTGCCCGAGATTTTGTTGAGTTGGTTGAAGATAATGTTCAT
CYP337B3v3_KM675665   (421) TTTTACATCATAGAAAAAAGTGCCCGAGATTTTGTTGAGCTGGTTGAAGATAATGTTCAT
CYP337B3v4_KM675666   (421) TTTTACATCATAGAAAAAAGTGCCCGAGATTTTGTTGAGTTGGTTGAACATAATGCTTGT
CYP337B3v5_KX958388   (421) TTTTACATCATAGAAAAAAGTGCCCGAGATTTTGTTGAGTTGGTTGAAGATAATGTTCAT
CYP337B3v6_KX958389   (421) TTTTACATCATAGAAAAAAGTGCTCGAGATTTTGTTGAGTTGGTTGAAGATAATGTTCAT
CYP337B3v7_KX958390   (421) TTTTACATCATAGAAAAAAGTGCCCGAGATTTTGTGGAATTGGTTGAACACAATGCTCAT
CYP337B3v8_KX958391   (421) TTTTACATCATAGAAAAAAGTGCCCGAGATTTTGTTGAGTTGGTTGAACATAATGCTTGT
 CYP337B3_Olathe-2    (421) TTTTACATCATAGAAAAAAGTGCCCGAGATTTTGTTGAGTTGGTTGAAGATAATGTTCAT
 CYP337B3_Olathe-6    (421) TTTTACATCATAGAAAAAAGTGCTCGAGATTTTGTTGAGTTGGTTGAAGATAATGTTCAT
                             481                                                    540
CYP337B3v1_JQ995292   (481) CTGCGAAAGAAACCGTTCAAACTTATGACCAGATACACTACAGCGTCTATTAGTGCTGCT
CYP337B3v2_KJ636466   (481) CTGCGAAAGAAACCGTTCAAACTTATGACCAGATACACTACAGCGTCTATTAGTGCTGCA
CYP337B3v3_KM675665   (481) CTGCGAAAGAAACCGTTCAAACTTATGACCAGATACACTACAGCGTCTATTAGTGCTGCA
CYP337B3v4_KM675666   (481) CTGCAAAAGGTTCCATTCAATCTGGTAAGCAGATACACCACAGCATCGATCAGTGCTGCT
CYP337B3v5_KX958388   (481) CTGCGAAAGAAACCGTTCAAACTTATGACCAGATACACTACAGCGTCTATTAGTGCTGCA
CYP337B3v6_KX958389   (481) CTGCGAAAGAAACCGTTCAAACTTATGACCAGATACACTACAGCGTCTATTAGTGCTGCA
CYP337B3v7_KX958390   (481) CTGCGAAAGGTTCCATTCAATTTGATAAGCAGATACACCACAGCATCGATCAGTGCTGCT
CYP337B3v8_KX958391   (481) CTGCAAAAGGTTCCATTCAATCTGGTAAGCAGATACACCACAGCATCGATCAGTGCTGCT
 CYP337B3_Olathe-2    (481) CTGCGAAAGAAACCGTTCAAACTTATGACCAGATACACTACAGCGTCTATTAGTGCTGCA
 CYP337B3_Olathe-6    (481) CTGCGAAAGAAACCGTTCAAACTTATGACCAGATACACTACAGCGTCTATTAGTGCTGCA
                             541                                                    600
CYP337B3v1_JQ995292   (541) GTATTCGGTATAGATACTCAAGTAAAGAGTACCATGGAATCACCATTCGTTGAATTGGCA
CYP337B3v2_KJ636466   (541) GTATTTGGTATAGATACACAAGTAAAGAGTACCATGGAATCACCATTCGTTGAATTGGCA
CYP337B3v3_KM675665   (541) GTATTTGGTATAGATACACAAGTAAAGAGTACCATGGAATCACCATTCGTTGAATTGGCA
CYP337B3v4_KM675666   (541) GTATTCGGTATAGATACTCAAGTAAAGAGTACCATGGAATCACCATTCGTTGAATTGGCA
CYP337B3v5_KX958388   (541) GTATTTGGTATAGATACTCAAGTGAAGAGTACCATGGAATCACCATTCGTTGAATTGGCA
CYP337B3v6_KX958389   (541) GTATTTGGTATAGATACTCAAGTAAAGAGTACCATGGAATCACCATTCGTTGAATTGGCA
CYP337B3v7_KX958390   (541) GTATTCGGTATAGATACTCAAGTAAAGAGTACCATGGAATCACCATTCGTTGAATTAGCA
CYP337B3v8_KX958391   (541) GTATTCGGTATAGATACTCAAGTAAAGAGTACCATGGAATCACCATTCGTTGAATTGGCA
 CYP337B3_Olathe-2    (541) GTATTTGGTATAGATACACAAGTAAAGAGTACCATGGAATCACCATTCGTTGAATTGGCA
 CYP337B3_Olathe-6    (541) GTATTTGGTATAGATACTCAAGTAAAGAGTACCATGGAATCACCATTCGTTGAATTGGCA
                             601                                                    660
CYP337B3v1_JQ995292   (601) TTTAGAGCTTTACGACCATCGTTTATTCAAAATGTAATAGTTGTTATTGCAAATACTTTC
CYP337B3v2_KJ636466   (601) TTTAGAGCTTTACGACCATCGTTTATTCAAAATGTAATAGTTGTTATTGCAAATACTTTC
CYP337B3v3_KM675665   (601) TTTAGAGCTTTACGACCATCGTTTATTCAAAATGTAATAGTTGTTATTGCAAATACTTTC
CYP337B3v4_KM675666   (601) TTTAGAGCTTTACGACCATCGTTTATTCAAAATGTAATAGTTGTTATTGCAAATACTTTC
CYP337B3v5_KX958388   (601) TTTAGAGCTTTGCGACCATCGTTTATTCAAAATGTAATAGTTGTTATTGCAAATACTTTC
CYP337B3v6_KX958389   (601) TTTAGAGCTTTACGACCATCGTTTATTCAAAATGTAATAGTTGTTATTGCAAATACTTTC
CYP337B3v7_KX958390   (601) TTTAGAGCTTTACGACCATCGTTTATTCAAAATGTAATAGTTGTTATTGCAAATACTTTC
CYP337B3v8_KX958391   (601) TTTAGAGCTTTACGACCATCGTTTATTCAAAATGTAATAGTTGTTATTGCAAATACTTTC
 CYP337B3_Olathe-2    (601) TTTAGAGCTTTACGACCATCGTTTATTCAAAATGTAATAGTTGTTATTGCAAATACTTTC
 CYP337B3_Olathe-6    (601) TTTAGAGCTTTACGACCATCGTTTATTCAAAATGTAATAGTTGTTATTGCAAATACTTTC
                             661                                                    720
CYP337B3v1_JQ995292   (661) CCTAGATTGTACAAACTCTTGCAGTTGAAACTTTTTGGTGAACATGAAGAATTTTTTGTG
CYP337B3v2_KJ636466   (661) CCTAGATTGTACAAACTCTTGCAGTTGAAACTTTTTGGTGAACATGAAGAATTTTTTGTG
CYP337B3v3_KM675665   (661) CCTAGATTGTACAAACTCTTGCAGTTGAAACTTTTTGGTGAACATGAAGAATTTTTTGTG
CYP337B3v4_KM675666   (661) CCTAGATTGTACAAACTCTTGCAGTTAAAACTTTTTGGTGAACATGAAGAATTTTTTGTG
CYP337B3v5_KX958388   (661) CCTAGATTGTACAAACTCTTGCAGTTGAAACTTTTTGGTGAACATGAAGAATTTTTTGTG
CYP337B3v6_KX958389   (661) CCTAGATTGTACAAACTCTTGCAGTTGAAACTTTTTGGTGAACATGAAGAATTTTTTGTG
CYP337B3v7_KX958390   (661) CCTAGATTGTACAAACTCTTGCAGTTGAAACTTTTTGGTGAACATGAAGAATTTTTTGTG
CYP337B3v8_KX958391   (661) CCTAGATTGTACAAACTCTTGCAGTTGAAACTTTTTGGTGAACATGAAGAATTTTTTGTG
 CYP337B3_Olathe-2    (661) CCTAGATTGTACAAACTCTTGCAGTTGAAACTTTTTGGTGAACATGAAGAATTTTTTGTG
 CYP337B3_Olathe-6    (661) CCTAGATTGTACAAACTCTTGCAGTTGAAACTTTTTGGTGAACATGAAGAATTTTTTGTG
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                             721                                                     780
CYP337B3v1_JQ995292    (721) GGTGCAGTGAAAACTGTTTTAGAAAGTAGGAGGCATGATACTACTAAAAGATATGATTTT
CYP337B3v2_KJ636466    (721) GGTGCAGTGAAAACTGTTTTAGAAAGTAGGAGGCATGATACTACTAAAAGATATGATTTT
CYP337B3v3_KM675665    (721) GGTGCAGTGAAAACTGTTTTAGAAAGTAGGAGGCATGATACTACTAAAAGATATGATTTT
CYP337B3v4_KM675666    (721) GGTGCAGTGAAAACTGTTTTAGAAAGTAGGAGGCATGATACTACTAAAAGATATGATTTT
CYP337B3v5_KX958388    (721) GGTGCAGTGAAAACTGTTTTAGAAAGTAGGAGGCATGATACTACTAAAAGATATGATTTT
CYP337B3v6_KX958389    (721) GGGGCAGTGAAAACTGTTTTAGAAAGTAGGAGGCATGATACTACTAAAAGATATGATTTT
CYP337B3v7_KX958390    (721) GGTGCAGTGAAAACTGTTTTAGAAAGTAGGAGGCATGATACTACTAAAAGATATGATTTT
CYP337B3v8_KX958391    (721) GGTGCAGTGAAAACTGTTTTAGAAAGTAGGAGGCATGATACTACTAAAAGATATGATTTT
  CYP337B3_Olathe-2    (721) GGTGCAGTGAAAACTGTTTTAGAAAGTAGGAGGCATGATACTACTAAAAGATATGATTTT
  CYP337B3_Olathe-6    (721) GGGGCAGTGAAAACTGTTTTAGAAAGTAGGAGGCATGATACTACTAAAAGATATGATTTT
                             781                                                     840
CYP337B3v1_JQ995292    (781) ATTGAGATTTGCTTGGAACTACAGAAGAATGGAATAATGCAGGACTTCTCAACTGGATAT
CYP337B3v2_KJ636466    (781) ATTGAGATTTGCTTGGAACTACAGAAGAATGGAATAATGCAGGACTTTTCAACTGGATAT
CYP337B3v3_KM675665    (781) ATTGAGATTTGCTTGGAACTACAGAAGAATGGAATAATGCAGGACTTCTCAACTGGATAT
CYP337B3v4_KM675666    (781) ATTGAGATTTGCTTGGAACTACAGAAGAATGGAATAATGCAGGACTTCTCAACTGGATAT
CYP337B3v5_KX958388    (781) ATTGAGATTTGCTTGGAACTACAGAAGAATGGAATAATGCAGGACTTCTCAACTGGTTAT
CYP337B3v6_KX958389    (781) ATTGAGATTTGCTTGGAACTACAGAAGAATGGAATAATGCAGGACTTTTCAACTGGATAT
CYP337B3v7_KX958390    (781) ATTGAGATTTGCTTGGAACTACAGAAGAATGGAATAATGCAGGACTTCTCAACTGGATAT
CYP337B3v8_KX958391    (781) ATTGAGATTTGCTTGGAACTACAGAAGAATGGAATAATGCAGGACTTCTCAACTGGATAT
  CYP337B3_Olathe-2    (781) ATTGAGATTTGCTTGGAACTACAGAAGAATGGAATAATGCAGGACTTTTCAACTGGATAT
  CYP337B3_Olathe-6    (781) ATTGAGATTTGCTTGGAACTACAGAAGAATGGAATAATGCAGGACTTTTCAACTGGATAT
                             841                                                     900
CYP337B3v1_JQ995292    (841) AAATTGGAGCCGACCGACGAACTGATGGCTGCTCAAGCATTCTTCTTTTTTGTCGCTGGT
CYP337B3v2_KJ636466    (841) AAATTGGAGCCGACCGACGAACTGATGGCTGCTCAAGCATTCTTCTTTTTTGTGGCTGGT
CYP337B3v3_KM675665    (841) AAATTGGAGCCGACCGACGAACTGATGGCTGCTCAAGCATTCTTCTTTTTTGTGGCTGGT
CYP337B3v4_KM675666    (841) AAATTGGAGCCGACTGACGAACTGATGGCTGCTCAAGCATTCTTCTTTTTTGTGGCTGGT
CYP337B3v5_KX958388    (841) AAATTGGAGCCAACCGACGAACTGATGGCTGCTCAAGCATTCTTCTTTTTTGTGGCTGGT
CYP337B3v6_KX958389    (841) AAATTGGAGCCGACCGACGAACTGATGGCTGCTCAAGCATTCTTCTTTTTTGTGGCTGGT
CYP337B3v7_KX958390    (841) AAGTTGGAGCCGACCGACGAACTGATGGCTGCTCAAGCATTCTTCTTTTTTGTGGCTGGT
CYP337B3v8_KX958391    (841) AAATTGGAGCCGACTGACGAACTGATGGCTGCTCAAGCATTCTTCTTTTTTGTGGCTGGT
  CYP337B3_Olathe-2    (841) AAATTGGAGCCGACCGACGAACTGATGGCTGCTCAAGCATTCTTCTTTTTTGTGGCTGGT
  CYP337B3_Olathe-6    (841) AAATTGGAGCCGACCGACGAACTGATGGCTGCTCAAGCATTCTTCTTTTTTGTGGCTGGT
                             901                                                     960
CYP337B3v1_JQ995292    (901) GCAGACACCTCTGCTAACACAATGCATTATTCTTTGTTAGAGCTGTCAAACAATCCAAAA
CYP337B3v2_KJ636466    (901) GCAGACACCTCTGCTAACACAATGCATTATTCTTTGTTAGAGCTGTCAAACAATCCAAAA
CYP337B3v3_KM675665    (901) GCAGACACCTCTGCTAACACAATGCATTATTCTTTGTTAGAGCTGTCAAACAATCCAAAA
CYP337B3v4_KM675666    (901) GCAGACACCTCTGCTAACACAATGCATTATTCTTTGTTAGAGCTGTCAAACAATCCAAAA
CYP337B3v5_KX958388    (901) GCAGACACCTCTGCTAACACAATGCATTATTCTTTGTTAGAGCTGTCAAACAATCCAAAA
CYP337B3v6_KX958389    (901) GCAGACACCTCTGCTAACACAATGCATTATTCTTTGTTAGAGCTGTCAAACAATCCAAAA
CYP337B3v7_KX958390    (901) GCAGACACCTCTGCTAACACAATGCATTATTCTTTGTTAGAGCTGTCAAACAATCCAAAA
CYP337B3v8_KX958391    (901) GCAGACACCTCTGCTAACACAATGCATTATTCTTTGTTAGAGCTGTCAAACAATCCAAAA
  CYP337B3_Olathe-2    (901) GCAGACACCTCTGCTAACACAATGCATTATTCTTTGTTAGAGCTGTCAAACAATCCAAAA
  CYP337B3_Olathe-6    (901) GCAGACACCTCTGCTAACACAATGCATTATTCTTTGTTAGAGCTGTCAAACAATCCAAAA
                             961                                                    1020
CYP337B3v1_JQ995292    (961) ATCTTGGCAAAACTACATGAGGAAATTGACAAAGTTTTCGAAGGCGGAGCTGGGGAACTA
CYP337B3v2_KJ636466    (961) ATCTTGGCAAAACTACATGAGGAAATTGACAAAGTTTTCGAAGGCGGAGCTGGGGAACTA
CYP337B3v3_KM675665    (961) ATCTTGGCAAAACTACATGAGGAAATTGACAAAGTTTTCGAAGGCGGAGCTGGGGAACTA
CYP337B3v4_KM675666    (961) ATCTTGGCAAAACTACATGAGGAAATTGACAAAGTTTTCGAAGGCGGAGCTGGGGAACTA
CYP337B3v5_KX958388    (961) ATCCTGGCAAAACTACACGAAGAAATTGACAAAGTTTTCGAAGGCGGAGCTGGGGAACTA
CYP337B3v6_KX958389    (961) ATCTTGGCAAAACTACATGAGGAAATTGACAAAGTTTTCGCAGGTGGAGCTGGGGAACTA
CYP337B3v7_KX958390    (961) ATCTTGGCAAAACTACATGAGGAAATTGACAAAGTTTTCGAAGGCGGAGCTGGGGAACTA
CYP337B3v8_KX958391    (961) ATCTTGGCAAAACTACATGAGGAAATTGACAAAGTTTTCGAAGGCGGAGCTGGGGAACTA
  CYP337B3_Olathe-2    (961) ATCTTGGCAAAACTACATGAGGAAATTGACAAAGTTTTCGAAGGCGGAGCTGGGGAACTA
  CYP337B3_Olathe-6    (961) ATCTTGGCAAAACTACATGAGGAAATTGACAAAGTTTTCGCAGGTGGAGCTGGGGAACTA
                             1021                                                   1080
CYP337B3v1_JQ995292   (1021) ACTTATAATGACATTGATAAGTTACAATATTTAGATCAGGTTATAAATGAAGCAATGAGA
CYP337B3v2_KJ636466   (1021) ACTTATAATGACATTGATAAGTTACAATATTTAGATCAGGTTATAAATGAAGCAATGAGA
CYP337B3v3_KM675665   (1021) ACTTATAATGACATTGATAAGTTACAATATTTAGATCAGGTTATAAATGAAGCAATGAGA
CYP337B3v4_KM675666   (1021) ACTTATAATGACATTGATAAGTTACAATATTTAGATCAGGTTATAAATGAAGCAATGAGA
CYP337B3v5_KX958388   (1021) ACTTATAATGACATTGATAAGTTACAATATTTAGATCAGGTTATAAATGAAGCAATGAGA
CYP337B3v6_KX958389   (1021) ACTTATAATGACATTGATAAGTTACAATATTTAGATCAGGTTATAAATGAAGCAATGAGA
CYP337B3v7_KX958390   (1021) ACTTATAATGACATTGATAAGTTACAATATTTAGATCAGGTTATAAATGAAGCGATGAGA
CYP337B3v8_KX958391   (1021) ACTTATAATGACATTGATAAGTTACAATATTTAGATCAGGTTATAAATGAAGCAATGAGA
  CYP337B3_Olathe-2   (1021) ACTTATAATGACATTGATAAGTTACAATATTTAGATCAGGTTATAAATGAAGCAATGAGA
  CYP337B3_Olathe-6   (1021) ACTTATAATGACATTGATAAGTTACAATATTTAGATCAGGTTATAAATGAAGCAATGAGA
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                                      1081                                                1140
CYP337B3v1_JQ995292   (1081) AAGTATCCTCCCATAGGTGTCATGCAAAGATTGTGTACTAAAGATACAGTTTTACCGTCT
CYP337B3v2_KJ636466   (1081) AAGTATCCTCCAGTAGGTGTCATGCAAAGATTGTGTACTAAAGATACAGTTTTACCTTCT
CYP337B3v3_KM675665   (1081) AAGTATCCTCCAGTAGGTGTCATGCAAAGATTGTGTACTAAAGATACAGTTTTACCTTCT
CYP337B3v4_KM675666   (1081) AAGTATCCTCCAGTAGGTGTCATGCAAAGATTGTGTACTAAAGATACAGTTTTACCTTCT
CYP337B3v5_KX958388   (1081) AAGTATCCTCCAGTAGGTGTCATGCAAAGATTGTGCACTAAAGATACAGTTTTACCTTCT
CYP337B3v6_KX958389   (1081) AAGTATCCTCCAGTAGGTGTCATGCAAAGATTGTGTACTAAAGATACGGTTTTACCTTCT
CYP337B3v7_KX958390   (1081) AAGTATCCTCCAGTAGGTGTCATGCAAAGATTGTGCACTAAAGATACAGTTTTACCTTCT
CYP337B3v8_KX958391   (1081) AAGTATCCTCCAGTAGGTGTCATGCAAAGATTGTGTACTAAAGATACAGTTTTACCTTCT
 CYP337B3_Olathe-2    (1081) AAGTATCCTCCAGTAGGTGTCATGCAAAGATTGTGTACTAAAGATACAGTTTTACCTTCT
 CYP337B3_Olathe-6    (1081) AAGTATCCTCCAGTAGGTGTCATGCAAAGATTGTGTACTAAAGATACAGTTTTACCTTCT
                                      1141                                                1200
CYP337B3v1_JQ995292   (1141) GGTATACCCATAGCAAAGGGTAACACAATAATGATTCCAGTGTTCGGTCTTCACAGAGAT
CYP337B3v2_KJ636466   (1141) GGTATACCCATAGCAAAGGGTAACACAATAATGATACCAGTGTTCGGTCTTCACAGAGAC
CYP337B3v3_KM675665   (1141) GGTATACCCATAGCAAAGGGTAACACAATAATGATTCCAGTGTTCGGTCTTCACAGAGAC
CYP337B3v4_KM675666   (1141) GGTATACCCATAGCAAAGGGTAACACAATAATGATTCCAGTGTTCGGTCTTCACAGAGAC
CYP337B3v5_KX958388   (1141) GGTATACCCATAGCAAAGGGTAACACAATAATGATTCCAGTGTTCGGTCTTCACAGAGAC
CYP337B3v6_KX958389   (1141) GGTATACCCATAGCAAAGGGTAACACAATAATGATACCAGTGTTCGGTCTTCACAGAGCC
CYP337B3v7_KX958390   (1141) GGTATACCCATAGCAAAAGGTAACACAATAATGATTCCAGTGTTCGGTCTTCACAGAGAC
CYP337B3v8_KX958391   (1141) GGTATACCCATAGCAAAGGGTAACACAATAATGATTCCAGTGTTCGGTCTTCACAGAGAC
 CYP337B3_Olathe-2    (1141) GGTATACCCATAGCAAAGGGTAACACAATAATGATACCAGTGTTCGGTCTTCACAGAGAC
 CYP337B3_Olathe-6    (1141) GGTATACCCATAGCAAAGGGTAACACAATAATGATACCAGTGTTCGGTCTTCACAGAGAC
                                      1201                                                1260
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CYP337B3v2_KJ636466   (1201) GAAAAATACTTTGATGACCCACACGTATTTGATCCGGATAGATTTTCACCAGAAAACGTA
CYP337B3v3_KM675665   (1201) GAAAAATACTTTGATGACCCACACGTATTTGATCCGGATAGATTTGCACCAGAAAACGTA
CYP337B3v4_KM675666   (1201) GAAAAATACTTTGATGACCCACACGTATTTGATCCGGATAGATTTGCACCAGAAAACGTA
CYP337B3v5_KX958388   (1201) GAAAAATACTTTGATGACCCACATGTATTTGATCCGGATAGATTTTTACCAGAAAACGTA
CYP337B3v6_KX958389   (1201) GAAAAATACTTTGATGACCCCCATGTATTTGATCCGGATAGATTTTCACCAGAAACCGTA
CYP337B3v7_KX958390   (1201) GAAAAATACTTCGATGACCCACATGTATTTGATCCGGATAGATTTTCACCAGAAATGTA
CYP337B3v8_KX958391   (1201) GAAAAATACTTTGATGACCCACACGTATTTGATCCGGATAGATTTGCACCAGAAAACGTA
 CYP337B3_Olathe-2    (1201) GAAAAATACTTTGATGACCCACACGTATTTGATCCGGATAGATTTTCACCAGAAAACGTA
 CYP337B3_Olathe-6    (1201) GAAAAATACTTTGATGACCCACATGTATTTGATCCGGATAGATTTTCACCAGAAAACGTA
                                      1261                                                1320
CYP337B3v1_JQ995292   (1261) TCCAAAATCAAGAATTACGCTTATTTACCTTTTGGTGAAGGAAACCGCATTTGTATTGGT
CYP337B3v2_KJ636466   (1261) TCCAAAATCAAGAATTATGCTTATTTACCTTTTGGTGAAGGAAACCGCATTTGTATTGGT
CYP337B3v3_KM675665   (1261) TCCAAAATCAAGAATTATGCTTATTTACCTTTTGGTGAAGGAAACCGCATTTGTATTGGT
CYP337B3v4_KM675666   (1261) TCCAAAATCAAGAATTATGCTTATTTACCTTTTGGTGAAGGAAACCGCATTTGTATTGGT
CYP337B3v5_KX958388   (1261) TCCAAAATCAAGAATTATGCCTATTTACCTTTTGGTGAAGGAAACCGCATTTGTATTGGT
CYP337B3v6_KX958389   (1261) TCCAAAATCAAGAATTATGCTTATTTACCTTGTGGTGAAGGAAACCGCATTTGTATTGGT
CYP337B3v7_KX958390   (1261) TCCAAAATCAAGAATTATGCTTATTTACCTTTTGGTGAAGGAAACCGCATTTGTATTGGT
CYP337B3v8_KX958391   (1261) TCCAAAATCAAGAATTATGCTTATTTACCTTTTGGTGAAGGAAACCGCATTTGTATTGGT
 CYP337B3_Olathe-2    (1261) TCCAAAATCAAGAATTATGCTTATTTACCTTTTGGTGAAGGAAACCGCATTTGTATTGGT
 CYP337B3_Olathe-6    (1261) TCCAAAATCAAGAATTATGCTTATTTACCTTTTGGTGAAGGAAACCGCATTTGTATTGGT
                                      1321                                                1380
CYP337B3v1_JQ995292   (1321) GAGTA----TTAAACATTTATACATATGTATTGTTAATATTG-TAAATATA---------
CYP337B3v2_KJ636466   (1321) GAGTACCTATTAAACATCTATACATATGTATTGTTAATCTTCATATATATAAAAATGAAT
CYP337B3v3_KM675665   (1321) GAGTA----TTCAACATTTACTTATAACT-------TAATT-TAAATATA---------
CYP337B3v4_KM675666   (1321) GAGTA----TTCAACATTTACTTATAACT-------TAATT-TAAATATA---------
CYP337B3v5_KX958388   (1321) GAGTA----CTAAACATTTACTTATACATAT---------A----ATATA---------
CYP337B3v6_KX958389   (1321) GAGTACCTATTAAACATCTATACATATGTATTGTTAATCTTCATATATATAAAAATGAAT
CYP337B3v7_KX958390   (1321) GAGTA----TTAAACATTTATACATATGTATTGTTAATATTG-TAAATATA---------
CYP337B3v8_KX958391   (1321) GAGTA----TTCAACATTTACTTATAACT-------TAATT-TAAATATA---------
 CYP337B3_Olathe-2    (1321) GAGTACCTATTAAACATCTATACATATGTATTGTTAATCTTCATATATATAAAAATGAAT
 CYP337B3_Olathe-6    (1321) GAGTACCTATTAAACATCTATACATATGTATTGTTAATCTTCATATATATAAAAATGAAT
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                                      1381                                                   1440
CYP337B3v1_JQ995292  (1367) ---TATGTGTAACTCATAC------------------------ATTT-------------
CYP337B3v2_KJ636466  (1381) TGCTGTTCGTTAGTCTTACTAAAACTCGAGTATGGCTGGACCGATTTGGCTTATTTTGGT
CYP337B3v3_KM675665  (1359) ---TTTTTGTAACTT-TAT------------------------ATTT-------------
CYP337B3v4_KM675666  (1359) ---TTTTTGTAACTT-TAT------------------------ATTT-------------
CYP337B3v5_KX958388  (1354) ---TTTTTGTAACATTTGTAA-----------------C----ATTT-------------
CYP337B3v6_KX958389  (1381) TGCTGTTCGTTAGTCTTACTAAAACTCGAGTATGGCTGGACCGATTTGGCTTATTTTGGT
CYP337B3v7_KX958390  (1367) ---TTTGTGTAACTCATAC------------------------ATTT-------------
CYP337B3v8_KX958391  (1359) ---TTTTTGTAACTT-TAT------------------------ATTT-------------
 CYP337B3_Olathe-2   (1381) TGCTGTTCGTTAGTCTTACTAAAACTCGAGTATGGCTGGACCGATTTGGCTTATTTTGGT
 CYP337B3_Olathe-6   (1381) TGCTGTTCGTTAGTCTTACTAAAACTCGAGTATGGCTGGACCGATTTGGCTTATTTTGGT
                                      1441                                                   1500
CYP337B3v1_JQ995292  (1387) ------AAGATTGTAGTG--------AAGGCATAAAT-----------------------
CYP337B3v2_KJ636466  (1441) GTTAAAATGTTTGTAGAGGTCCAGGGAAGGTATAAACGATACGAAGTTTGCGGGATCAGC
CYP337B3v3_KM675665  (1378) ------AAGGTTCTAGAG--------AAGGCATAAAT-----------------------
CYP337B3v4_KM675666  (1378) ------AAGGTTCTAGAG--------AAGGCATAAAT-----------------------
CYP337B3v5_KX958388  (1377) ------AAGGTTCTAGAG--------AAGGCATAAAT-----------------------
CYP337B3v6_KX958389  (1441) GTTAAAATGTTTGTAGAGGTCCAGGGAAGGTTTAAACGATACGAAGTTTGCGGGATCACC
CYP337B3v7_KX958390  (1387) ------AAGATTCTAGTG--------AAGGCATAAAT-----------------------
CYP337B3v8_KX958391  (1378) ------AAGGTTCTAGAG--------AAGGCATAAAT-----------------------
 CYP337B3_Olathe-2   (1441) GTTAAAATGTTTGTAGAGGTCCAGGGAAGGTATAAACGATACGAAGTTTGCGGGATCAGC
 CYP337B3_Olathe-6   (1441) GTTAAAATGTTTGTAGAGGTCCAGGGAAGGTTTAAACGATACGAAGTTTGCGGGATCACC
                                      1501                                                   1560
CYP337B3v1_JQ995292  (1410) ------------------------------CTTATTTAGCTTTGATCAGTTATTCTGAA
CYP337B3v2_KJ636466  (1501) TAGTATTGTAAATATATTTGTGTAACTTATACTTGTTTAGCTTTGATCAGTTATTCTAAA
CYP337B3v3_KM675665  (1401) ------------------------------CTTATTTAGCTTTGATCAGTTATTCTAAA
CYP337B3v4_KM675666  (1401) ------------------------------CTTATTTAGCTTTGATCAGTTATTCTAAA
CYP337B3v5_KX958388  (1400) ------------------------------CTTATTTAGCTTTGATCAGTTATTCTAAA
CYP337B3v6_KX958389  (1501) TAGTATTGTAAATATATTTGTGTAACTTATACTTATTTAGCTTTGATCAGTTATTCTAAA
CYP337B3v7_KX958390  (1410) ------------------------------CTTATTTAG---------------------
CYP337B3v8_KX958391  (1401) ------------------------------CTTATTTAGCTTTGATCAGTTATTCTAAA
 CYP337B3_Olathe-2   (1501) TAGTATTGTAAATATATTTGTGTAACTTATACTTGTTTAGCTTTGATCAGTTATTCTAAA
 CYP337B3_Olathe-6   (1501) TAGTATTGTAAATATATTTGTGTAACTTATACTTATTTAGCTTTGATCAGTTATTCTAAA
                                      1561                                                   1620
CYP337B3v1_JQ995292  (1439) GTAGGTACCTAGTACGCAATGGGCGTGCTAGTCTTTTTATGGCCCAAAACAATTGTTCAA
CYP337B3v2_KJ636466  (1561) GAAGGTACCTATTACGCAATGTGCGTCCTAGTCTTTTTATGGGATCAAAACAATTGTTCAA
CYP337B3v3_KM675665  (1430) GTAGGTACCTAGTACGCAATGGGCGTGCTAGTCTTTTTATGGCCCAAAACAATTGTTCAA
CYP337B3v4_KM675666  (1430) GTAGGTACCTAGTACGCAATGGGCGTGCTAGTCTTTTTATGGCCCAAAACAATTGTTCAA
CYP337B3v5_KX958388  (1429) GAAGGTACCTAGTATGCAATGGGCGTGCTAGTCTTTTTATGGCCTAAAGCAATTGTTCAA
CYP337B3v6_KX958389  (1561) GAAGGTACCTATTACGCAATGTGCGTCCTAGTCTTTTTATGGATCAAAACAATTGTTCAA
CYP337B3v7_KX958390  (1419) ---G-TACCTAGTACGCAACGGGCGTGCTAGTCTTTTTATGGTTCAAAACAATTGTTCAA
CYP337B3v8_KX958391  (1430) GTAGGTACCTAGTACGCAATGGGCGTGCTAGTCTTTTTATGGCCCAAAACAATTGTTCAA
 CYP337B3_Olathe-2   (1561) GAAGGTACCTATTACGCAATGTGCGTCCTAGTCTTTTTATGGATCAAAACAATTGTTCAA
 CYP337B3_Olathe-6   (1561) GAAGGTACCTATTACGCAATGTGCGTCCTAGTCTTTTTATGGATCAAAACAATTGTTCAA
                                      1621                                                   1680
CYP337B3v1_JQ995292  (1499) TGAACGGTCATAATCTTCCATACTTATTCCACCCCATTCATTCAATCATTGTCTCATAGT
CYP337B3v2_KJ636466  (1621) TGATCGACCATAATCTTCAATACTTATTCTACCCCATTCATTCAATCATTGTGTCATATT
CYP337B3v3_KM675665  (1490) TGAACGGTCATAATCTTCCATACTTATTCCACCCCATTCATTCAATCATTGTCTCATATT
CYP337B3v4_KM675666  (1490) TGAACGGTCATAATCTTCCATACTTATTCCACCCCATTCATTCAATCATTGTCTCATATT
CYP337B3v5_KX958388  (1489) TGATCGACCATAATCATCAATACTTATTCCACCCCATTCATTCAATCATTGTCTCATATT
CYP337B3v6_KX958389  (1621) TGATCGACCATAATGATCACTACTTATTCTACCCCATTCATTCAATCATTGTCTCATAGT
CYP337B3v7_KX958390  (1475) TGATCGACCATAATCATCAATACTTATTCTACCCCATTCATTCAATCATTGTCTCATAGT
CYP337B3v8_KX958391  (1490) TGAACGGTCATAATCTTCCATACTTATTCCACCCCATTCATTCAATCATTGTCTCATATT
 CYP337B3_Olathe-2   (1621) TGATCGACCATAATCTTCAATACTTATTCTACCCCATTCATTCAATCATTGTGTCATATT
 CYP337B3_Olathe-6   (1621) TGATCGACCATAATGATCACTACTTATTCTACCCCATTCATTCAATCATTGTCTCATAGT
                                      1681                                                   1740
CYP337B3v1_JQ995292  (1559) AAGTAGTCATAAAAATACATAAATGAATAGTTATCATTCCTTTTGTTTAGTTTT-ACTAA
CYP337B3v2_KJ636466  (1681) AAGAAGTCATAAAAATACATATATGAATAGTTATCATTCCCTTTGTTTAGTTTT-ACTAA
CYP337B3v3_KM675665  (1550) AAGTAGTCATAAAAATACATAAATGAATAGTTATCATTCCCTTTGTTTAGTTTT-ACTAA
CYP337B3v4_KM675666  (1550) AAGTAGTCATAAAAATACATAAATGAATAGTTATCATTCCCTTTGTTTAGTTTT-ACTAA
CYP337B3v5_KX958388  (1549) AAG-AGTCATAAAAATACATAAATGAATAGTTATCATTCCCTTTGTTTAGTTTT-ACTAA
CYP337B3v6_KX958389  (1681) AAGTAGTCATAAAAATACATAAATGAATGGT-ATCATTCCCTTTGTTTAGTTTTTACATA
CYP337B3v7_KX958390  (1535) AAGTAATCATAAAAATACATAAATGAATGGTTATCATTCCCTTTGTTTAGTTTT-ACTAA
CYP337B3v8_KX958391  (1550) AAGTAGTCATAAAAATACATAAATGAATAGTTATCATTCCCTTTGTTTAGTTTT-ACTAA
 CYP337B3_Olathe-2   (1681) AAGAAGTCATAAAAATACATATATGAATAGTTATCATTCCCTTTGTTTAGTTTT-ACTAA
 CYP337B3_Olathe-6   (1681) AAGTAGTCATAAAAATACATAAATGAATGGT-ATCATTCCCTTTGTTTAGTTTT-ACATA
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CYP337B3v1_JQ995292   (1618)  TTGCATCATCCGATAAATCAGTGAGTGATCTGATAATGCATTATTTAATTTA--------
CYP337B3v2_KJ636466   (1740)  TTGCATCATCCGATAAATGAGTGAGTGATCTGATAATGCATTATTTAATTTTTTAATTTG
CYP337B3v3_KM675665   (1609)  TTGCATCATCCGATAAATCAGTGAGTGATCTGATAATGCATTATTTAATTTA--------
CYP337B3v4_KM675666   (1609)  TTGCATCATCCGATAAATCAGTGAGTGATCTGATAATGCATTATTTAATTTA--------
CYP337B3v5_KX958388   (1607)  TTGCATCATCCGATAAATGAGTGAGTGATCTGATAATGCATTATTTAATTTTTTAATTTA
CYP337B3v6_KX958389   (1740)  TTGCATCATCCGATAAATGAGTGAGTGATCTGATAATGCATTATTTAATTTA--------
CYP337B3v7_KX958390   (1594)  TTGCATCATCCGATAAATGAGTGAGTGATCTGATAATGCATTATTTAATTTA--------
CYP337B3v8_KX958391   (1609)  TTGCATCATCCGATAAATCAGTGAGTGATCTGATAATGCATTATTTAATTTA--------
 CYP337B3_Olathe-2    (1740)  TTGCATCATCCGATAAATGAGTGAGTGATCTGATAATGCATTATTTAATTTTTTAATTTG
 CYP337B3_Olathe-6    (1739)  TTGCATCATCCGATAAATGAGTGAGTGATCTGATAATGCATTATTTAATTTA--------
                              1801                                                    1860
CYP337B3v1_JQ995292   (1670)  AATGATAATGACGGCCTAATCCGGTTATCATTAATTATTT-AATCATTAGTTAGCAAATA
CYP337B3v2_KJ636466   (1800)  AATGATAATGACGGCCTAATTCGGTTATCATAAATCATTA-AATCATTAGTTAGCAAATA
CYP337B3v3_KM675665   (1661)  AATGATAATGACGGCCTAATTCGGTTATCATTAGTTATTT-AATCGTTAGTTAGCAAATA
CYP337B3v4_KM675666   (1661)  AATGATAATGACGGCCTAATTCGGTTATCATTAGTTATTT-AATCGTTAGTTAGCAAATA
CYP337B3v5_KX958388   (1667)  AATGATAATGACGGCCTAATTCGGTTATCATTAATCATTTTAATCATTAGTTAGCAAATA
CYP337B3v6_KX958389   (1792)  AATGATAGTGACGGCCTAATTCGGTTATCATTAATCATTT-AATCATTAGTTAGCAAATA
CYP337B3v7_KX958390   (1646)  AATGATTATGACGGCCTAATTCGGTTATCATGAATCATTTTAATCATTAGTTAGCAAATA
CYP337B3v8_KX958391   (1661)  AATGATAATGACGGCCTAATTCGGTTATCATTAGTTATTT-AATCGTTAGTTAGCAAATA
 CYP337B3_Olathe-2    (1800)  AATGATAATGACGGCCTAATTCGGTTATCATAAATCATTA-AATCATTAGTTAGCAAATA
 CYP337B3_Olathe-6    (1791)  AATGATAGTGACGGCCTAATTCGGTTATCATTAATCATTT-AATCATTAGTTAGCAAATA
                              1861                                                    1920
CYP337B3v1_JQ995292   (1729)  TTTTTCTTTAATCTTGGCTTATCTCGACAAACTGTATACCTAGTACTAATTATTCGTCTA
CYP337B3v2_KJ636466   (1859)  TTTTTCTTTAATCTTTGCTAATCTTGACAAACTTTATACCTAGTACTAATTATTAGTTAT
CYP337B3v3_KM675665   (1720)  TTTTTCTTTAATCTTGGCTTATCTTGACAAACTTTATACCTAGTACTAATTGTTTGTCTG
CYP337B3v4_KM675666   (1720)  TTTTTCTTTAATCTTGGCTTATCTTGACAAACTTTATACCTAGTACTAATTGTTTGTCTG
CYP337B3v5_KX958388   (1727)  TTTTTCTTTAATCTTGGCTTATCTTGACAATCTTTATACCAAGTAA-AATTGTTTGTTTG
CYP337B3v6_KX958389   (1851)  TTTTTCTTTAATCTTGGCTTATCTTGACAAA----ATACCTAGTACTAATTGTTTGTTTG
CYP337B3v7_KX958390   (1706)  TTTTTCTTTAATCTTGGCTTATCTTGACAAACTTTATACCTAGTACTAATTGTCTGTGTT
CYP337B3v8_KX958391   (1720)  TTTTTCTTTAATCTTGGCTTATCTTGACAAACTTTATACCTAGTACTAATTGTTTGTCTG
 CYP337B3_Olathe-2    (1859)  TTTTTCTTTAATCTTTGCTAATCTTGACAAACTTTATACCTAGTACTAATTATTAGTTAT
 CYP337B3_Olathe-6    (1850)  TTTTTCTTTAATCTTGGCTTATCTTGACAAA----ATACCTAGTACTAATTGTTTGTTTG
                              1921                                                    1980
CYP337B3v1_JQ995292   (1789)  TTTATTTTTTCCTATTATTATGTATCCCT-------ATCTCAGGTGCGTCGT--TTTAAT
CYP337B3v2_KJ636466   (1919)  TTTGACTATTCCTACTTATCCCTATTTATT------ATCTCAAGTGCGTATTTGTTTAAT
CYP337B3v3_KM675665   (1780)  TTTATTTTTACCTATTATTATGTATCCCT-------ATCTCAGGTGCGTTGT--TTTAAA
CYP337B3v4_KM675666   (1780)  TTTATTTTTACCTATTATTATGTATCCCT-------ATCTCAGGTGCGTTGT--TTTAAA
CYP337B3v5_KX958388   (1786)  TTTATTTTTACCTATAACTATTTATCCCTATTTATTATCTCAAGTGCGTATTTGTTTAAT
CYP337B3v6_KX958389   (1907)  TTTATTTTAACCTATAACTATTTATCCCTATTTATTATCTCAAGTGCGTATTTGTTTAAT
CYP337B3v7_KX958390   (1766)  TTTACCTTTTACTATTTATCCCTATTTGTT------ATCTCAAGTG--------TATAAT
CYP337B3v8_KX958391   (1780)  TTTATTTTTACCTATTATTATGTATCCCT-------ATCTCAGGTGCGTTGT--TTTAAA
 CYP337B3_Olathe-2    (1919)  TTTGACTATTCCTACTTATCCCTATTTATT------ATCTCAAGTGCGTATTTGTTTAAT
 CYP337B3_Olathe-6    (1906)  TTTATTTTAACCTATAACTATTTATCCCTATTTATTATCTCAAGTGCGTATTTGTTTAAT
                              1981                                                    2040
CYP337B3v1_JQ995292   (1840)  TATAGTACCTACGACAATAGTTTACAACAAAGGTATAAGTT--ACTATGGAAATAGTCTG
CYP337B3v2_KJ636466   (1973)  AGTAGTATTTACGACAATAGTTTACCACAAAGTTATATAAG-TACTATGTAAATAGTCTG
CYP337B3v3_KM675665   (1831)  AATAGTATTTACGACAATAGTTTACCACAAAGTTATATAATGCACTATGTAAATAGTCTG
CYP337B3v4_KM675666   (1831)  AATAGTATTTACGACAATAGTTTACCACAAAGTTATATAATGCACTATGTAAATAGTCTG
CYP337B3v5_KX958388   (1846)  AGTAGTATTTACGACAATAGTTTACCACAAAGTTATATAAG-TACTATGTAAATAGTCTG
CYP337B3v6_KX958389   (1967)  AGTAGTATTTACGACAATAGTTTACCACAAAGTTATATAAA-TACTATGTAAATAGTCTG
CYP337B3v7_KX958390   (1812)  TATAGTACTTACGACAATAGTTTACCACAAAGTTATATAATGTAGTATGTAAATAG----
CYP337B3v8_KX958391   (1831)  AATAGTATTTACGACAATAGTTTACCACAAAGTTATATAATGCACTATGTAAATAGTCTG
 CYP337B3_Olathe-2    (1973)  AGTAGTATTTACGACAATAGTTTACCACAAAGTTATATAAG-TACTATGTAAATAGTCTG
 CYP337B3_Olathe-6    (1966)  AGTAGTATTTACGACAATAGTTTACCACAAAGTTATATAAA-TACTATGTAAATAGTCTG
                              2041                                                    2100
CYP337B3v1_JQ995292   (1898)  AAGTTGATAAAACAACGACTAGTCTCTACC--------------TGCAGTAGTTTGTACA
CYP337B3v2_KJ636466   (2032)  CAGTTGATAAAACAACTACTAGTCTCTACCTGAG----------TGCAGTGGTTTG---A
CYP337B3v3_KM675665   (1891)  AAGTTGATAAAACAACGACTAGTCTACATGAG-----------TGCAGTGGTTTGTACA
CYP337B3v4_KM675666   (1891)  AAGTTGATAAAACAACGACTAGTCTACATGAG-----------TGCAGTGGTTTGTACA
CYP337B3v5_KX958388   (1905)  CAGTTGATAAAACAACTACTAGTCTCTACCTGAG----------TGTAGTGGGTTTGTACA
CYP337B3v6_KX958389   (2026)  AAGTTGACAAAACAGCGACTAGTTTACCTGAG----------TGCAGTGGTTTGTACA
CYP337B3v7_KX958390   (1868)  AAGTTGATAAAACAACGACTAGTCTCTACCTGAGTGCAGTGGCACGCAGTGGTTTGTACA
CYP337B3v8_KX958391   (1891)  AAGTTGATAAAACAACGACTAGTCTACATGAG-----------TGCAGTGGTTTGTACA
 CYP337B3_Olathe-2    (2032)  CAGTTGATAAAACAACTACTAGTCTCTACCTGAG----------TGCAGTGGTTTG---A
 CYP337B3_Olathe-6    (2025)  AAGTTGACAAAACAGCGACTAGTTTACCTGAG-----------TGCAGTGGTTTGTACA
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                              2101                                                              2160
CYP337B3v1_JQ995292  (1944) CAATAT----TAATATTCTGG-TTTCATCCGACTTATTGAATTACGTCTCTATTACATAC
CYP337B3v2_KJ636466  (2079) CAATACCGATTAATATTCTGG-TTTCATCTGACTTATTGAATTACGTCCCTATTACATAC
CYP337B3v3_KM675665  (1939) CAATATCTATTAATATTCTGG-TTTCATCTGACTTATTGAATTACGTCGCTATAACATAC
CYP337B3v4_KM675666  (1939) CAATATCTATTAATATTCTGG-TTTCATCTGACTTATTGAATTACGTCGCTATAACATAC
CYP337B3v5_KX958388  (1955) CAATAT----TATTATTCTGGGTTTCATCTGACTTATTGAATTACGTCGCTATAATAAAC
CYP337B3v6_KX958389  (2074) CAATACCTATTAATATTCTGG-TTTCATCTGACTTATTGAATTACGTCCCTATTACATAC
CYP337B3v7_KX958390  (1928) CAATAT----TAATATTCTGG-TTTCATCTGACTTATTGAATTACGTCCCTAATACATAC
CYP337B3v8_KX958391  (1939) CAATATCTATTAATATTCTGG-TTTCATCTGACTTATTGAATTACGTCGCTATAACATAC
 CYP337B3_Olathe-2   (2079) CAATACCGATTAATATTCTGG-TTTCATCTGACTTATTGAATTACGTCCCTATTACATAC
 CYP337B3_Olathe-6   (2073) CAATACCTATTAATATTCTGG-TTTCATCTGACTTATTGAATTACGTCCCTATTACATAC
                              2161                                                              2220
CYP337B3v1_JQ995292  (1999) AATGTCTTT------ATCTAACACTGTAGGGTTATTTTATAACTAGGTGCCACCTGCGGT
CYP337B3v2_KJ636466  (2138) AAGGTCTCT------ATCTAACACTGTAGGTTTATTTTATAACTAGCTTGCGCCAGCGGT
CYP337B3v3_KM675665  (1998) AAGGTTTTT------ATCTAATACTGCACGGTTATATTATAACTAGCTTCCGCCAGTGGT
CYP337B3v4_KM675666  (1998) AAGGTTTTT------ATCTAATACTGTACGGTTATATTATAACTAGCTTCCGCCAGTGGT
CYP337B3v5_KX958388  (2011) AAGGTCTAGCACTAGATCTAGCACTGTACCGTTATATTATAACTAGCTGCTGCCAGCAGT
CYP337B3v6_KX958389  (2133) AAGGTCTTT------ATCTAACACTGTAGTGTTATTTTATAACTAGCTTCCGCCAGCGGT
CYP337B3v7_KX958390  (1983) AAGGTCTTT------ATCTAACACTGTAGGTTTATTTTATAACTAGGTGCTTCCAGCGGT
CYP337B3v8_KX958391  (1998) AAGGTTTTT------ATCTAATACTGTACGGTTATATTATAACTAGCTTCCGCCAGTGGT
 CYP337B3_Olathe-2   (2138) AAGGTCTCT------ATCTAACACTGTAGGTTTATTTTATAACTAGCTTGCGCCAGCGGT
 CYP337B3_Olathe-6   (2132) AAGGTCTTT------ATCTAACACTGTAGTGTTATTTTATAACTAGCTTCCGCCAGCGGT
                              2221                                                              2280
CYP337B3v1_JQ995292  (2053) TTAATTCTCAACTCATATTGCGCTCACATAAAAA--TTAGCATCGATAATAATGTGGCTA
CYP337B3v2_KJ636466  (2192) TTAATTCTCAACCTA---------CACATAAAA---GTAGCATCAATAATAATACAGCTA
CYP337B3v3_KM675665  (2052) TTAACTCTCAACCCA---------CACATAAAAA--GTAGCATCGATTATAATGTTGCTG
CYP337B3v4_KM675666  (2052) TTAACTCTTAACCCA---------CACATAAAAA--GTAGCATCGATTATAATGTTGCTG
CYP337B3v5_KX958388  (2071) TTAACTCTAAACCCATATCACGCACACATATAAATAGTTGCATCGATAATAATGTGGCTA
CYP337B3v6_KX958389  (2187) TTAACTCTCAACCTA---------CACATAAAA---GTAGCATCAATAATAATGTGGCTA
CYP337B3v7_KX958390  (2037) TTAACTCTCAACCTA---------CACATAAAA---GTAGCATCGATAATGAGCTGCCTA
CYP337B3v8_KX958391  (2052) TTAACTCTCAACCCA---------CACATAAAAA--GTAGCATCGATTATAATGTTGCTG
 CYP337B3_Olathe-2   (2192) TTAATTCTCAACCTA---------CACATAAAA---GTAGCATCAATAATAATACAGCTA
 CYP337B3_Olathe-6   (2186) TTAACTCTCAACCTA---------CACATAAAA---GTAGCATCAATAATAATGTGGCTA
                              2281                                                              2340
CYP337B3v1_JQ995292  (2111) CTTAACACTACAAGAATTTCTCAAATTACCCCAGCTATCCCAGGTT--------------
CYP337B3v2_KJ636466  (2240) CTTAACACTATAAGAATTTCTCAAATCACCCCAGTTATCCCAGGTT--------------
CYP337B3v3_KM675665  (2101) CTTAACACTTTAAGAATTTCTCAAATTACCCCAGCTATCCCAGGTT--------------
CYP337B3v4_KM675666  (2101) CTTAACACTTTAAGAATTTCTCAAATTACCCCAGCTATCCCAGGTT--------------
CYP337B3v5_KX958388  (2131) TTTAACACTGAAAAAAATTCTCGAATCACCCCAGTTATTCCAGGTTGAAGCAAACAAACT
CYP337B3v6_KX958389  (2235) TTTAACACTGAAAAAAAATCTCAAATTACCCCAGCTATCCCAGGTT--------------
CYP337B3v7_KX958390  (2085) CTTACCACTATAAGAATTTCTCAAATTACCTCAGCTATCCCAGGTT--------------
CYP337B3v8_KX958391  (2101) CTTAACACTTTAAGAATTTCTCAAATTACCCCAGCTATCCCAGGTT--------------
 CYP337B3_Olathe-2   (2240) CTTAACACTATAAGAATTTCTCAAATCACCCCAGTTATCCCAGGTT--------------
 CYP337B3_Olathe-6   (2234) TTTAACACTGAAAAAAAATCTCAAATTACCCCAGCTATCCCAGGTT--------------
                              2341                                                              2400
CYP337B3v1_JQ995292  (2157) ---CAGATATAATGGTTCAGGCATAGA---------CGATAATGATAACTGAGATACTTT
CYP337B3v2_KJ636466  (2286) -----------------------------------------AAAACTGAGATA-TTT
CYP337B3v3_KM675665  (2147) ---CAGATATAATGGTTCAGGTATAGA---------TGATGATGATAACTGAGATACTTT
CYP337B3v4_KM675666  (2147) ---CAGATATAATGGTTCAGGTATAGA---------TGATGATGATAACTGAGATACTTT
CYP337B3v5_KX958388  (2191) TTTCAGCTTTAAAATATTAGTCATCTACTAATATTTTAATAATGATATTTGAGATA-TTT
CYP337B3v6_KX958389  (2281) ---CAGATATAATGGTTCAGGTATAGA---------TGATGATGATACCTTAGGTA-TTT
CYP337B3v7_KX958390  (2131) ---CAGATATAATGGTTCAGGCATAGA---------TGATGATGATAACTCAGATA-TTT
CYP337B3v8_KX958391  (2147) ---CAGATATAATGGTTCAGGTATAGA---------TGATGATGATAACTGAGATACTTT
 CYP337B3_Olathe-2   (2286) ---AA------------------------------------AACTGAGATA-TTT
 CYP337B3_Olathe-6   (2280) ---CAGATATAATGGTTCAGGTATAGA---------TGATGATGATACCTTAGGTA-TTT
                              2401                                                              2460
CYP337B3v1_JQ995292  (2205) TTT--ATGTTCTAAAGTACTTTTCCATCTTGTTCCAGGTGTACGCTTCGCTCGCCTCCAA
CYP337B3v2_KJ636466  (2301) TTT--ATGTTCTAAAGTACTTTTCCGTCTTGTTCCAGGTGTACGCTTCGCTCGCCTCCAA
CYP337B3v3_KM675665  (2195) TTTTTATGTTTTAAAGTACTTTTCAATCTTGTTCCAGGTGTACGCTTCGCTCGCCTCCAA
CYP337B3v4_KM675666  (2195) TTTTTATGTTTTAAAGTACTTTTCAATCTTGTTCCAGGTGTACGCTTCGCTCGCCTCCAA
CYP337B3v5_KX958388  (2250) TTT--ATGTTCTAAAGTACTTTTACATCTTGTTCCAGGTGTACGCTTCGCTCGCCTCCAA
CYP337B3v6_KX958389  (2328) TTT--ATGTTCTCAAGTACGATTCCATCTTGTTCCAGGTGTACGCTTCGCTCGCCTCCAA
CYP337B3v7_KX958390  (2178) TTT--ATATTCTAAAGTACTTTTCCATCTTGTTCCAGGTGTACGCTTCGCTCGCCTCCAA
CYP337B3v8_KX958391  (2195) TTTTTATGTTTTAAAGTACTTTTCAATCTTGTTCCAGGTGTACGCTTCGCTCGCCTCCAA
 CYP337B3_Olathe-2   (2301) TTT--ATGTTCTAAAGTACTTTTCCGTCTTGTTCCAGGTGTACGCTTCGCTCGCCTCCAA
 CYP337B3_Olathe-6   (2327) TTT--ATGTTCTCAAGTACGATTCCATCTTGTTCCAGGTGTACGCTTCGCTCGCCTCCAA
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                                            2461                                                          2520
CYP337B3v1_JQ995292    (2263)  GTGAAAGCGGGTCTCGCCTGGCTGTTACGTCGTTTTACCTTAGTCGAACAGGACAATTGC
CYP337B3v2_KJ636466    (2359)  GTGAAAGCGGGTCTCGCCTGGCTGTTACGTCGTTTTACCTTAGTCGAACAGGACAATTGC
CYP337B3v3_KM675665    (2255)  GTGAAAGCGGGTCTCGCCTGGTTGTTACGTCGTTTTACTCTAGTCGAACAGGACAATTGC
CYP337B3v4_KM675666    (2255)  GTGAAAGCGGGTCTCGCCTGGTTGTTACGTCGTTTTACTCTAGTCGAACAGGACAATTGC
CYP337B3v5_KX958388    (2308)  GTGAAAGCGGGTCTCGCCTGGCTGTTGCGTCGTTTTACTCTAGTCGAACAGGACAATTGC
CYP337B3v6_KX958389    (2386)  GTGAAAGCGGGTCTCGCCTGGCTGTTACGTCGGTTTACCTTAGTTGAACAGGACAATTGC
CYP337B3v7_KX958390    (2236)  GTGAAAGCGGGTCTCGCCTGGCTGTTACGTCGTTTTACCTTAGTCGAACAGGACAATTGC
CYP337B3v8_KX958391    (2255)  GTGAAAGCGGGTCTCGCCTGGTTGTTACGTCGTTTTACTCTAGTCGAACAGGACAATTGC
  CYP337B3_Olathe-2    (2359)  GTGAAAGCGGGTCTCGCCTGGCTGTTACGTCGTTTTACCTTAGTCGAACAGGACAATTGC
  CYP337B3_Olathe-6    (2385)  GTGAAAGCGGGTCTCGCCTGGCTGTTACGTCGGTTTACCTTAGTTGAACAGGACAATTGC
                                            2521                                                          2580
CYP337B3v1_JQ995292    (2323)  ATACCAGAATTCGAGAAAAGTCCATTTGGCCTCCGAAGTCCCGATGCTTGTTATGAATTA
CYP337B3v2_KJ636466    (2419)  ATACCAGAATTCGAGAAAAGTCCATTTGGCCTCCGAAGTCCCGATGCTCGTTATGAATTA
CYP337B3v3_KM675665    (2315)  ATACCAGAATTCGAGAAAAGTCCATTTGGCCTCCGAAGTCCCGATGCTCGTTATGAATTA
CYP337B3v4_KM675666    (2315)  ATACCAGAATTCGAGAAAAGTCCATTTGGCCTCCGAAGTCCCGATGCTCGTTATGAATTA
CYP337B3v5_KX958388    (2368)  GTACCAGAATTCGAGAAAAGTCCATTCGGTCTACGAAGTCCCGATGCTCGTTATGAATTA
CYP337B3v6_KX958389    (2446)  ATACCAGAAATCGAGAAAAGTCCATTTGGTCTACGAAGCCCGGATGCTCGTTATGAATTA
CYP337B3v7_KX958390    (2296)  ATACCAGAATTTGAGAAAAGTCCATTCGGTCTACGAAGTCCCGATGCTCGTTATGAATTA
CYP337B3v8_KX958391    (2315)  ATACCAGAATTCGAGAAAAGTCCATTCGGTCTACGAAGTCCCGATGCTCGTTATGAATTA
  CYP337B3_Olathe-2    (2419)  ATACCAGAATTCGAGAAAAGTCCATTTGGCCTCCGAAGTCCCGATGCTCGTTATGAATTA
  CYP337B3_Olathe-6    (2445)  ATACCAGAATTCGAGAAAAGTCCATTTGGTCTACGAAGCCCGATGCTCGTTATGAATTA
                                            2581           2598
CYP337B3v1_JQ995292    (2383)  AAGTTAAGAGACATATAA
CYP337B3v2_KJ636466    (2479)  AAGTTAAGAGACATATAA
CYP337B3v3_KM675665    (2375)  AAGTTAAGAGACATATAA
CYP337B3v4_KM675666    (2375)  AAGTTAAGAGACATATAA
CYP337B3v5_KX958388    (2428)  AAGTTAAGAGACATATAA
CYP337B3v6_KX958389    (2506)  AAGTTAAGAGACATATAA
CYP337B3v7_KX958390    (2356)  AAGTTAAGAGACATATAA
CYP337B3v8_KX958391    (2375)  AAGTTAAGAGACATATAA
  CYP337B3_Olathe-2    (2479)  AAGTTAAGAGACATATAA
  CYP337B3_Olathe-6    (2505)  AAGTTAAGAGACATATAA
```

Figure S4. Alignment of reference genomic DNA sequences of cytochrome P450 337B (CYP337B3 gene alleles v1 through v8 and CYP337B3 alleles identified from Olathe, CO population of *Helicoverpa zea*. Identical and conserved nucleotide positions are shown in black text and nucleotide polymorphisms, insertions, and deletions are shown with grey background. Alignment gaps are indicated with a hyphen (-).

```
                                        1                                                          60
CYP337B3v2_KJ636466        (1)  ATGTTGTTCGTAATATTACTCACGATATTAATAGTACTGTGCTCAATAGTGCTCCATTTC
CYP337B3_Olathe-2          (1)  ATGTTGTTCGTAATATTACTCACGATATTAATAGTACTGTGCTCAATAGTGCTCCATTTC
                                        61                                                         120
CYP337B3v2_KJ636466       (61)  AAGTTCACAAACAGCAAATACTGGAAAAAGAAGAACATTATCCAGATAAAAGATTTGACA
CYP337B3_Olathe-2         (61)  AAGTTCACAAACAGCAAATACTGGAAAAAGAAGAACATTATCCAGATAAAAGATTTGACA
                                        121                                                        180
CYP337B3v2_KJ636466      (121)  TTCACCTTTCTGTTCAACAAGCAATCGATGCCAGAACTAATCAAATCGATTTACGATAAA
CYP337B3_Olathe-2        (121)  TTCACCTTTCTGTTCAACAAGCAATCGATGCCAGAACTAATCAAATCGATTTACGATAAA
                                        181                                                        240
CYP337B3v2_KJ636466      (181)  CATGATGAACCGTATATTGGAACGACGTCGGCGACAATACCAACGCTCATTATAAAGAAC
CYP337B3_Olathe-2        (181)  CATGATGAACCGTATATTGGAACGACGTCGGCGACAATACCAACGCTCATTATAAAGAAC
                                        241                                                        300
CYP337B3v2_KJ636466      (241)  CTCGATGATATTCAAGCAGTGTTAGCTGGTGACTTCCAAAGTTTCTACAGTCGAGGAATA
CYP337B3_Olathe-2        (241)  CTCGATGATATTCAAGCAGTGTTAGCTGGTGACTTCCAAAGTTTCTACAGTCGAGGAATA
                                        301                                                        360
CYP337B3v2_KJ636466      (301)  ATAACCAGTCCAAACGATGTGTTAGCTGATAATTTGTTATTAATGGACGACTTCAAAAAA
CYP337B3_Olathe-2        (301)  ATAACCAGTCCAAACGACGTGTTAGCTGATAATTTGTTATTAATGGACGACTTCAAAAAA
                                        361                                                        420
CYP337B3v2_KJ636466      (361)  TGGAAACTCATACGACAAAAACTCACTCCAATTTTCACTAGTGCGAAACTCAAAAACATG
CYP337B3_Olathe-2        (361)  TGGAAACTCATACGACAAAAACTCACTCCAATTTTCACTAGTGCGAAACTCAAAAACATG
                                        421                                                        480
CYP337B3v2_KJ636466      (421)  TTTTACATCATAGAAAAAAGTGCCCGAGATTTTGTTGAGTTGGTTGAAGATAATGTTCAT
CYP337B3_Olathe-2        (421)  TTTTACATCATAGAAAAAAGTGCCCGAGATTTTGTTGAGTTGGTTGAAGATAATGTTCAT
                                        481                                                        540
CYP337B3v2_KJ636466      (481)  CTGCGAAAGAAACCGTTCAAACTTATGACCAGATACACTACAGCGTCTATTAGTGCTGCA
CYP337B3_Olathe-2        (481)  CTGCGAAAGAAACCGTTCAAACTTATGACCAGATACACTACAGCGTCTATTAGTGCTGCA
                                        541                                                        600
CYP337B3v2_KJ636466      (541)  GTATTTGGTATAGATACACAAGTAAAGAGTACCATGGAATCACCATTCGTTGAATTGGCA
CYP337B3_Olathe-2        (541)  GTATTTGGTATAGATACACAAGTAAAGAGTACCATGGAATCACCATTCGTTGAATTGGCA
                                        601                                                        660
CYP337B3v2_KJ636466      (601)  TTTAGAGCTTTACGACCATCGTTTATTCAAAATGTAATAGTTGTTATTGCAAATACTTTC
CYP337B3_Olathe-2        (601)  TTTAGAGCTTTACGACCATCGTTTATTCAAAATGTAATAGTTGTTATTGCAAATACTTTC
                                        661                                                        720
CYP337B3v2_KJ636466      (661)  CCTAGATTGTACAAACTCTTGCAGTTGAAACTTTTTGGTGAACATGAAGAATTTTTTGTG
CYP337B3_Olathe-2        (661)  CCTAGATTGTACAAACTCTTGCAGTTGAAACTTTTTGGTGAACATGAAGAATTTTTTGTG
                                        721                                                        780
CYP337B3v2_KJ636466      (721)  GGTGCAGTGAAAACTGTTTTAGAAAGTAGGAGGCATGATACTACTAAAAGATATGATTTT
CYP337B3_Olathe-2        (721)  GGTGCAGTGAAAACTGTTTTAGAAAGTAGGAGGCATGATACTACTAAAAGATATGATTTT
                                        781                                                        840
CYP337B3v2_KJ636466      (781)  ATTGAGATTTGCTTGGAACTACAGAAGAATGGAATAATGCAGGACTTTTCAACTGGATAT
CYP337B3_Olathe-2        (781)  ATTGAGATTTGCTTGGAACTACAGAAGAATGGAATAATGCAGGACTTTTCAACTGGATAT
                                        841                                                        900
CYP337B3v2_KJ636466      (841)  AAATTGGAGCCGACCGACGAACTGATGGCTGCTCAAGCATTCTTCTTTTTTGTGGCTGGT
CYP337B3_Olathe-2        (841)  AAATTGGAGCCGACCGACGAACTGATGGCTGCTCAAGCATTCTTCTTTTTTGTGGCTGGT
                                        901                                                        960
CYP337B3v2_KJ636466      (901)  GCAGACACCTCTGCTAACACAATGCATTATTCTTTGTTAGAGCTGTCAAACAATCCAAAA
CYP337B3_Olathe-2        (901)  GCAGACACCTCTGCTAACACAATGCATTATTCTTTGTTAGAGCTGTCAAACAATCCAAAA
                                        961                                                        1020
CYP337B3v2_KJ636466      (961)  ATCTTGGCAAAACTACATGAGGAAATTGACAAAGTTTTCGAAGGCGGAGCTGGGGAACTA
CYP337B3_Olathe-2        (961)  ATCTTGGCAAAACTACATGAGGAAATTGACAAAGTTTTCGAAGGCGGAGCTGGGGAACTA
                                        1021                                                       1080
CYP337B3v2_KJ636466     (1021)  ACTTATAATGACATTGATAAGTTACAATATTTAGATCAGGTTATAAATGAAGCAATGAGA
CYP337B3_Olathe-2       (1021)  ACTTATAATGACATTGATAAGTTACAATATTTAGATCAGGTTATAAATGAAGCAATGAGA
                                        1081                                                       1140
CYP337B3v2_KJ636466     (1081)  AAGTATCCTCCAGTAGGTGTCATGCAAAGATTGTGTACTAAAGATACAGTTTTACCTTCT
CYP337B3_Olathe-2       (1081)  AAGTATCCTCCAGTAGGTGTCATGCAAAGATTGTGTACTAAAGATACAGTTTTACCTTCT
                                        1141                                                       1200
CYP337B3v2_KJ636466     (1141)  GGTATACCCATAGCAAAGGGTAACACAATAATGATACCAGTGTTCGGTCTTCACAGAGAC
CYP337B3_Olathe-2       (1141)  GGTATACCCATAGCAAAGGGTAACACAATAATGATACCAGTGTTCGGTCTTCACAGAGAC
                                        1201                                                       1260
CYP337B3v2_KJ636466     (1201)  GAAAAATACTTTGATGACCCACACGTATTTGATCCGGATAGATTTTCACCAGAAAACGTA
CYP337B3_Olathe-2       (1201)  GAAAAATACTTTGATGACCCACACGTATTTGATCCGGATAGATTTTCACCAGAAAACGTA
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                              1261                                              1320
CYP337B3v2_KJ636466  (1261) TCCAAAATCAAGAATTATGCTTATTTACCTTTTGGTGAAGGAAACCGCATTTGTATTGGC
  CYP337B3_Olathe-2  (1261) TCCAAAATCAAGAATTATGCTTATTTACCTTTTGGTGAAGGAAACCGCATTTGTATTGGC
                              1321                                              1380
CYP337B3v2_KJ636466  (1321) CTCCAAGTGAAAGCGGGTCTCGCCTGGCTGTTACGTCGTTTTACCTTAGTCGAACAGGAC
  CYP337B3_Olathe-2  (1321) CTCCAAGTGAAAGCGGGTCTCGCCTGGCTGTTACGTCGTTTTACCTTAGTCGAACAGGAC
                              1381                                              1440
CYP337B3v2_KJ636466  (1381) AATTGCATACCAGAATTCGAGAAAAGTCCATTTGGCCTCCGAAGTCCCGATGCTCGTTAT
  CYP337B3_Olathe-2  (1381) AATTGCATACCAGAATTCGAGAAAAGTCCATTTGGCCTCCGAAGTCCCGATGCTCGTTAT
                              1441            1464
CYP337B3v2_KJ636466  (1441) GAATTAAAGTTAAGAGACATATAA
  CYP337B3_Olathe-2  (1441) GAATTAAAGTTAAGAGACATATAA
```

Figure S5. Alignment of the mRNA reference sequences of cytochrome P450 337B3 allele v2 (KJ636466.1) and CYP337B3 allele v2 identified from Olathe, CO population of *Helicoverpa zea*. Identical and conserved nucleotide positions are shown in black text and nucleotide polymorphisms, insertions, and deletions are shown with grey background. Alignment gaps are indicated with a hyphen (-).

```
                            1                                                  60
CYP337B3v6_KX958389    (1) ATGTTGTTCGTGATATTACTCACGATATTAATAGTACTGTGCTCAATAGTGCTCCATTTC
  CYP337B3_Olathe-6    (1) ATGTTGTTCGTAATATTACTCACGATATTAATAGTACTGTGTTCAATAGTGCTCCATTTT
                            61                                                 120
CYP337B3v6_KX958389   (61) AAGTTCACAAACAGCAAATACTGGAAAAAGAAGAACATTATCCAGATAAAAGATTTGACA
  CYP337B3_Olathe-6   (61) AAGTTCACAAACAGCAAATACTGGAAAAAGAAGAATATAATACAGATAAAAGATTTGACA
                            121                                                180
CYP337B3v6_KX958389  (121) TTCACCTTTCTGTTCAACAAGCAATCGATGCCAGAACTAATCAAATCGATTTACGATAAA
  CYP337B3_Olathe-6  (121) TTCACCTTTCTGTTCAACAAGCAATCGATGCCAGAACTAATCAAATCGATTTACGATAAA
                            181                                        *       240
CYP337B3v6_KX958389  (181) CATGATGAACCGTATATTGGAACGACGTCCGCGACAATACCAACGCTCATTATAAAGAAC
  CYP337B3_Olathe-6  (181) CATAATGAACCGTATATTGGAACGACGTCGGCGACAATACCAACGCTCATTTTAAAGAAC
                            241                                                300
CYP337B3v6_KX958389  (241) CTCGATGATATTCAAGCAGTGTTAGCTGGTGACTTCCAAAGTTTCTACAGTCGAGGAATA
  CYP337B3_Olathe-6  (241) CTCGATGATATTCAAGCAGTGTTAGCTGGTGACTTCCAAAGTTTCTACAGTCGAGGAATA
                            301                                                360
CYP337B3v6_KX958389  (301) ATAACCAGTCCAAACGATGTGTTAGCTGATAATTTGTTATTAATGGACGACTTCAAAAAA
  CYP337B3_Olathe-6  (301) ATAACCAGTCCAAACGATGTGTTAGCTGATAATTTGTTATTAATGGACGACTTCAAAAAA
                            361                                                420
CYP337B3v6_KX958389  (361) TGGAAACTCATACGACAAAAACTCACTCCAATTTTCACTAGTGCGAAACTCAAAAACATG
  CYP337B3_Olathe-6  (361) TGGAAACTCATACGACAAAAACTCACTCCAATTTTCACTAGTGCGAAACTCAAAAACATG
                            421                                                480
CYP337B3v6_KX958389  (421) TTTTACATCATAGAAAAAAGTGCTCGAGATTTTGTTGAGTTGGTTGAAGATAATGTTCAT
  CYP337B3_Olathe-6  (421) TTTTACATCATAGAAAAAAGTGCTCGAGATTTTGTTGAGTTGGTTGAAGATAATGTTCAT
                            481                                                540
CYP337B3v6_KX958389  (481) CTGCGAAAGAAACCGTTCAAACTTATGACCAGATACACTACAGCGTCTATTAGTGCTGCA
  CYP337B3_Olathe-6  (481) CTGCGAAAGAAACCGTTCAAACTTATGACCAGATACACTACAGCGTCTATTAGTGCTGCA
                            541                                                600
CYP337B3v6_KX958389  (541) GTATTTGGTATAGATACTCAAGTAAAGAGTACCATGGAATCACCATTCGTTGAATTGGCA
  CYP337B3_Olathe-6  (541) GTATTTGGTATAGATACTCAAGTAAAGAGTACCATGGAATCACCATTCGTTGAATTGGCA
                            601                                                660
CYP337B3v6_KX958389  (601) TTTAGAGCTTTACGACCATCGTTTATTCAAAATGTAATAGTTGTTATTGCAAATACTTTC
  CYP337B3_Olathe-6  (601) TTTAGAGCTTTACGACCATCGTTTATTCAAAATGTAATAGTTGTTATTGCAAATACTTTC
                            661                                                720
CYP337B3v6_KX958389  (661) CCTAGATTGTACAAACTCTTGCAGTTGAAACTTTTTGGTGAACATGAAGAATTTTTTGTG
  CYP337B3_Olathe-6  (661) CCTAGATTGTACAAACTCTTGCAGTTGAAACTTTTTGGTGAACATGAAGAATTTTTTGTG
                            721                                                780
CYP337B3v6_KX958389  (721) GGGGCAGTGAAAACTGTTTTAGAAAGTAGGAGGCATGATACTACTAAAAGATATGATTTT
  CYP337B3_Olathe-6  (721) GGGGCAGTGAAAACTGTTTTAGAAAGTAGGAGGCATGATACTACTAAAAGATATGATTTT
                            781                                                840
CYP337B3v6_KX958389  (781) ATTGAGATTTGCTTGGAACTACAGAAGAATGGAATAATGCAGGACTTTTCAACTGGATAT
  CYP337B3_Olathe-6  (781) ATTGAGATTTGCTTGGAACTACAGAAGAATGGAATAATGCAGGACTTTTCAACTGGATAT
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                                    841                                              900
CYP337B3v6_KX958389    (841) AAATTGGAGCCGACCGACGAACTGATGGCTGCTCAAGCATTCTTCTTTTTTGTGGCTGGT
   CYP337B3_Olathe-6   (841) AAATTGGAGCCGACCGACGAACTGATGGCTGCTCAAGCATTCTTCTTTTTTGTGGCTGGT
                                    901                                              960
CYP337B3v6_KX958389    (901) GCAGACACCTCTGCTAACACAATGCATTATTCTTTGTTAGAGCTGTCAAACAATCCAAAA
   CYP337B3_Olathe-6   (901) GCAGACACCTCTGCTAACACAATGCATTATTCTTTGTTAGAGCTGTCAAACAATCCAAAA
                                    961                                             1020
CYP337B3v6_KX958389    (961) ATCTTGGCAAAACTACATGAGGAAATTGACAAAGTTTTCGCAGGTGGAGCTGGGGAACTA
   CYP337B3_Olathe-6   (961) ATCTTGGCAAAACTACATGAGGAAATTGACAAAGTTTTCGCAGGTGGAGCTGGGGAACTA
                                   1021                                             1080
CYP337B3v6_KX958389   (1021) ACTTATAATGACATTGATAAGTTACAATATTTAGATCAGGTTATAAATGAAGCAATGAGA
   CYP337B3_Olathe-6  (1021) ACTTATAATGACATTGATAAGTTACAATATTTAGATCAGGTTATAAATGAAGCAATGAGA
                                   1081                                             1140
CYP337B3v6_KX958389   (1081) AAGTATCCTCCAGTAGGTGTCATGCAAAGATTGTGTACTAAAGATACGGTTTTACCTTCT
   CYP337B3_Olathe-6  (1081) AAGTATCCTCCAGTAGGTGTCATGCAAAGATTGTGTACTAAAGATACAGTTTTACCTTCT
                                   1141                                             1200
CYP337B3v6_KX958389   (1141) GGTATACCCATAGCAAAGGGTAACACAATAATGATACCAGTGTTCGGTCTTCACAGAGCC
   CYP337B3_Olathe-6  (1141) GGTATACCCATAGCAAAGGGTAACACAATAATGATACCAGTGTTCGGTCTTCACAGAGAC
                                   1201                                             1260
CYP337B3v6_KX958389   (1201) GAAAAATACTTTGATGACCCCCATGTATTTGATCCGGATAGATTTTCACCAGAAACCGTA
   CYP337B3_Olathe-6  (1201) GAAAAATACTTTGATGACCCACATGTATTTGATCCGGATAGATTTTCACCAGAAACGTA
                                   1261                                             1320
CYP337B3v6_KX958389   (1261) TCCAAAATCAAGAATTATGCTTATTTACCTTGTGGTGAAGGAAACCGCATTTGTATTGGC
   CYP337B3_Olathe-6  (1261) TCCAAAATCAAGAATTATGCTTATTTACCTTTTGGTGAAGGAAACCGCATTTGTATTGGC
                                   1321                                             1380
CYP337B3v6_KX958389   (1321) CTCCAAGTGAAAGCGGGTCTCGCCTGGCTGTTACGTCGGTTTACCTTAGTTGAACAGGAC
   CYP337B3_Olathe-6  (1321) CTCCAAGTGAAAGCGGGTCTCGCCTGGCTGTTACGTCGGTTTACCTTAGTTGAACAGGAC
                                   1381                                             1440
CYP337B3v6_KX958389   (1381) AATTGCATACCAGAAATCGAGAAAAGTCCATTTGGTCTACGAAGCCCGGATGCTCGTTAT
   CYP337B3_Olathe-6  (1381) AATTGCATACCAGAATTCGAGAAAAGTCCATTTGGTCTACGAAGCCCCGATGCTCGTTAT
                                   1441             1464
CYP337B3v6_KX958389   (1441) GAATTAAAGTTAAGAGACATATAA
   CYP337B3_Olathe-6  (1441) GAATTAAAGTTAAGAGACATATAA
```

Figure S6. Alignment of the mRNA reference sequences of cytochrome P450 337B3 allele v6 (KX958389.1) and CYP337B3 allele v6 identified from Olathe, CO population of *Helicoverpa zea*. Identical and conserved nucleotide positions are shown in black text and nucleotide polymorphisms, insertions, and deletions are shown with grey background. Alignment gaps are indicated with a hyphen (-). A to T transversion at the nucleotide position 232 leading to the amino acid substitution I78L is marked with an asterisk (*).