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Prichard et al.

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(54) **MARKERS TO PREDICT MACROCYCLIC LACTONE DRUG RESISTANCE IN *DIROFILARIA IMMITIS*, THE CAUSATIVE AGENT OF HEARTWORM DISEASE**

(71) Applicants: **Elanco US Inc.**, Indianapolis, IN (US);
McGill University, Montreal (CA)

(72) Inventors: **Roger K. Prichard**, Quebec (CA);
Catherine Bourguinat, Quebec (CA);
Timothy G. Geary, Quebec (CA)

(73) Assignees: **Elanco US Inc.**, Indianapolis, IN (US);
McGill University, Montreal (CA)

(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 0 days.

This patent is subject to a terminal disclaimer.

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(65) **Prior Publication Data**

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Related U.S. Application Data

(60) Division of application No. 15/887,164, filed on Feb. 2, 2018, now Pat. No. 11,414,703, which is a continuation of application No. 14/896,736, filed as application No. PCT/US2014/044000 on Jun. 25, 2014, now Pat. No. 10,000,811.

(60) Provisional application No. 61/839,545, filed on Jun. 26, 2013.

(51) **Int. Cl.**

C12Q 1/68 (2018.01)

C07H 21/04 (2006.01)

C12Q 1/6883 (2018.01)

C12Q 1/6888 (2018.01)

(52) **U.S. Cl.**

CPC **C12Q 1/6883** (2013.01); **C12Q 1/6888** (2013.01); **C12Q 2600/124** (2013.01); **C12Q 2600/136** (2013.01); **C12Q 2600/156** (2013.01)

(58) **Field of Classification Search**

None

See application file for complete search history.

(56)

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Primary Examiner — Jeanine A Goldberg

(74) *Attorney, Agent, or Firm* — Barnes & Thornburg LLP

(57)

ABSTRACT

Disclosed are nucleic acid molecules from the genome of *Dirofilaria* spp. nematodes that contain single nucleotide polymorphisms related to reduced responsiveness of the nematodes to macrocyclic lactones. In one example, the species of *Dirofilaria* is *Dirofilaria immitis* (the agent of heartworm in animals). Also disclosed are methods for determining the responsiveness of *Dirofilaria* spp. nematodes to macrocyclic lactones, methods for selecting a treatment to treat an animal infected with *Dirofilaria* spp. nematode, and kits for determining the responsiveness of *Dirofilaria* spp. nematodes to macrocyclic lactones.

16 Claims, 29 Drawing Sheets

Specification includes a Sequence Listing.

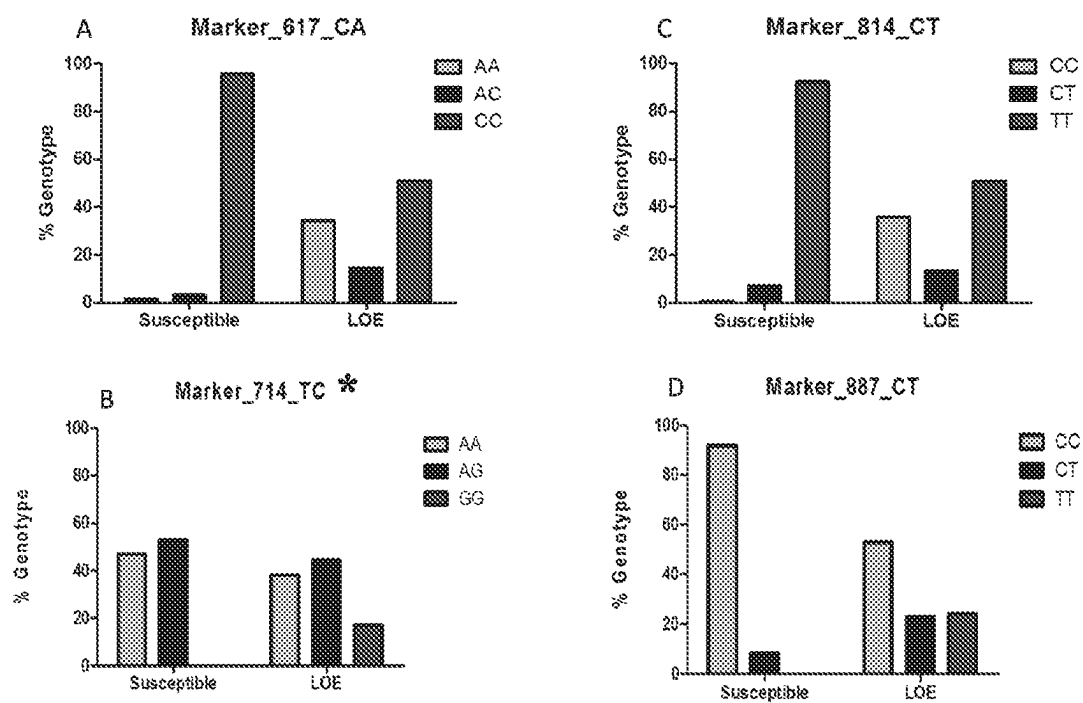


Figure 1

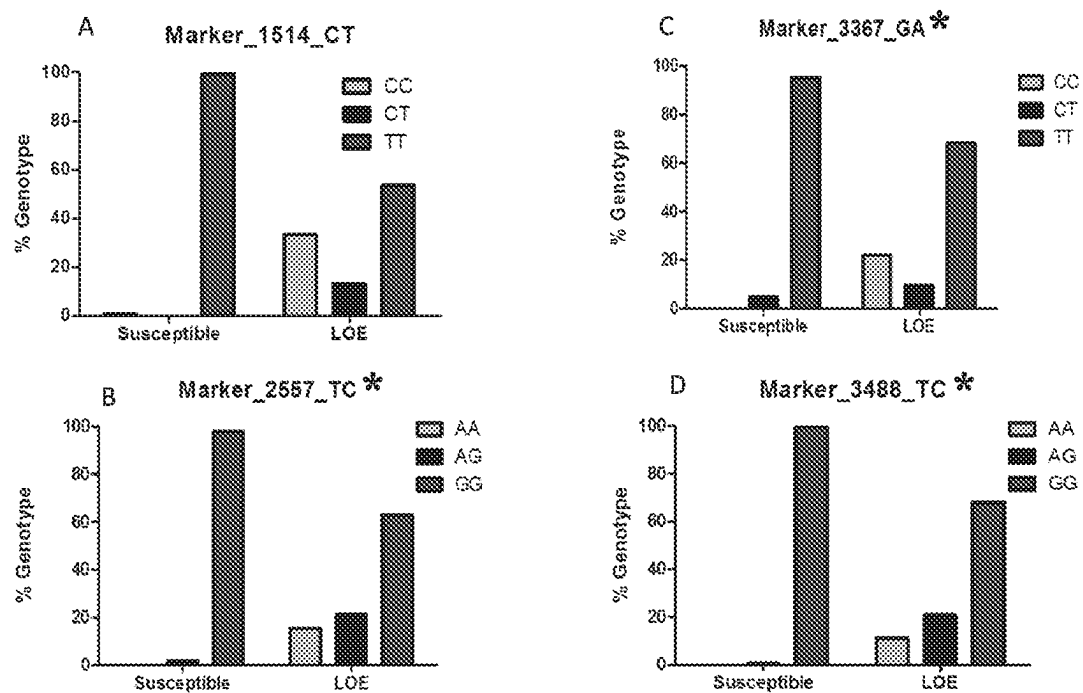


Figure 2

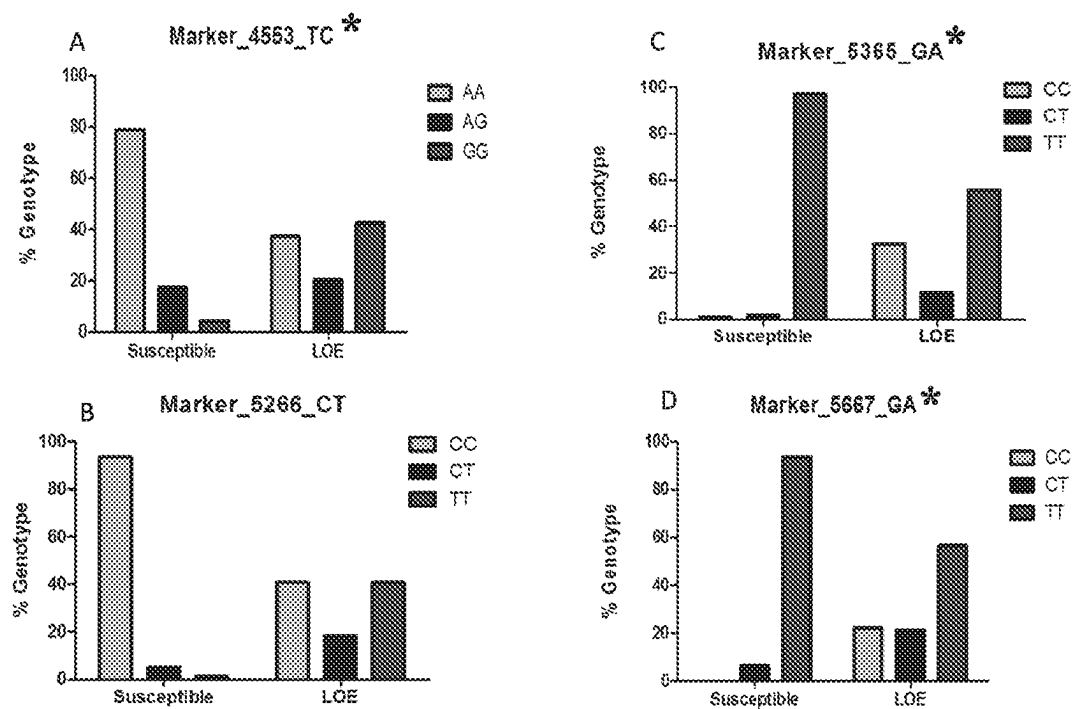


Figure 3

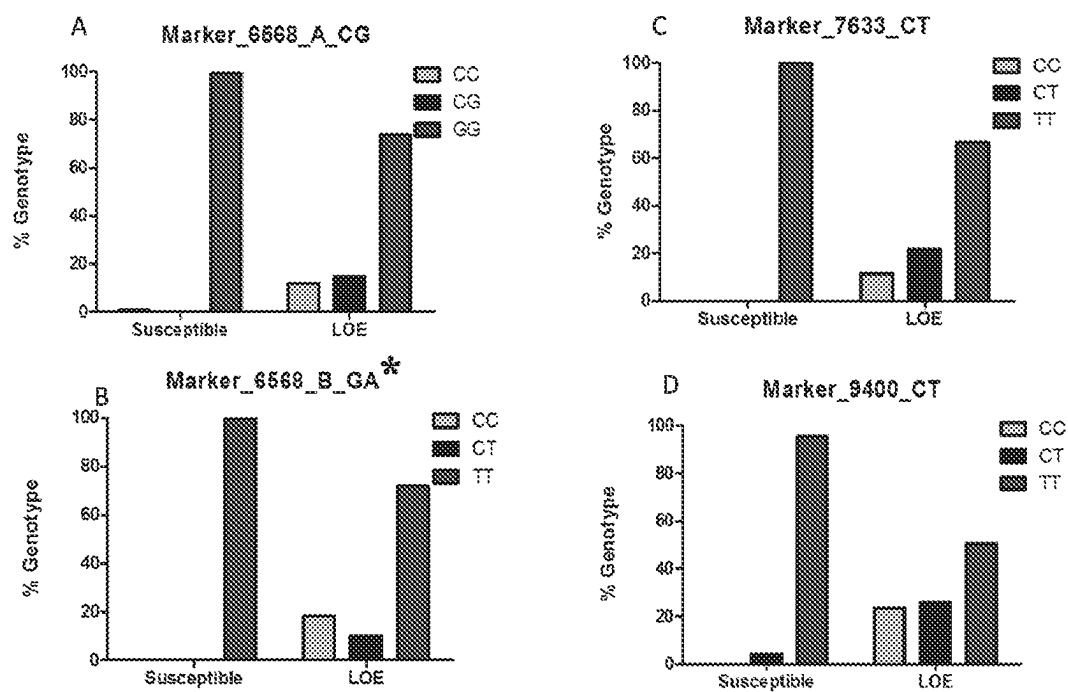


Figure 4

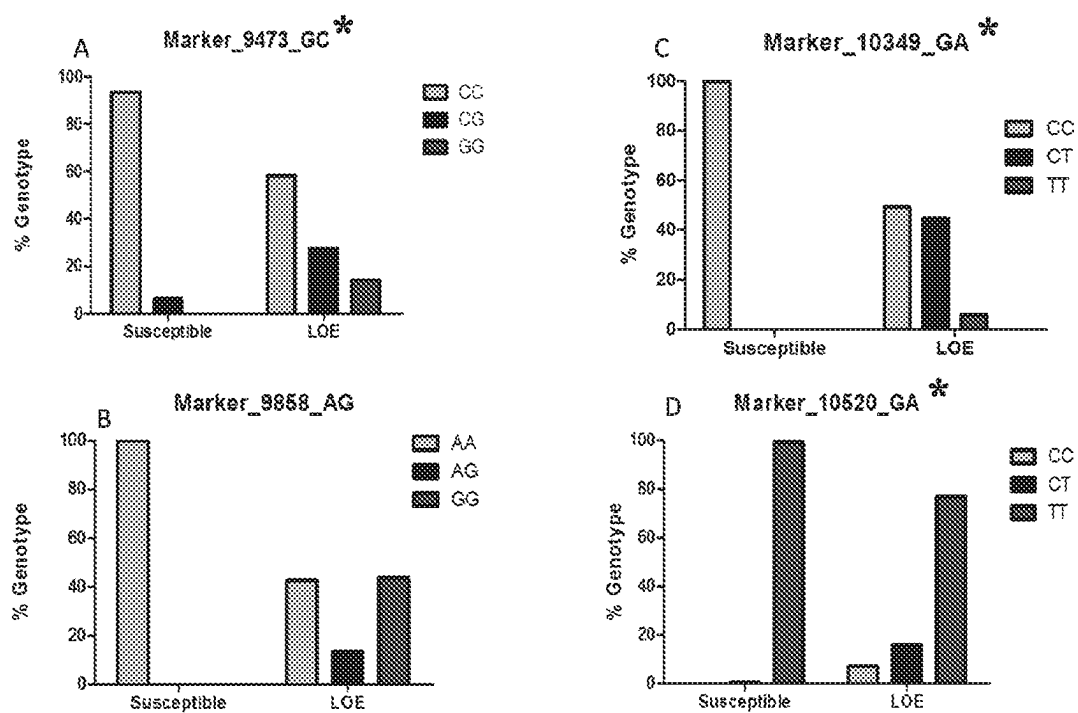


Figure 5

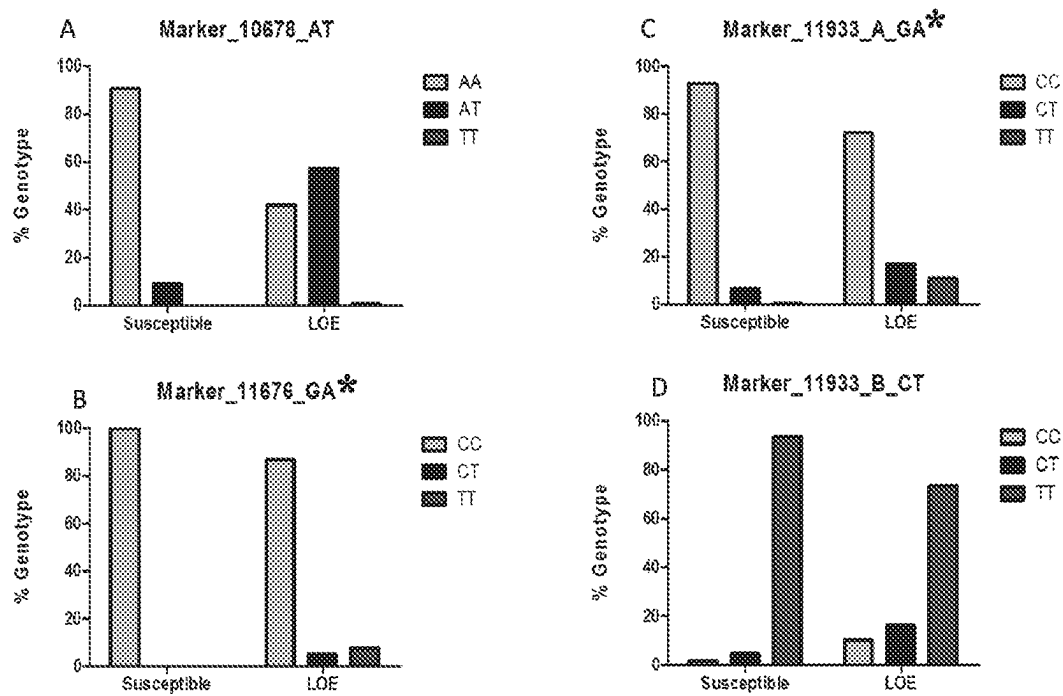


Figure 6

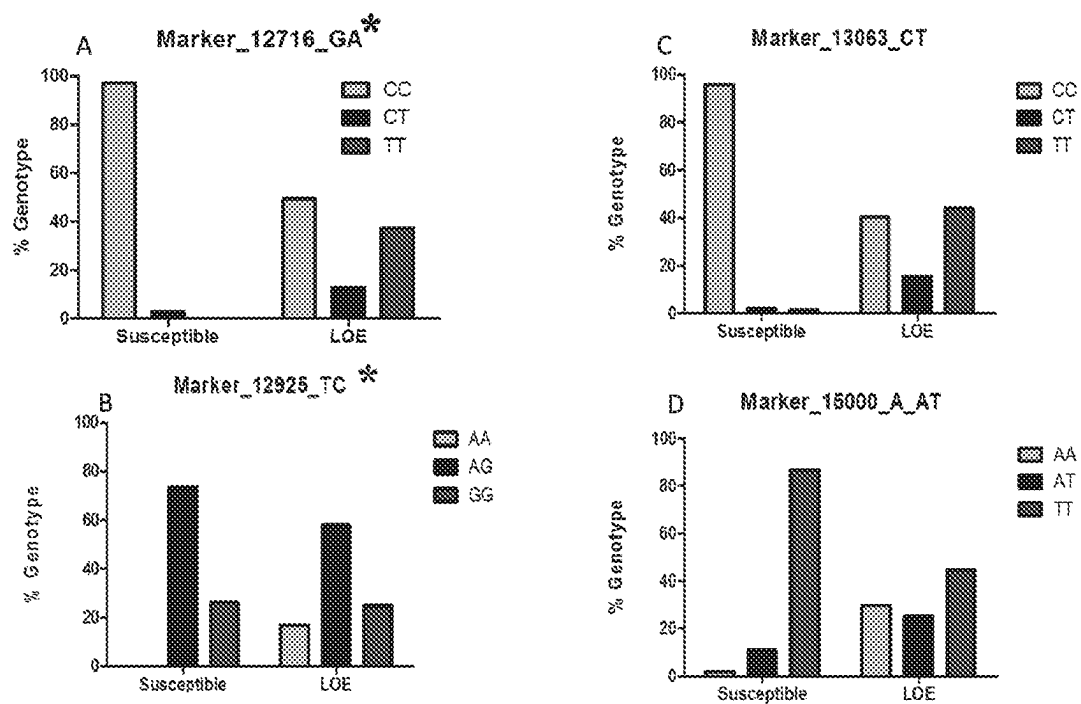


Figure 7

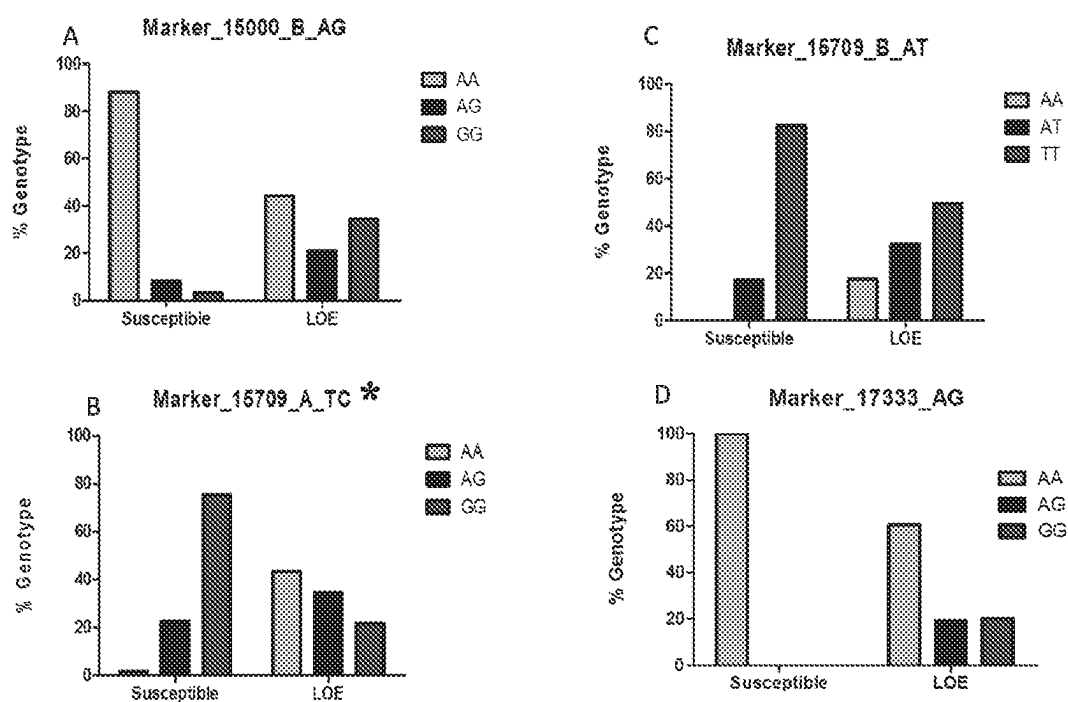


Figure 8

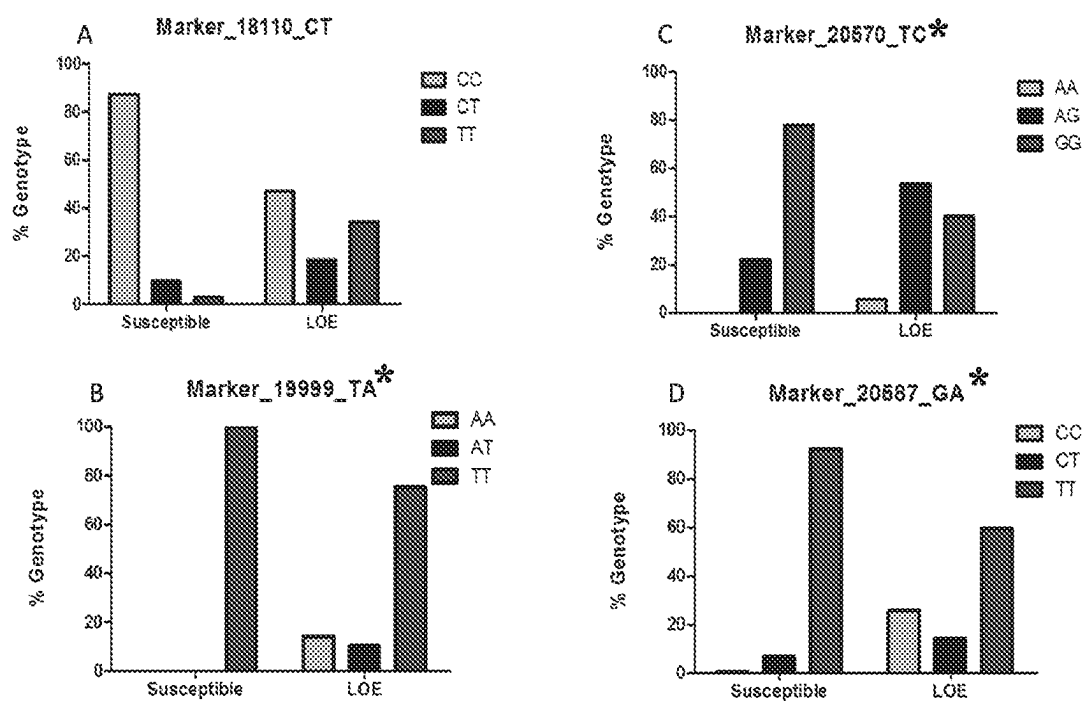


Figure 9

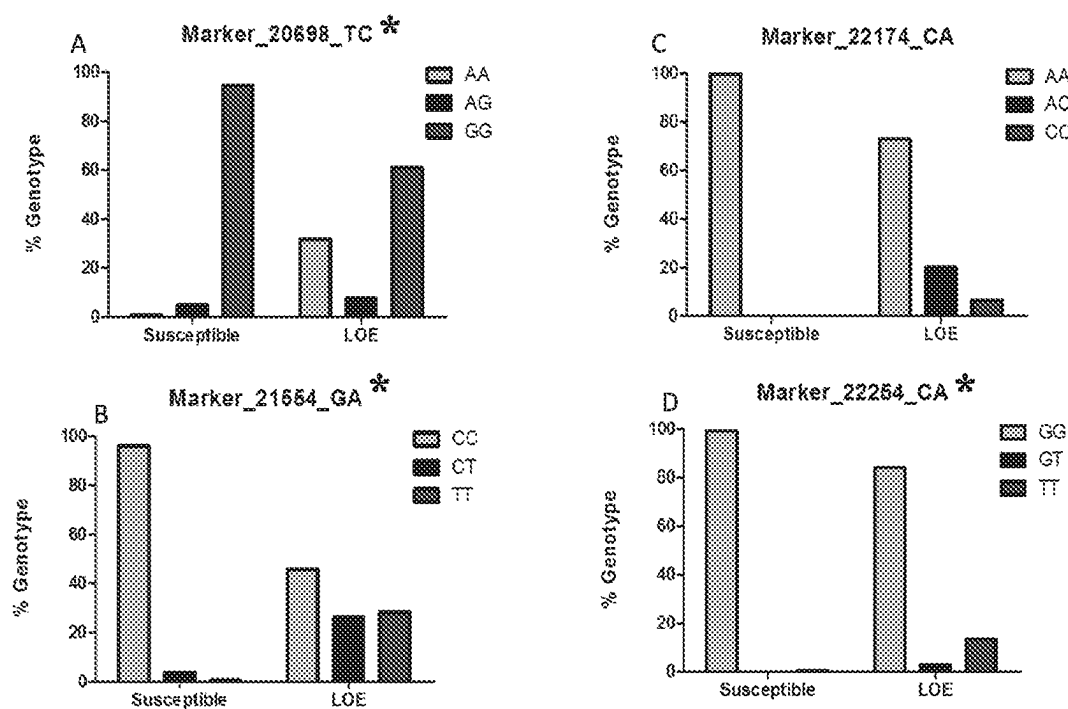


Figure 10

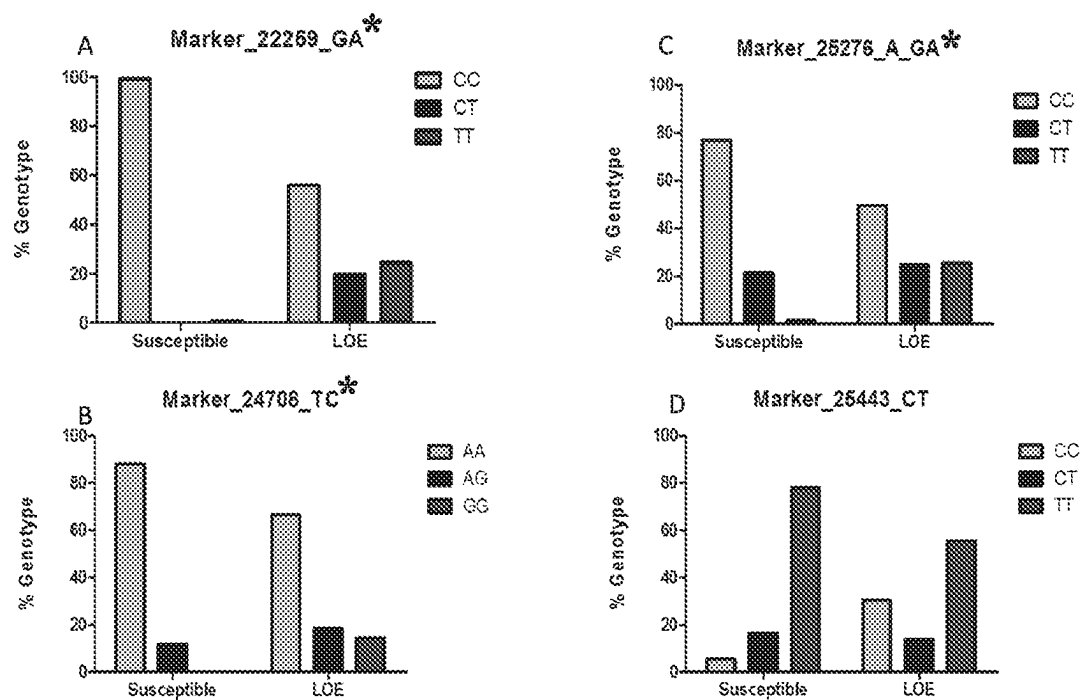


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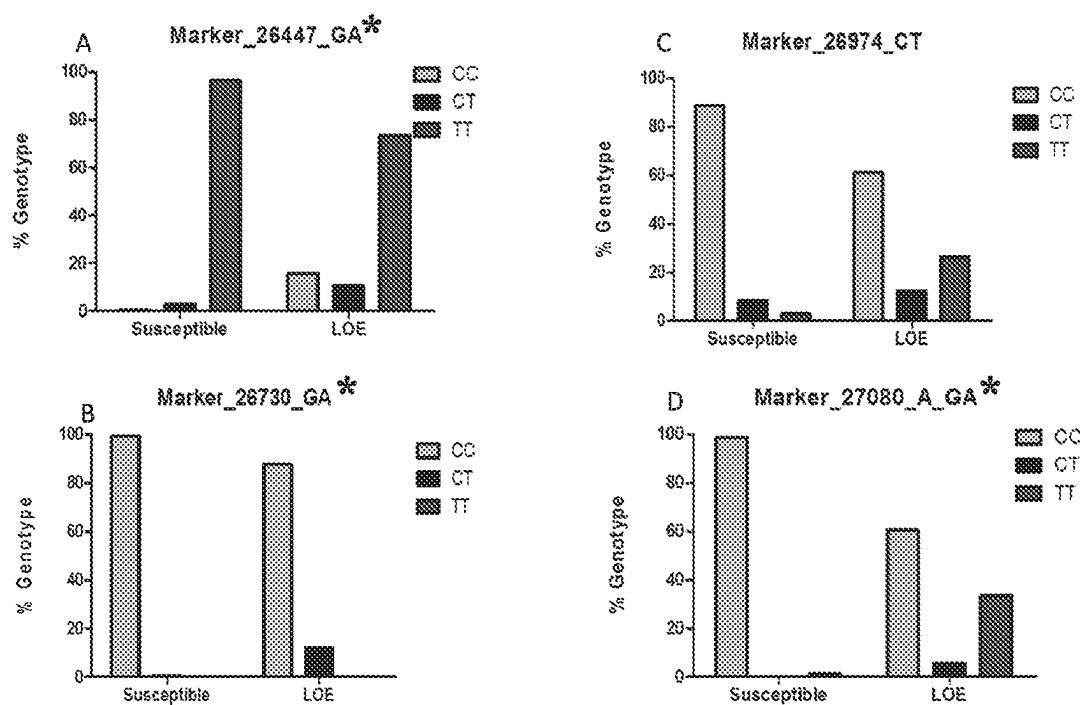


Figure 12

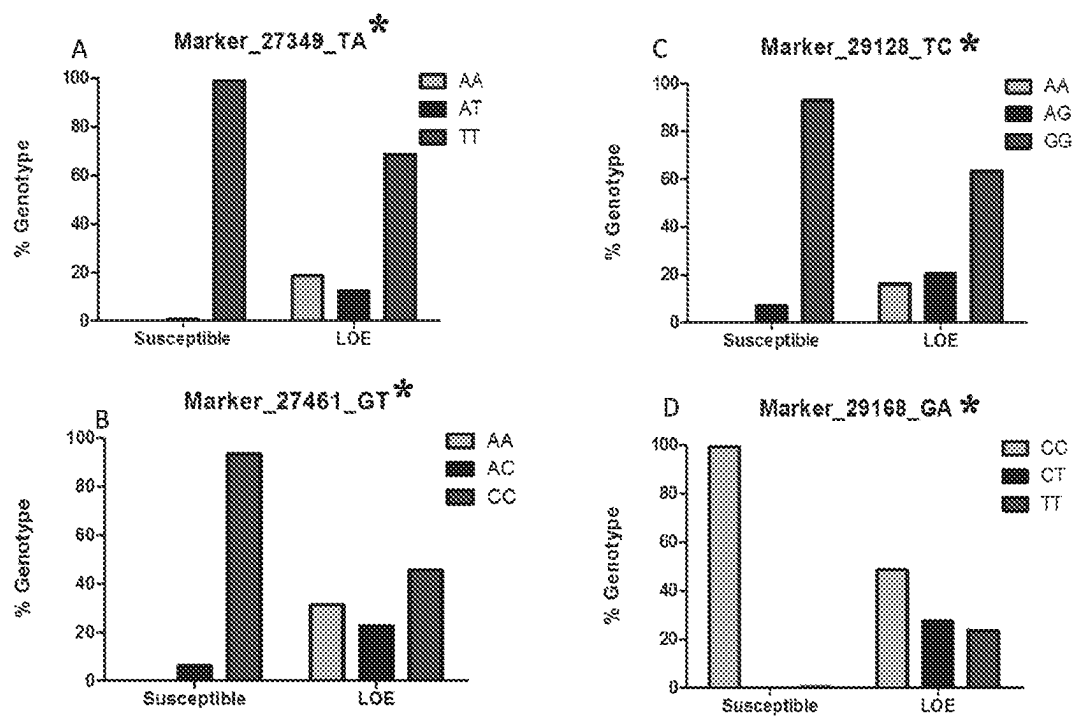


Figure 13

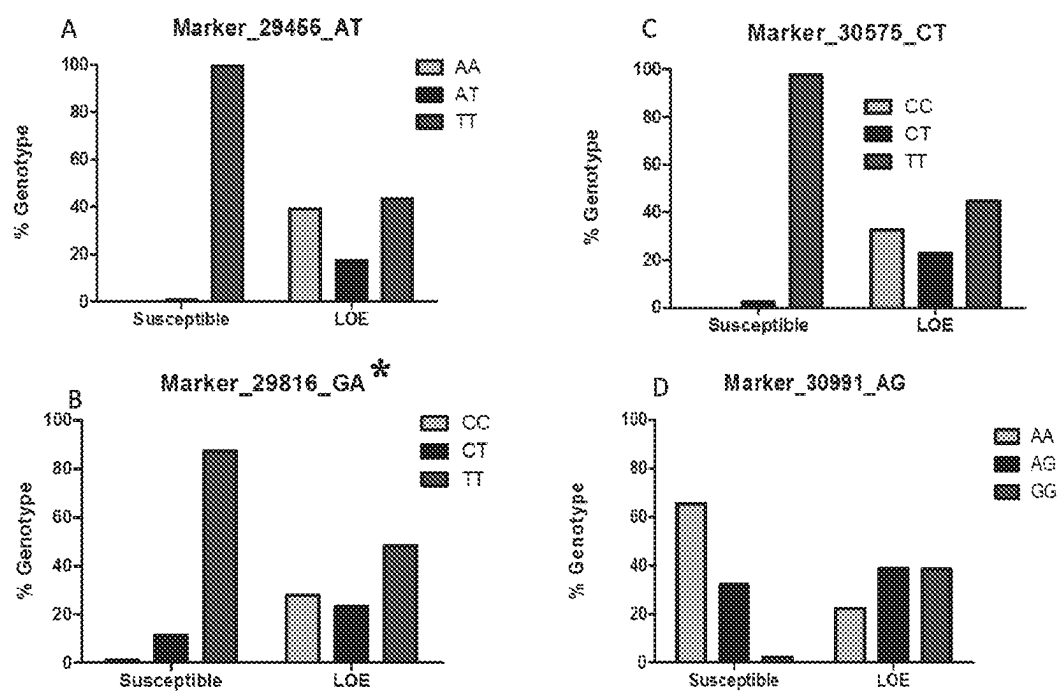


Figure 14

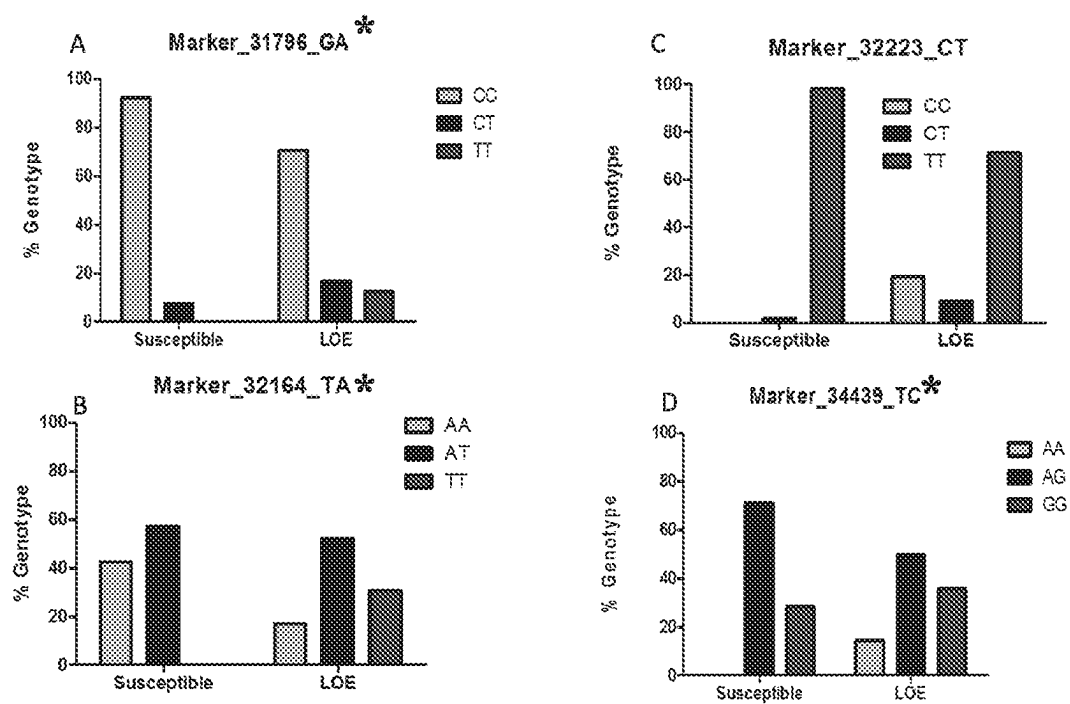


Figure 15

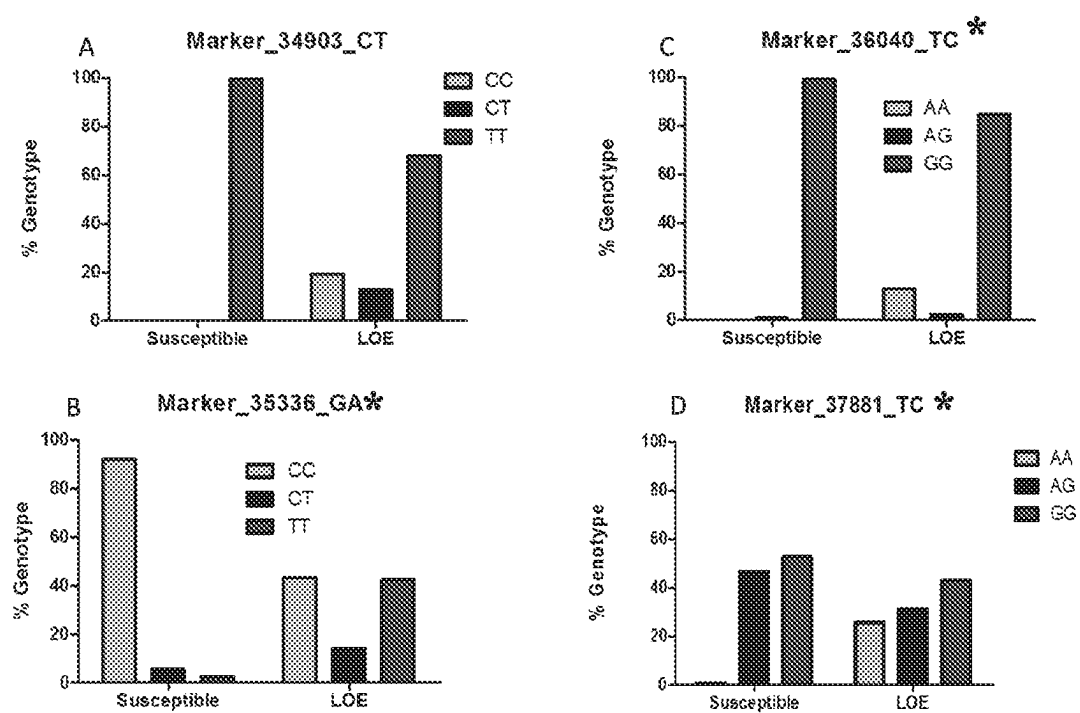


Figure 16

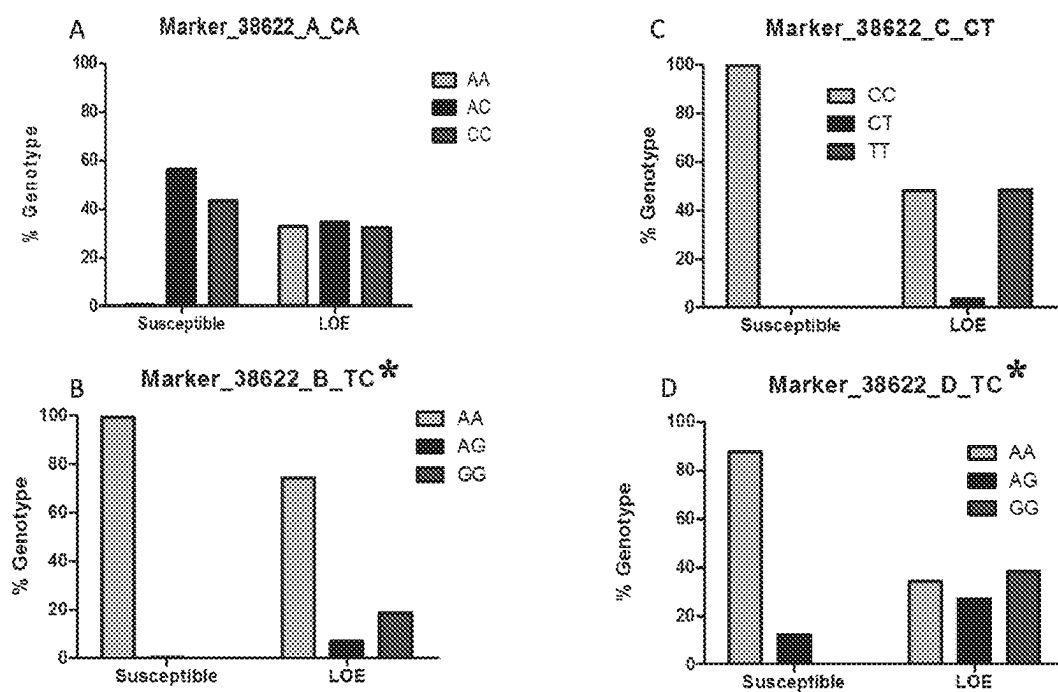


Figure 17

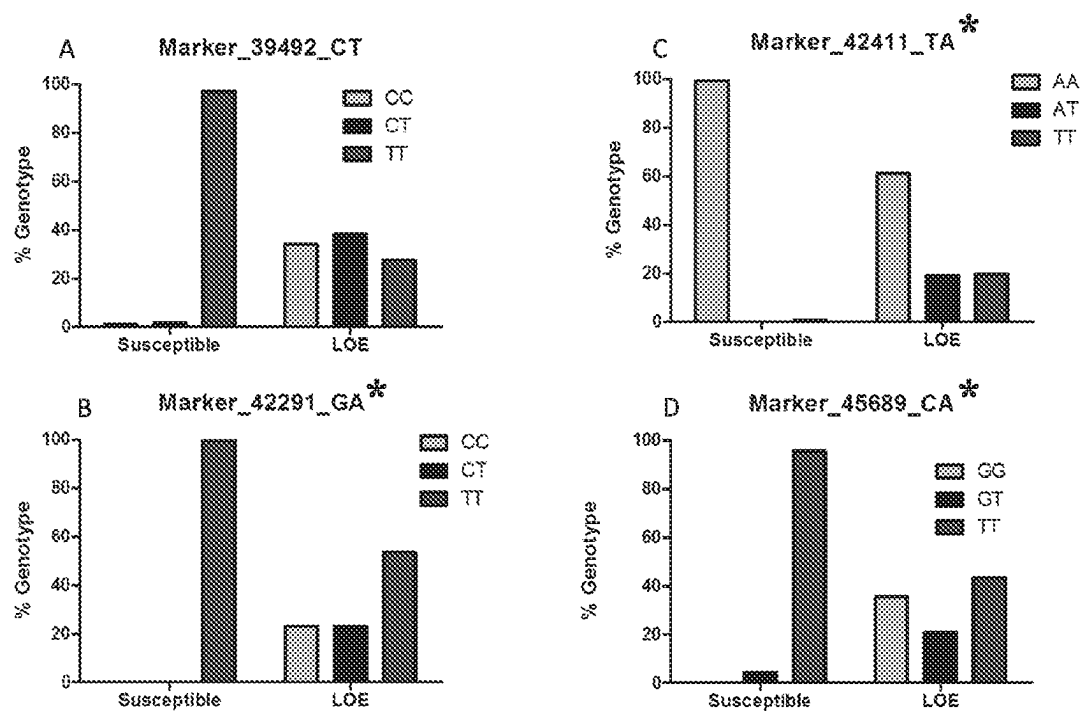


Figure 18

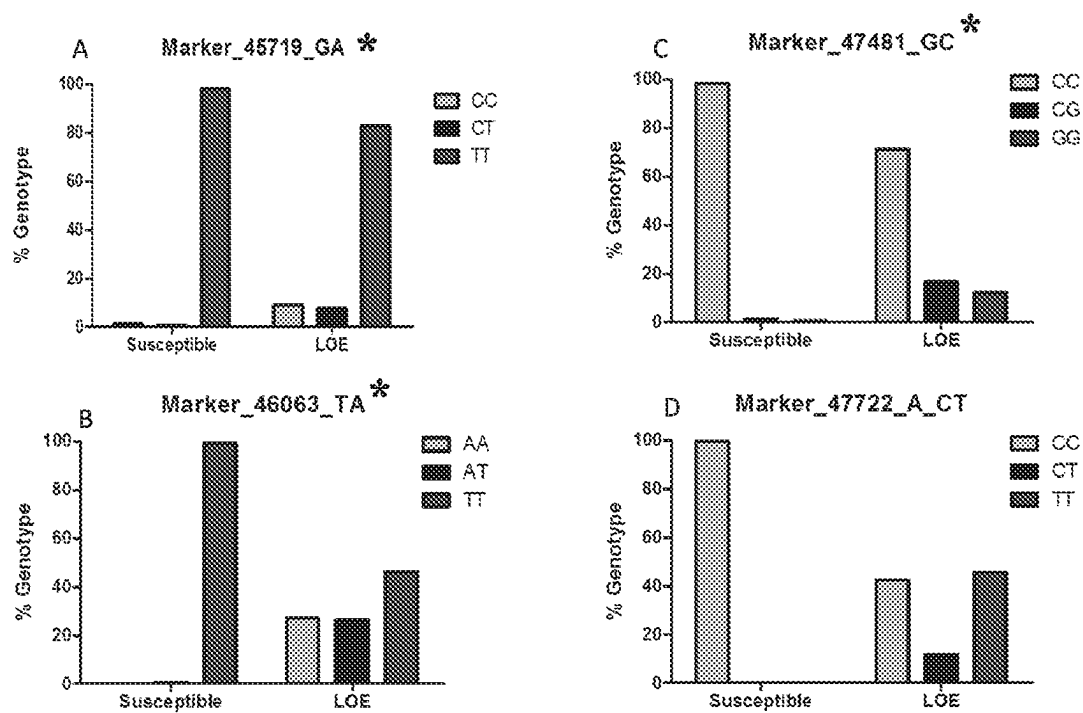


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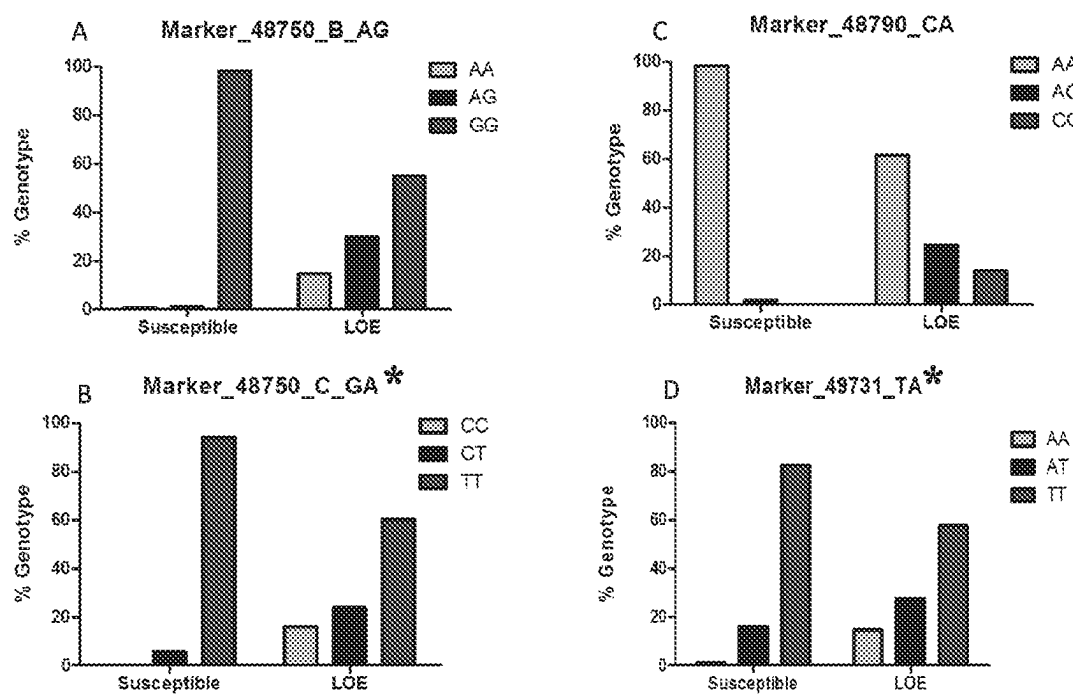


Figure 20

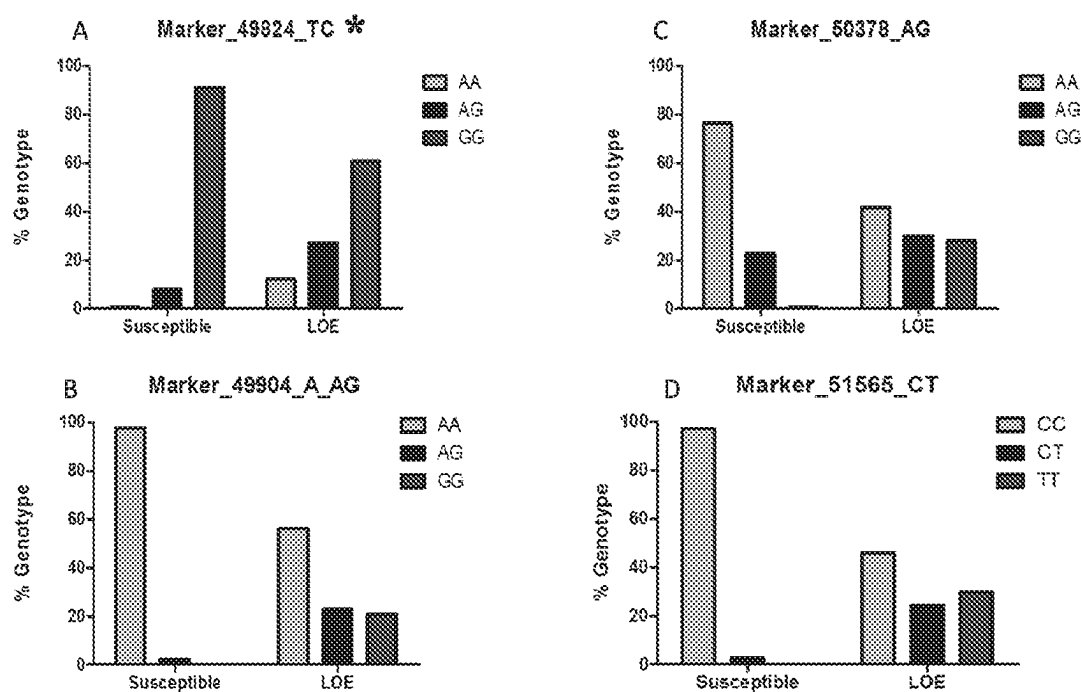


Figure 21

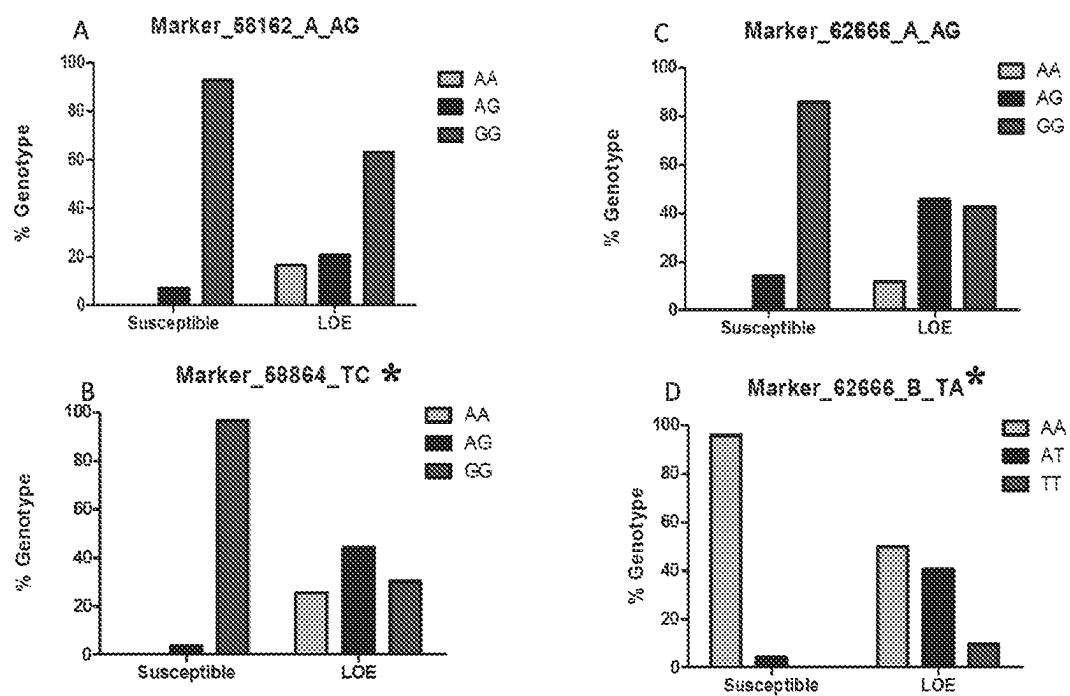


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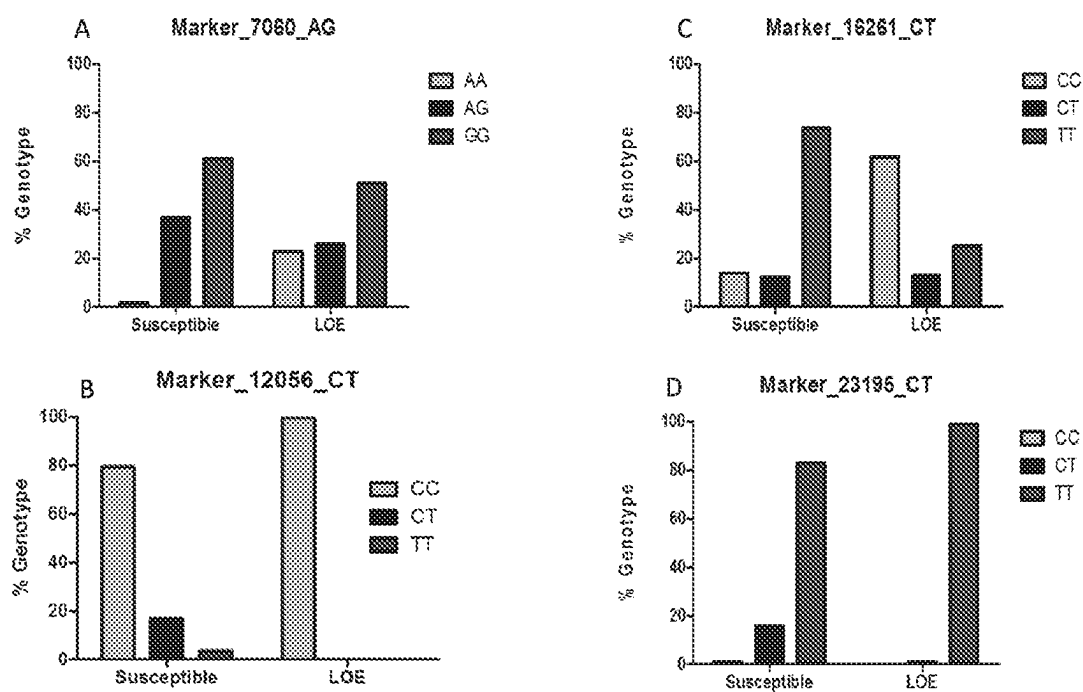


Figure 23

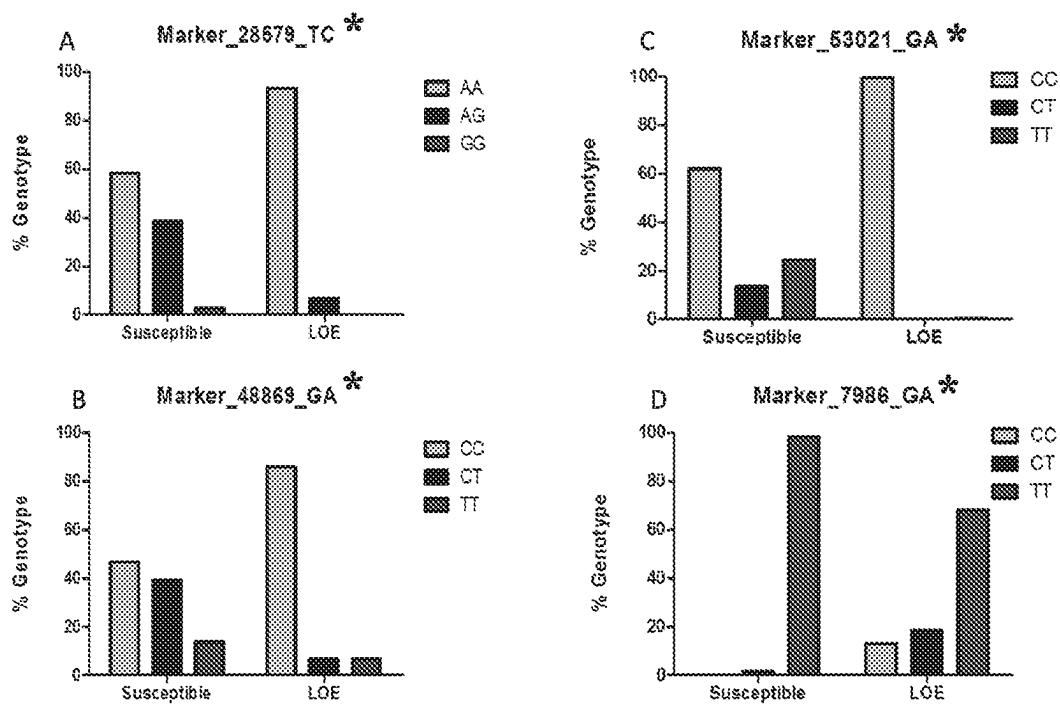


Figure 24

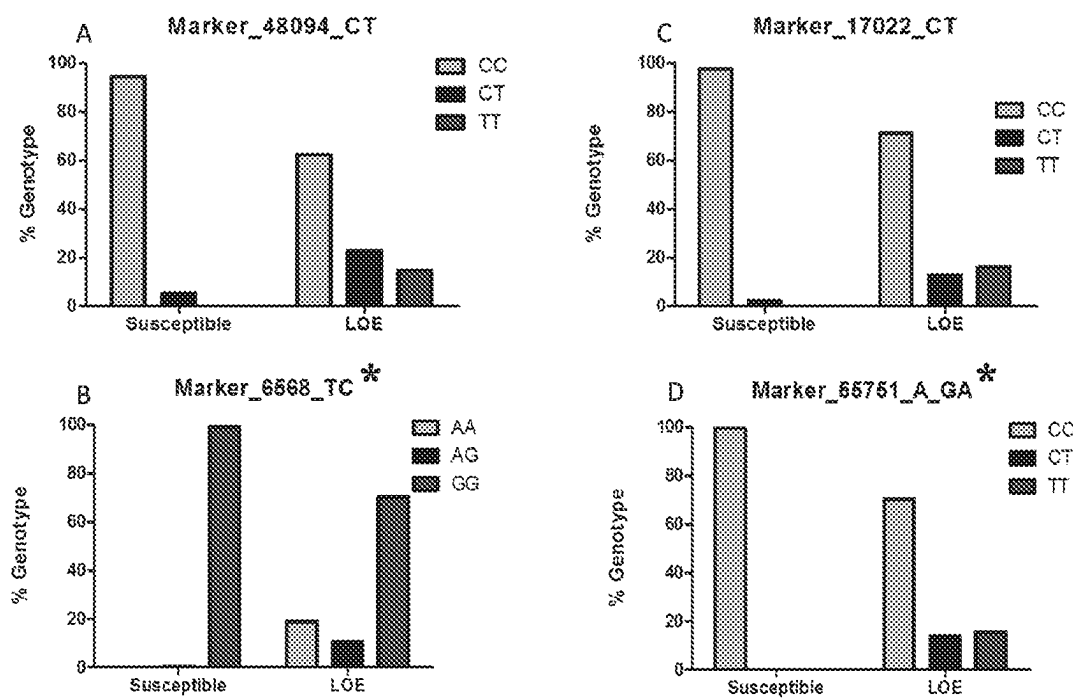


Figure 25

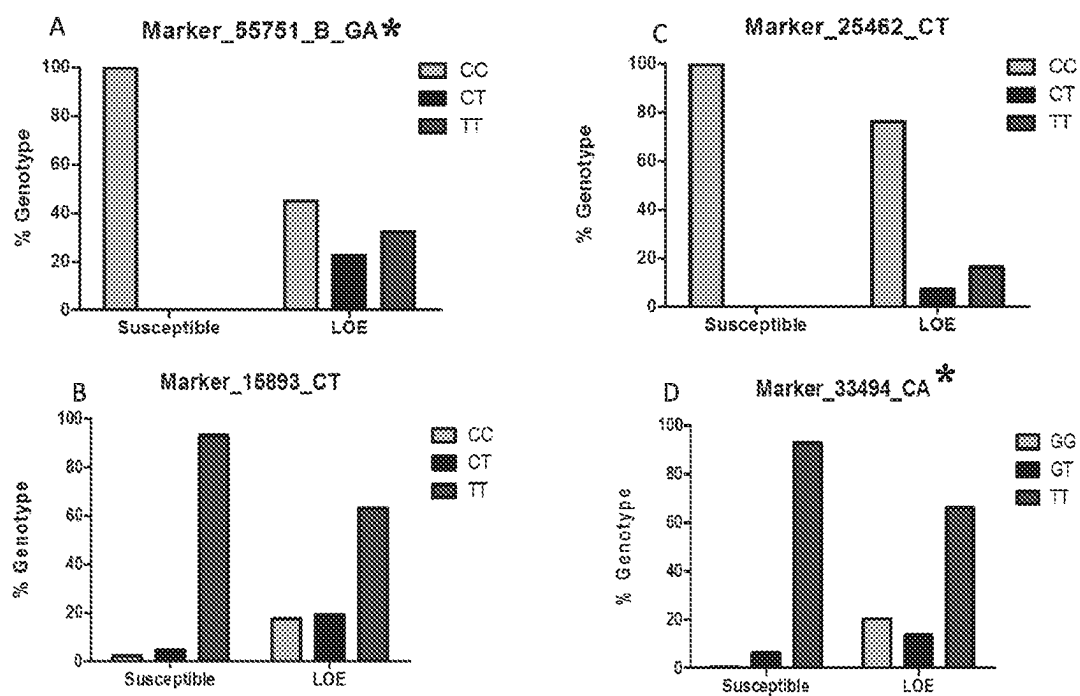


Figure 26

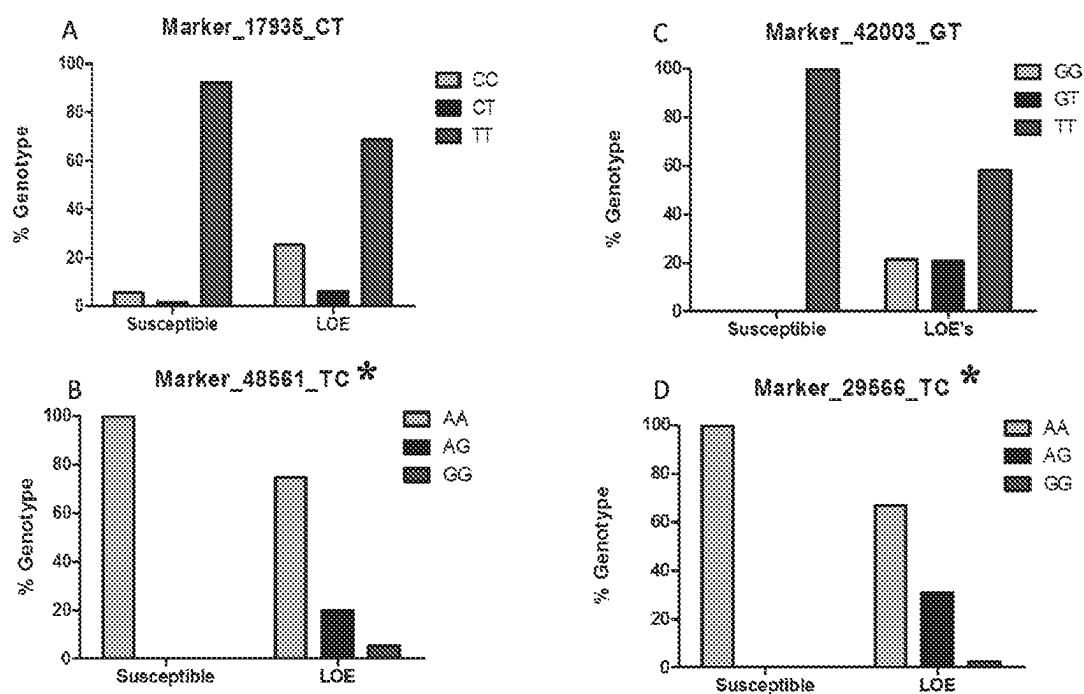


Figure 27

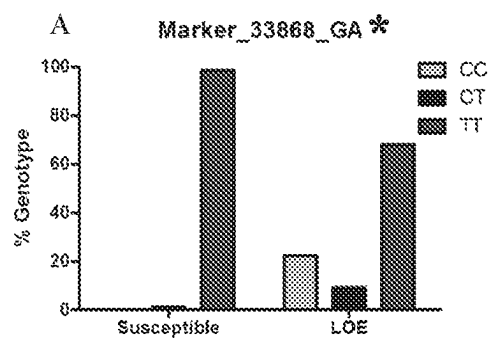
**Figure 28**

Table 1. Genotype frequencies for markers representing SEQ ID NOs: 110-127

SNP Loci	% Genotype Frequency Susceptible			% Genotype Frequency Confirmed Resistant			Comparison Susceptible/Confirmed Resistant	% Genotype Frequency Confirmed Resistant + LOE			Comparison Susceptible/Confirmed Resistant + LOE
	CC	CT	TT	CC	CT	TT	p-value	CC	CT	TT	p-value
MARKER_31307*			100.0%	2.9%	11.7%	85.4%	6.3E-05	8.7%	8.7%	82.6%	5.7E-06
MARKER_26225*		0.7%	99.3%	1.3%	48.3%	50.3%	3.7E-21	1.9%	47.2%	50.9%	1.2E-23
MARKER_47722_B*	6.5%	1.3%	92.3%	22.7%	33.7%	43.6%	5.0E-20	18.9%	23.5%	57.6%	2.9E-14
MARKER_58162_B	0.7%	1.5%	97.8%	26.7%	18.6%	54.7%	1.8E-16	30.7%	14.7%	54.6%	1.0E-18
	AA	AG	GG	AA	AG	GG		AA	AG	GG	
MARKER_17709*	100.0%			74.1%	19.0%	6.8%	4.3E-02	67.3%	17.5%	15.1%	NS
MARKER_47141*	100.0%			56.7%	43.3%		4.7E-23	68.8%	27.7%	3.5%	3.5E-16
MARKER_48750_A	100.0%			54.9%	28.7%	16.5%	1.3E-15	54.1%	24.8%	21.0%	1.9E-17
MARKER_63962	100.0%			87.7%	11.7%	0.6%	1.0E-03	81.9%	11.8%	6.2%	1.7E-05
MARKER_6372	90.2%	2.3%	7.5%	20.2%	49.7%	30.1%	1.8E-32	35.8%	32.9%	31.3%	2.0E-26
MARKER_15611*	90.5%		9.5%	53.3%	26.7%	20.0%	9.3E-14	47.7%	15.9%	36.4%	6.9E-19
	AA	AT	TT	AA	AT	TT		AA	AT	TT	
MARKER_46432			100.0%	0.8%	15.0%	84.2%	8.2E-05	3.2%	10.3%	86.5%	3.0E-04
MARKER_29594	1.2%	8.7%	90.1%	12.7%	32.9%	54.4%	1.5E-12	12.4%	20.8%	66.8%	1.4E-08
	CC	CG	GG	CC	CG	GG		CC	CG	GG	
MARKER_26784			100.0%	16.8%	7.2%	76.0%	1.4E-07	10.1%	4.4%	85.4%	1.0E-04
MARKER_51661	100.0%			45.5%	39.4%	15.2%	2.7E-23	48.9%	29.0%	22.1%	2.7E-24
MARKER_7819*	94.9%	1.9%	3.2%	45.2%	39.2%	15.7%	3.1E-21	53.6%	23.5%	23.0%	3.1E-19
MARKER_26704*	90.4%	4.5%	5.1%	70.2%	27.4%	2.4%	2.5E-08	65.8%	22.7%	11.5%	2.2E-09
	AA	AC	CC	AA	AC	CC		AA	AC	CC	
MARKER_14329	1.1%	6.1%	92.8%	6.4%	14.0%	79.7%	9.9E-04	17.4%	20.4%	62.2%	1.0E-13
	GG	GT	TT	GG	GT	TT		GG	GT	TT	
MARKER_56169			100.0%	16.0%	1.3%	82.7%	5.0E-03	21.8%	1.1%	77.1%	4.8E-04

For markers designated with an asterisk (), the genotype indicated shows analysis of the reverse complement of the sequences shown as SEQ ID NOs: 110-127.

Figure 29

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MARKERS TO PREDICT MACROCYCLIC LACTONE DRUG RESISTANCE IN *DIROFILARIA IMMITIS*, THE CAUSATIVE AGENT OF HEARTWORM DISEASE

The present application is a divisional application of U.S. patent application Ser. No. 15/887,164, filed Feb. 2, 2018, which is a continuation application of U.S. patent application Ser. No. 14/896,736, filed Dec. 8, 2015, which is the U.S. National Stage filing under 35 U.S.C. § 371 of International Application No. PCT/US14/44000, filed Jun. 25, 2014, which claims benefit of priority to U.S. Provisional Application 61/839,545, filed Jun. 26, 2013; all of which are incorporated herein by reference in their entirety.

REFERENCE TO SEQUENCE LISTING SUBMITTED ELECTRONICALLY

Incorporated by reference in its entirety is a computer-readable nucleotide/amino acid sequence listing submitted concurrently herewith and identified as follows: as a 8 kilobytes xml file named "78045-366383_ST26.xml", created on Apr. 13, 2023.

FIELD OF THE INVENTION

Disclosed are genetics related to macrocyclic lactone (ML) endectocide resistance in nematode parasites (e.g., *Dirofilaria immitis*). Single nucleotide polymorphisms within the genome of *D. immitis* are disclosed that, singly or in combination, correlate with reduced responsiveness of the parasites to MLs. Also disclosed are methods for detection of these parasites, methods for treatment of these parasites, and methods and kits for determination of responsiveness of these parasites to MLs.

BACKGROUND OF THE INVENTION

Dirofilariasis is a parasitic disease of animals and occasionally in humans, which may result from infection by a species of *Dirofilaria* such as *D. immitis*, *D. repens*, *D. tenuis*, *D. ursi*, *D. subdermata*, *D. lutrae*, *D. striata* and *D. spectans*.

Dirofilaria immitis (heartworm) is a parasitic nematode that commonly infects dogs, foxes, wolves, coyotes, and cats. Heartworms may cause serious vascular damage and may be fatal, especially in highly active animals.

The life cycle of *D. immitis* is well known (reviewed in McCall et al., Adv. Parasitol. 66:193-285, 2008). In brief, a mosquito may become infected when it draws blood from an infected host (e.g. a dog). In the mosquito, microfilariae (mf) develop to the infective larval stage. When the infected mosquito feeds, it may transmit larvae to a new host (e.g. another dog). In the new host, the larvae continue to mature for eight to ten weeks, after which time they move to the right side of the lungs and the pulmonary artery, where they become adult. Adult worms mate and females produce eggs, which develop in utero into the long thin embryos (microfilariae) that are released into the bloodstream. A mosquito that takes in the circulating mf when it draws blood from the infected host starts the cycle again.

D. immitis may be found wherever its vector, the mosquito, is found. Generally, *D. immitis* may be found on a world-wide basis, but are very common in areas with mild and warm climates.

Macrocyclic lactones (MLs) are often prescribed as therapeutics or prophylactics in the management of *D. immitis* in

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veterinary applications. Example MLs include ivermectin (IVM), milbemycin oxime (MO), moxidectin (MOX) and selamectin (SLM). However, resistance to MLs is common in a variety of parasitic nematodes and appears to be developing in *D. immitis*. A number of tests have been described for the detection of anthelmintic resistance in nematodes of livestock and horses, including, faecal egg count reduction test, the egg hatch test, microagar larval development test and molecular tests based on benzimidazole resistance (reviewed in Coles et al., Veterinary Parasitology 136:167-185, 2006). Prichard et al. (European patent EP 0979278) describes a P-glycoprotein sequence in *Haemonchus contortus* which may be useful for the diagnosis of ML resistance in parasitic nematodes. However, there remains a need for methods to detect *D. immitis* (heartworms) that are resistant to a ML.

SUMMARY OF THE INVENTION

Genetic variations (e.g., SNPs) have been discovered in the genomes of *Dirofilaria* spp. nematodes that relate to reduced responsiveness of the nematodes to macrocyclic lactones. In one example, the nematode is *Dirofilaria immitis* (the agent of heartworm in animals). In one example, the macrocyclic lactones are ivermectin, selamectin, milbemycin oxime or moxidectin.

Methods for determining the responsiveness of a *Dirofilaria* spp. nematode to a macrocyclic lactone are disclosed. In one example, the method involves determining the genotype of the nematode at a polymorphic site in a nucleic acid molecule that includes one or more of SEQ ID NOs: 1-127 from the nematode. In one example, the nucleic acid molecule possesses at least 80% sequence identity to one or more of SEQ ID NOs: 1-127. In other examples, the nucleic acid molecule possesses at least 90% or at least 95% sequence identity to one or more of SEQ ID NOs: 1-127. In one example, the nucleic acid molecule includes a fragment having a length of at least 100 nucleotides of one or more of SEQ ID NOs: 1-127 and includes the polymorphic site. In another example, the nucleic acid molecule includes a fragment having a length of at least 50 nucleotides of one or more of SEQ ID NOs: 1-127 and includes the polymorphic site. In one example, the nucleic acid molecule includes a fragment having a length of at least 100 nucleotides and that possesses at least 95% sequence identity to one or more of SEQ ID NOs: 1-127 and includes the polymorphic site.

In one embodiment of the method, the presence of an alternative nucleotide at the polymorphic site in the nucleic acid molecules indicates that the nematode is likely to be resistant to the macrocyclic lactone. In one embodiment, the method may include isolating the nucleic acid molecule from the nematode, and optionally purifying the nucleic acids prior to determining the genotype of the nematode. In one embodiment of the method, the genotype of the nematode is determined by DNA sequencing, hybridization-based methods including with allele specific oligonucleotides, microarray analysis, enzyme-based methods, single strand conformational polymorphism (SSCP), high resolution melt (HRM) or approaches based on PCR, RT-PCR, or qRT-PCR.

Isolated nucleic acid molecules comprising one or more of SEQ ID NOs: 1-127 are disclosed. In one example, the nucleic acid molecule possesses at least 80% sequence identity to one or more of SEQ ID NOs: 1-127. In other examples, the nucleic acid molecule possesses at least 90% or at least 95% sequence identity to one or more of SEQ ID NOs: 1-127. In one example, the nucleic acid molecule includes a fragment having a length of at least 100 nucleotides

tides of one or more of SEQ ID NOs: 1-127 and includes the polymorphic site. In another example, the nucleic acid molecule includes a fragment having a length of at least 50 nucleotides of one or more of SEQ ID NOs: 1-127 and includes the polymorphic site. In one example, the nucleic acid molecule includes a fragment having a length of at least 100 nucleotides and that possesses at least 95% sequence identity to one or more of SEQ ID NOs: 1-127 and includes the polymorphic site.

Kits for determining the responsiveness of a *Dirofilaria* spp. nematode to a macrocyclic lactone are disclosed. In one example, the kit contains a probe capable of determining the genotype of the nematode at a polymorphic site of one or more of SEQ ID NOs: 1-127. The probe may be an oligonucleotide, a primer or an aptamer. Using the kit, the genotype of the nematode may be determined, for example, by DNA sequencing, hybridization-based methods including using allele specific oligonucleotides, microarray analysis, enzyme-based methods, single strand conformational polymorphism (SSCP), high resolution melt (HRM) or approaches based on PCR, RT-PCR, or qRT-PCR.

Methods for selecting a treatment to treat an animal infected with a *Dirofilaria* spp. nematode are disclosed. In one example, the method involves determining the genotype of the nematode at a polymorphic site in a nucleic acid molecule that includes one or more of SEQ ID NOs: 1-127 and selecting the treatment based on the genotype of the nematode. In one example, the nucleic acid molecule possesses at least 80% sequence identity to one or more of SEQ ID NOs: 1-127. In other examples, the nucleic acid molecule possesses at least 90% or at least 95% sequence identity to one or more of SEQ ID NOs: 1-127. In one example, the nucleic acid molecule includes a fragment having a length of at least 100 nucleotides of one or more of SEQ ID NOs: 1-127 and includes the polymorphic site. In another example, the nucleic acid molecule includes a fragment having a length of at least 50 nucleotides of one or more of SEQ ID NOs: 1-127 and includes the polymorphic site. In one example, the nucleic acid molecule includes a fragment having a length of at least 100 nucleotides and that possesses at least 95% sequence identity to one or more of SEQ ID NOs: 1-127 and includes the polymorphic site.

In one embodiment, the method involves treating the animal with one or more alternative agents when an alternative nucleotide is found at the polymorphic site. Alternative agents may include one or more of an arsenic-based therapy, diethylcarbamazine, and antibiotics. In one embodiment, the method may include isolating the nucleic acid molecule from the nematode, and optionally purifying the nucleic acids prior to determining the genotype of the nematode. In one embodiment of the method, the genotype of the nematode is determined by DNA sequencing, hybridization-based methods including with allele specific oligonucleotides, microarray analysis, enzyme-based methods, single strand conformational polymorphism (SSCP), high resolution melt (HRM) or approaches based on PCR, RT-PCR, or qRT-PCR.

BRIEF DESCRIPTION OF THE DRAWINGS

FIGS. 1-28 illustrate the genotype frequencies for the SNP within each of the indicated markers, for susceptible and LOE isolates. The graphs are representative of markers that are also designated as SEQ ID NOs: 1-109 within the application. For markers designated with an asterisk(*), the

genotype indicated shows analysis of the reverse complement of the sequences shown as SEQ ID NOs: 1-109 within the application.

FIG. 1 illustrates the genotype frequencies for the SNP within Marker 617 (SEQ ID NO: 1), Marker 714 (SEQ ID NO: 2), Marker 814 (SEQ ID NO: 3), and Marker 887 (SEQ ID NO: 4).

FIG. 2 illustrates the genotype frequencies for the SNP within Marker 1514 (SEQ ID NO: 5), Marker 2557 (SEQ ID NO: 6), Marker 3367 (SEQ ID NO: 7), and Marker 3488 (SEQ ID NO: 8).

FIG. 3 illustrates the genotype frequencies for the SNP within Marker 4553 (SEQ ID NO: 9), Marker 5266 (SEQ ID NO: 10), Marker 5365 (SEQ ID NO: 11) and Marker 5667 (SEQ ID NO: 12).

FIG. 4 illustrates the genotype frequencies for the SNP within Marker 6568_A (SEQ ID NO: 13), Marker 6568_B (SEQ ID NO: 14), Marker 7633 (SEQ ID NO: 15), and Marker 9400 (SEQ ID NO: 16).

FIG. 5 illustrates the genotype frequencies for the SNP within Marker 9473 (SEQ ID NO: 17), Marker 9858 (SEQ ID NO: 18), Marker 10349 (SEQ ID NO: 19), and Marker 10520 (SEQ ID NO: 20).

FIG. 6 illustrates the genotype frequencies for the SNP within Marker 10678 (SEQ ID NO: 21), Marker 11676 (SEQ ID NO: 22), Marker 11933_A (SEQ ID NO: 23), and Marker 11933_B (SEQ ID NO: 24).

FIG. 7 illustrates the genotype frequencies for the SNP within Marker 12716 (SEQ ID NO: 25), Marker 12925 (SEQ ID NO: 26), Marker 13063 (SEQ ID NO: 27), and Marker 15000_A (SEQ ID NO: 28).

FIG. 8 illustrates the genotype frequencies for the SNP within Marker 15000_B (SEQ ID NO: 29), Marker 15709_A (SEQ ID NO: 30), Marker 15709_B (SEQ ID NO: 31), Marker 17333 (SEQ ID NO: 32).

FIG. 9 illustrates the genotype frequencies for the SNP within Marker 18110 (SEQ ID NO: 33), Marker 19999 (SEQ ID NO: 34), Marker 20570 (SEQ ID NO: 35), and Marker 20587 (SEQ ID NO: 36).

FIG. 10 illustrates the genotype frequencies for the SNP within Marker 20698 (SEQ ID NO: 37), Marker 21554 (SEQ ID NO: 38), Marker 22174 (SEQ ID NO: 39), and Marker 22254 (SEQ ID NO: 40).

FIG. 11 illustrates the genotype frequencies for the SNP within Marker 22259 (SEQ ID NO: 41), Marker 24708 (SEQ ID NO: 42), Marker 25276_A (SEQ ID NO: 43), and Marker 25443 (SEQ ID NO: 44).

FIG. 12 illustrates the genotype frequencies for the SNP within Marker 26447 (SEQ ID NO: 45), Marker 26730 (SEQ ID NO: 46), Marker 26974 (SEQ ID NO: 47), and Marker 27080_A (SEQ ID NO: 48).

FIG. 13 illustrates the genotype frequencies for the SNP within Marker 27349 (SEQ ID NO: 49), Marker 27461 (SEQ ID NO: 50), Marker 29128 (SEQ ID NO: 51), and Marker 29168 (SEQ ID NO: 52).

FIG. 14 illustrates the genotype frequencies for the SNP within Marker 29455 (SEQ ID NO: 53), Marker 29816 (SEQ ID NO: 54), Marker 30575 (SEQ ID NO: 55), and Marker 30991 (SEQ ID NO: 56).

FIG. 15 illustrates the genotype frequencies for the SNP within Marker 31796 (SEQ ID NO: 57), Marker 32164 (SEQ ID NO: 58), Marker 32223 (SEQ ID NO: 59), and Marker 34439 (SEQ ID NO: 60).

FIG. 16 illustrates the genotype frequencies for the SNP within Marker 34903 (SEQ ID NO: 61), Marker 35336 (SEQ ID NO: 62), Marker 36040 (SEQ ID NO: 63), and Marker 37881 (SEQ ID NO: 64).

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FIG. 17 illustrates the genotype frequencies for the SNP within Marker 38662_A (SEQ ID NO: 65), Marker 38662_B (SEQ ID NO: 66), Marker 38622_C (SEQ ID NO: 67), and Marker 38622_D (SEQ ID NO: 68).

FIG. 18 illustrates the genotype frequencies for the SNP within Marker 39492 (SEQ ID NO: 69), Marker 42291 (SEQ ID NO: 70), Marker 42411 (SEQ ID NO: 71), and Marker 45689 (SEQ ID NO: 72).

FIG. 19 illustrates the genotype frequencies for the SNP within Marker 45719 (SEQ ID NO: 73), Marker 46063 (SEQ ID NO: 74), Marker 47481 (SEQ ID NO: 75), and Marker 47722_A (SEQ ID NO: 76).

FIG. 20 illustrates the genotype frequencies for the SNP within Marker 48750_B (SEQ ID NO: 77), Marker 48750_C (SEQ ID NO: 78), Marker 48790 (SEQ ID NO: 79), and Marker 49731 (SEQ ID NO: 80).

FIG. 21 illustrates the genotype frequencies for the SNP within Marker 49824 (SEQ ID NO: 81), Marker 49904_A (SEQ ID NO: 82), Marker 50378 (SEQ ID NO: 83), and Marker 51565 (SEQ ID NO: 84).

FIG. 22 illustrates the genotype frequencies for the SNP within Marker 58162_A (SEQ ID NO: 85), Marker 58864 (SEQ ID NO: 86), Marker 62666_A (SEQ ID NO: 87), and Marker 62666_B (SEQ ID NO: 88).

FIG. 23 illustrates the genotype frequencies for the SNP within Marker 7060 (SEQ ID NO: 89), Marker 12056 (SEQ ID NO: 90), Marker 16261 (SEQ ID NO: 91), and Marker 23195 (SEQ ID NO: 92).

FIG. 24 illustrates the genotype frequencies for the SNP within Marker 28579 (SEQ ID NO: 93), Marker 48869 (SEQ ID NO: 94), Marker 53021 (SEQ ID NO: 95), and Marker 7986 (SEQ ID NO: 96).

FIG. 25 illustrates the genotype frequencies for the SNP within Marker 48094 (SEQ ID NO: 97), Marker 6568 (SEQ ID NO: 98), Marker 17022 (SEQ ID NO: 99), and Marker 55751_A (SEQ ID NO: 100).

FIG. 26 illustrates the genotype frequencies for the SNP within Marker 55751_B (SEQ ID NO: 101), Marker 15893 (SEQ ID NO: 102), Marker 25462 (SEQ ID NO: 103), and Marker 33494 (SEQ ID NO: 104).

FIG. 27 illustrates the genotype frequencies for the SNP within Marker 17935 (SEQ ID NO: 105), Marker 48561 (SEQ ID NO: 106), Marker 42003 (SEQ ID NO: 107), and Marker 29566 (SEQ ID NO: 108).

FIG. 28 illustrates the genotype frequencies for the SNP within Marker 33868 (SEQ ID NO: 109).

FIG. 29 presents Table 1 which displays genotype frequencies for markers representing SEQ ID NOs: 110-127.

DETAILED DESCRIPTION OF THE INVENTION

Definitions

Herein, “macrocyclic lactones” or “MLs” means products, or chemical derivatives thereof of soil microorganisms that belong to the genus *Streptomyces* including, but not necessarily limited to, avermectins and milbemycins. These molecules are used to treat species of endo- and ectoparasites in a wide range of hosts. Avermectins in use include, without limitation, ivermectin, abamectin, doramectin, eprinomectin and selamectin. Available milbemycins include, without limitation, milbemycin oxime and moxidectin. Macrocyclic lactones have a potent, broad antiparasitic spectrum at low dose levels. They are active against many immature nematodes (including hypobiotic larvae) and arthropods. A single therapeutic dose may persist in concentrations suffi-

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cient to be effective against incumbent nematode infections for prolonged periods after treatment.

Macrocyclic lactone (ML) heartworm preventatives were developed for the treatment of dogs and cats, which were not already infected, to prevent establishment of adult infections by targeting the developing L3/L4 stages. Macrocyclic lactones also have effects on the microfilarial stage (L1). Macrocyclic lactone endectocides such as ivermectin (IVM), milbemycin oxime (MO), moxidectin (MOX) and selamectin (SLM) are used during the transmission season for chemoprophylaxis for heartworm in dogs and cats.

Herein, “responsiveness” means that a nematode responds following exposure to a macrocyclic lactone (ML). In embodiments of the invention, a nematode may respond by being sensitive or resistant to a ML. Sensitivity or sensitive to a ML means that the macrocyclic lactone adversely affects the exposed *D. immitis* nematode. For example, a ML may be lethal or sub-lethal to the *D. immitis* nematode, shorten its life-span or inhibit its ability to reproduce. Resistance is the reduction in effectiveness of a drug, herein MLs, in curing a disease or improving symptoms (e.g., eradicating heartworm organisms from a dog). AD. *immitis* nematode may be ML resistant if the drug meant to neutralize it is ineffective, less effective or has reduced effectiveness. AD. *immitis* nematode may also be ML resistant if the drug, at a specific dose that is meant to neutralize it, has reduced effect. In embodiments of the invention, responsiveness of a nematode to a macrocyclic lactone may be determined in vivo or in vitro.

Herein, “loss of efficacy” or “LOE” means that there is at least a perceived decrease in responsiveness of nematodes to MLs. The perceived decrease in responsiveness may be perceived or may be actual. In one example, the decrease in responsiveness of nematodes to MLs may be real, in which case the nematodes may be said to be resistant to MLs. In another example, the decrease in responsiveness of nematodes to MLs may be perceived and not real. For example, in the case where a dog infected with heartworm is treated with MLs, for the purpose of eliminating heartworm from the dog, the dog owner may not be compliant in properly administering the MLs to the dog. In such a case, the heartworm infection may not be eliminated from the dog because sufficient doses of MLs were not administered, for example. The dog owner, or other observer, may mistakenly believe that MLs were compliantly administered to the dog (e.g., the owner believes s/he administered MLs as directed but, in reality, missed administrations, administered inadequate dosages, etc.) and, because the heartworms were not eliminated from the dog, the heartworm parasites are resistant to MLs. In at least some of these cases, heartworms are not eliminated from the dog because of the lack of compliance. In these cases, continued presence of heartworm may not be due to ML resistance of the heartworm organisms (i.e., the decrease in responsiveness of the heartworm parasites is perceived and not real). In cases of LOE, generally there is no confirmation that the heartworm infection is actually resistant to MLs.

Herein, “resistant” or “confirmed resistant” generally means that the heartworm organisms were shown to have at least reduced responsiveness to MLs. In one example, dogs infected with heartworm are treated with MLs, using a regime known to normally rid dogs of heartworm infection (i.e., compliance of the ML treatment is not in question), but the treatment does not rid the dog of heartworm organisms. Such heartworm organisms, which would normally be eliminated from the dogs by the compliant treatment, are not

eliminated because of their reduced responsiveness to ML. Such heartworm organisms are said to be resistant to the MLs.

In one example, a *D. immitis* nematode may be said to be resistant to a ML if less than about 93%, less than about 91%, less than about 89%, less than about 87%, less than about 85%, less than about 83%, less than about 81%, less than about 79%, less than about 77%, less than about 75%, less than about 73%, less than about 71%, less than about 69%, less than about 67%, less than about 65%, less than about 63%, less than about 61%, less than about 59%, less than about 57%, less than about 55%, less than about 53%, less than about 51%, less than about 49%, less than about 47%, less than about 45%, less than about 43%, less than about 41%, less than about 39%, less than about 37%, less than about 35%, less than about 33%, less than about 31%, less than about 29%, less than about 27%, less than about 25%, less than about 23%, less than about 21%, less than about 19%, less than about 17%, less than about 15%, less than about 13%, less than about 11%, less than about 9%, less than about 7%, less than about 5%, less than about 3%, less than about 1% or if 0% of nematodes died following exposure to a LD95 (a lethal dose or concentration of a drug that should have killed 95% of *D. immitis* nematodes) dose or concentration of a macrocyclic lactone.

In another embodiment, a *D. immitis* nematode may be said to be sensitive to a macrocyclic lactone if at most about 5%, at most about 4%, at most about 3%, at most about 2%, at most about 1% or if 0% of nematodes survived following exposure to a LD95 (a lethal dose or concentration of a drug that should have killed 95% of *D. immitis* nematodes) dose or concentration of a macrocyclic lactone.

Herein, “nucleic acid”, “nucleotide sequence” or “nucleic acid molecule” may refer to a polymer of DNA and/or RNA which may be single or double stranded and optionally containing synthetic, non-natural or altered nucleotide bases capable of incorporation into DNA or RNA polymers. “Nucleic acids”, “nucleic acid sequences” or “nucleic acid molecules” may encompass genes, cDNA, DNA (e.g. genomic DNA) and RNA encoded by a gene. Nucleic acids or nucleic acid sequences may comprise at least 3, at least 10, at least 100, at least 1000, at least 5000, or at least 10000 nucleotides or base pairs.

“Nucleic acids”, “nucleic acid sequences” or “nucleic acid molecules” may be modified by any chemical and/or biological means known in the art including, but not limited to, reaction with any known chemicals such as alkylating agents, browning sugars, etc.; conjugation to a linking group (e.g. PEG); methylation; oxidation; ionizing radiation; or the action of chemical carcinogens. Such nucleic acid modifications may occur during synthesis or processing or following treatment with chemical reagents known in the art.

Herein, an “isolated nucleic acid molecule” may refer to a nucleic acid molecule that does not occur in nature as part of a larger polynucleotide sequence; and/or may be substantially free from any other nucleic acid molecules or other contaminants that are found in its natural environment. As used herein, an “isolated nucleic acid molecule” may also encompass recombinantly or synthetically produced nucleic acid molecules.

Herein, the term “identity” or “identical” refers to sequence similarity between two or more polynucleotide molecules, at one position in within molecules, or at more than one position within the molecules. Identity can be determined by comparing each position in the aligned sequences. A degree of identity between nucleic acid sequences is a function of the number of identical or

matching nucleic acids at positions shared by the sequences, for example, over a specified region. Optimal alignment of sequences for comparisons of identity may be conducted using a variety of algorithms, as are known in the art. In one example, sequence identity may be determined using the well-known and publicly available BLAST algorithm (e.g. BLASTn and BLASTp). In another embodiment, the person skilled in the art can readily and properly align any given sequence and deduce sequence identity/homology by mere visual inspection.

Herein, “single nucleotide polymorphisms” or “SNPs” refer to genetic variations (or non-identity) at specific locations in a genome (i.e., polymorphic site). Generally, at a specific position in a genome, the identity of a nucleotide may be invariant or constant. At some positions in a genome, however, the identity of a nucleotide may not be invariant. At such positions, there may be a nucleotide present at the position at a relative higher frequency than other nucleotides, when the genomes of different individuals within a population are analyzed. The nucleotide most commonly found at such a position may be referred to as the wild-type nucleotide at this position. However, there may be one or more other nucleotides found at this position at relatively lower frequencies. These nucleotides may be referred to as alternative nucleotides. The frequencies by which the alternative nucleotides are found may vary. In one example, the SNPs described herein may play a role in responsiveness of nematodes to MLs. In one example, the SNPs may identify or tag a region of a genome that may play a role in responsiveness of nematodes to MLs (i.e., the SNP itself is not directly involved in the altered responsiveness to MLs but may be genetically linked to genetic changes that are involved in altered responsiveness). In one example, presence of one or more of the disclosed SNPs may indicate that the parasite whose genome contains the one or more SNPs is less responsive to MLs compared to parasites that do not have the SNPs.

As used herein, the term “polymorphic site” may refer to a region/specific location in a nucleic acid at which two or more alternative nucleotide sequences are observed in a significant number of nucleic acid samples from a population of individuals. A polymorphic site that is one nucleotide in length may be referred to herein as a “single nucleotide polymorphism” or a “SNP.”

Herein, “marker” or “markers” generally refer to nucleic acid sequences that can contain one or more SNPs. These nucleic acid sequences can be of different lengths.

Herein, “genotype” refers to the genetic constitution of a cell, an organism, or an individual (i.e. the specific allele makeup of the individual) usually with reference to a specific character under consideration. In the context of this application, genotype generally refers to identity of nucleotides at positions of SNPs. In one example, aGG genotype may mean that at a specific position of a gene (e.g., a polymorphic site) which has two alleles, the nucleotide at the same location in each allele is G (guanine). Alleles are alternative DNA sequences at the same physical locus, which may or may not directly result in different phenotypic traits, but generally within the context of this application, correlate with decreased responsiveness of parasites to MLs. In any particular diploid organism, with two copies of each chromosome, the genotype for each gene comprises the pair of alleles present at that locus, which are the same in homozygotes and different in heterozygotes.

Suitable approaches for use in determining genotype are known in the art and may include, without limitation, PCR, RT PCR, qRT PCR, SSCP and hybridization with allele

specific oligonucleotides. Other approaches may include nucleic acid hybridization to DNA microarrays or beads, restriction fragment length polymorphism (RFLP), terminal restriction fragment length polymorphism (t-RFLP), amplified fragment length polymorphism (AFLP), and multiplex ligation-dependent probe amplification (MLPA).

Herein, “consists essentially of” or “consisting essentially of” means that the nucleic acid sequence may include one or more nucleotide bases, including within the sequence or at one or both ends of the sequence, but that the additional nucleotide bases do not materially affect the function of the nucleic acid sequence.

Genomes and SNPs

In one aspect, the invention relates to isolated nucleic acid molecules possessing at least 80% sequence identity to SEQ ID NOs: 1-127, over their entire length, and comprising the alternative nucleotides at the location of the SNP (i.e., polymorphic site), the alternative nucleotides indicated by the underlined nucleotide in SEQ ID NOs: 1-127, as disclosed in this application. The alternative nucleotides generally have a lower frequency of occurrence at the indicated positions within the sequences, as shown in FIGS. 1-29. In one embodiment of the invention, the genome of a nematode parasite, or a population of parasites, may contain one or more of the alternative nucleotides at the polymorphic sites shown in SEQ ID NOs: 1-127. The presence of these alternative nucleotides generally correlates with reduced sensitivity of the parasites to MLs as compared to parasites that do not contain the alternative nucleotides.

In another aspect, the invention relates to isolated nucleic acid molecules comprising, consisting of, or consisting essentially of the sequence depicted in SEQ ID NOs: 1-127.

A nucleic acid molecule of the invention may comprise a sequence corresponding to that of SEQ ID NOs: 1-127 over their length, and containing the alternative nucleotide at the SNP site (i.e., polymorphic site). In embodiments of the invention, the nucleic acid sequence may be at least about 80%, at least about 81%, at least about 82%, at least about 83%, at least about 84%, at least about 85%, at least about 86%, at least about 87%, at least about 88%, at least about 89%, at least about 90%, at least about 91%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99% or 100% identical to SEQ ID NOs: 1-127, but that was isolated from a nematode having the alternative nucleotide at the position in each sequence shown by the underlined nucleotide as disclosed in this application.

In other embodiments, the nucleic acid molecule of the invention may comprise a part of, or fragment of, SEQ ID NOs: 1-127 that also contains the polymorphic site and the alternative nucleotide at the polymorphic site. In various examples, the fragment of SEQ ID NOs: 1-127 may be 5, 20, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180, 200, 220, 240, 260, 280, 300 or more nucleotides in length.

A nucleic acid molecule of the invention may be derived from a *D. immitis* nematode containing one or more of SEQ ID NOs: 1-127 as disclosed in this application. As used herein, “derived from” may refer to a nucleic acid molecule that was isolated from a natural source, e.g. a *Dirofilaria immitis* nematode. It may also refer to a nucleic acid molecule that is man-made, e.g. recombinantly or synthesized on the basis of a nucleic acid molecule isolated from a *D. immitis* nematode.

Detection of SNPs

SNPs may be detected by any method that can determine the identity of a nucleotide at a specific position in a genome (e.g., polymorphic site) and that allows for comparison of the identities of nucleotides at the specific genome position between individuals or populations of individuals. Differences in the identities of nucleotides at a specific position may be indicative of a SNP.

A variety of methods may be used to detect SNPs. In one example, hybridization-based methods can be used. Hybridization-based methods generally rely on hybridizing complementary DNA probes to the site containing the SNP. In one method, dynamic allele-specific hybridization (DASH) relies on differences in melting temperatures resulting from mismatched base pairing. By designing probes that differentially hybridize based on nucleotide changes in target genomes, SNPs can be detected.

In one example of a hybridization-based method, molecular beacons can be used. Molecular beacons are single-stranded nucleotide probes, with a fluorochrome at one end and a fluorochrome quenching molecule at the other end, that can form a stem-loop structure and place the fluorochrome and quenching molecule in close proximity to one another. In absence of hybridization of a molecular beacon to a genome region, the fluorochrome will be quenched, due to its close proximity to the quenching molecule. When the molecular beacon hybridizes to a genome region, the fluorochrome generally will not form a stem-loop structure. Under these conditions, the fluorochrome will fluoresce, due to the increased distance to the fluorochrome from the quenching molecule.

In one example of a hybridization-based method, oligonucleotide microarrays, which are high-density arrays containing hundreds of thousands of probes, are used for hybridization to SNPs. By comparing differential hybridization to redundant probes, it is possible to detect SNPs.

In one example of detecting SNPs, enzyme-based methods may be used. In one example of an enzyme-based method for detecting SNPs, restriction endonucleases are used to digest a genomic DNA. By determining the fragment lengths that result from the digest, it can be determined whether certain sites within a genome fail to be cleaved by the endonuclease due to a nucleotide change (e.g., alternative nucleotide) in the sequence recognized by the endonuclease.

In one example of an enzyme-based method for detecting SNPs, PCR (polymerase chain reaction)-based methods are used. In one example of this, two primer pairs are designed such that only one of them will function to amplify a site containing a SNP, depending on whether the SNP is present. The sizes of the amplified products are distinguishable, therefore informing which primer pair functions, and whether the SNP is present.

In one example of an enzyme-based method for detecting SNPs, nucleotide probes are designed to hybridize to a genomic site and produce a mismatch, whether or not a SNP is present at the specific genomic site. An endonuclease (e.g., Flap endonuclease) that cleaves one of the probes, depending on whether a mismatch exists, is used. Using fluorochromes and quenching molecules, attached to one or more of the probes, SNPs can be detected.

In one example of an enzyme-based method for detecting SNPs, primer extension is used. In this method, primers are hybridized to genome DNA immediately upstream of the SNP. DNA polymerase is then used to extend the primer in a mini-sequencing reaction. The sequencing reaction determines the presence of a SNP.

In one example of an enzyme-based method for detecting SNPs, the 5'-nuclease activity of Taq DNA polymerase is used. A TAQMAN™ assay is performed concurrently with a PCR reaction. The method is set up so the PCR reaction will extend through a site containing a SNP, and release a fluorochrome from a probe hybridizing to the SNP region, depending on whether the probe contains a mismatch due to presence of the SNP.

In one example of an enzyme-based method for detecting SNPs, DNA ligase is used to ligate two probes, one hybridizing to a SNP site in a genome, depending on whether the SNP is present, and a second probe hybridizing adjacent to the SNP site. If both probes hybridize to the genome without mismatches, ligase will connect the two probes, which can be measured.

Other methods of detecting SNPs exist, including for example, detection of single-stranded conformation polymorphisms, temperature gradient gel electrophoresis to detect duplex mismatches due to SNPs, denaturing high performance liquid chromatography to detect mismatched duplexes, high resolution melting analysis, use of mismatch-binding proteins, and others.

In one example of detecting SNPs, a biological sample comprising a *D. immitis* nematode may be obtained from a subject. The subject may be, without limitation, a dog, fox, wolf, coyote or cat. In the context of the invention, a biological sample may be any sample (e.g. bodily fluid, excrement, organ, tissue, etc) from a subject. The biological sample may be from a subject that is known to have, or is suspected of having, a *D. immitis* nematode infection. The *D. immitis* nematode may be isolated from the biological sample with standard separation methods and techniques.

A nucleic acid sample may be isolated or obtained from a *D. immitis* nematode prior to use. Methods of isolating nucleic acids from organisms and tissues are known. Such methods may include, but are not limited to, traditional DNA extraction, with proteinase K digestion followed by phenol chloroform extraction, sodium hydroxide extraction, and physical disruption, followed by purification, e.g. by cesium chloride centrifugation or high performance liquid chromatography (HPLC); or the use of commercial kits. A skilled person would appreciate that different approaches may be used to isolate a nucleic acid sample from an adult *D. immitis* nematode in comparison to a microfilaria. In an embodiment of the invention, the nucleic acid sample comprises genomic DNA.

The nucleic acid sequences of the nucleic acids from the parasite may be determined using any one of numerous methods known in the art. In some techniques, sequences of separate pieces of the genome are assembled into linear whole genome representations of the parasite using computer-based methods. In one example, massive parallel sequencing may be used. Massive parallel sequencing (also called “next-generation sequencing”) may encompass various high-throughput DNA sequencing methods. One such method is the HiSeq2000 system from ILLUMINA®.

Through comparison of sequences from separate parasites or parasite populations (e.g., comparison of a consensus or reference genome obtained from parasites sensitive to MLs with a consensus or reference genome obtained from parasites resistant to MLs), presumptive SNPs can be identified.

The presumptive SNPs can be analyzed further. In one example, high-throughput SNP analysis using multiplex PCR and MALDI-TOF mass spectrometry (SEQUENOM® analysis) was used. Generally, this system uses extension of an oligonucleotide primer or probe using chain terminating nucleotides to product different sized PCR products for each allele of a SNP. The different sized PCR products are analyzed using MALDI-TOF mass spectrometry.

Disclosed SNPs

In one example, genetic markers from *D. immitis* include the sequences below (SEQ ID NOs: 1-109), where the underlined nucleotides (i.e., the polymorphic sites) indicate the nucleotide position within the fragment that correlates with resistance to MLs (i.e., the alternative nucleotide). In these sequences, the nucleotide at the underlined position is generally different than the nucleotide found at this position in organisms that are not resistant to MLs (wild-type). In the sequences below, the nucleotide underlined in the indicated sequence is the alternative nucleotide which correlates with resistance to MLs. In the heading for each sequence, the nucleotide change from wild-type to the alternative nucleotide (alternative correlates with ML resistance) at the polymorphic site is shown (e.g., C in wild-type and A in the alternative sequence is designated as C→A). The genotype frequencies for each SNP at the polymorphic sites are shown in FIGS. 1-28. In FIGS. 1-28, for markers designated with an asterisk (*), the graph presents the genotypes of the reverse complement sequence, as compared to the nucleotide sequence presented in SEQ ID NOs: 1-109.

MARKER 617 (SEQ ID NO: 1): C→A
AACATAACATATTGAACTGAATCCTGCAACAGTTCTCTTATAACGTGAACCATACTAAATTTAGAGAAAATATG
AAAAAGAAAAATAAGTTGCTTTTGCTCGTGCAACCAACTCTAATACCCAGGAAATCAAGAAGTGATAATGAGTAATGT
CATCATTAGATTCAGTAATTGGTGACACTATCAATATTATTATTATTACTTAAAAATACGACGACCACTTATCGT
AACTTAAAGCATGCATAATACGACTGTCTATCATATTACATTTCTTCAAGTTCGTATTGGACAAGTGATT

MARKER 714 (SEQ ID NO: 2): C→T
GACAAGCGTTGACGGGAGAGACGATATAATAATAAGAAGGCATTGGGTATCAGAAGGCACAATCCAATTATAAATG
CCAAGGCAAAATGAATAAAATTTATGCTGACGATTGTGATCAATTACGAAGAATTTCCGATCGGCTCGAATCTTTGTT
TGTATGTGCACTACTGTTAACTTAATCTTTGTTTTATATACTTTTTCGTGTCATATATAATATATTCATGTCAACTG
ATACGTTATGATGTTTTTTTGTAATTAAGTTGATCGGAACCTGAAGTCTATTTCAAATTTAAGAAAT

MARKER 814 (SEQ ID NO: 3): T→C
TTTTAGGAAAATGGTGACTGTAGAGAGATATTATCGGAACGACAAGTCCACTTCGAACGGGTCTTTTATTGTCGAC
GGATTGTGAACCAAGTTTGGCATTCAATGACAGGTAGCTATTTTCCATCATCCCATTTTGTATTAGTGAAG

- continued

CAAGTCATGAGTCGAAAGAAAATCTCAAAAGAAAAAATGAAATTTTCAGGTTCAAAGGACTGCGTCCATTATTCGCA
CTGGTTGATGAGAACGTACAGATTCAGAGCGGCAATGCTGCACAGTATCTTTTGTTCACCTCTGAAT

MARKER 887 (SEQ ID NO: 4): C→T
TCGATTAAAAATTATCATCGATAAAATTTCTAAAATTTATTTTAGTAAAATTATTATTATTTTGATGAATAAGTTAAC
AAAAAAATTTTAATAACTTTTTGATTGCGCCAAAAATCTAATTCGTTAAAAAGTCGTCCAAACAGATATCGCTTGTT
CGATGAAAATGTCGGTTGTTAGAAAAATCAAAATGGTTCAAATAATTTTCCAGAACGTTGAAAAAATATTCCTT
TGTATCGGATAAATAACCATTACAATTTTCCACTCGTGTGTCATGTGTTTCTCGACAAAAATCAGCTAA

MARKER 1514 (SEQ ID NO: 5): T→C
TCAACAGAAATCGAGATTCCAAAAAGTTTCTACAAATACCTTAATTATCAATGGATATTTAGTTTTGTATCTGTTA
TCATAAGTTCTGCTTCTTACAGATTAAAAATGTCCAAGAATTTTTTACTATTCAAATGAGGGAAATAAAAAACCA
TGCCAATAATATCCAGAACTACATACATCTTTCTTTTTTCGAAGCTCATCTATTCCGGCCGAAAAAATGAAGAAC
ATTAAATTTCTTAAAGATAGTCTTAGCCTTTTCTTGACCCTATCTTAAGTGTGAGCGCTAAAATGT

MARKER 2557 (SEQ ID NO: 6): T→C
AATAGTCGTCTACTTCTTTGACTTTATAATTCGAGAATCTTATGTAGTCCTTCACTTTACCTTCTTCTGTCG
AACTAAGAATTACAGCATTATTTTCGAATTTAATGTGTAAAAGACAATAGCAGATTTTGTAAATTTGTGTTAACCTC
ACTTTATATTTTCGCTTCATATCGTGACAGAGAATTACTATTTAGAGAGTATTACTTGTCAACAGAGAATCTCCAGA
AAGATTTTTATTTACGTCGGAAAAATGGACAAAAATGGTTTCTTATCATTAGCACTGATAGCTAGTTTCC

MARKER 3367 (SEQ ID NO: 7): G→A
TATCTCTTGTGTGTGTTCTGCATTGTATCAAGTGGGTAAATTTTGCTTTAGACGTTGACTTATTGTCTTTTTTAA
GTTATATTCTAGTCCATGTTTTCTCTTGCAAATATTTTTTCCGCCGCTATGATTCAATTGTTTTGTTGTAAC
CTCTATTAAGTTGCTTTTAGTTTGAATTGTATCAAAATTTCAAACATTTAAATACGCACTAGCACTATTTTTCTT
ATCTCAATTAAGCGAATCCCGAACAAGATTTAATCGATTTCCGAATCACAATTAATCACTGGAAAAAC

MARKER 3488 (SEQ ID NO: 8): T→C
ATTTTCTTAAACAAATCATTTTCAACGAAAAACATTAAGAGTGTAAAATAAAATGGTGATATTGATAAGAAAT
TAATTCACCTGCATATCAATCTTGTAGCGCCATTTCTTAGCAAGTTCTATAGCAGCTCGATCCATATCACCTT
CTTGCTCTAATGTCAATCCGGTCCCGAATTTTTTTTATTTTGCCATTCTTCATCTTTTTTTTATTTTACTGAT
ATAGCTATAGACCTTTCTCCCGTGCATGCTGTAGGCCTGTTCTGATATACAGGCTTGTGAACCACTG

MARKER 4553 (SEQ ID NO: 9): C→T
TTCTGGGGTAGTTATACGGAATTTAGACAATGAAGAGAATCAAAAAACATGCGATTTTCAACAGAGGAACCTTGG
TACTTTTGCTCGACTTACTTTATTTTAAACCCATACAAAAATAAATGTTTCATTGATTGATATTGTCGTAATAA
AATTAGAGCTTCAACATTAGGATTTTAATAACCTTCAATTTATTTTCAAGATTTAAGAACTTACGTATGGATGGAGA
AAATATAAAGAAATGGCGATGACAAATAAGATTTGCTATGAAAAAATAATGCCACAAGATCCGAATGCA

MARKER 5266 (SEQ ID NO: 10): C→T
TTTATGAACAAAATAATAAAATTTAGGATAACAGATATCAATTTCTTTTAGCTATAAATATACGCTTCGATTGAAA
AAAGCTTTCAAATTATAATTAAGGCATACGTTACGATATAGACAATTAAGTCGACATTAATTATTTGAAATATTTTA
AATTTTTTCTCTTTCTTTTTTCTATTCTCTTCCAAAGTGTCAAATAGTTATGAAATGTGAGAGCTAAAATGAT
AATATTATTCAAGTTTATTACCTAATCTTTTATCACCTCATTTCTTATCATTTATCTGAAAACTAATC

MARKER 5365 (SEQ ID NO: 11): G→A
ATGTTGAATTTTAAATGAACTTTTTCGGTGCATAAGCATTACAGATCTGTAAGCTGTGCAACCTGTTTCTTTGT
AAATGAACAAAGATCATTTATGTTTCCAGCGTCGATTTGACCTGGATAAATGTGGTACCAAAAGTAGATGACGA
GAGGTAAGTGCAACAAAAATGCACAAAAATGATTTTGATGCACTCAAATCATTTTAAAGTTTGTGCAATTTCCAT
TTATAGTTTCGTGATCGGTTGTTATTCATCAACTGATTTTGTTTGTGTTTTTGTGACTTATATTTCAT

MARKER 5667 (SEQ ID NO: 12): G→A
TTTGACATTTTCAATACCTTACAACTCATCTCCAGCACCAATTTACAATATCGCTGCCTAAATAAAGAAATTTAT
TCGGATATGAGACTGTAGTTTTTCATTCCGTACCAATCATAGTAGAACAGATCTATAGCATGGTGTCTACTAAAGTT

ATTAGAGCCAAGGATGGTATCACATGTAAACTGCAATTTTGCTATTTGTTTAAAGCAAAATAAGAAATAAAATATTTTC

- continued

GTTCTTATTCTTTAATTTATTTTCATCAGATGGCTTTGTTATACCATAATTGTAAATCTGTCATATCTTAATTGCGCA

ATAGCCCAAGATTCTTGTATATCTTACATTTACAATTTATTTTCTTATTCTAGTTTGAATTATA

MARKER 11676 (SEQ ID NO: 22): A→G

AATAGCTACTCACAGCTTAAGTTAACTAATGGATTCTTGAATTTATTTAAGCGTGTAGTTAAGCGATTAATATGATG

GATGCCCAAGATCGCTTTGTCTTATAGTTTGTCTCGACAGAAAGGATGCATTGTTGTCTTGAATTTGTTCAGGGA

AAATTAATAGGTTTCTTTCAATGACTCCTATTAAATTTTTTTGAATTTAGGCTTGCATTGCGTGTCTGATCCACT

ATTAGCACGTACGGGTATCGCAGTGCCATGTGATGCAGCACTATGCAAAAACCACTCCATGTCACCTG

MARKER 11933 A (SEQ ID NO: 23): A→G

TCTGTTGTAAGTTTCACAAATCCAGTTAATTTAAGCTCAGCTTATTTGAAATTTTCAACAAAATTACGAAAATTACTT

TCTCGGTTCAATTTTTTCAACCACCAATATTTAGCATAATTGGCCTGAAATCGTCAAAGTTTACAAACTTTTGTTC

AGCAATCTTCTTACTCTTACAATAAACATGATTAACCTTGTCTGCATACCAATCTCGTTTATAGCAAATCTTTTC

AAAAAACATTGCTACAAATTTTATATCGCATCATTTCAACACGCATAATTATTTTTCATATATGAAAA

MARKER 11933 B (SEQ ID NO: 24): T→C

TTCACAAATCCAGTTAATTTAAGCTCAGCTTATTTGAAATTTTCAACAAAATTACGAAAATTACTTTCTCGGTTCAAT

TTTTTCAACCACCAATATTTAGCATAATTGGCCTGAAATCGTCAAAGTTTACAAACTTTTATTAGCAATCTCCTC

TTACTCTTACAATAAACATGATTAACCTTGTCTGCATACCAATCTCGTTTATAGCAAATCTTTTCAAAAAACATTG

CTACAAATTTTATATCGCATCATTTCAACACGCATAATTATTTTTCATATATGAAAAACCATATTATAA

MARKER 12716 (SEQ ID NO: 25): A→G

ATTAAGCTCTGAACCAAGACTGTTGGTTAAATAAAGATCTATTTTAGTTATACATCTAACATTAAAGGTTTTCGT

ACGGAACAAGTAGGTTTGATAATTTTCATGTAAGTAAAGAACACCTGTGAAAGGGATCAGTAAAAATTTGGGGGA

TGTCAGCACGAAATATGAAGCTGAGTGTTTTGTACCCAAAAGTTTTTCAAATCTGCGAAATAACGAGAGGTGTAATG

ATCGTTTTTAACCAATTTTTTGATTCTAATCCTTCCCACAGTTTTGAAATTCAGTAAGCATTTCTTTT

MARKER 12925 (SEQ ID NO: 26): T→C

TTGCAACAAATCAATAATAAAAGACTTGCGGCTAACAATATATTTGATTCTTTTTTACCGTTATTATTATGACAGGT

AATAATAGTATTACAAGCATTTTGTAGGTGCAATTTTTTCAATTCAAATTTCTTAATTCATTATTTCTTCCTTT

CCTTAATAAATAGTCTTTCATTTAAGAATTAACTTTTTGAAATCTTAAATGAGAAGACACAAAAGATTCCGGATAA

TTTTGCATCATCTTTCTATTTTCGCGTTAGTATTTTATGTTTTCAACAGATTTTATGATTTAACTATA

MARKER 13063 (SEQ ID NO: 27): C→T

GATAAAATGGGTTCTTGTCAAGCTCATTTGGCATATCTTCGTCTTCTATATTTATATCCTTAAATATCTTCTCTTTT

TTCAAATTTTCTTCCCAGCTTTTCCATATCGACCTCTTCTTCATAAATTTATCTTCCCTATTGCGCTCATTTT

TGACTTTTTCATCCGTTTCATCCTTATTTTTCTTTTTTTCATCTCCTATTTTACCTTTTCTTTATCAACTTCTATCT

TAACTTTCTCAATGTTTTTTTTTATTTCTTTCATCTTTTTGTTTTCTTCTATTGACATACATAACAAA

MARKER 15000 A (SEQ ID NO: 28): T→A

TTTTACGAACAATTATTTTCATAAAAGATTTCGTATTTTGTATTAGTTTTTAAGAATTTTTTTTTATTATTTTAGCCA

ACAAATATATTTTTCAAATTTGTTAAATTTGAAATTATAAATTTCAACTAAAAAAGCAAAAAGCTAAGCCAATAG

AAATAACATACATGTGTAATATAAAATATAAAGTATTCGAAATGAAATCAAAGTTTCATAACAAAAACAAAAAT

ATTCTAACCTTTTAGATTTTCATCAAAACTTCACTAAAAAGTTAAATTTAAATTTTCAAATTTGTTATACA

MARKER 15000 B (SEQ ID NO: 29): A→G

CGAACAAATTTTCATAAAAGATTTCGTATTTTGTATTAGTTTTTAAGAATTTTTTTTTATTATTTTAGCCAACAAA

TATATTTTTCAAATTTGTTAAATTTGAAATTATAAATTTCAACTAAAAAAGCAAAAAGCTAAGCCATTAGAGATA

ACATACATGTGTAATATAAAATATAAAGTATTCGAAATGAAATCAAAGTTTCATAACAAAAACAAAAATATTCT

AACCTTTTAGATTTTCATCAAAACTTCACTAAAAAGTTAAATTTAAATTTTCAAATTTGTTATACAATGAT

MARKER 15709 A (SEQ ID NO: 30): T→C

TCAAAGACAAAATGAAGAACTTAACAAAAAAGGCCAATAAATAAAGGCTATTTCGTGAAAAATCTAAAAA

AGATCTGTTCTTCGAATCAAGTGATTCTTCTACTACATTCGTGTTGTAATCTTACTTGTATACAGTCCCCAGT

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TTTTCGACGATAAAAAACATTTTCGATAAGTGAGTTTGAATTAATTGAATTTTAAAGATCATAAAAAATAAAATCAAA

ATAAAAAGACCAAAATTAAGTCTGATAATTCAGAAAAACACAATAATAATATACAAATAATAAAAACT

MARKER 15709 B (SEQ ID NO: 31): T→A

AAATAATTCATAATTTCTCATCATCAAATTATTTTCGTACAATCGATAAATCAACGATTATAATAGCGAAGAGAATG

AAAAATTAATGTGGTGCACAGTATACGGACCCCATATACAATGTTCAACAGAGATGAACATTTTTTTCTATTAAAGT

TTTCTGTTTCGGCGAAAGAAAGACACTTTCTAACGATGCTTTCCCTCCCAACTCCCCTTGCAATGATAGAGGATGCAGC

CAAGATTCGTCTGACTCAAGCAGCATCACTCAACCGGCCATCACTTCGGGACCTTTTTCCCTGCCTTTTA

MARKER 17333 (SEQ ID NO: 32): A→G

CATTCGGAATGACCGCTATGAATATCAATTAGCAGATATTAATCGTGAATTAAGCACATTGGTGGAAATTTTACGA

CCAAATCGAATTTCAAAAAATGCTACACTTGCAACATCAGCAACCATTGCAACATATAACAGTACTTCGATGCGTAA

TGTA AAAAGAAATGTAATGCATCTGAAAGCTGAAAATTCATCTGATATATTGAAGCAAAAGGTAAGATTATTTTTA

AGATATCATTCTTGATGCTCTCATAATTTCTACATCAAATTTAATCAAACGATTCAATTTATGTTCAATT

MARKER 18110 (SEQ ID NO: 33): C→T

TTCTTGTTGTACCTATCATAGATGATACTTAAGTACCAATAGCAATAGTGCAACGATGCAAGGATTCTGATTAATG

ATTATAAAAGTTTAACCAATCTTCTTCATTCTTCTAATCAAGAGAAAAAAAATGAGAACATTTTATGACATTTG

AAGAAAGGCAATTTATCGCTGAAAATCTACTGCGATATGGAAGTATCAGATAGAGAAAAATAATATTAATAATG

ATTTCATACGAAAAATGATAAAGATAATAATTTACATTTTGGTGCTTTACTGATATGATTGGAGTATT

MARKER 19999 (SEQ ID NO: 34): T→A

CGATATTTTTTGGAGCAATCAAACCTTTTTGGGAAATCATTGATGTCACAAGCATGGTTTGAGAAATTTTTTCCG

AATTAGTTCTGCTAAAAATACTCCAAATGAGTCTAGTGGAATTAAGCTAAGCACCTTAAGTAAGTTGAGAAAAACGT

TTCCATTTGACTAACAAGGCTAGTATATCGACATGAGACAGAAATGGTTATTACTTCACTCACTTCATGAAGCGAAT

ACGAAATATCTGTTCACTTTAGTTTCAATCTACTATTTTACCAATAAACGTGTTCTTTTCCGGATAAAT

MARKER 20570 (SEQ ID NO: 35): T→C

TCTTAATTGATTTTCTTAACCGAAACACTTGTCTTGATTACTGTGCTGTACTTTATCTTATTAATTAATAATTT

CCATGACCACTTCATACCATTGACCATCAAACCTTTGATGAAGTTTATGTGTGAAGTGCCAAACAATCATTCACTCCCT

TCAGTTTAACTTATTGCTGGTCAAATTCATAAAAAATGCAAATTATCAAGCAGATAGTAATTCAGTGAACGTAGCGTA

TTCTCGAAATTTCTTCTCTTGATTTACCTTATATAGAACACGTATATTTGTAGCATATATTCAATAT

MARKER 20587 (SEQ ID NO: 36): G→A

TTTCTGAGTTTGCGTTACAGCGCCAAATCTTCACGGAGATAGATAAAATACTTATCGTGAAATTTTGGCGCCATGAT

TTAAAAAACACGGAGATAAAAAATAAATGCTTATCGGTGATAATTTAGCGCCATAATATGAATGAATTGAAAAACA

ATTTGAGTAGAAACATGACATAGAGTTTTCGTTTTCTGGCTACGAAAATGGATGAATTTTCTGGAATCGAATTCAG

TCAAAGAAATAGGAACGTTGTTACTAAATGATCGAAAAGCTTTCTAAATTAATTTATGACGTCTAAG

MARKER 20698 (SEQ ID NO: 37): T→C

ATCTAAATCTTCGTTTATAGTGGTAAGACTTCCATTGCTGCATTCTTGCAAATTAAGCTGTTGAAATACTTTTT

TTTTTGATAGATTTCCAATTTAATCATATTATAAGAAGAATTAATTTGGAATAGAAATTTTAAATCATTAAACTTT

AAGTTTTAAACTAATATAAGTTATGCAGATTTTCGCGAAAAAGTCTCATTTGTTAATTCAAATTATCCAAAATGTAA

TAATTTTATAAATCAAATTTAACTACTACTAATCTCTGAAGTCAGGAGCCAGTAGCAACAACGTAAT

MARKER 21554 (SEQ ID NO: 38): A→G

AACTTTACATTATATATCAATTTTTTTTTTATTTGTTGTTTTTAGAAATTTGAAAATGGGTACTAATCAGTGTCTAT

TTGCAGCCTCTTAGACCTCTTTATAACGACCGATTTCGATGAAATACGTCTCAATATGCCAGTTTATTGTTTCGGGT

GGAGAATGTTTTCAAAGTTGCTGAAGTGATGAAGTATAGTGAGAATGCACCTTATTCAGCACCATTAAAGAAGTAAA

TTTTTGCTTTGGAATTTGACAAAGACAAAGCAGGAAGTTGACAACGATGTTCTGATGAAACGGTTTCGA

MARKER 22174 (SEQ ID NO: 39): A→C

GTCTATTTTGGCTGTCTCTAATAATTCATTTGTAACTTTTGAAATATGATAAATGTAGAAATTTTTCTTCCTG

GTCTATAATAGTTTAATAATGTGTTGTAGTAATAGTTTGGTGCCGTTGAAATATTTCAATGATATGCTATCGCAAA

- continued

ATTAGGAATTCAAATCAAGGTTACAAGATAATTCAAAACAAACACGTAAAAATGAAATAATTTCTTCTTCTTACT

TACCAACAGGCATATCATCATCATCTCAAATTCATGACTATATTTAACATTGTCATATTTGAATAATC

MARKER 22254 (SEQ ID NO: 40): C→A

CGACGCAAAAATCTTTCAAATTGTCACCCAGTTCCTAAGTGATTCCAATGATGTTGGTAAACATTCTGCATGATGT

ACCGGGTAATGAAC TACCAAGTTGTTTTTGCTTTTAATACAAC TCGCAAAGATTCTGAAAACCATGAAATTAAGAA

AGATTAAATAATCTGAACTCTTTTTTTCATTTTTCCTTGAACCTTAGCAATATACTGAGTTGGATAAAATTTAGAAA

CGAAATTTGCAAAATTTATTCAGTAAATTCAGGAAAAC TCGGTTTCGGTATTCTAAATATAAATAGATA

MARKER 22259 (SEQ ID NO: 41): A→G

GTTTCTTTGGTTTATCTCAGTAAGATTTGGGCGGAAATTCAGTTATACTTTTCATTTCCATGTGCTGTTTAAATT

TCTTCCATATTAGTATAATTTTCAAATAATGTAGCGTCACTGGTTTATTTAAGGATAACAGGTTGGACTGCAGTGG

CTGAGAAGTGTCTTGCCGGTCAATTGTTTGGTGGTGATCAACTTGTACGAGTTACTGATATCGACATATATAATACA

CGGCAAAATCCATTGTTTTTCAGTACTGCATCAAAACGGGATTATCGGTACTTTGTAAATCGCAGTAT

MARKER 24708 (SEQ ID NO: 42): C→T

GACCCCTGCTCACAAGGCAGTTCACACAGACAATCACACATCTAATCACACACATCAACTCATCCGACGTAGGCTAT

CAATAAGGAAAATTCATTGCTTTATCGTCTAAGTGAATAAACATCTACATAATGAAATTATTCGCCACTATGAC

AACTAATATCGCCCAATGCAAATATTTGTCTCAGAGTTATTCCTTTTAAACAGCTGTTGAACGAATAGATAGGACGT

CATGTGGATGATCTACTTGTTCAAAGGTTGAGGTAACACATGAAACACATGAAACCGGTAATTTAAAA

MARKER 25276 A (SEQ ID NO: 43): A→G

AAAGAATGTCAGCAAGATGTGGAAAATCGATTACTATAGTTGAAGTATGAATCGAAGAGGTTTTTTTAAATCTAA

GAGAACAATAATCGGCAAGAGAAAGTTGAGTAACCTATTTTGCCTTGTTTTAGTCAATTTATAATATGCGGTT

AATTGTGTTAAAGAAAGTACAAGGTATGAAATCTAAGCCAAGAAATAAGAGAAAACAGCTAATGATTATTTCTGCAT

TTTTTCTTTTTCGACACAACTTGAACCGAATCAATGAACTAGTAATCAGATTTTGATTATTGCTT

MARKER 25443 (SEQ ID NO: 44): T→C

TTAGATTTTGCTGAAGCATTGTTGTTAGATCGATGAAAATATAATTATGAGAGATTTGTTGAAATTCAGCAACAA

AATTATTATTCATGCTTTCATGCTGTCAGTTTTGTTTTATTTCTTCTTTGACATCGGTTATATTTTGTCTTCCAA

CAATATAAAAAAAATATAATCAATTGGTAATCAAATTTAAACTCTAATTGTTAGCTCCCTAAATCAGCTTTAAA

AAAATAATTGCTTAATTGGTATTGCTACTATTAGCAAACTGAAACTATCCTTTTCTCGAATGGTGAAC

MARKER 26447 (SEQ ID NO: 45): G→A

ATGAGCTGATATTTGATATGCATATTAAAAATAGGGTAAATTACATTAGTTAGATATCGTTCGATAAAATTAATTA

GAAAAAATGTTTACCAATTAGATCGCAATGATGTAATAATTTACAGTATTTTATTTCTTAAGATTATTTGCAAAAT

CAAAAATATGCTTTATGAAAAATAATTTTCTGTGTAAGAACAAGGGACCGATTCACTTGATTTATTCGCAACAAT

CGAAATTCAAAATTAGTAATTTTAAATATTGCTTTATTCAAACCATACCAATAATAATTTGAGAGATTT

MARKER 26730 (SEQ ID NO: 46): A→G

ATTGATTGATTCAAATAAGAAATTTAAATTATTTCCCTTTTTTTCAAAGATTTAACAATATTATTTATTTGATC

TCCTCGTTCGTTCTTATCTTTTGATTATCAATCCATCCTCCTCCATCATATAGCTAATTTATTTTTCGATCGTAA

ATCAATTGATGTATGATTGATTTCTTGATTATAAAAAGTTAGAAGAATTGAATTGCTTAAATTTAATTATTGATAAT

GAAATATTATTATATTTCAAATGATACGAAGAAATATGACGATGATAAGAGAAAATATGATATTTATC

MARKER 26974 (SEQ ID NO: 47): C→T

TACGATAAGTTATTTTATTTTACACATCTCCATCCTTGACTAGTGTCGGTGCCGACTGTCGACTTGAACCGACAAC

CTACTAATTACAAGTCAGTTGCTCTACCCAATTGAGCTAAGCCGCCATCTAGAATGTGCGACCCCGTCGTGGTACA

TCTTCTATAATCGTTTGGTATTCAGGACTCTCTTCTTTCGTGGGTGGAGGATCTTGATACAGTTGACTATTAATAAT

AGGGCCTTTGTTAGTCTGTTACAACCTATAGACAAAGGCGACAATTTTAGCTTACATCTTACGTTATGC

MARKER 27080 A (SEQ ID NO: 48): A→G

ATGGTAGAAAAATATATGAAAAATATCATACTAAAAATATAACAGATTGTTATAAGGTATGGTTAAGAATTTACA

ACAATTGATTATTTATGATAAAAAAAGTAAATCAGTGAATCATTAGATAGTTATGATAAGCAGTTTGTAT

- continued

TCGGTAAAGCGAATGATTAGAGGAATTATGGGACGAAACGCTATAACCTATTCTCAAACCTTTAATGAGTATGACG

TGTCTTGCTTGCTTAAATTTATTTCAATGATCATTTCACTTTACAGTATGATCATGATTAGACTTGAA

MARKER 27349 (SEQ ID NO: 49): T→A

TTAGTATCGATATTATCACAAATGATATCACTTTTCATCAATACTGGATACGATTTTATTAGTATCATAATTTGTGG

CTCGCATTCCGAAAGTTTACACGTAGAAGATTAACTGCAATATGATTATTTTATCATTTTCGAATATCCAACCT

TGAAATAATTGAAAAATGTTGAAAAATTTGAAAAATGTTAAACAAAATATTACAAAAATATCAAATGAAATTAAT

AACTGTCCATTTCAAAAAAGAAGAAAAATTATGAAATTACCAATTAACACAGGACTTATTAATTAAT

MARKER 27461 (SEQ ID NO: 50): G→T

TGTGGAAATAAGTACAATTAATGCTGTTTCGCTTAATAATATTATTTTCATTCTTGGCTTTTTTTTCTTCCCCG

TGATATTATAAATATAGTTTTTAAATTTTAAACAAATCGTCATAATTATTTAAAAAATACTGAGGTGAGTAAATGTA

ATTGGTTGCTGGAAAAAGTGGGTGATGAGAGGTGAATGAAAGCAGAATAGTTTATGATTGCATCAAATTCCTCC

TTAATCTGTGATTAAATCAAACAAACCCGAAAGTTTCTTCTTCGCCTTTTTCTTCTCTTTGTTTCA

MARKER 29128 (SEQ ID NO: 51): T→C

CGAAATCCGCCGCGTGCATTACTTTGCGCTTGTTGATTACGACGCATTTGTTTCGTCGTGATAACCTTATCAATCAT

CATACGTCGCTTACGTATGCAATCAACATCGCCAGTTAGGCTGAAATCAAATGGATGGCGATGATATCAAAAACAAA

AATAAGGAGTATTTGCTGAATCATTTCTTTTTCTGTATTATTATCAAAATTTCTCCTTTCCATTGTTTCCTTCTTA

ATCAAGTGAATGCTCATTTTCATTTTGAATAATCCAACGTAATAATCCCCATATTCCTCAATTACTTTC

MARKER 29168 (SEQ ID NO: 52): A→G

AGAAATATTAACTTTGAAAGATGTGACATGTTCTGTAACAAAAGCCCAAAATTCGACTGCTGCGCTTGAAGTA

AAATTTGGAATATGCTACATCAGTAGTGAACAGATGGTTCGATAAATAGTGGTAAGTATGGGAATCCTAGGAAT

AGATGGGAATGTATTTAGATATAAAATTTGATGCATATTTTCATAGTTGATTATATCTACGATCACACGTTGAATA

TTCTAAAAGCAAACGTGAATTAATACTAATGAATTTGAAAATTTCCAAGAATTAAATTTGTAACAAAA

MARKER 29455 (SEQ ID NO: 53): T→A

ATTGTCAGGAATGAGAAGCAAGTTTGGATACTTAAGGGATGAATGGAACACATACATGGCAGAAATGTTAGTAAT

CAAACCATTTAAATTACTTAGCCACTATGCTAACTTTCTAGAAGTATGGTTGAACGTTTAAAAACCTTCGCAAAAA

TTGTATTAGATTATCTTAATCTTCCCTACATCAAAACAGAGAATTTTGTCTACGACGTGAGTCTGCATGTATTAA

GGAAGTTCGTATCATGACGTAAATATCCTGAGTGATTATTGAATTGAGAAATGAGCTTTTTCATTTGG

MARKER 29816 (SEQ ID NO: 54): G→A

ATATGAGTGTTACATGTGTACGTTACATGTAATATTATATGTTATATGTAAAAATGTCATGTATAGCATCTATTCA

CGTGTACGTACACGTATATACATATACATTGATACTTAATACGTATACGCATGAATGAACAGATATTATATATTT

ACGTACACTAGACTCACATGTACCTCTGTATACGCATACATGTACAGATATATGTTTGACATACGTAAATTCATATA

TGCTTTTATTATGCTTATATTAATGTACATACATGCCTTATATTTTCGTTGTTATAACACATAAA

MARKER 30575 (SEQ ID NO: 55): T→C

GAAATATAAATTAGCTGAAATATATGCGAGGTAAAGCACACAGAAGAAATTAACCTAAGGTAATATATTGTAAGAAT

TTTTATATTCGCGCACCTAATAATTTTAGACGCATATGCCAGTATTTGAACTGGTAGCGCTGTTCTGACTTG

CTGTTGTCCATGTTATGTATATGATACCATTCCTAAATACTTTTGCGGCTGTGGTTTCCAGTGTTGATGTGACTGGT

ATGATGCCTAACACTGGATCCTTCCATCTGCGGCATTTTGTGAAATTCCTATTGATGTGAGCTGTTTA

MARKER 30991 (SEQ ID NO: 56): A→G

CAACTGTGAATCATAAACATTACTTAAATTAATGAAGCTAGTTAACGACAAATATATTTTTTATGTATCAGTGCTA

TCATATAACATAAAAACTTACTTTCATTAATAAATGAGCTCAAATATTGACTTTTGTCCAAAATGCTCAAATGTCTG

TCATAATATTTGAAATGAAGATAATTTACGCTTTTTCGAAGCCTCCTCTCACGTCTTTTAAATCTTCTTTCTTCTTC

TTGCTCTAATGGTTCTGCGAAAAACACGGTGCAATAATCACTTTCCATAATTTATACAGTACATAAGC

MARKER 31796 (SEQ ID NO: 57): A→G

CTGCTTAACCTCTTTTCATTTTTTCAGAGAATCTTCTCTAAAATTTGTGAATTGATCCAAACCAAGAATATGGATAATG

TGATTGCAATTCCTGGAATTTAGATTTTGAGAGTTTGAAGTTTTTAAAGAGATTGAATTTCTGTGACCTTCTGGTA

- continued

TATTTGATGTCATTTCCGGATGCGTATTTTGGCGAAATTTTGGCCTCACTGCAATCTTGTTAAAAAGTCAAAAAA

ATTCATCGTAGAATTTCCGGTTTACCTGATATTACTGGAAATCTCTGATCTTTGTTCTAGATTGCTGT

MARKER 32164 (SEQ ID NO: 58): A→T

ATAAAGAATTTGCAACTCTGTATACCTTTTGCAGTGCAAAAGCGGATGAATTCCTCACTGCAGTGTGACAGATTCC

TTTGATAAAATGCTTCGTTCTTATGTAACTTGGAAATTCGCGTAGTTATGCTTTTGCTAGTTGAAAAATGTTCTG

CTCTTGTAACATGCAAAAAGAGATTATCTTTGTTCTATTATGGAAAGATTCTTTTGAAATTTTGACGACTGAGAA

GACAAATTTTATCCCACTTGTCATCTGCAATAAAAAATTTTCTGACCTGTTTCTTAACCTTCCAAGT

MARKER 32223 (SEQ ID NO: 59): T→C

AAAATCAAATCAATATGATCAGATAACTCATACTTATCTTACTGAAAATTCCTCATTCAAGGAAATAAATAATTGC

AATTCCTGATTCGATCATGGATGATTTTCAAGCAAATTACCAATGATATCTATCGATAACGATTACAGCATACAGC

TATAACTTATTATTGATTGAATTGATGAAAAATAATTTACCAGAAATTTATCAATGTTTATCTCATTGCAGTATACG

ATGTTTAGTGTGACAACTTTTCTTGGAAATAATTGTGCATAAATCATTGATTGCATTTAGTATTGGA

MARKER 34439 (SEQ ID NO: 60): T→C

TCCTGCCACATCTTTCTACTTTAGATAATCAACAGGAGTTAGTTGAAAGAGAAGACTAGGAACAGTTGCAACTTC

TGAATCTTTCTGACTTTCTTTCGTTTTGTAAATTATTTATTGTATAAATTTAAAATTCGAAGAGAAAATAATCCAAG

GTCCAACTTCTTTTCTGTAGTTCTTGCGAATGCTCCATCAAAATGCAAAAATATGATTAGAATTCTGATGGAAAT

TAACAAAATCGATTAGATAAGAAAAGTACAAAACAGAACTAACTTTTCTCCCATTTTCATATTATAG

MARKER 34903 (SEQ ID NO: 61): T→C

TCATTGCTTTAATACCTTTTAAACGAGAATTTTCTCGATCAAAATAAGATCTGCAATTGATATACGTCAATAAGCGAA

CATTAGCTGATTACACGCTAATATTACATATGATGAACGTTGTAAGCGTCATACATCAACATATATCCATCCGAT

AAATAATGACCACTACACATTGCTACCAACCATCTATCCCGCCACTATTTGAAATGAACTGAGAAGGAGTTATCGA

CACAGGCTTCCTAGCAACCAACAAAAGACGAGACAGATGAATAGATAGACAGACAGACGAACATACAA

MARKER 35336 (SEQ ID NO: 62): A→G

AGATTCTGGTTATTATTGTATTTCTGATTTATTTAATCCCACTTAAAGATTCATTGGCTATTGTTTAGCATCTATA

TCAATTTTATAAATAAATAGTAATACCTGATGAAAAGCAATAAATAATTAGATGCAATTTTAAATTAGATACAGTTT

GATGGAAAACATTGAAGCCATGTACAACATAATTTATGCATGTTGAATTATGCATGCATAATTAATTTATGCATGACA

GCAAGTTTGGTATAAAATTAATTTTGTATGAAGATAAAATTTTATAAATAATGATAATAATGCTGGTAA

MARKER 36040 (SEQ ID NO: 63): T→C

ATTATTGAAAAGAATAATGTAGCTAATTAGTTGAAGCTGTTAAAAGTAAAGCTAAAAAGATGATGGAAATTATTCGT

ATAAACATCTTTGTAAACAAACAGTCATTTCTGTGAATAACAATTATAATTATAAACAATACTTTTCAAGACAAT

AAAAAATTAGGAAGCATTGTTGTGATAATCAATAGTTGATAGACTGTCAATGTATTTTATCAGTCGTGCTGCTTT

TTTTCCCTTTCTGACTCATTATTTTATTATTATTGATAGAATGTCAATATTCTAGTCATTTGTTAT

MARKER 37881 (SEQ ID NO: 64): T→C

ATCTTAACCTTGCTTTAAACAAATAAATTAACAGCCCAATGTTCCAAGAAAAAAGATAAGTTAAAAGTGGGGTGT

CCAAAAATTTATGAATTGAATTGGACAGTTATTTCAGATCCTGAAAATACGCTTCTCTGATCACTGCAAAATATCCCG

ATAAATAAGTGAACATTAGGTTAATCTTAATTTTCCCTTAACCTTCCCTAGCCTTTTTTAAATTTTGGATTATTCA

AGCATTTTTATTGCGGTATCGTTTTTGTAAAAAAAAGTATAATTCAACATTCAGGCTCGACGTTATG

MARKER 38622 A (SEQ ID NO: 65): C→A

AATTATAAAAAAGGAATACGATAAAATATCTATTTTTTGAACTAATCAAACATATTCCTCACTGCTCACCGG

ATAGTTGCTTTCTAATTTTACATTAAGAAATATATTTTTTTTTTCAATAAGGAAAGTTATGCAGACTAGGAGAATT

CTACTCTGAAGAAGAGATAAGCATGTTAGAATTATTAAAACTATGGAAATATCCTTAAAGAAATGCCATATAGTAGC

TCTGATTTTCAAAAAAAGCAAAAAACAAAATAACAAATCTGCTCAATTGAAATAAAAACTTTCCT

MARKER 38622 B (SEQ ID NO: 66): C→T

TAAAAATATCTATTTTTTGAACTAATCAAACATATTCCTCACTGCTCACCGGATAGTTGCTTTCTAATTTTACATTA

AGAAATATATTTTTTTTTTCAATAAGGAAAGTTATGCAGACTAGGAGCATCTACTCTGAAGAAGAGATAAGTATG

- continued

TTAGAATTATTTAAATCTATGGAAATATCCTTAAAGAAATGCCTATAGTAGCTCTGATTTGAAAAAAAAAGCAAAA

AACAAAAATAACAAATTCGTCTCAATTGAAATAAAAACTTTCCCTTCAACTTCCAGCATCACTGCTGTGA

MARKER 38622 C (SEQ ID NO: 67): C→T

AACTGCTAAAAAATTGAACTAGTGTAGATTGATAAGTGGGAGATTAAACCAATTGTGTATTGGCCCGTTAAT

TAGTGACTCTGAATAGCTATGGCGAATCGTATAGTGTGTACCGACGACGTATCTATCAAATGCTGCCTTGTAAAA

TTTCGATGATAGTTTATGTGCCTATTATAGTTGTAACGAGTAACGGAGAATAAGGTTTCGACTCCGGAGAGGGAGCC

TGAGTTGCCACATTCAAGGAAGGAAGCAGTCGCGAAGATTACCCACTCTTAGAATGAGGAAAGAGTGAC

MARKER 38622 D (SEQ ID NO: 68): C→T

GAAAACTAAGAAGTAAGTGAAATTTCTAAGTTCTTCCAGAAAGGTTAGATCCAATATTTGTTTTTCATTTAGCAT

TTTTATCCAATGAAAAATGTGCCCAATAAACTTGTATATAGTATTGCATTTAAAACTTCAGAAAGCACAATGAG

ATCTAAGCTCAGAAATATGACGAATACCAATCCTTTTCCTAGTCTTACCGCTTCTTAACTTTGTGTCGCTTTATAA

AAATTAATAATAAAAGTTGAACAAATGGGAATTACATCATTTTCATCTGAATGTTTATTTCCCTATTCT

MARKER 39492 (SEQ ID NO: 69): T→C

CTTCCCTAGCTATGCCTTTTCGTCACTTAAGCTTCNNNNNNNNNTCTAGCTACGTATCGTTATCATTATGCTTCT

TTAGCTACGTTTCTCCATCATTTATGCTTCTAAGCTACGTATCTTCATCACTTACGCTTCCCTAGCTATGTCCTTT

CGTCACTTAAGCTTCTTTGGCTGCGTGTCTTCATCATTAATCTTCTTTAGCTACGTATCGTTATCATTACGCTTCC

TTAGCTACGTCTTTCCATCATTTATGCTTCCCAAGCTACGTATTTTCATCATTTATGCTTCCCTAGATA

MARKER 42291 (SEQ ID NO: 70): G→A

GATCTTAAATTCATATGAACTTCTTCTGCATGGTATTGTTTCCACAGAATATAATGACAAATAGCAACAGTATTGG

TTATATAAAAAATTGACTGCAGCAGGATTATATTTCAAGTTCTTTTAATTTTCATTTATTTATTCTTTTCATTTACTT

TTACTGTTTTTATGTTTTTCTTCTTTAAAAAATATGATTTCTCTCACTGTTCTCTTTTCATCTATCTATATTTATTG

ATAATGCTTATATGATACTAGCTAAAGGGAAATAAAGTTTCAGTCATCATAGCTTCATTTTAGTAAA

MARKER 42411 (SEQ ID NO: 71): A→T

CTATACTAATCAGTCCACTATCCATTTTtaggttgcaaaagttgcaatgacggtttgatttcatcctccaatgcaat

TTTgagtcctcaatctcgagagatagatcgatcgcttttagcttgatttagcttggttaatggttgagggatattgg

gcagaaattctgtcaagcgttacttaatgaaatagtaaatgatcactgatatttattgttaatgatacttgagctct

ctagattatgaaactggaaggttttcgatagaataatcgatacatatattagaatcgacttctttttttc

MARKER 45689 (SEQ ID NO: 72): A→C

TCATCTTTTTCACATTTCAATTAATCATCATTTTATCAATTCCTATTTTAAACAAATCTTTTCAAATATCTCTC

TTTCTTCTCTTTTGTTTTCCGCTTATTCATTCTAATGATGAACAGATGTAGAAAAATTGCATTCTATTGCTCACT

ACAATTTTGAGTAGAATATATTTAATTATTTGATTCGAGACAGATGGTTATAGCCTTTAGCTTCAGCTTCTCGTTCA

AATTAAGTACTTGTGACCTTTCCAAGTACCATTAAAGCTTTCCTGCGTTTCCTAATTAGAAAAAAGG

MARKER 45719 (SEQ ID NO: 73): G→A

GCATTTTAAGTTAAAGTATCACGCTGCATGACACCTCACGTTTGCTATCTCAAATTGAGTAGGTTAGAATCTTTT

TTGGCTACTATTCAAATATTAATAATAAATTGCTGCAACAGATTTCACACCGGAAAAAATTAATTTTCTAGCA

ATGTTTTAACTCCCTTATTAATATTTATAGAAAATCGACTACTTAAAAAGAATTGACTAACATTTCTGAATCTCTG

CAGAGATTATAGATGGATTAGCATCCTACAAGTTTTATCTTTTGCTATATTCCATTATTTTTTA

MARKER 46063 (SEQ ID NO: 74): T→A

GATAAGACGCTTATTTTGTAAATAATCAAAAATTAATTAATATAGAAGTAAGATCTTGATAATAATTAATAGCTC

AAATTTCTTAATGAGAATATGTTCCAGGATGAAGATGAAGTGAAGAAATTGATAGATTGAGGAAGCAATTGCTAATT

GAAACAGAACAGCTCGTTTCCAATTCTCTTAAAGATTTACTGAAGAAAAATTTATTATCCACTTGAAGAAGCTATTGA

TCTCAAAATTCATCAGAAATTAATTCAACAAATTGCTGCCTTGTTGAAGTGTATTAGTATCTTGGATAA

MARKER 47481 (SEQ ID NO: 75): C→G

ACCGCAAAATACCTAAAAATTTCTATAACAACGATTAAACACGGCCTCGAACTGGAAGCATATTAATCCATGCGTGGC

TCAAACCTCAATCATAAAGACAAGATCTAGAGATCAACACAAAATGGTGAATTGTTACCTATCGTTGCTAAAGTTT

CGAAAGCTAAGCATGCTTGCAGCTTTGCCAAGATGCTGCATGCTACGGCTAGCAAAGAAAAATCAGCATTGCTTAATAATGCTGTA

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ATTATTACATCGCTTTTTTTTAAATCTTTTCTAAAATTAAACTGAATAATCAACTATTGCTATTGCTTTATCTT

ATTTTTTATCAACAAAATTCGAGGAAACAAATCGCTTATCAGAATAATTGTTTTGATCAACAAATAAAG

MARKER 58162 A (SEQ ID NO: 85): G→A

CAATCCCAAAATTCAGTGTGTCGGCGGGTCAGCGAAGGGAAGTTTGAACCGAGGGTATGTACAAATTGTGATAAT

TTTGTGATGACGTAGTAAATTTTCATAGTTTTGCATGCTTTAATGTTGATAGTCGCACAATCCTACGTTGATTAAATT

TAGCTATTAGATATCCTACTAAATTATGTTGTTTCATAATTTTTGTTTTTAAATGCTCCACTTATATTTTCAGGTTG

TGCAGTGTCTACAATAGGGGTTATGACGGCAATGATGTCCAATGGGAGTGTAAGCGGAAATGAGCAATC

MARKER 58864 (SEQ ID NO: 86): T→C

TCAGATAAATGTATTGATGTTAATTCAAAGAAGAAAAAATAATCAGTAGAATATGAATCGAATAATATTCATAC

AACCAGTTTATTCATTATTATTCACTTTTAACGTCTAAATGACGTAGCTACGCTTTTTTCTCGCTTCAAGCCTTT

ACTGACCAAGATTAATGTACATTCTGTTGAACAAGATTAATCGACATTCTATCGATCAAGATCAAGCTTTTACTGAT

CAAGATTAATAATGACATTCTTCTGTTGATCAAGATTAATCGACATTCCATTGATCAAGATTAATCGAC

MARKER 62666 A (SEQ ID NO: 87): G→A

CTCTCTAAAACCTATTGGTCACTAACTTGCACTGACTAAAACTATTGGTCATCAGACTTGTGATTCATTGAAAAG

ACCGTTAGCCGCTAAAATTATGATTCATAAAAAAATCTATTGATCATTAAATCTGTAATCATTGAGAACTACAA

TCATTGGTCATTAAGTTTGTGCTCTCTAAAACCTATTGGTCATTAACTGACTAAAACTATTGGTCACTGAACCTA

GAGTCTATTAAAAAAAATCATTGTATCAATAAATTTATTGTTTACTATCAAATCCATTGATTACTGA

MARKER 62666 B (SEQ ID NO: 88): A→T

TCTAAAACCTATTGGTCACTAACTTGCACTGACTAAAACTATTGGTCATCAGACTTGTGATTCATTGAAAAGACC

GTTAGCCGCTAAAATTATGATTCATAAAAAAATCTATTGATCATTAAATCTGTAATCATTGAGAACTGCATTCA

TTGGTCATTAAGTTTGTGCTCTCTAAAACCTATTGGTCATTAACTGACTAAAACTATTGGTCACTGAACCTAGAG

TCTATTAAAAAAAATCATTGTATCAATAAATTTATTGTTTACTATCAAATCCATTGATTACTGAATA

MARKER 7060 (SEQ ID NO: 89): G→A

AAAATGTATCAAATCTTCGATGCCATAAATTATACAGACTTGATTGGCATTTTTTCTAACTTTCATCATGAACCAT

TCTATTTCTAAATTGATCCATTACAAAATCAACTTTGTGATATCATCAATCTCAGTCATAACGAGAAATAATGATAA

TATAAAGCGACTATCATTTGAATTTCTGAATATTCAAGATGTAATTACATCTTTTTTTAATGTAATCAAAATTC

TTGCCATCAATAATTTTTCAACATATGCTTTCATCGACTGCCTTATGCAGATCGTAATGATGACAGCCA

MARKER 12056 (SEQ ID NO: 90): T→C

ATTGATTAAAAAGAAATCAACATTAAATTTTTGATATAGTCGAGAAATCCTTCGTGATAATTCTTTTAGACAATTCT

TTACTACTAACTTGTATTACTTGCTTATTATTTGTCTAAAGATACTAACTATTGTGTCAGTGGAATTTATGATCTTG

GCATTATTGCATATAACGCTTTCCTAAAATCTGAAATTTTTCAGTATTTTAAAACTAAGACGATTATTAAATATTA

CTCAAAGCTTAGAAGTTTGATTATACTAATCAAATCAAAATTTTCATCAGCGATTTTTGTTGTGTCATT

MARKER 16261 (SEQ ID NO: 91): T→C

ATTTTTTCCAGCAGAAATGTGCATCAAAAATCCATTTTTGATATCCTCTTCATCGAACTTGCTCCTGAATCCAGAG

AACAACGAAGAATGTGTAATCTATTTTCAGTAGCCTGCTCATTGTGCAATTCAGCGACTTTATTCTGTGCTTCAAG

CTAACTTCTTCATTATGCCACTCCTCTCTCGCTATTTTTTCGCTATCTAATTCAAAATCCTCGTCTGAAACGGA

ATCAACTCCTGACGATGTACTCGACACTGATAATATTTTCATGCCGATTTTTCTCTCAAACGAATCTTT

MARKER 23195 (SEQ ID NO: 92): C→T

GAATGAAGAGCAAAAAATAGTCAGCACCCTGCAATAAAAAACAGCATCTCCGTAAAAATGATTGAATTGATTCCC

GAAATACGAGTTTATCAAATTGAGAATTATGCAAATTAATTATCAGCATGCAGATTACTGATTTTATATCTCTCAT

ACCGAAATTAAGGTGATGTTTTCCATTCTTTGTTTCCACAATGTCTTCTTTGTGAATCGTTTTGGATCAACTATTA

ATCCGATCGAATCAATCCTCCAAATATGAGTTTATTCAACGTAACAAAACATTGTCCGAGATAATCAAA

MARKER 28579 (SEQ ID NO: 93): T→C

TGGAATTTTCGAAATCGAAAGGATGAAGAAAAAGGATCCTTGATCTATACATTAAATATCACCATATCAACTAGCAT

GGCAAGTCAAAGTAATGTTATCATTTAAATAAAAAAGATGAATAGTAGGACTACAGGTTATATTGTTAAAAAGTCGAC

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AAATTTGGAGTAATTGACAGAGATCAACGATTAAATGTAATGGATGATCTTATCTTCTTTTTTCAACTACGCCAAAA

TGAAAAATAACAATTGAATTTGTGCGAATAAGAACTAACATTTTGAAAAAAGATTGAACATTTATAAAT

MARKER 48869 (SEQ ID NO: 94): G→A

GGTTGGATCATTATCGACAGAACTTTAGAGTTTCTTGATAAGGACGAAAAGAAGCAGCACCATTGCTGATCTAAAC

AAGGAAAAAAGACCTTTTTTGGAATATTGAAGTTTTTACTGATAGGTGCGTGCTGTGTACTGTGGGCATAAGTACAA

GCTTCATGCTCCGAGCGTGAATACGTGCTGCATGCATACATATGCAGTAAAGGTGCGTGTGCTATTGCTCAATAAGT

GTATAAATGCTGCTTTTCTTGATAGTTAAATATTTTGTGTTTCATTTTTTCCGCTATTCAAATAAAT

MARKER 53021 (SEQ ID NO: 95): G→A

GTTGGGATTTGAGACTCTCACTCGTGTGCTTTCACAGTGATATCTGAATCGAAGTCACAAGCAGGTATGAATGCAT

AACAACATAATCCATTGCAGAAACAAGGCAAACTGAGAAGCTCGAGCAATATAGCTATAGAAGCTGGTACCACAG

ATGACATTACATGGTATTTCCATTTTCAGCTTCACAAACATTGTAAATAGCTTGCTTCGATGATTCAATATCTCGTTC

TACGATATTTCTTAAAGTAATTTTTATTATTGAAGTATAGATTACATCCATGTTCTATCTATCATTTTC

MARKER 7986 (SEQ ID NO: 96): G→A

TGTTCTGAACATCTCTTTTGATTATCTTTTAAATCCTCCATTATTTTCGTTTTTTTCGTTGTGAATTAATATTG

TTTGCTTTGATTGAGATGATATTTTCGGATCGTAAATAGATGGCATCGGCATAAGCGTATTGAGAAGCATTCAATG

GTGCACTCTTGCTTCTTTTTTTTTGAAATCTTTCTCGATAATCAAATAAGTGCAGGATGCCAATCATTAAACAATTT

CGTTCACATTTTTTCAGTCTTATTCTTATAACACCACATCTCATTTGCAATTTTGTGCGCAATGATTTT

MARKER 48094 (SEQ ID NO: 97): C→T

TTTTTTCGAGGTCACTCTGGAATAATAATCATATTTTAAAAAGACATAAAATAAAAAATATGTATATATAAGAAAA

TTTTTACTCTGAATTTCTTAAGAAAATTCTCGATTCTGTTTTCCATAAATTCGGAATATGTTGTCCCTGAATTAAG

AATTCGATTCCTTGACACCATTATTTTCGTCTAGTTCCTGTGTGAACAATGTAACCTGGAAATGAACACATAAACTG

TAATATTTTGAGCTTAAAAATAATTATGAGGATGCGAACTGAAGATATTCATAAATGTTTAAAAA

MARKER 6568 (SEQ ID NO: 98): T→C

GTCCATGCATTGCTTTTCGGAAGTTAGTGTAGATTGAGTGAATATTTAATACCAGTCTCTTCTAATTCAAAAGAGC

CTCCCATTTCTTTTTTCAGTTTCAGTCTCTGAATCAGAGCGTGAATCTACCACTCCATTGCCGAAAACAGCTCGAT

GTATTTCTGCTACGTAGTGTTTAGAATTGGCGTATGCCACTTGCTCATTATTCGCGCATGAAGTGTAACGTGAAT

AGAATGATACTACTGTTAGAAGAGAATGCGTTCACTTTATTTAACATTATACTGATTTCATTTCTTCTTT

MARKER 17022 (SEQ ID NO: 99): C→T

AGTGAAACGAGAAAAACAGAAGAAGAGATAGCACATCAAGATCGTGAGAAATTAATTAGACAAGAAAAGCTCGTCT

TACACAAATATATCAGGTTTTCTTTTTCTTGCTTTTCGAAAGTTATTTGAATTATCTCATTCTTTGAATTTTATAAG

AAATAATTTAATTTTTTTTTGAAATTTTGCCTATTGAGCTCTAAATTTTGTAAGTTTTCTAGGATGATGTTAGC

AAAGCAAAAAGAAATCCAAAAGTGATGGTAACAAACAGGAAGATTTATAGTGAGGTACGATAATACG

MARKER 55751 A (SEQ ID NO: 100): A→G

TAGACAATATCATCCTTCTTTTTTTTCTGCTCAATTTCTCTGCTCATTGCTTTGATGATAATGGTAGGTGGTATAAT

GAAACGAATAGATAATTGATGTTGCGAAACATTTGCTGTTAAATTTGAGTAAAGAAATTGACCTTTTGTCTTTGTGT

TGGATGTTTAGCTTCATTTTCTTCTGTTTCATTGTCATATTCATTCTCTCAAACTTCTTGCTTAGCGATGCTAATA

TAAATACTGGAAGAATGCCTTTGCTTTGTTTTAGTTGTAAATCATACCAAGGTATTTTTTGCAAAAT

MARKER 55751 B (SEQ ID NO: 101): A→G

AAGATGAACTAAAAAAATTATTTGAAAAAAGAAAATAAATTAATGAAATAAAGCAAAAATGAACAAACCGT

ATTAATTTTAAACAATAACAATATCGAAATCGAAAAATGGACTATTATGATGAACATATTTTCAAAATGTGAA

GGTCAAAGTTGTTTCAATTATGATAAATACAATTTAAATAAGATTAAGCTAACAAATAAGTTGAGCAAATTGATG

AAACAACAAATCAGAATATATTACAGAAAATGATATAACATGAAAAATATATTAGACCAATTATTTTTA

MARKER 15893 (SEQ ID NO: 102): T→C

TTGAAGTTTTGAGATAAATTTGATAAAAAATGTTCTATGAATTTCTCAAATTTCAATTAGTGATACTTATTTGAA

GGTAATTATGCCTGATTGAATCTTCAATATCAACAAAATGAAAATTTTAGTATGATTGTTAACTCATACACCTCTAA

- continued

TTAAAGGTATTTCTTTATCCCATGAAATGAAAAATTTATTAAGAACTTAGAAAGCTACGGTATGCCTTTGATGCAAA

AGAAAGATTCATTTTCATTAATCATGTTTAAAAAAGAGCAAGAGCAAAAGGTGATGAAAGTTTTT

MARKER 25462 (SEQ ID NO: 103): C→T

TTCTATACGAAATATTTGTCTGCCATAAATCTACTCAGGAACGATACATCAAAACATAAGTACGCTTGCTCTTTA

TTTTTCGTTTGAATAAATAGATCATTTTCGCACTTACATTTCAATTTCAATTGCTTTATTCATATCTTTCTGTT

TTTACTTACTGGTATTTAACAGTCGTTGTTTCAATTTAATGATCTATGAAACACCATTTAATTGATTTGGACTAA

CTTTTCGACAAGCAAGATTTAAATTTGTCTTCAGATACAGTTATAAATTTACATTGAAGATAAATGAA

MARKER 33494 (SEQ ID NO: 104): A→C

TAACGATCTGTATATCAATGAATAATATTCAAGTTCATGTTGACTCGATATGAGATAGAATTACAATTTTGAACA

AGATAATCTCAACAGCTATTTTCAAGAATAGTTAAATTAGGATACCATTTCAAAGAACTTTAAAAATGATTCCAT

ACATTAATGCTTTTTGTGTTTTTCGCTCTCGACCAGAATCCAGGAATTGTCCATTATCATCAATTTGATTAACTTTTA

TCTTTATTCTAATTTCTCAACATTTCTCTAATTGATATTAGTTTCAATTTTAAATAAGTAAAAATTTA

MARKER 17935 (SEQ ID NO: 105): T→C

ATAATGTGTTATTTGATCAAGGATTTTTAGTTACCTACCAGATGGAAAAAAGCAAGTTTACGAAACAGAAGTTAG

CATCAACTTTTCATCCATGGTTACACCGTATATAATCCAATCGACTCATACTTTATGTTGATCTGATTTTATAGCAGA

TAACTAGTTACCTTGCTCAGCAGCAGCTAAATCCTTTCTATTGCTTAATAACAGAAATATTTTTCATTAACAAAGA

AATTATACCTCGTGTGTTGACATTTCAATTTTAAATTTTCGTTCCAAAATGAAAAAGCTTCGTCGGAAAT

MARKER 48561 (SEQ ID NO: 106): C→T

ATTATTTTGTAGTTTTTCATTTTTTGTAGTTCAATTTTCCTTTGCTTATTTTAAATATGCCATTCTTTATTGAGCTCA

TAGCGAATGCATATGTTTCATTAATTTTTTGTAGTTACAGTTACAAATTTCTCAATTTCTCTTAATCATTTTTTTTTC

AAAAATAGTCTGAGCACTCAACCATTTCATTCAACAATTGCAGCTTTTTTTTATGGAGCCTTGTCAAATTATCAATTC

GTTTCCATGTTTATTATTGAAATAATAACGGTATTTAGGATAACGAAGTTCGCTTAGCTTCTTTGACT

MARKER 42003 (SEQ ID NO: 107): T→G

AAAAATTCAGGTAATGAGATCAGTAATTTTTTTGGTCACTTTGCTGTTTCTTATCAGCTCATTGTTATCCATATCA

AATGAGCGAAAGTGTGTATCACATATTGGCAGAGTGTAATCTATGAAGATTTTTCGCTATCAAAGTAATTATGAGAGA

ACTGATAATTTTATTTTAAAGTAGTAGAAAACCTCGAATTAAGCTAATAAATAATCGGTTGATATCCATGAAATGAAT

TACTAATGAAATGGATAATTGAGTAATAACAAATGATATTTCATGAAGAAAGGCAGGTTTTTTTTAATAG

MARKER 29566 (SEQ ID NO: 108): C→T

TATACTTAAACAAGAAATACAATTAATGCCAATAGCAGAGTGAAACTTCTGAAAAATAATGAGTTGAACTGGTAA

AATTAACATTTTATTAGAAATTTTCAGAACTTATGACTCCTCATGGCACTATCACAAAATGTTTGAATAAATTTGAC

AGCTCGCGTCGATTGCAAAAATCATGATTCCTGATATTTAGTATCGAACATGTGACAAATAATATAAGACCTAACC

ATAAAGCACTGAAACAACCTCGCGGAAACAAAAATTAATTTGCATAAACACGGAATACGATCAGAAAAAT

MARKER 33868 (SEQ ID NO: 109): G→A

GAATTTTTTTAGAAAGCTTGAAGTCGAGAATATTAGAGACTATATCGAAGACTTAAATAATCCTGGTAATCTTCTGT

ATGAATCAAAATTAACCTCGAACAGAACCATTCAGCACATCAGAGATAATTTCATGGAATGAACTAGCCAATCAGAG

CGTTGTAAAGAAGAAAGTTATGAAATGACCTTAAATCAATTTAAAGCATGTCCTCGCCATATAAGCGTTGAAAAG

TTAGGATAGAATCAATTATCAAAAAATATGTTAACTAGATCTTATCAATCAAAACATCAGAAGGAAAA

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In another example, genetic markers from *D. immitis* include the sequences below (SEQ ID NOs: 110-127), where the underlined nucleotides (i.e., the polymorphic sites) indicate the SNP nucleotide position within the fragment that correlates with resistance to MLs (i.e., the alternative nucleotide). Those markers were identified after genotype frequencies comparison between susceptible individuals and confirmed ML resistant individuals. In these sequences, the underlined nucleotide at the SNP position is generally different than the nucleotide found at this position in organisms that are susceptible to MLs (wild-type). In the sequences below, the nucleotide at the SNP position in the indicated

sequence correlates with resistance to MLs. In the heading for each sequence, the nucleotide change from wild-type to the alternative nucleotide (alternative nucleotide correlates with ML resistance) at the polymorphic site is shown.

MARKER 31307 (SEQ ID NO: 110): A→G

ATATGATAATAGTGAAACAATTCATCACAATAAATATTATCGATTAGG

65 AGATAAATTAACTTATGATGCCTCAATTTGGTCAACAATATATATTTGC

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TATTAGCATTTTTATTAATCGTTTTTATCTGACTTGACATAAATTGAA
 ATAGAAAAAATGAATCTGTTCCCTTGTTAGATTTTCTCTAAAAATTCT
 TGAAATACAAATAATTTCTTAAATTTCAATATTTCTACATAATGTATTG
 CGACAAAAATGCTAATGATTGGCTTATTATTATTTTCAATAATTTTTTA
 ATCAAA
 MARKER 26225 (SEQ ID NO: 111): A→G
 AGCTCGAAGATCGACAAAATTTGTTTCAGCTTGTTCCTTGAGGCTTTA
 GTCTGAAAGACACTTAAAGTATAAACAAATTATATTCAAAAAATCTT
 ATTTTGCAATTTGCGTCTTAATTTTGTCTTTTGCAAAGTTTTTCCGAG
 CAAGTTTTTCTATCTTCGAAAAGATTATATCAATTAAAAATTTCAATTTA
 AGCAATCATTGCTCTTCGAGTTTCTGTTTCAGCAAATAAATATCACCA
 CCACGACGCTGTGGAAGAAAGAAACGCCTTTCCCAATTTCTCGTCTCA
 ACTTTT
 MARKER 47722 B (SEQ ID NO: 112): A→G
 TAAGAAAGCTGGGAGATTTTCCAAAACACTATTTCCACGATTTGTTG
 TTTTCTATGATCAATCTTAATCAAACCTCTGAAATTTCTCAATTTTCGA
 TTTCTATCCAACCTCTACATATTTTTTTAGAAAATTCATATTTAGCAAA
 GCTGAGTGTAGAAATAATTCATACTTGCAATTCATTTTCTTAAATTTT
 CGAATTTCTTAAAAAGTATTTTCAAATTACCTACCAATTTTGATTGGAA
 AATTCGTGGATGCTAAAAATTCAAATCAAATAGTTAAACAGTATTCCT
 AATTGT
 MARKER 58162 B (SEQ ID NO: 113): T→C
 AATTTAAAAACACATCGACATTTTGCAGTACGGTAATGATTGTTTACA
 GTAACATAATGTGTCCTACGGTAGTAATACTCGTGTACGTAATGAATGA
 GTATAGTGACCGGATATTTCTTCACTAGTAGGCAATATTAAGAAGTAT
 TTTCATTTTCATATTTCTATCTAAAATAAACCGATAAAATGGTTTTTGAA
 TTATTACTTTTTGATTGTTATTTTTTGATCCTAAATTTGAAATACTGT
 AATAATTTAGCTAATTTCTATGATTCTATTCAATATGCTTAAATTAATA
 TTCTAA
 MARKER 17709 (SEQ ID NO: 114): T→C
 TCGTATTTGTTGTATGTAATATAGAAATATTGTTTAAATTCATATGTA
 GAAAAAATTTCTANNNNNNNNNNAATTAATTACATATTAACCTCGTATTT
 GTTGATGTAATATAGAAATATTGTTTAAATTCATATGTAGAAAAAAT
 TTCCATAATAAAGACGAACAGCATTATATAATTATCAATGATAAGTTGAA
 ATTAATTCATCAATGATAAGTTGAAATTAATTTATTGAAATAATTTCT
 TTGAAATTCGAATATAGACGAGAATTTTTTTTTTTTGCTAATCGTTTA
 TCAAT
 MARKER 47141 (SEQ ID NO: 115): T→C
 TCTAGCAATATAAATTACAAGAAATATGCCGTCCAAGTATTTTCAAGATTT
 ATTATTAATTTGGATAATAATACATTGTAATACTGCGTATTTCTGGATT
 ATTATGCACTGCATAATAACATGCAATTTCTGTCTACATATCGCGAATAA
 ACGCCAAAAGATTTCTCGATAAAAGAAAATATAAGAATTCGTAATGAA
 TGTGTGTGTCAGAGATATGTGTTAATTCATAAGTCAAGATGTTGTAAATC

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GATCCATATTAGTAATCATATTTACGTGCTCGTAAATAAAGCGGTGAT
 TCTTGT
 5 MARKER 48750 A (SEQ ID NO: 116): A→G
 ATCGAAAAAGATGATCTGATGACGGAAGCGAAATGTCTGCAGAAGCT
 AAGATGACGGAAGAAAAAGTGAAGAAATGAAAGAAGAGCTGGTAAAA
 CTCAGAAGGAATGTAAAACCTGGAGAATCGAAAAAGATGATCTGATGAC
 10 GGAGGGCGAAATGTCTAAAGAAGCTAAGATGTGCGAAGAAAAAGTGAA
 GAAATGAAAGAAGAGCTGATAAAAACCTCAGAAGGAATGTAAAACGGAAG
 AATCGAAAAAGACGATCTGACGACAGAAGCGCAAAAATCTGAAGTAGA
 15 TGAGCC
 MARKER 63962 (SEQ ID NO: 117): A→G
 ACTAATGATAAGAAACGAGCCGACGATTTTAGGAAATGAATAATAACG
 ACATGACACAACCATTGTTAGAAAATTGATAGTACTGATAATAAAGCTA
 20 GTTATAGAAAATTGATAATAATAATAAAATTTGCTGGTAGCAATGTCTA
 GAAGTGATAATAAAATTAATGATAGCAATGGATTAGCAATGATAATTA
 AACTGATGATAGCGAATGGATTAGTAATGATAATAAAATTTGATGATAGC
 25 AAATGACTAATAATGGTAATAAAAGTTAATGCTAGTGATAACTTGTATT
 TTAAGT
 MARKER 6372 (SEQ ID NO: 118): A→G
 30 ACAGTTTATAGTTACAATATTTCTCCGTGACTAACTGTATTTTACAAC
 TATAATTATAGATTACAAAATATATTATAGTAGTTTATAATTACAGTA
 TTCTTAAGTGAATAACTATACTTTACAGCTTACAGTTACAGTAGTTTTC
 35 TATGTTTTTGAATATTAATTTTACATGGTTTTTCTAGTTTTCAGTTTCA
 AAATTTTCAGATATTTTATGTGTTAAAGCAAATATATTTCGAGATATAA
 AAAGTACTGGTCATATCTTACAATTCATCCTTCTATATTGGAAAGAA
 40 TTGAGT
 MARKER 15611 (SEQ ID NO: 119): T→C
 GTATTGGGACCGCGTATCGGAAATCTGAAAGAAGTCTTTAACAGTATT
 TTAAATGAATAATTCAAATCGTTACTTCTTAATATATTAATTTATGCGT
 45 ATATATGCAGTACATAGCATTGCTTAAATTTCTATTTTTCCGCGTTAA
 AACCTATGTAAGATAAGGGAGGTGATTGTATCTGCGCCGTACTCCTTG
 TTTTAATCTACCTGCTTGTGTATATCCTCCACATATTGTAACGTGACG
 50 TTCACATTTGCATATATAGTAAGGGCATCGTTGTCTCCAGAAGAGATAT
 ATTATC
 MARKER 46432 (SEQ ID NO: 120): T→A
 GCTGCCCGAATGTTACAATTAGGACGAAAGTAAAAGTAGTTGACTGTAG
 55 GTATGACGATAAAGGAAAAATTTGTATCTTAAGACTTTACAATTTCTAA
 ATATTACGTGTTTTATCGTGCTAACATCACGAATTCATATTCACAAAA
 AAAATTTTGTAGAACTCCATCTGGTTTGGATGAATTTGCTACAGTTGAA
 60 CTGGATGATGGAACGAAATTGCAACATCTCTTATTGTTAGTATTTTCT
 AAATCTGTGAAATTTTGCACCGGCATTATGTTTAAATTAATTTTGG
 AGAAAG
 65 MARKER 29594 (SEQ ID NO: 121): T→A
 AAATAAGCAATCCGAAAGTATTACATATACGGACTAAATATTGCCATT

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CATTCCGGGAGTATACCATTGCAACCATTGGTATTTTCATTGTGATCGAGAA
 AACTAGTTTTTGTAGTTTGGGATAAAGAGAAATGGAGAGAGGAACTTTT
 ATGATCAATTTCTTTACGTACTGAAATTCATTTCTATGGATGTTCTTTT
 TCTATTTTCATTCTCCTCAGCAAATACAGTCCGAACAGTCATCAAATAAG
 TCTAAAAGGCATGAATAATATAAATCATCAGCAACTTTTTAAATGAATGC
 TTATTA
 MARKER 26784 (SEQ ID NO: 122): G→C
 ATTTCTATAACATCTCTTGCATTGATTAATTTAACATGTTGCAATAAA
 TATTTCTTACTTTTGAATGTATCATTTACTAGAAAAAACTTCAATCGAG
 GAAATAAGTTTTAAAAATAAATTCATATTTGAATTCATGTCAGTTCAAAA
 ATTCTATTACTATAATACATGTCTCTTGGTGTATCTTTTTTCTTTT
 AAATAATACAATCAACGGTTTCTCTAAATTTTCATAGACATCATATTTT
 AAAAAAATGCATTTGAAATTTTTCGAAATCAATGAACCTAATTGAT
 GAAAAA
 MARKER 51661 (SEQ ID NO: 123): C→G
 GCATGTGTATGTAGTATTTCTTTGTAACAACATATCTAATCTGTCTGT
 CCTTTAACATTATAGAATAGTCAGTTAGTCCGCTATTATTTTAAATAA
 CAAAATATCTCACTTAACTTCCATTCTTTCTCTAAATAATTTGTTTCG
 CTAGATCTTTCTCTATAATTTTCAAATTTTCAAAATGAATTAATCTTTT
 ATTTATATATGTGTATGTATGTGTATGTATGTGTACGTTGCATAT
 ATGTATATGTATGTGTATGTGTATGTATGTATATGTATATGTGTGT
 TGTGTG
 MARKER 7819 (SEQ ID NO: 124): G→C
 TATGCATAATGTGCGACCACCAATAATGTCTTCAAACCATAATTATGC
 AGAAATAAATTTTTTCCAGAAATAATTTTTTTTTTTTACATATACTTC
 CGATCTGTGAGAAAATACATTTGAAGTGAAGTGTGAAGCAATGCTACTT
 TTTCAAACAACATTGTGAAATGGATTAAACGCACCAATGGAGCAAGA
 GATCGTAAGTTTCGTTCCGCATGTCTGTGGCAACGTGTAACCATCCG
 TTAACGATATATGATGTAAAGCCGACACACCCAAATTAATCCATTA
 TAAACA
 MARKER 26704 (SEQ ID NO: 125): G→C
 AAATGGATCGTATTCACCTCGTAAGAACTTAGTGAACGAAAAATCAAAC
 CATCACAAATACTTTACTTTTTTTCTTTTTTACTAAACACACTATCCT
 ATGAAAACAAAATGTCCAAATAGATTTCATATGATAATGAACTGTGAAGT
 TATCCAATCTATCAGTTCTCGAAGAGGGAATAAATAAAACATTAAGCA
 ACCCACCAGTCTTCGCTGACCATCTCCTTCTTATTAGCAAGAAGCAAA
 TCTTGTGGTGATATTTCTGCAACCATCTGCAAAATAAAGCACGAAAAAT
 TAAGGA
 MARKER 14329 (SEQ ID NO: 126): C→A
 TTTGATATGCAATCAACTAACCAATCAGAATTCATATGATCTGTATAA
 ATTTCTTCAATATCGTGCATCAATTCGACATCATATTTTGACAGTGATG
 CTACCTTTTTAGCCGTATTTTCGAAAAATATGAATTCACACAGCTGCGT
 CCAAAAATTAAGGCTGTAGCAAGTCCAGCAACAACAGCCCTACAAC

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GAAATTTCTAAAACTGGTTCACGTGCTTATCATTAAATAATTTCAACAC
 TATCACTATCTCCACATGAACCTGATCGATTATAATTTAGTAGAACTGA
 5 AAAAAA
 MARKER 56169 (SEQ ID NO: 127): T→G
 ACAAATTCGTTTAAATATGGATTACATTGAAATGCTGAAATAAAGTG
 10 GAAATATTGAAAAGCATTTTACAATATTTGTTAACAACATTATATTTAA
 AGAATATACACCTTGGTTTAAATGGTAAAAATAATCTCAAGAATTTTCAT
 TAGGTTAATTTTTTTTTTATTTATTTATATTACAAAAAATGTAAAAGA
 15 AAACAAAAACAACAATAATAACGGTGACAACAACAATAATAATAAC
 AAAACTATTTGTTGTGATTTTGCAGCATGTAGTGTAGTGGGGATCTTTTG
 GAGCGA

The genotype frequencies for each SNP (SEQ ID NOs: 110-127) at the polymorphic sites are shown in FIG. 29 (Table 1). In one analysis, genotype differences of susceptible individuals were compared with confirmed resistant individuals. In a second analysis, genotype differences of susceptible individuals were compared with grouped confirmed resistant and LOE individuals.

Kits and Methods

In embodiments of the invention, probes of the invention may be provided to a user as a kit. A kit of the invention may contain one or more probes of the invention. For example, a kit may comprise a probe capable of determining the genotype of a nematode at a SNP position in one of the fragments disclosed herein. The kit may further comprise one or more reagents, buffers, packaging materials, instructions for using the kit and containers for holding the components of the kit.

A probe of the invention may be one or more molecules that are capable of binding to, or associating with, the nucleic acid sample to determine the genotype of the nematode at one or more specific positions (e.g., polymorphic site) in the fragments disclosed herein. For example, probes may be used to determine whether a wild-type or alternative nucleotide is present at the SNP position of one or more of the fragments disclosed herein. An example probe may be a nucleic acid molecule or oligonucleotide. Example probes may contain a label or labels. Example labels may include radioactive labels, enzymatic labels and/or fluorescent labels.

An oligonucleotide used as a probe or primer may comprise any size, shape and composition that is suitable for use in the context of the invention. Preferably, an oligonucleotide of the invention may comprise DNA, RNA, synthetic nucleotides, non-natural nucleotides, altered nucleotides, or combinations of one or more thereof. In one embodiment, an oligonucleotide of the invention may comprise locked nucleic acids and/or peptide nucleic acids.

In embodiments of the invention, an oligonucleotide may comprise a sequence of at least 5, at least 10, at least 15, at least 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 70, at least 75, at least 80, at least 85, at least 90, at least 95, at least 100, at least 125, at least 150, at least 175, at least 200, at least 250, or more nucleotides.

In embodiments of the invention, an oligonucleotide may encompass, without limitation, a primer or more than one primer, e.g. a primer pair, such as a forward primer and a reverse primer.

A primer may be an oligonucleotide that may be used to initiate DNA replication. Typically, a primer is a short oligonucleotide that may be about 10, about 15, about 20, about 25, about 30, about 35, about 40, about 45, about 50, about 55, about 60, about 65, about 70, about 75, about 80, about 85, about 90, about 95, about 100 or more nucleotides.

A primer may be used as part of an approach to detect the genotype of a nematode at a specific location of a gene. For example, a primer may be useful in amplifying DNA such as by PCR, RT-PCR and qRT PCR, for subsequent analysis, such as by Southern blot, sequencing, HRM (high resolution melt) or SSCP (single strand conformational polymorphism).

As used herein, an "aptamer" may be a nucleic acid or a peptide molecule that binds to a specific molecular target. For example, in solution, a chain of nucleotides may form intramolecular interactions that fold the aptamer into a complex three-dimensional shape. The shape of that aptamer allows it to bind tightly against the surface of its target molecule. Because of the diversity of molecular shapes that exists for nucleotide and amino acid sequences, aptamers may be obtained for a wide array of molecular targets, including, but not limited to, nucleic acid molecules, enzymes, membrane proteins, viral proteins, cytokines, growth factors, and immunoglobulins.

A probe of the invention may be prepared according to standard techniques known to a skilled person. For example, a probe may be produced synthetically, recombinantly or may be isolated from a natural source. In one embodiment, the source may be a biological source, for example, from a microorganism (e.g. a bacteria or a virus), an animal (e.g. a mouse, a rat, a rabbit, a goat, or a human), or a plant.

In the context of the invention, "a probe" may mean one probe or more than one probe. One or more types of probes may be simultaneously used in methods of the invention. Probe design and production are known in the art. Generally, a probe may be produced recombinantly, synthetically, or isolated from a natural source, e.g. from a cell, an animal or a plant. However, a skilled person would appreciate that probe production may depend on the type of probe at issue. A preferred probe may be a nucleic acid molecule (e.g. a primer), with or without a fluorophore or dye. A probe may be linear or in the form of a hairpin, with a fluorophore, with or without a quencher or another fluorophore (e.g. for FRET analysis). It could also be an antibody that specifically recognizes the DNA (or protein) sequence. Another probe could be based on a RNA molecule. What would be preferred may depend on technical considerations, stability, cost, ease of use, etc.

In embodiments of the invention, probes of the invention may be provided to a user as a kit. A kit of the invention may contain one or more probes of the invention.

Uses of the Methods and the Kits

Methods of the invention and kits to carry out the methods may have research, medical and industrial applications. The invention finds broad application in the management of heartworms in infected animals and in detecting ML resistant *D. immitis* nematodes in an area. Representative, non-limiting applications of the invention may include the detection, quantification and/or diagnosis of the existence of individuals or populations of *D. immitis* that are not susceptible to normal doses of ML for prophylaxis or therapy. In one embodiment, the ability to detect and quantify nucleic acid molecules of the invention is valuable insofar as it will instruct a practicing veterinarian to alter chemotherapeutic regimens for animals infected with *D. immitis* nematodes that have decreased responsiveness to MLs. Identification of

ML resistant *D. immitis* nematodes may instruct a veterinarian to switch from ML therapy alone to therapy that may include an alternative agent or alternative agents, such as an adulticide (e.g. arsenic based drugs), diethylcarbamazine, antibiotics such as tetracycline, and combinations of one or more thereof in order to achieve cure and/or to minimize the spread of the resistant strain. Alternatively, a veterinarian may adjust the dosage of a ML and/or treatment regimen using a ML in the treatment of an animal infected with a ML resistant nematode. Typical recommended dose rates for ML preventatives include, for example, 6 µg/kg for ivermectin; 500 mg/kg for milbemycin oxime; 3 µg/kg (monthly) moxidectin; and 6 mg/kg for selamectin. A veterinarian may also combine one or more of the treatment approaches and therapies noted above in any combination suitable to treat an animal infected with a *Dirofilaria* spp. nematode, e.g. a ML resistant *D. immitis* nematode. For example, a veterinarian may treat such an animal with an adulticide, such as an arsenic based drug, and then follow up with a microfilaricide, such as a ML or diethylcarbamazine.

In one instance, an arsenic based drug may be used to treat an animal infected with a ML resistant *D. immitis* nematode. An arsenic based drug may include, but is not limited to, melarsomine dihydrochloride. Melarsomine dihydrochloride may be used, for example, at a dose of 2.5 mg/kg, twice, 24 hours apart. This may be repeated in 4 months depending on the response to the first treatment and the condition, age, and use of the animal. However, a skilled person would understand that the dosage may vary depending on the severity of the infection. For example, an infected animal such as a dog with severe (class 3) disease may receive one dose and allowed to recover for a few months before receiving the complete set of 2 doses.

In another instance, diethylcarbamazine may be used to treat an animal infected with a ML resistant *D. immitis* nematode. Diethylcarbamazine may be used, for example, at a dose of 25 to 50 mg per pound of an animal. The duration of administration may depend on the condition being treated, response to the medication and the development of any adverse effects.

In another instance, an antibiotic may be used to treat an animal infected with a ML resistant *D. immitis* nematode. Said antibiotic may include, but is not limited to, tetracycline. A tetracycline, such as doxycycline, which targets the *Wolbachia* endosymbionts in *D. immitis* may be used, for example, at a dose of 10 mg/kg/day for 40 days.

In a further instance, another anthelmintic agent may be used. Such other anthelmintic agent may include, but is not limited to, acacisides. An acaciside may be used, for example, at a dose of 10 mg/kg/day for 7 days.

In another embodiment, the detection of *D. immitis* nematode populations with the above mentioned genotypes may instruct the use of alternative agents, such as diethylcarbamazine as a prophylactic to protect susceptible animals, e.g. dogs.

In one instance, diethylcarbamazine may be used to prevent an animal from becoming infected with a ML resistant *D. immitis* nematode. In this regard, diethylcarbamazine may be used, for example, at a dose of 3 mg per pound of an animal once daily.

In another embodiment, a kit of the invention may be useful in as a commercial product in the detection of ML resistant *D. immitis* nematodes. Such a product may be suitable for use by, without limitation, a veterinarian, a

physician, a pet owner, a farmer, a zoo keeper, an epidemiologist, or another consumer in need thereof.

EXAMPLES

The examples are for the purpose of illustrating an example and are not to be construed as illustrating limitations.

Example 1—Susceptible and LOE Populations of *D. immitis* Parasites Used in the Studies

The various susceptible and LOE populations of *D. immitis* used in these studies are described below.

- a. Susceptible isolates from Missouri, USA. Thirty five (35) *D. immitis* adult specimens were obtained from two dogs originating from an animal pound in Missouri. The history of the dogs prior to the animal pound is not known. The dogs were not subsequently treated. The *D. immitis* isolates were believed to be susceptible to ML heartworm preventatives.
- b. Susceptible isolates from Grand Canary, Spain. Seventy-one (71) *D. immitis* adult specimens were obtained from 12 dogs originating from a shelter on Grand Canary. The dogs were never exposed to ML heartworm preventatives and heartworm prevention is not practiced in this region of Grand Canary.
- c. Susceptible isolates from Grenada, WI. Ten (10) *D. immitis* adult specimens were obtained from 2 dogs originating from Grenada. The dogs were recruited from poor, remote areas of the island where ML heartworm prevention is not practiced.
- d. Susceptible isolates from Italy, Six (6) *D. immitis* adult specimens were obtained from the Po Basin in northern Italy. *D. immitis* seroprevalence in dogs from this area is reported to be approximately 60-70%. ML heartworm preventatives are commonly given to dogs in this area. But, there are no reports of LOE (loss of efficacy) in Italy.
- e. Loss of efficacy (LOE) isolate case 1. Microfilariae (mt) were isolated from a dog that was previously described (see Bourguinat et al.; W0201 1/120165). The dog was a male neutered Labrador mix, born in February, 2006, that weighed approximately 31 kg. He was a rescue dog from New Orleans, Louisiana, U.S.A., collected by the Boudreaux Rescue Crew, New Orleans, and subsequently transferred to Canada where he was adopted in January, 2008.

The dog was brought to the Main West Animal Hospital (MWAH) in Welland, Ontario on Jun. 6, 2008 (day 1) for a check-up. Blood collected from the dog tested positive with a heartworm antigen test (PETCHER® PF; IDEXX Laboratories, Westbrook, Maine) and contained microfilariae of *D. immitis*. On Jun. 11, 2008 (day 6), initial work-up (bloodwork, thoracic radiographs, physical exam, urinalysis) was performed. Auscultation revealed a mild increase in bronchovesicular sounds in the lungs and a grade III-IV/VI heart murmur. The remainder of the physical exam was unremarkable. Thoracic radiography revealed moderate right-sided heart enlargement and an interstitial lung pattern in the caudodorsal lung field. These examinations indicated a diagnosis of class 2 heartworm disease.

Adulticide treatment was initiated on Jun. 11, 2008 (day 6) with 2.5 mg/kg intramuscular melarsomine dihydrochloride (IMMITICIDE®; Merial Inc.). The treatment was followed by two intramuscular treatments with 2.5 mg/kg melarsomine dihydrochloride on July 9 and July 10 (days

34, 35). Over the following 90 days, in order to eliminate circulating mf, the dog was treated on one occasion with milbemycin oxime (MO) and on two occasions with IVM (see Table 2). On days 159 and 160, four months after the last dose of adulticide, the dog was again treated with 2.5 mg/kg melarsomine dihydrochloride intramuscularly. The subsequent diagnostic testing and microfilaricidal treatments are summarized in Table 2. During the treatment of the dog, several heartworm antigen tests were conducted, including DIROCHEK® (Synbiotics Corporation, San Diego, California) and PETCHER® (IDEXX Laboratories, Westbrook, Maine), which are microwell ELISA tests, and SNAP® PF (IDEXX Laboratories, Westbrook, Maine, a membrane format test designed for rapid in-clinic use (see Table 2).

To perform the Knott's test, 9 ml of 2% formalin and 1 ml blood (collected in EDTA) were mixed in a centrifuge tube. Centrifugation was performed in a LW Scientific EZ Swing SK centrifuge at 3000 rpm (604 m/s²) for 5 min. The supernatant fluid was discarded. A drop of 0.1% methylene blue solution was added to the pellet at the bottom of the centrifuge tube, mixed, and a drop of stained mixture examined under the microscope for *D. immitis* microfilariae. Table 2 indicates when this test was carried out and, when determined, the level of microfilaremia.

The dog was treated as follows. Two days after the last of three doses of melarsomine dihydrochloride in July 2008 (i.e., on day 37), the dog showed transitory signs consistent with death of adult heartworms (elevated rectal temperature, lethargy, cough, increased lung sounds). Beginning on day 41, these signs were managed with prednisone (Apo-Prednisone; Apotex, Toronto, ON, Canada), 1.3 mg/kg bid for 6 days. Following the administration of milbemycin oxime (MO) per os at 0.74 mg/kg on day 74, IVM per os at 50 ug/kg on day 95, and IVM per os at 200 ug/kg (4× the normal microfilaricidal dose rate) on day 125, the dog remained continually microfilaremic. On day 207, six weeks after the second treatment regimen of melarsomine dihydrochloride, on days 159 and 160, a Knott's test was still positive, so the dog was again treated with 200 µg/kg IVM per os. One month later, on day 242, a *D. immitis* antigen test was negative, which confirmed that the dog was free of adult worms. However, the dog was still microfilaremic. Thus, beginning on day 243, the dog was given MO per os at 0.74 mg/kg every 2 weeks on four occasions (see Table 2). Despite this, the dog remained microfilaremic on day 298. It was therefore administered MO per os at 1.1 mg/kg on days 298, 312, 326, 340 and 354. On day 356, blood was collected from the dog and examined: microfilariae were still present, and a *D. immitis* antigen test was still negative. On day 375, a blood sample was sent to Animal Health Laboratory, University of Guelph (AHLUG); microfilaremia was 6530 mf/ml, and an antigen test was still negative (see Table 2). As a result, beginning on day 384, the dog was administered MO per os at 2.0 mg/kg once daily for 7 days. On day 420, the dog had a microfilaremia of 355 mf/ml. On day 420, the dog was again treated with MO per os at 2.0 mg/kg, and this was continued once daily for 8 days. Despite this second high-dose regimen, on day 480, while still testing negative with a heartworm antigen test, the dog had a microfilaremia of 1810 mf/ml.

Blood was collected from the dog on day 706 and DNA was isolated from pooled microfilariae.

TABLE 2

Diagnostic testing and treatment history for dog between 2008 and 2009					
Date (day)	Antigen test Name-result (+ve or -ve)	Adulticide (melarsomine)* dosage	Microfilariae concentration in blood (mf/ml)	Microfilaricide drug dosage (PO)	Comments
2008					
June 6 (1)	PetChek +ve ^a		Knott's test +ve ^a		
June 11 (6)		2.5 mg/kg			Classified as Class 2 heartworm disease
July 9 (34)		2.5 mg/kg			
July 10 (35)		2.5 mg/kg			
August 18 (74)				MO, 0.74 mg/kg	
September 3 (90)			Knott's test +ve ^a		
September 8 (95)				IVM, 50 µg/kg	
October 6 (123)			Knott's test +ve ^a		
October 8 (125)				IVM, 200 µg/kg	
November 10 (158)			Knott's test +ve ^a		
November 11 (159)		2.5 mg/kg			
November 12 (160)		2.5 mg/kg			
December 12 (190)				MO, 0.74 mg/kg	
December 29 (207)			Knott's test +ve ^a		
December 30 (208)				IVM, 200 µg/kg	
2009					
February 2 (242)	SNAP -ve ^a		Knott's test +ve ^a ≥100 ^b		Interpretation: no adult heartworms
February 3 (243)				MO, 0.74 mg/kg	
February 17 (257)				MO, 0.74 mg/kg	
March 3 (271)			Knott's test +ve ^a ≥100 ^b	MO, 0.74 mg/kg	
March 17 (285)				MO, 0.74 mg/kg	
March 30 (298)			Knott's test +ve ^a ≥100 ^b	MO, 1.1 mg/kg	
April 13 (312)				MO, 1.1 mg/kg	
April 27 (326)				MO, 1.1 mg/kg	
April 28 (327)			Knott's test +ve ^a		
May 11 (340)				MO, 1.1 mg/kg	
May 25 (354)				MO, 1.1 mg/kg	
May 27 (356)	SNAP -ve ^a		Knott's test +ve ^a		no adult heartworm
June 8 (368)				MO, 1.1 mg/kg	
June 15 (375)	DiroChek -ve ^c		Knott's test +ve ^c 6530		no adult heartworm
June 24 (384)				MO, 2.0 mg/kg daily for 7 days	
July 30 (420)			Knott's test +ve ^c 355	MO, 2.0 mg/kg daily for 8 days	
September 28 (480)	PetChek -ve ^a		Knott's test +ve ^c 1810		

TABLE 2-continued

Diagnostic testing and treatment history for dog between 2008 and 2009					
Date (day)	Antigen test Name-result (+ve or -ve)	Adulticide (melarsomine)* dosage	Microfilariae concentration in blood (mf/ml)	Microfilaricide drug dosage (PO)	Comments
2010					
May 12 (706)					Microfilariae collected for DNA isolation

MO = milbemycin oxime (INTERCEPTOR®);

IVM = ivermectin (IVOMEC® Injection for cattle, sheep and swine, Merial Inc.);

*Adulticide = IMMITICIDE®;

^a= Main West Animal Hospital (i.e. test carried out in house);^b= Idexx Laboratories;^c= Animal Health Laboratory, University of Guelph.

f. LOE isolate case 2. Approximately 9000 pooled mf were obtained from a dog from Mechanicsville, Virginia, that had been treated with INTERCEPTOR® from 2004 to 2008. In May 2008, the dog was heartworm antigen positive and was placed on HEARTGARD® Plus (IVM/PYR) for slow kill treatment. In 2008, the dog was still positive for heartworm antigen and was still microfilaremic. From Dr Blagburn's (Auburn University) in vitro assay: LD9s concentration for susceptible mf produced only a 10.5% kill, and 2× LD9s produced a 13.6% kill of mf.

g. LOE isolate case 3. Pooled mf were obtained from low responder mf from an in vitro ivermectin susceptibility assay. The dog was a naturally infected client-owned animal, from Monroe, Louisiana, selected because it had been on ML heartworm preventative treatment. The veterinarian was convinced that compliance was not an issue. Patient records indicated that proper amounts of product had been provided to the client, based on numbers and weights of target animals in the household. The dog was microfilaremic despite the fact that it had been under ML heartworm prophylaxis.

h. LOE isolate case 4. Pooled mf were obtained from a dog that had the history as described below. This stray dog originated from Haywood County, Tennessee, USA, and presented as heartworm antigen positive to a local clinic on Jan. 21, 2011. The dog was neutered on Jan. 26, 2011. On Feb. 1, 2011, doxycycline (200 mg orally twice per day) and prednisone (1.5 mg tablet orally every other day) therapy was initiated and continued for 30 days. On February 2, March 3 and Mar. 4, 2011, an injection of melarsomine dihydrochloride (IMMITICIDE®) (2.5 mg/kg) were given. On February 2, March 3 and Apr. 1, 2011, an oral dose of milbemycin oxime (INTERCEPTOR®) (11.5 mg/tablet) was given. On Apr. 5, 2011, a Knott's test was performed and was positive; ivermectin was administered subcutaneously at a dose of 0.26 mg/kg. On Apr. 11, 2011, Knott's test was again positive; ivermectin was administered subcutaneously at a dose of 0.39 mg/kg. Knott's tests were again performed on both April 19 and 26, 2011 and were both positive. On May 2, 2011, Knott's test was again positive and a blood smear showed microfilariae; ADVANTAGE MULTI® (2.5% imidacloprid, 10% moxidectin) was administered to the dog. On May 5, 2011, a blood smear was positive for microfilariae; at this time, microfilariae were collected. The repeated adulticide treatment led to the assumption they the dog was free of adult parasites. On Jun. 11, 2011, 200 mg

of diethylcarbamazine was administered to the dog. No side effects of the treatment were noted. Within 7 days, the blood smear showed no mf. The dog was adopted on Aug. 18, 2011 and moved to Massachusetts.

i. LOE isolate case 5. Pooled mf were obtained from a dog originating from West Monroe, Louisiana, USA. This was a veterinarian's dog. The medical history implied compliant use of milbemycin oxime and there were several negative heartworm antigen tests at annual check-ups, until a positive heartworm antigen test and presence of mf in the blood on Sep. 25, 2008. An in vitro microfilaria sensitivity assay was performed (B. Blagburn laboratory, Auburn University, Alabama) on Nov. 19, 2008. The results of the assay indicated drug-resistant organisms. Mosquitoes were fed on infected blood samples from this original dog. L3 larvae were used to infect a second dog. At the time of infection, the second dog had been under treatment with ivermectin. Thereafter, at weekly intervals, the second dog received 1 dose of 3 µg ivermectin/kg, followed by 11 doses of 6 µg ivermectin/kg, followed by 4 doses of 12 µg ivermectin/kg, followed by 8 doses of 24 µg ivermectin/kg (interrupted for one week after the 4th dose). During the entire period of weekly dosing with ivermectin, the dog was remained positive for mf. Microfilariae were collected at 1 and 2 weeks after the last treatment were used in the analysis.

j. LOE isolate case 6. The samples correspond to the second passage of parasite that came from a dog originally from Earle, Arkansas, USA. The original isolate LOE-6 dog received milbemycin oxime in 2004 and 2005, ivermectin/pyrantel in 2006 and 2007, and ivermectin/praziquantel/pyrantel (IVERHART MAX™) in January 2008 and at the beginning of July 2008. The owner stated that she had been consistent with prophylaxis. This dog tested negative for heartworm antigen at annual check-ups in 2005, 2006 and 2007. This dog was positive for heartworm antigen and microfilaremic at the annual exam on Nov. 4, 2008. Results of the in vitro microfilaria assay (B. Blagburn laboratory, Auburn University, AL) on this dog suggested resistance. Dog-LOE-6, was experimentally infected on Nov. 16, 2009 with L3 larvae derived from mosquitoes fed with blood from the first passage. The first passage dog was experimentally infected on Feb. 24, 2009 with L3 larvae derived from mosquitos fed with blood from a naturally infected dog (the original isolate LOE-6 dog).

Example 2—DNA Isolation from Parasites Used in the Studies

Genomic DNA for the individual adult worms was extracted with DNEASY™ kit from Qiagen (Qiagen Inc, Mississauga, Canada). The genomic DNA extraction of individual mfwas extracted using QTAAMP® DNA Micro kit from Qiagen. To obtain enough DNA for analysis, the mfDNA was amplified using a REPLI-G® kit from Qiagen which allow amplifying the full genome from a very small amount of DNA. Mfwere isolated by filtration through polycarbonate membrane filters from freshly drawn blood.

Example 3—DNA Sequencing, Analysis and Identification of SNPs

The goal was to identify genetic changes (e.g., nucleotide variations) present in LOE heartworm populations that were not present in the susceptible heartworm populations. Nucleotide variations in any of the LOE populations, as compared to a reference genome obtained from the susceptible isolates, would indicate potential SNP markers.

Initially, the genomes from the heartworm populations identified in lettered paragraphs a-h of Example 2 above (susceptible isolates from Missouri, Grand Canary Island, Grenada and Italy; LOE isolates cases 1-4) were sequenced using the HISEQ™2000 system from ILLUMINA®. Table 3 shows the number of reads and the number of bases that were sequenced for each population. Not included in Table 3 is information from heartworm populations identified in paragraphs i and j (resistant isolates from LOE cases 5 and 6).

TABLE 3

Read information on isolates used for whole genome sequencing		
Isolates	Number of reads	Number of bases
1 - susceptible	85,097,000	17,019,400,000
2 - susceptible	78,242,862	15,648,572,400
3 - susceptible	80,687,895	16,137,579,000
4 - susceptible	75,515,617	15,103,123,400
5 - LOE-1	82,417,743	16,483,548,600
6 - LOE-2	74,261,369	14,852,273,800
7 - LOE-3	79,894,844	15,978,968,800
8 - LOE-4	75,477,318	15,095,463,600

The data generated from the ML susceptible samples (susceptible isolates from Missouri, Grand Canary Island, Grenada and Italy) were used to assemble the genome which was then used as the reference genome for the project. All of the individual fragments from the 4 susceptible populations were pooled together. Velvet aligner software (European Bioinformatics Institute) was used to assemble the genome. Reads were filtered by having the adaptor sequences removed/clipped, if found. Reads were trimmed at Q30 length 32 base pairs. A length of 32 base pairs is the Aligner seed default value and the number of reads was consistent with the default value. Table 4 describes the assembly of the reference genome used for the study.

TABLE 4

Information about the <i>D. immitis</i> genome assembly	
Number of contigs	22 966
50% of the contigs are longer than	28 928 bp
Length of longest contig	250 211 bp

TABLE 4-continued

Information about the <i>D. immitis</i> genome assembly	
Total bases in contigs	94 611 006 (94 Mb)
Number of contigs >1 kb	6654
Total bases in contigs >1 kb	90 045 376 bp (90 Mb)

Once the reference heartworm genome was obtained from sequences of the susceptible isolates/populations, then the genomes from the LOE populations were compared to the reference genome, to identify differences and possible SNPs. As part of this analysis, genetic loci containing the potential SNPs were shown not to be significantly different between the individual susceptible populations (i.e., between the susceptible isolates from Missouri, Grand Canary Island, Grenada and Italy), as well as not to be significantly different between the individual LOE populations (LOE 1-4), but were significantly different between the susceptible populations and the LOE populations. To perform this analysis, the software program called PoPoolation2 (Kofler et al. Bioinformatics 27: 3435-3436, 2011) was used. The program required the use of other programs, such as Perl, R, bwa, and Samtools. First, a synchronized file was generated, which contained the nucleotide frequencies for every population at every base in the reference genome, after filtering for base quality, in a concise format. The synchronized file generated with the PoPoolation2 program contained detailed nucleotide count information on loci for each of the populations. P-values were generated with Fisher's exact test for all the possible comparisons between populations. To identify loci associated with ML resistance, p-values needed to be simultaneously not statistically significant(>0.05) within all susceptible samples and within all the LOE samples, and statistically significant(<0.05) between all susceptible versus all LOE samples. Three hundred thirty eight loci met these criteria, including 12 that had a p-value of 10-5, Flanking regions of 1000 bp including each locus that was statistically different between the susceptible and LOE samples were analyzed by Blast (BlastN and BlastX) in NCBI and in the Broad Institute filarial genome database to remove loci located in mitochondrial, *Wolbachia* or *C. lupus familiaris* DNA. Loci located in reads with very high polymorphism(>2 nucleotides and/or indels) or low coverage(<10x) were removed from further analysis. Nucleotide counts for each locus of interest were analyzed individually for the pooled populations to ensure that the increase or decrease in nucleotide frequency was in the same direction for all the susceptible samples or for all the LOE samples. The loci that best met the criteria were retained for further genotype analysis on individual parasites to assess actual allele frequencies in populations that had been characterized in terms of ML response.

From these analyses, 186 loci were found to be significantly different between the susceptible and LOE samples. As this approach was based on reads and nucleotide frequencies of pooled samples, these loci were further studied (SNP genotyping) using individual (not pooled) populations. For this purpose, SEQUENOM® SNP frequency analysis was used. Table 5, below, shows the origins of the DNA used in this analysis.

TABLE 5

Description of isolates used for SEQUENOM® analysis			
	State and/or country of origin	# Individual adult worm	# Individual microfilaria
Susceptible samples = 181 isolates			
Sus1-Missouri	Missouri isolate, USA		49
Sus2-Missouri	Missouri isolate, USA		45
Grand Canary	Grand Canary, Spain	71	
Grenada	Grenada, WI	10	
Italy	Northern Italy	6	
Low responder samples = 244 Isolates			
LOE-1	New Orleans, LA, USA, moved to Ontario, Canada		56
LOE-2	Mechanicsville, VA, USA		35
LOE-3	Monroe, LA, USA		51
LOE-5	West Monroe, LA, USA		54
LOE-6	Earle, AR, USA		48

SEQUENOM® analysis is based on multiplex PCR and MALDI-TOF mass spectrometry. The SEQUENOM® analysis was used to evaluate the 186 loci using 425 individual samples (5 panels with 36-38 SNPs in each panel). Primer design for each SNP marker was based on a requirement that elongation primers be located in a non-polymorphic region 15 base pairs before or after the SNP of interest. All the genome calls were performed blinded (i.e., the sample origin and dog treatment history was not known during the analysis). A total of 79050 genotypes were analyzed. From the 186 potential loci, 109 were observed to have technical advantages to predict for ML loss of efficacy. The susceptible population carried more than 90% of the wild-type genotype while the LOE population had a significant lower genotype frequency of the wild-type genotype. These 109 loci are disclosed herein as SEQ ID NOs: 1-109.

Example 4—Additional SNPs from Confirmed Resistant Organisms

LOE samples, as described in Example 1, were presumed to be resistant to MLs because of the history of treatment of the dogs with MLs and the continued presence of heartworm organisms. However, despite the history of treatment, an alternative explanation to true ML-resistance of the parasites is owner non-compliance of ML treatment. Therefore, a study was performed under controlled ML treatment conditions, to eliminate the possibility of owner non-compliance in ML treatment, as a possible reason for presence of heartworm organisms in dogs.

Heartworm organisms used in the efficacy studies were derived from one identified as Jd2009 from Earle, Arkansas, USA. Jd2009 received monthly MO in 2004 and 2005, IVM/pyrantel in 2006 and 2007, and IVM/praziquantel/pyrantel in January 2008 until early July 2008. Jd2009 tested negative for HW antigen in 2005, 2006, and 2007. This dog was heartworm antigen positive and microfilaremic on Apr. 11, 2008 despite a history of compliance with HW preven-

tatives. Mf were obtained from the dog at this time with the consent of the owner and were sent to Auburn University, where the mf were examined for sensitivity to IVM in an in vitro concentration-response assay measuring migration (Blagburn, B., American Heartworm Society-13th Triennial State of the Heartworm Symposium, 2010). These mf were significantly less sensitive to IVM than mf obtained from a dog infected with a laboratory strain of *D. immitis* that was fully susceptible to the drug. The mf were used at Auburn University to infect mosquitoes to produce L3 that were used to infect dog Jd2009-1, which developed a patent infection. Mf from this dog were shown to be as resistant to ML as mf from Jd2009 in the in vitro migration assay.

L3s derived from mf harvested from Jd2009-1 were used at Auburn University to infect a second dog, Jd2009-2 and the dog was treated monthly with HEARTGARD PLUS® (0.006-0.013 mg/kg IVM) 9 consecutive times. Adult worms were recovered indicating that the Jd2009-2 isolate was resistant to IVM prophylaxis. In a second study, dogs were challenged with Jd2009-2 L3 on day 0 and treated monthly for 5 consecutive months with HEARTGARD PLUS® (0.007-0.009 mg/kg IVM; Study 1b). At necropsy on day 188, efficacy was 71.3%, confirming resistance to IVM prophylaxis in the Jd2009-2 isolate.

In another study, dogs were challenged with L3 on day 180 after PROHEART6® injection. At necropsy on day 150 after infection, efficacy was 21.6%, indicating that the Jd2009-2 was also resistant to the PROHEART6® long acting formulation of MOX, which has a claim for 100% protection for 180 days after treatment.

In another study, the confirmed IVM-resistant isolate Jd2009-2 was used to determine whether the resistance extended to other ML heartworm preventatives. None of the other ML heartworm preventatives (MOX, MO and SEL), given as monthly chemoprophylaxis as recommended, was fully effective, i.e., at least one dog in groups of four to six dogs on these heartworm preventatives became infected with *D. immitis* following treatment with each of these MLs used as recommended.

DNA from individual organisms from two Jd2009 isolates were used. DNA from individuals from one group, called RES-1, came from 4 dogs from the PROHEART6® study, described above. DNA from individuals from another group, called RES-2, came from 6 dogs from the HEARTGARD PLUS® study, described above.

DNA was isolated from 115 adult worms and 79 mf from the RES-1 and RES-2 populations, as described in Example 2, and were analyzed using SEQUENOM® SNP frequency analysis, as described in Example 3. From this analysis, 18 additional loci (out of the initial 186 loci) were significantly different between the susceptible and RES samples. These loci are disclosed herein as SEQ ID NOs: 110-127.

While example compositions, methods, and so on have been illustrated by description, and while the descriptions are in considerable detail, it is not the intention of the applicants to restrict or in any way limit the scope of the application. It is, of course, not possible to describe every conceivable combination of components or methodologies for purposes of describing the compositions, methods, and so on described herein. Additional advantages and modifications will readily appear to those skilled in the art. Therefore, the disclosure is not limited to the specific details, the representative apparatus, and illustrative examples shown and described. Thus, this application is intended to embrace alterations, modifications, and variations that fall within the scope of the application. Furthermore, the preceding description is not meant to limit the scope of the invention. Rather, the scope of the invention is to be determined by the appended claims and their equivalents.

SEQUENCE LISTING

Sequence total quantity: 127

SEQ ID NO: 1 moltype = DNA length = 300

FEATURE Location/Qualifiers

source 1..300

mol_type = genomic DNA

organism = *Dirofilaria immitis*

SEQUENCE: 1

```

aacataaaca tattgaactg aatcctgcaa acagtctctt tataacgtga accataacta 60
aathtagaga aaatatgaaa aagaaaaata agttgctttt gtcgctgcac caactctaata 120
acccaggaaa tcaagaagtg ataataagta atgtcatcat tagattcagt aattggtgac 180
actatcaata ttattattat tatacttaaa aatacgcaga ccacttatcg taacttaaaag 240
catgcataat acgactgtca tcatattaca tttcttcaag ttcgtattgg acaagtgtatt 300

```

SEQ ID NO: 2 moltype = DNA length = 300

FEATURE Location/Qualifiers

source 1..300

mol_type = genomic DNA

organism = *Dirofilaria immitis*

SEQUENCE: 2

```

gacaagcggt gacgggagag acgatataat aataaagaag gcattgggta tcagaaggca 60
caatccaatt ataaatgccg aggcacaaatg aataaaattt atgctgcaga ttgatcaaat 120
tcagaagaat ttcgatcggt ctgcaatctt tgtttgtatg tgcactactg ttaacttaata 180
ctttgtttta tatacttttg cgtgtcatat ataataatatt catgtcaact gatacgttat 240
gatgtttttt tgtaaatata gttgatcgga aacctgaagt ctatttcaaa ttaagaaat 300

```

SEQ ID NO: 3 moltype = DNA length = 300

FEATURE Location/Qualifiers

source 1..300

mol_type = genomic DNA

organism = *Dirofilaria immitis*

SEQUENCE: 3

```

ttttaggaaa atggtgactg tagagagata ttatcggaac gacaaggtcc acttcgaacg 60
ggtcttttat tgtcgacgga ttgtgaacca agttttggca ttcataatga caggtagcta 120
ttttccatc atcccatctt tgtattagtg caagcaagtc atgagtcgaa agaaaatctc 180
aaaagaaaaa aatgaaattt cagggtcaca ggactgcgtc cattattcgc actgggtgat 240
gagaacgtac agattccaga gcggcaatgc tgcacagtat cttttgtttc acttctgaat 300

```

SEQ ID NO: 4 moltype = DNA length = 300

FEATURE Location/Qualifiers

source 1..300

mol_type = genomic DNA

organism = *Dirofilaria immitis*

SEQUENCE: 4

```

tcgattaaaa attatcatcg ataaaaattt aaaaatttatt ttagtaaaat tattattatt 60
ttgatgaata agttaacaaa aaaattttta taactttttg attcgcaaaa aatctaattc 120
gttaaaaagt cgttccaaac agatatcgct tgttcgatga aaatgtccgg ttgttagaaa 180
atcataaatt ggttcaaatg attttccaga acgttcgaaa aaatattccc ttgtatcgga 240
taaataacca ttacaatttt ccactcgtgt tgcattgtgt tctcgacaaa aatcagctaa 300

```

SEQ ID NO: 5 moltype = DNA length = 300

FEATURE Location/Qualifiers

source 1..300

mol_type = genomic DNA

organism = *Dirofilaria immitis*

SEQUENCE: 5

```

tcaacagaaa tcgagattcc aaaaagtctt ctacaaatc ttaattatca atggatattt 60
agttttgtta tctgttatca taagtctctg tctttacacg attaaaaatg tccaagaatt 120
ttttactatt caaatgaggg aaataaaaaa ccaatgccaa taatatccag aaactacata 180
catctttctt ttttcgaagc tcatctattc cggccgaaaa caatgaagaa cattaaaaat 240
cttaaaagat agtcttagcc ttttccttga ccactatctt aactgtcagc gctaaaatgt 300

```

SEQ ID NO: 6 moltype = DNA length = 300

FEATURE Location/Qualifiers

source 1..300

mol_type = genomic DNA

organism = *Dirofilaria immitis*

SEQUENCE: 6

```

aatagtcgtc tcaattacttt ttgactttta taattcgaga atcttatgta gtccttcact 60
ttacccttct tctgtcgaaac taagaattac agcattattt tcgaatttaa tgtgtaaaag 120
acaatagcag attttgtaat tttgtgttaa cctcacttta tatttcgctt catatcgtga 180
cagagaatta ctatttcaga gagtattact tgtcaccaga gaatctccag aaagattttt 240
atttagctcg gaaaaatggac aaaaatgggt tcttatcatt agcactgata gctagttttc 300

```

SEQ ID NO: 7 moltype = DNA length = 300

FEATURE Location/Qualifiers

source 1..300

mol_type = genomic DNA

organism = *Dirofilaria immitis*

-continued

SEQUENCE: 7
 tatctcttgt tgtgtgttct gcattgtatc aaagtgggta aattttgctt tagacgttga 60
 cttattgtct tttttaagtt atattctagt ccatgttttt ctctttgcaa atattttttt 120
 ccgcgccta tgattcattg tttgtttgt aactctctat taagttgctt ttagtttgaa 180
 ttgtatcaaa atttcaaaac tttaaaatac gcactagcac tattttttct tatctcaatt 240
 aagcgaatcc cggaacaaga tttaatcgat ttccgaatca caattaaatc actggaaaac 300

SEQ ID NO: 8 moltype = DNA length = 300
 FEATURE Location/Qualifiers
 source 1..300
 mol_type = genomic DNA
 organism = *Dirofilaria immitis*

SEQUENCE: 8
 attttcctta acaaatcatt ttcaaacgaa aaaacattaa aaagtgttaa aataaaatgg 60
 tgatattgat aagaaattaa ttcaacctgc atatcaattc ttgtagcggc cattttctta 120
 gcaagttcta tagcagctcg atccatatca ctttcttgct ctaatgtcaa ttccggttcc 180
 ggaaattttt ttattttgccc attcttcac ttttttttat tttttactga tatagctata 240
 gaccctttct cccgtgcatg cctgtaggcc tgttctgata tacaggcttg tgaaccactg 300

SEQ ID NO: 9 moltype = DNA length = 300
 FEATURE Location/Qualifiers
 source 1..300
 mol_type = genomic DNA
 organism = *Dirofilaria immitis*

SEQUENCE: 9
 ttctggggta gttatacgga aaattagaca atgaagagaa tcaaaaaaca tgcgattttc 60
 aaacagagga actttgttac ttttgctcgc acttacttta ttttaaaacc catacaaaat 120
 aaatgtttca tttgattgat attgtcgtac taataattag agcttcaaca ttaggatttt 180
 aataaccttc aatttatttc agaatttaag aaacttacgt atggatggag aaaatataaa 240
 gaatggcgat gacaaataag attgtctatg aaaaaactaa tgccacaaga tccgaatgca 300

SEQ ID NO: 10 moltype = DNA length = 300
 FEATURE Location/Qualifiers
 source 1..300
 mol_type = genomic DNA
 organism = *Dirofilaria immitis*

SEQUENCE: 10
 tttatgaaca aaaataataa aaattaggat aacagatatc aattttcttt agctataaat 60
 atacgcttcg attgaaaaaa gctttcaaat tataattaag gcatacgtaa cgatatagac 120
 aattaagtcg acattaattt ttgaaatat tttaaatatt tttctctttc tttttttcta 180
 ttctcttcca aagtgatcaa tagttatgaa attgtcagaa gctaaaatga taatattatt 240
 caagtttatt acctaattct ttatcacctc atttcttacc atttatctga aaatctaatt 300

SEQ ID NO: 11 moltype = DNA length = 300
 FEATURE Location/Qualifiers
 source 1..300
 mol_type = genomic DNA
 organism = *Dirofilaria immitis*

SEQUENCE: 11
 atgttgaatt tttaatgaaa ctttttcggt gcataagcat tacagatctg taagctgtgc 60
 aaaccctggt tctttgtaaa ttgaaacaaa gatcatttat tgtttccagc gtcgatttga 120
 cctggataaa atagcatggt gtcctactaa aagtagatg acgagaggtg agtgcaaca aaatgcacaa 180
 aaatgatttt gatgcactca aatcattttt aagttttgtg caattttcca ttttatagtt 240
 tctgtgatcg ttgttatcca tcaacttgat tttgtttgtt tttgtgact tatatttcat 300

SEQ ID NO: 12 moltype = DNA length = 300
 FEATURE Location/Qualifiers
 source 1..300
 mol_type = genomic DNA
 organism = *Dirofilaria immitis*

SEQUENCE: 12
 tttgacactt tcagatacct tacaaaactca tctccagcac ccaatttaca atatcgctgc 60
 ctaaaataag aatttattcg gatatgagac tgtagttttc attccgtacc aatcatagta 120
 gaacagatct atagcatggt gtcctactaa agttgtgact ggctattaag tatgtgggtg 180
 tttttacgtg tgcgtgggtg tttgtgcgtg tgtgcgtgtg cgtttctgca catattttcg 240
 tgcgcggtgt ctgtgtgtgt ccgtttgat atgccgagtg tagctgtgtg tatgttcttg 300

SEQ ID NO: 13 moltype = DNA length = 300
 FEATURE Location/Qualifiers
 source 1..300
 mol_type = genomic DNA
 organism = *Dirofilaria immitis*

SEQUENCE: 13
 cactcataat atacctgtca acaaaactcag aaacttgaat aaaatgacgc aaaaatgaca 60
 aaaacatttt atcaaccttt tcttcatcac tcccccgcat ttccaatttt ctccaaaact 120
 gtttttgtcg tgtacaaaag tcatcagcca cttcattttc ttcaagatgg ttcgagacgc 180
 cattcttga ttcacccctt atttcaactg tttccgaagt cccagcagtt gaagctgaac 240
 ctagcattta taccaccacc cgaatgtcaaa aaatgacagc ggtcagagaa tacgaatttc 300

-continued

SEQ ID NO: 14 moltype = DNA length = 300
 FEATURE Location/Qualifiers
 source 1..300
 mol_type = genomic DNA
 organism = *Dirofilaria immitis*

SEQUENCE: 14
 gctaggtcaa cagttggttt atttggactt atacgatatt aaacataata tcgcctcata 60
 tacacagaaa tatcaaaaaa acgaacacag ctaaatcgaa gaatacgaac aaatgtttta 120
 aaaattatat taaatctttt aatgctctct acaatgtcgt atcttccctt ttgtctgtat 180
 ttctcctttc gttccaccac tgctatttct catgcctttg aactatgggt ctcgttgcgt 240
 cgaattgtcc tcgaaactgt tgtttctgtc gaattacgtc gaactgctgg actttgtcgg 300

SEQ ID NO: 15 moltype = DNA length = 300
 FEATURE Location/Qualifiers
 source 1..300
 mol_type = genomic DNA
 organism = *Dirofilaria immitis*

SEQUENCE: 15
 atatctcact ttgacataa attgaagtgg cactgatttg aatgaaatga taaataaaat 60
 aaagacgaca aggtagtggg aaaaaaaaga ggagaaaaca ccgtttagtt ttggatgcaa 120
 gctcgaaatct gagttttctt gcaaaccgta cactgatcaa ttttcttaca caaacataag 180
 aaaaaagaaa gtgattttac tgtagctgta tcgtataatt caaatcatat atatatatgt 240
 ttcaataatc tatacattta tgtatatatt tttttgaatg gaacagtga tgaatttaaa 300

SEQ ID NO: 16 moltype = DNA length = 300
 FEATURE Location/Qualifiers
 source 1..300
 mol_type = genomic DNA
 organism = *Dirofilaria immitis*

SEQUENCE: 16
 acaaatgccg tcgggagaga aatatcgctt gcgtactgat cacattggcg gtatcacttc 60
 tttgaaaact ccagctggta ttgtgtatca tttcatgcaa tacgctattt ttgatcgaat 120
 atgtcgacgg cgtagtgttt cattttccaa cgcactctac gttgcgtgta tggatgatga 180
 cggacaatta ttggaattga aagttcagca tcgattgcat tccgtaacct tgaacgtga 240
 catatatggg agagtatgtc aaataacttc agatggcgaa aatattttct tcgaatatgg 300

SEQ ID NO: 17 moltype = DNA length = 300
 FEATURE Location/Qualifiers
 source 1..300
 mol_type = genomic DNA
 organism = *Dirofilaria immitis*

SEQUENCE: 17
 ataatatata ttccattgga taatatTTTT catattatgt gatgtttgaa attttctgca 60
 attgtacatc tccgattaaa aacttttatt atccgtactg gagaattttg cttttttttg 120
 acggtttgtt caataagtgt tcaatatatt gtctgcctta gtaaaacctt tctaatacat 180
 ccgttcgaat tggaaagtga aagttcagca tcattctttt agtgaggtgt ttaagttgtt 240
 caatagatat tatttagaac gatctcaatt aaaatcttct gaatgatttt atgtttttat 300

SEQ ID NO: 18 moltype = DNA length = 300
 FEATURE Location/Qualifiers
 source 1..300
 mol_type = genomic DNA
 organism = *Dirofilaria immitis*

SEQUENCE: 18
 gcagcacatt gcacacagta aactgcaaac tgaattaaga gatattgggt tgaattattt 60
 ctaatttaaa aggatataat aaatgacttt gatgattgtt gattttaagg tatctcgga 120
 gactccatca gtctcagttg tctagcaatc gctataggta ctaaaagaaa agaaaagatg 180
 tctcgttatt cactttgaaa tgtacatata aaatcatttt gtcgtatgaa attaagtata 240
 ttatgtctaa tcgtatcatt cgaaatgaat ttactgtcac tgttagaact atttaggcag 300

SEQ ID NO: 19 moltype = DNA length = 300
 FEATURE Location/Qualifiers
 source 1..300
 mol_type = genomic DNA
 organism = *Dirofilaria immitis*

SEQUENCE: 19
 agagttcaat cgccaagtgt ttctttttct cgctcgcaga gatcaaaacg gtgttggtta 60
 tacactcatt catcagctgt tgatagacat ctcttagaat ttcagtgctt ttctggatga 120
 aaacattatt tctcaaacat gacacttaag gacaatagtg cgtgacttct ttgttaacgt 180
 acacgagaaa acaaaacaga tgatgcttgt tatcttggtg ataaatgtgt attcagaata 240
 atgttatata tctttgcgtg acaaatatca ttctgttata cttcggatac gcctttttat 300

SEQ ID NO: 20 moltype = DNA length = 300
 FEATURE Location/Qualifiers
 source 1..300
 mol_type = genomic DNA
 organism = *Dirofilaria immitis*

SEQUENCE: 20
 aactttactt gaactttttt ggtgttcaat ttggaatatt ataccaacca ttcagaagac 60

-continued

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tgtatataga aatgaacctt caagaattaa tcgaaatttt tattaaaaac ttttatttga 120
atatttcatt attttaaactc attactattt gcagtatat attagatcta atgtagaaaa 180
aaaaatcaga tggcaaaaat aatatcatag gtttggtttt aaaattcatt gcaaaattca 240
gtgcgccgtt ccagtcgctc gtaattacc cttacccctgag ctttacaaaa agaattgctt 300

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SEQ ID NO: 21      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

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SEQUENCE: 21
aggtatctag atagcataat aaattactac acaaaccgat ggaaacgcaa gtttgccgtt 60
gcgtgttgat acaaaatatt agagccaagg atgggtatcac atgtaaaact gcaattttgc 120
tatttggtta aagcaaaataa gaaaataata ttctgttctt attctttaat ttatttcac 180
agatggcttt gttataccat aattgtaaat ctgtcatatc ttaattgcgc aatagcccaa 240
gattcttgta tattcttaca ttccacaatt tattttctta ttctagttt tagaattata 300

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```

SEQ ID NO: 22      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

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SEQUENCE: 22
aatagctact cacagcttaa gttaactaat ggattcttga atttatttaa gcgtgtagtt 60
aagcgattaa attactttct gcccagaatc gctttgtctt atagttttgt ctgcacagaa 120
aggatgcatt ttgtgtctga atttgttcaa gggaaaatta aataggtttc ttcaaatgac 180
tcctattaaa tttttttgaa tttaggcttg cattgcgtgt tctgatccac tattagcacg 240
tacgggtatc gcagtgccat gtgatgcagc actatgcaa aaccacctcc atgtcacttg 300

```

```

SEQ ID NO: 23      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

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SEQUENCE: 23
tctgttgtaa gtttcacaat ccagttaatt taagctcagc ttatttgaaa ttttcaacaa 60
aattacgaaa attactttct tttcaaccac ccaaatattt agcataattg 120
gcctgaaatc gtcaaaagttt acaaaacttt gtccagcaat cttctcttac tcttacaata 180
aacatgatta actgtcgtc ataccaatct cgtttatagc aaattctttt caaaaaaaca 240
ttgtacaaa ttttatatcg catcatttca acacgcataa ttatttttca tatatgaaaa 300

```

```

SEQ ID NO: 24      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

```

```

SEQUENCE: 24
ttcacaatcc agttaattta agctcagctt atttgaaatt ttcaacaaaa ttacgaaaat 60
tactttctcg gttcattttt ttcaaccacc aaatatattg cataattggc ctgaaatcgt 120
caaagtttac aaacttttat tcagcaatct cctcttactc ttacaataaa catgattaac 180
ttgtcgtcat accaatctcg tttatagcaa attcttttca aaaaacatt gctacaaatt 240
ttatatcgca tcatttcaac acgcataatt atttttcata tatgaaaaac catattataa 300

```

```

SEQ ID NO: 25      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

```

```

SEQUENCE: 25
attaactctg aacccaaaga ctgttggtta aaataaagat ctattttagt tatacatcta 60
acattaaagg ttttcgtacg gaaacaagta ggtttgataa ttttcatgta actgtaaaga 120
acacctgtga aagggatcag taaaatttgg gggatgtagc acggaaatat gaagctgagt 180
gttttgatcc caaaagtttt tcaaatctgc gaaataacga gaggtgtaat gatcgttttt 240
aaccaaatth tttgattcta atccttccca cagttttgaa attcagtaag catttctttt 300

```

```

SEQ ID NO: 26      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

```

```

SEQUENCE: 26
ttgcaacaaa tcaataataa aagacttgcg gctaacaata tatttgattc tttttaccg 60
ttattattat gacaggtaat aatagtatta caagcatatt tgtaggtgtc aattttttca 120
attcaaatth tcttaattca ttatttcttc ctttccttaa taaatagtct ttccatttaa 180
gaattaactt tttgaaatct ttaatgagaa gacacaaaag attccggata attttgcac 240
atcttttcta tttcgcgtta gtattttatg ttttcaacag atttttatga tttaactata 300

```

```

SEQ ID NO: 27      moltype = DNA length = 300
FEATURE           Location/Qualifiers

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-continued

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source                1..300
                      mol_type = genomic DNA
                      organism = Dirofilaria immitis

SEQUENCE: 27
gataaaatgg gttcttgta agctcatttg gcatactctt gtcttctata tttatatacct 60
ttaatatctt ctcttttttc aaattttcct tcccgacgtt ttccatatcg acctctttct 120
tcataaatat atcttctctca ttgacctcat tttttgactt ttcacccgtt tcatccttat 180
ttttcttttt ttcactctct attttacctt ttcctttatc aacttctatc ttaactttct 240
caatgttttt tttattttct ttcactcttt tgttttcttc tattgacata ctataacaaa 300

SEQ ID NO: 28          moltype = DNA length = 300
FEATURE               Location/Qualifiers
source                1..300
                      mol_type = genomic DNA
                      organism = Dirofilaria immitis

SEQUENCE: 28
ttttacgaac aattatttca taaaagattc gtatttttga ttagttttta agaatttttt 60
tttattattt ttagccaaca aatatatttt tcaaaattgt taaatttgaa attataaatt 120
tcaactaaaa aaaagcaaaa agctaagcca atagaataaa catacatgtg taatataaaa 180
tataaagtat tcgaaatgaa aatcaaagtt tcataacaaa aaacaaaaaa tatttcaacc 240
ttttagattt catcaaaact tcactaaaaa gttaaattta aattttcaaa ttgttatata 300

SEQ ID NO: 29          moltype = DNA length = 300
FEATURE               Location/Qualifiers
source                1..300
                      mol_type = genomic DNA
                      organism = Dirofilaria immitis

SEQUENCE: 29
cgaacaatta tttcataaaa gattcgtatt tttgattagt ttttaagaat ttttttttat 60
tatttttagc caacaaatat atttttcaaa attgtttaat ttgaaattat aaatttcaac 120
taaaaaaaag caaaaagctca agccattaga gataacatac atgtgtaata taaaataaaa 180
agtattcgaa atgaaaatca aagtttcata acaaaaaaca aaaaatatcc taacctttta 240
gatttcatca aaacttcact aaaaagttta attttaaatt tcaaatgtgt atacaatgat 300

SEQ ID NO: 30          moltype = DNA length = 300
FEATURE               Location/Qualifiers
source                1..300
                      mol_type = genomic DNA
                      organism = Dirofilaria immitis

SEQUENCE: 30
tcaaagacaa aatgaagaac ttaacaaaaa aaaggccaat aaataaaggc tatttcgtga 60
aaaatctaaa aaaaaaaaga tctgttcctt tcgaatcaag tgattcttcc tactacattc 120
gtgttgtaat tcttacttgt atacagtccc cagtttttcg acgataaaaa acatttcgat 180
aagtgaagtt gaattaattg aattttaaaa gatcataaaa ataaaatcaa aataaaaaaga 240
ccaaaattaa gtcgataaat tcagaaaaac acaataataa atatacaaat aataaaaaact 300

SEQ ID NO: 31          moltype = DNA length = 300
FEATURE               Location/Qualifiers
source                1..300
                      mol_type = genomic DNA
                      organism = Dirofilaria immitis

SEQUENCE: 31
aaataattca ctaattttct atcatcaaat tatttcgtac aatcgataaa tcaacgatta 60
taatagcgaa gagaatgaaa attaatgttg tgcacagtat acggacccca tatacaatgt 120
tcaacagaga tcttacttgt ttttctatta aagttttctg ttccggcgaa gaaagacact 180
ttctaacgat gctttctctc caactcccct tgcaatgata gaggatgcag ccaagattcg 240
tcgactcaag cagcatcact caaccggcca tcacttcggg acctttttcc ctgcctttta 300

SEQ ID NO: 32          moltype = DNA length = 300
FEATURE               Location/Qualifiers
source                1..300
                      mol_type = genomic DNA
                      organism = Dirofilaria immitis

SEQUENCE: 32
cattgcgaat gaccgctatg gaatatcaat tagcagatat taatcgtgaa ttaagcacat 60
tggtggaatt tttacgacca aatcgattt caaaaaatgc tacacttgca acatcagcaa 120
ccattgcaac atataacagt acttcgatgc gtaattgtaa aaagaaatgt aatgcattcg 180
aaagctgaaa attcatctga tatattgaag caaaaggtaa gattattttt aagatatcat 240
tcttgatgct ctcataattt ctacatcaaa tttaatacaa cgattcattt atgttcattt 300

SEQ ID NO: 33          moltype = DNA length = 300
FEATURE               Location/Qualifiers
source                1..300
                      mol_type = genomic DNA
                      organism = Dirofilaria immitis

SEQUENCE: 33
ttcttgttgt acctatcata gatgataact taagtaccaa tagcaatagt gcaacgatgc 60
aaggattctg attaatgatt ataaaagttt aaccaatctt cttcatcct tctaataaag 120
agaaaaaaaa atgagaacat ttttatgaca ttgaagaaa ggcaatttat cgctgaaaat 180

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tctactgcga tatggaagta tcagatagag aaaataaata ttaaaatatg gatttcatac 240
gaaaaatgat aaaagataat aattttacatt ttggtgcttt actgatatga ttggagtatt 300
```

```
SEQ ID NO: 34      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis
```

```
SEQUENCE: 34
cgatattttt tggacgaatc aaaccttttt gggaaatcat ttgatgtcac aagcatgggt 60
tgagaaattt ttttccgaat tagttctgct aaaaatactc caaatgagtc tagtggaatt 120
aagctaagca ccttaagtaa gttgagaaaa acgtttccat ttgactaaca aggctagtat 180
atcgacatga gacagaaatg gttattactt cactcacttc atgaagcgaa tacgaaatat 240
ctgttcactt tagtttcaat ctactatttt accaataaac gtgttctttt ccggataaat 300
```

```
SEQ ID NO: 35      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis
```

```
SEQUENCE: 35
tcttaattga ttttcttaac tcgaaacact tgtcttgatt actgtgtctg actttatctt 60
attaaattaa ataatttcca tgaccacttc ataccattga ccatcaaaact ttgatgaagt 120
ttatgtgtga agtgccaaac aatcattcat ccttcagttt taacttattg ctgggtcaaat 180
tcataaaaaa caaaattatc aagcagatag taattcagtg aacgtagcgt attctcgaaa 240
tttttttctt tgtatttacc ttatatagaa caacgtatat ttgtagcata tattcaatat 300
```

```
SEQ ID NO: 36      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis
```

```
SEQUENCE: 36
tttctgagtt tgcgttacag cgccaaatct tcacggagat agataaaata cttatcgtga 60
aattttggcg ccatgattta aaaaacacgg agataaaaaa aaaatgctta tcgggtgataa 120
tttagcgcca taatatgaat gaattgaaaa aacaatttga gtagaaacat gacatagagt 180
tttcgttttc tggctacgaa aatggatgaa tttttctgga atcgaaattca gtcaaagaaa 240
taggaacggtt ttacttaaat gatcgaaaag cttttctaaa ttaaatatat gacgtctaag 300
```

```
SEQ ID NO: 37      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis
```

```
SEQUENCE: 37
atctaaatct tcggtttata gtggaagac ttccatttgc tgcattcttg caaattaagc 60
tgttgaaatc actttttttt ttgatagatt tccaatttaa tcatattata agaagaatta 120
atctcgaata gaatttttaa atcatttaaa ctttaagttt taaaactaat ataagttatg 180
cagatttcgc gaaaaagtct catttggtta ttcaattatt ccaaaatgta ataattttat 240
aaattcaaat ttaaactact actaacttct gaagtcagga gccagtagca acaacgtaat 300
```

```
SEQ ID NO: 38      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis
```

```
SEQUENCE: 38
aactttacat ttatatccaa ttttttttta ttttgtttgt ttttagaaat ttgaaaatgg 60
gtactaatca gtgtcatttg cagcctctta gaccctcttt ataacgaccg attcgatgaa 120
atcgtcatc aatattgcag ttattgttc ggggtggagaa tgttttcaaa agttgctgaa 180
gtgatgaagt atagttagaa tgcaccttat tcagcaccat taagaagtaa atttttgctt 240
tggaatttga caaagacaaa gcaggaagtt gacaacgatg ttctgatgaa acggtttcga 300
```

```
SEQ ID NO: 39      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis
```

```
SEQUENCE: 39
gtctattttg gctgtcttct aataattcat tttgtaacct tttgaaatat gataaatgta 60
gaaatttttt cttctcggtc tataatagtt taataatgtg ttgtagtaat agttttgggt 120
ccgttgaaat atttcaatga tatgctatcg caaaattagg aattcaaatc aagggtacaa 180
gataattcaa aaacaaacaa cgtaaaaatg aaataatttc ttcttcttac ttaccaacag 240
gcatacatc atcatcctca aattcatgac tatatttaac attgtcatat ttgaataatc 300
```

```
SEQ ID NO: 40      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
```

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                                organism = Dirofilaria immitis
SEQUENCE: 40
cgacgcaaaa atcttttcaaa ttgtcaccca gttctctaa gattccaat gatgttggtta 60
aacattctgc atgatgtacc gggtaaatga ctaccaagtt gttttttgct ttaatacaaa 120
ctcgcaaaaga ttctgaaaac catgaaatta agaaagatta aaataatctg aactcttttt 180
ttcatttttct cttgaactta gcaataact gagttggata aaatttagaa acgaaatttc 240
gcaaatttat tcagtaaat caggaaaact cggtttcggt attctaaata taaatagata 300

SEQ ID NO: 41      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

SEQUENCE: 41
gtttcttttg tttatctcag taagatttgg gcggaaattt cagttatact tttcatttcc 60
atgtgctggt ttaaatttct tccatattag tataattttc aaataattgt agcgtcactg 120
gtttatttaa ggataacagg ttggactgca gtggctgaga agtgtcttgc cggtaattg 180
tttgttggtg atcaacttgt acgagttact gatatcgaca tatataatac acggcaaat 240
ccattcggtt tcagtactgc atcaaaaacg ggattatcgg tactttgtaa atcgcagtat 300

SEQ ID NO: 42      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

SEQUENCE: 42
gaccctgct cacaaggcag ttcccacaga caatcacaca tctaatacaca cacatcaact 60
catccgagct aggcatacaa taaggaaaat tgcattgctt tatcgtctaa ctgtaataaa 120
catctacata atgaaatttat ttgcgactga tgacaactaa tatcgcccaa tgcaaatatt 180
tgtctcagag ttattccctt ttaacagctg ttgaacgaat agataggacg tcagtgggat 240
gatctacttg tttcaaaggt tgaggtaaca catgaaacac atgaaaacgg taatttaaaa 300

SEQ ID NO: 43      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

SEQUENCE: 43
aaagaatggt cagcaagatg tggaaaatcg attactatag ttgaagtatg aatcgaagag 60
gtttttttta attctaagag aacgaataat cggcaaaagag aaagttaggt aaccttattt 120
tgctttgttt tcagtcaatt tataatatgc ggttaattgt gttaaagaaa gtacaaggta 180
tgaaatctaa gccaagaat aagagaaaac agctaataat tatttctgca tttttcttt 240
ttcgacacaa acttgaagac agaatacaat gaactagtaa tcagattttg attattgctt 300

SEQ ID NO: 44      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

SEQUENCE: 44
ttagattttg ctgaagcatt gttgggttaga tcgatgaaaa tataattatg agagattttg 60
ttgaaattca gcaacaaaaa aaaatgttta ccaattagat cgcaatgatg taaaatttca 120
cttctttgac atcggttata tttttgtctt ccaacaatat aaaaaaaaaa ttataatcaa 180
ttggtaataa aattaaact ctaattgtta gtcacctaaa tcagctttta aaaaaataat 240
gcttaattgg tatttgctac tattagcaaa ctgaaactat ccttttctcg aatggtgaac 300

SEQ ID NO: 45      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

SEQUENCE: 45
atgagctgat atttgatag catattaaaa atagggtaaa ttacattaag ttagatatcg 60
ttcgataaaa ttaattagaa aaaatgttta ccaattagat cgcaatgatg taaaatttca 120
cgtattttta ttcttaagat ttatttgcaa aattcaaaaa tatgtcttat gaaaaataat 180
atttctgtgt aagaacaagg gaccgattca cttgatttat tcgcaacaaa tcgaaattca 240
aaattagtaa ttttaaatat tgctttattc aaaccatacc aataataatt tgagagattt 300

SEQ ID NO: 46      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

SEQUENCE: 46
attgattgat tcaataaaga aatttaaatt atttccctt tttttcaaaa gatttaacaa 60
atattattta ttgatctcc tcgttcggtt ttactttttt gattatcaat ccatcctcct 120
ccatcatata gctaatttat tttttgcac gttaatcaat tgatgtatga ttgatttctt 180
gattataaaa agttagaaga attgaattgc ttaaatttaa ttattgataa tgaaatatta 240
ttatatttca aaatgatacg aagaaatatg acgatgataa gagaaaatat gatatttatc 300

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SEQ ID NO: 47      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

SEQUENCE: 47
tacgataagt tattttat ttacacatct catccttgac tagtgctcgt gccgactgtc 60
ggacttgaac cgacaaccta ctaattacaa gtcagttgct ctaccaaat gagctaagcc 120
ggccatctag aatgtgctgac cccgtcgtgg tacatcttct ataatcgttt ggtattcagg 180
actctcttct ttcgtgggtg gaggatcttg atacagttga ctattaaaaa tagggccttt 240
gttagtctgt tacaactcat agacaaaggc gacaatttta gcttacatct tacgttatgc 300

SEQ ID NO: 48      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

SEQUENCE: 48
atggtagaaa attatatgaa aaaatatcat actaaaaata taacagattg ttataaggta 60
tgggttaaga atttacaaca attgattatt tatgataaaa aaaaaaaaag taaatcagtg 120
aatcatthaag atagtattga taagcagttt gtattcggta aagcgaatga ttagaggaat 180
tatgggagca aacgtctata acctattctc aaacttttaa tgagtatgac gtgtcttgct 240
tgcttaaaat tatttcaatg atcatttcac tttaccagta tgatcatgat tagacttgaa 300

SEQ ID NO: 49      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

SEQUENCE: 49
ttagtatcga tattatcaca aatgatatca ctttcatcaa tactggatac gattttatta 60
gtatcataat tttgtggctc gcattccgaa agttttacac gtagaagatt aacctgcaat 120
atgatttatt ttatcatttt cgaatatcca actttgaaat aattcgaaaa tgttgaaaaa 180
ttttgaaaaa ttgttaacaa aaattacaaa aaatatcaaa tgaaattaaa taactgtcca 240
tttcaaaaaa agaagaaaaa ttatgaaatt accaattaaa aacaggactt attaatataa 300

SEQ ID NO: 50      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

SEQUENCE: 50
tgtggaaata aagtacaatt aattgctggt cgcttaataa tattattttc attcttggtc 60
ttttttttct ttccccgtga tattataaaa tatagttttt taattttaac aaatcgctcat 120
aattatttaa aaaatactga ggtgagtaaa tgtaattggt tgctggaaaa aaagtgggtg 180
atgagagggtg aatgaaagca gaatagttaa tgattgcac aaatttcctc cttaactctgt 240
gattaaaatc aaacaaaacc cgaaaagttt cttcttcgcc ttttcttctc cttgttttca 300

SEQ ID NO: 51      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

SEQUENCE: 51
cgaaatccgc cgcgtgcatt accttgcgct tgttgattac gacgcatttg ttcgtcgttg 60
ataaccttat caatcatcat acgtccgtta cgtatgcaat caacatcgcc agttaggctg 120
aaatcaaatg gatggcgatt atatcaaaaa caaaaataag gagtatttgc tgaatcattt 180
ctttttctgt attattatca aaattttctc ctttccattg ttctcttctt aatcaagtga 240
atgctcattt cattttgaaa taatccaacg taataattcc ccatattccc aattactttc 300

SEQ ID NO: 52      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

SEQUENCE: 52
agaaatatta aactttgaaa agatgtgaca tgttctgtaa caaaagccca aaatttcgac 60
tgctgcggct tgaagtaaaa ttttggaata tgctacatca gtagtgcaac agatggttcg 120
ataaatagtg gtaagtgatg ggaatcctag gaatagatgg gaattgtatt tcagatataa 180
atttgatgca tattttcata gttgattata tctacgatca cacgttgaat attctaaaaa 240
caaaactgtaa ttaactaatt gaatttgaaa atttccaaga attaaaattg gtaacaaaaa 300

SEQ ID NO: 53      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

SEQUENCE: 53

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attgtcagga atgagaagca agttttggat acttaaggga tgaatggaac acatacatgg 60
cagaaaatgt tagtaatacaa accatttaaa ttacttagcc actatgctaa actttctaga 120
agtatgggtg aacggtttaa aaccttcgca aaaattgtat tagattatct taatcttccc 180
tacatcaaaa cagagaattt ttgttctacg acgtgagtct gcatgtatta aggaagtctg 240
tatcatgacg taaatatcct gagtgattat tgaattcaga aaatgagctt ttctatttgg 300

```

```

SEQ ID NO: 54      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

```

```

SEQUENCE: 54
atatgagtgt tacatgtgta cgttacatgt aaatattata tggtatatgt aaaaatgtca 60
tgtatagcat ctattcacgt gtacgtacac gtgtatatac atatacattg atacttaata 120
cgtatacgca tgaatgaaca gatattatat atttacgtac actagactca catgtacctc 180
tgtatacgca tacatgtaca gatataatgt tgacatacgt aaattcatat atgcttttat 240
ttatgcttat ataatgtgc acatacatgc cttatatttt cgttgttata aacacataaa 300

```

```

SEQ ID NO: 55      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

```

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SEQUENCE: 55
gaaaataaaa ttagctgaaa atatatcgca ggtaaaagcac acagaagaat taacttaagg 60
taatatattg taagaatttt tatattcgcc gcacctaaata atttttagac cgcatacgcc 120
cagtatttga aactggtagc gctgttcgta cttgctgttg tccatgttat gtatatgata 180
ccattcctaa aactttttgc ggctgtggtt tccagtgttg atgtgactgg tatgatgcct 240
aacaactggat ccttccatct gcggcatatt gttgaaattc ttattgatgt gagctgttta 300

```

```

SEQ ID NO: 56      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

```

```

SEQUENCE: 56
caactgtgaa tcataaacat tacttaaatt aatgaagcta gttaacgaca aatatatttt 60
tttatgtatc agtgctatca tataacataa aaacttactt tcattaataa atgagctcaa 120
atattgactt ttgtccaaaa tgctcaaaat gtcgtcataa tatttgaagt gaagataatt 180
tcacgctttt cgaagctccc tctcacgtct tttaattctt ttttcttctt cttgctctaa 240
tggtctcgcg aaaaaccacg gtgcaataat cactttccat aatttatata gtacataagc 300

```

```

SEQ ID NO: 57      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

```

```

SEQUENCE: 57
ctgcttaact cttttcattt ttcagagaat cttctctaaa attgtgaatt gatccaaacc 60
aaagaatatg gataatgtga ttcgaaattc tggaaatttag attttgagag ttttgaagtt 120
tttaaagaga ttgaatttct gtgaccttct ggtatatttg atgtcaattc gggatgcgta 180
tttttgccga aaatttttgc cctcactgca atcttggtta aagtcaaaaa aattcaatcg 240
tagaatttct ggtttacctg atattactgg aaatctctga tctttgttct agattgctgt 300

```

```

SEQ ID NO: 58      moltype = DNA length = 285
FEATURE           Location/Qualifiers
source            1..285
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

```

```

SEQUENCE: 58
ataaagaatt tgcaactctg tatacctttt tgcagtgcaa aagcggatga attcttcaact 60
gcagtggtgac agattccttt gataaaaatt cttcgttctt atgtaaaact ggaaattctc 120
ggtagttatg cttttgctag ttgaaaatgt tctgctcttg taaaacatgc aaaaagagat 180
tatctttgtt ctattatgga aagattcttt tgaaaatttg acgactgaga agacaaaatt 240
tatcccaact tgtcatctgc aataaaaaatt tttcctgacc tgtttt 285

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```

SEQ ID NO: 59      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

```

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SEQUENCE: 59
aaaatcaaat caatatgatc agataactca tacttatctt actgaaaatt cctcattcaa 60
gggaaataaa taattgcaat tcttgattcc gatcatggat gattttcaag caaattacca 120
atgatatacta tcgataacga ttacagcata cagctataac ttattattga ttgaattgat 180
gaaaataatt ttaccagaaa tttatcaatg ttatctcat tgcagtatac gatgtttagt 240
gtgacaacac tttttcttgg aataattgtg cataaatcat tgattgcatt tagtattgga 300

```

```

SEQ ID NO: 60      moltype = DNA length = 300

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FEATURE                      Location/Qualifiers
source                      1..300
                             mol_type = genomic DNA
                             organism = Dirofilaria immitis

SEQUENCE: 60
tcctgccac attcttctta ctttagataa tcaacaggag ttagttgaaa gagaagacta 60
ggaacagttg caacttctga atcttcttga ctttctttcg ttttgtaaat tatttatttg 120
tataaattta aaattcgaag agaaaataat caaggtccaa cttctttttc tgttagtctt 180
tgcaaatgct ccatcaaaat gcaaaaatat gattagaatt ctgatggaaa ttaacaaaat 240
cgattagata agaaaagtac aaaacagaaa ctaacttttt ctccattttt catattatag 300

SEQ ID NO: 61               moltype = DNA length = 300
FEATURE                      Location/Qualifiers
source                      1..300
                             mol_type = genomic DNA
                             organism = Dirofilaria immitis

SEQUENCE: 61
tcattgcttt aatacttttt aacgagaatt ttctcgatca aaataagatc tgcaattgat 60
atcgtctaata aagcgaacat tagctgtatt acacgctaata attcacatat gatgaacgtt 120
gtaagcgtca tacatcaaca tatatccatc cgataaataa tgaccactac acattgctac 180
caaccatcct atcccgccac tatttgaaat gaactgagaa ggagttatcg acacaggcct 240
cctagcaacc aaacaaaaga cgagacagat gaatagatag acagacagac gaacatacaa 300

SEQ ID NO: 62               moltype = DNA length = 300
FEATURE                      Location/Qualifiers
source                      1..300
                             mol_type = genomic DNA
                             organism = Dirofilaria immitis

SEQUENCE: 62
agattctggt tattattgta ttctcgattt atttaatccc aacttaaaaga ttcattggct 60
attgtttagc atctatatca attttataaa taaatagtaa tacctgatga aaagcaataa 120
ataattagat gcaaatattta attagataca gtttgatgga aaacattgaa gccatgtaca 180
actaatttat gcatgttgaa ttatgcatgc ataattaatt tatgcatgac agcaagtttg 240
gtataaaatt aattttgtat gaagataaaa ttttataaat atgataata atgctggtaa 300

SEQ ID NO: 63               moltype = DNA length = 300
FEATURE                      Location/Qualifiers
source                      1..300
                             mol_type = genomic DNA
                             organism = Dirofilaria immitis

SEQUENCE: 63
attattgaaa agaataatgt agctaattag ttgaagctgt taaaagtaaa gctaaaaaga 60
tgatggaaat tattcgtata aacattcttt gtaaacaaac agtcatttct gtgaataaac 120
aattataatt ataacaataa cttttcaaga caataaaaaa attaggaagc attgtgtgta 180
taatcaatag ttgatagact gtcaatgcat ttttatcagt cgtgctgctt tttttccctt 240
tcttgactca tttattttat tatttattga tagaatgtca atattctagt catttgttat 300

SEQ ID NO: 64               moltype = DNA length = 300
FEATURE                      Location/Qualifiers
source                      1..300
                             mol_type = genomic DNA
                             organism = Dirofilaria immitis

SEQUENCE: 64
atcttaactt gctttaaaca aataaattaa aacagcccaa tgttocaaga aaaaaagata 60
agttaaaagt ggggtgtcca aaaatttatg aattgaattg gacagttatt cagatcctga 120
aaatcagctt cctcgatcac tgcaaatatt cccgataaat aagtgaacat taggttaatc 180
ttaattttcc cttaactttc cttagccttt tttaaatttt tggattatc aagcattttt 240
attgcggtat cgtttttgta aaaaaaaaaa tataattcaa cattcaggct cgacgttatg 300

SEQ ID NO: 65               moltype = DNA length = 300
FEATURE                      Location/Qualifiers
source                      1..300
                             mol_type = genomic DNA
                             organism = Dirofilaria immitis

SEQUENCE: 65
aattaataaa aagaaaggaa tacgataaaa tatctatttt ttgaaactaa tcaaacatat 60
tcctcactgc tcaccggata gttgctttct aattttacat taagaaatat attttttttt 120
ttcaataagg aaagttatgc agactaggag aattctactc tgaagaagag ataagcatgt 180
tagaattatt aaaatctatg gaaatcctct taaaagaatg cctatagtag ctctgatttc 240
gaaaaaaaaa gcaaaaaaca aaataacaaa ttctgctcaa ttgaaataaa aaactttcct 300

SEQ ID NO: 66               moltype = DNA length = 300
FEATURE                      Location/Qualifiers
source                      1..300
                             mol_type = genomic DNA
                             organism = Dirofilaria immitis

SEQUENCE: 66
taaaatatct atttttgtaa actaatcaaa catattcctc actgctcacc ggatagttgc 60
tttctaattt tacattaaga aatatatttt tttttttcaa taaggaaagt tatgcagact 120

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aggagcattc tactctgaag aagagataag tatgttagaa ttattaaaa ctatggaaat 180
atccttaaaa gaatgcctat agtagctctg atttcgaaaa aaaaagcaaa aaacaaaata 240
acaaattctg ctcaattgaa ataaaaaact ttccctcaac ttccagcatc actgctgtga 300

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SEQ ID NO: 67      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

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SEQUENCE: 67
aactgctaaa aaattgaaac tagtgtaga ttgataagtg ggcagattaa aaccaattgt 60
gttattggcc cgtaatttag tgactctgaa tagctatggc gaatcgtata gtgttgtagc 120
gacgacgtat ctatcaaatg tctgccttgt taaatttcga tgatagttaa tgtgcctatt 180
atagttgtaa cgagtaacgg agaataaggt ttcgactccg gagagggagc ctgagttgcc 240
acattcaagg aaggaagcag tcgcaagat taccactct tagaatgagg aaagagtgc 300

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SEQ ID NO: 68      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

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SEQUENCE: 68
gaaaactaag aagtaagtga aatttctaag ttctttccca gaaaggtag atccaatatt 60
tgttttcatt ttagcatttt tatccaatga aaaaatgtgc caataaatac ttgtatatag 120
tattgcattt aaaaacttca gaaagcacaa tgagatctaa gctcagaat atgacgaata 180
ccaatccctt tcctagtctt accgcttctt aacttttctg tcgctttata aaaattaaaa 240
ataaaaagtt gaacaatggg aattacatca ttttcactct aatggtttat ttctattct 300

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SEQ ID NO: 69      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

```

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SEQUENCE: 69
cttcctagc tatgcctttt cgtaacttaa gcttcnnnnn nnnnntctag ctacgtatcg 60
ttatcattta tgcttcttta gctacgtttc tccatcattt atgcttccta agctacgtat 120
cttcacactt tacgcttccc tagctatgtc ctttcgtcac ttaagcttct ttggctgcgt 180
gtcttcacat ttaactctct ttgactacgt atcgctatca tttacgcttc cttagctacg 240
ctttccatc atttatgctt cccaagctac gtattttcat catttatgct tccttagata 300

```

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SEQ ID NO: 70      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

```

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SEQUENCE: 70
gatcttaaaa ttctatgaaa cttctctctg atggtattgt ttccaacaga atataatgac 60
aatagcaaca gtattgggta tataaaaaata ttgactgcag caggattata ttccaagttc 120
ttttaatttc atttatttat tctttcattt acttttactg tttttatggt ttctctcttt 180
aaaaaatatg atttctctca ctgttctctt tcatctatct atatttatgt gataattgct 240
tatatgataa ctagctaaag ggaataaac tttcagtcac catagcttca ttttagtaaa 300

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SEQ ID NO: 71      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

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SEQUENCE: 71
ctataactaat cagtcocacta tccattttta ggttgcaaaa gttgcaatga cggtttgatt 60
tcatcctcca atgcaatttt gagtctcaat ctcgagagat agatcgatcg cttttagctt 120
gatttagctt gggttaagtgt gtgagggata ttgggcagaa attctgtcaa gcgttactta 180
atgaaatagt aaatgatcac tgatatatat tgytaatgat acttgagctc tctagattat 240
gaactggaag gttttcgata gaaataatcg atacatatat tagaatcgac ttcttttttc 300

```

```

SEQ ID NO: 72      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

```

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SEQUENCE: 72
tcactctttt cacatttcat ttaatcatca ttttatcaat tcctattttt aaacaaattc 60
ttttcaaata ttctctcttt cttctctctt ttgttttccg cttattcatt ctaatgatga 120
acagatgtag aaaatttgca tttctattgt cactacaatt ttgagttaga tatatttaat 180
tatttgattc gagacagatg gttatagcct ttagcttcag cttctcgctt aaattaagta 240
cttgtagact ttccaagtac cattaaagct ttctgcgctt tcctaattag aaaaaaagg 300

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SEQ ID NO: 73      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300

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mol_type = genomic DNA
organism = Dirofilaria immitis

SEQUENCE: 73
gcattttaag ttaaaagtat cacgctgcat gacacctcac gtttgcctac tcaaattgag 60
taggttagaa tctttttttg gctactattc aaatattaat aataaattgc tgcaaacaga 120
tttcacaccg gaaaaaattt aaatttttct agcaatgttt taactccctt attaaatatt 180
tatagaaaat cgactactta aaaagaattg actaacattt ctgaatctct gcagagattt 240
atagatggat tagcatccta caagttttta tcttttttgc atatttccat tattttttta 300

SEQ ID NO: 74      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

SEQUENCE: 74
gataagacgt cttattttgt aataattcaa aaattaatta atatagaagt aagatcttga 60
taataaattaa tatgctcaaa tttcttaatg agaatatgtt caggatgaag atgaagtga 120
agaaattgat agattgagga agcaattgct aattgaaaca gaacagctcg ttccaattc 180
tcttaaagat ttactgaaga aaatttatta tccacttgaa gaagctattg atctcaaat 240
tcatcagaaa ttaattcaac aaattgctgc cttgttgaa tgatttagta tcttgataa 300

SEQ ID NO: 75      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

SEQUENCE: 75
accgcaaaat acctaaaaat ttctataaca acgattaaca cggcctcgaa ctggaagcat 60
attaatccat gcgtggctca aacttcaatc ataaagacaa gatctagaga tcaacacaaa 120
atgggtgaatt gttaccctat cgctgctaaa gtttgagaga aaaaagtctg aaatcaagta 180
gtacacacaaa ttaagttaat attaagaaat caatttagta ctgaatttaa acaaatgaaa 240
ttttacgata aataaaaaaa gtacctgata aaacagcgct ctcctgttat tccattgct 300

SEQ ID NO: 76      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

SEQUENCE: 76
tataagacta gtaaacagat cgtaatatata taaatatcga ttttatttta aattttcgaa 60
aacttccaaa tctatcgata tgaaattaaa gatcaatttt taatttccat aatatattta 120
gattctatcc caacatcact catctttatg tcaacttatt taattctctt attaacatta 180
tatttcttgt ttacaatgat aaattttatc aattttctaa tatgatagaa catcttcatc 240
atctgaagat atgcttttct catctttgta acaattcgta tcgcttctga ttttactttc 300

SEQ ID NO: 77      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

SEQUENCE: 77
gttttattat tgcttattga atagtataaa taacactttg atatgatatt gttttgttgc 60
gatcattgta ttgattataa ccttaattaa acgaggatat tatgggaaat gtatttatta 120
caaaattaaa tatgaaaggt tgaagtcttg acgaaacttt caaacacatt tctcgaattt 180
tctctgcaaa aatatcgtaa cgatttttgg aaattatgaa gtccaagaat tcaatcgaga 240
gttcgccatg tcactttggc tagtttcgtt tgtttttaat atttcaatca aaagtcaatt 300

SEQ ID NO: 78      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

SEQUENCE: 78
ccttgatata tgttcttgac atcgttgata agaaggtcac cgtagtgttc ggtgagcgag 60
atggaaattgg actcagggtt attctccgtt ttttccatgt ttttgaattt tagagagaaa 120
ataatgtttg tctgaatggt tagcaactaa attagttttt aagttatcag gaactcgaag 180
tatcttcttt tgcacttctt taaccttttt catcaaattt ttaacagta acaagatttt 240
tttgagaatt ttcaaaaatat ttttgacttc tgatgatatt tgatgagaaa accatcactg 300

SEQ ID NO: 79      moltype = DNA length = 300
FEATURE           Location/Qualifiers
source            1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

SEQUENCE: 79
agagtattat tatacatgat gatgatgatg atgatgatga tgatgatgat gatgatatta 60
tgatgatgat gatgatgatg atatgatgat gatgatgata atgataatga tgatgatgat 120
gattaattgc ttatttttaa tgattgataa ctttaaaaga aatcattgaa atttgatcga 180
ataaaaattt tcttaaaaaa agcatttgct atttatatag taaacctata aaaaattact 240

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SEQUENCE: 86
 tcagataaat tgtatttgat gtttaattcaa agaagaaaaa aataatcagt agaatatgaa 60
 tcgaataata ttcatacaac cagttttattc attattatttc actttttaacg tctaaatgac 120
 gtagctacgc tttttttctc gctttcaagc ctttactgac caagattaat gtacattctg 180
 ttgaacaaga ttaatcgaca ttctatcgat caagatcaag cttttactga tcaagattaa 240
 taatgacatt cttctgttga tcaagattaa tcgacattcc attgatcaag attaatcgac 300

SEQ ID NO: 87 moltype = DNA length = 300
 FEATURE Location/Qualifiers
 source 1..300
 mol_type = genomic DNA
 organism = *Dirofilaria immitis*

SEQUENCE: 87
 ctctctaaaa cctattggtc actaaacttg cactgactaa aaactattgg tcatcagact 60
 tgtgattcat tgaaaagacc gtttagccgct aaaattatga ttcactaaaa aaaatctatt 120
 gatcattaaa tctgtaatca ttgagaaact acaatcattg gtcattaaagt ttgtgctctc 180
 taaaacctat tggcatttaa actgactaaa aactattggg cactgaacct agagtctatt 240
 aaaaaaaaaa tcattgtatc aataaattta ttgtttacta tcaaatccat tgattactga 300

SEQ ID NO: 88 moltype = DNA length = 300
 FEATURE Location/Qualifiers
 source 1..300
 mol_type = genomic DNA
 organism = *Dirofilaria immitis*

SEQUENCE: 88
 tctaaaaact attggtcact aaacttgcac tgactaaaaa ctattgggtca tcagacttgt 60
 gattcattga aaagaccggt agccgctaaa attatgattc actaaaaaaa atctattgat 120
 cattaaatct gtaataacg agaaactgca ttcattggtc attaagtttg tgctctctaa 180
 aacctattgg tcattaaact gactaaaaac tattgggtcac tgaacctaga gtctattaaa 240
 aaaaaaatca ttgtatcaat aaatttattg ttactatca aatccattga ttactgaata 300

SEQ ID NO: 89 moltype = DNA length = 300
 FEATURE Location/Qualifiers
 source 1..300
 mol_type = genomic DNA
 organism = *Dirofilaria immitis*

SEQUENCE: 89
 aaaaatgtatc aaattctctg atgccataaa ttatacagac ttgattggca ttttttctaa 60
 ctttcatcat gaaccattct atttctaaat tgatccatta caaaatcaac ttgtgatata 120
 catcaatctc agtcataacg agaaataatg ataataataa gcgactatca ttggaatttc 180
 ctgaatatcc aagatgtaat tacatctttt ttttaatgta atcaaaattt cttgccatca 240
 ataatttttc aacatatgct ttcatcgact gccttatgca gatcgtaatg atgacagcca 300

SEQ ID NO: 90 moltype = DNA length = 300
 FEATURE Location/Qualifiers
 source 1..300
 mol_type = genomic DNA
 organism = *Dirofilaria immitis*

SEQUENCE: 90
 attgattaaa aagaatcaac attaaatttt tgatatagtc gagaaatcct tcgtgataat 60
 tcttttagaa caattcttta cactaaactt gtatttactt gcttattatt tgtctaaaga 120
 tactaaatct ttgtcagtggt aatttatgat cttggcatta ttgcataata cgctttccta 180
 aaatctgaaa tttttcagta ttttaaaaaa taagacgatt attaaatatt actcaagact 240
 tagaactttg attatactaa tcaaatcaaa aatttcatca gcgatttttg ttgtgtcatt 300

SEQ ID NO: 91 moltype = DNA length = 300
 FEATURE Location/Qualifiers
 source 1..300
 mol_type = genomic DNA
 organism = *Dirofilaria immitis*

SEQUENCE: 91
 attttttcca gcagaattgt catcaaaaat cccatttttg atatcctctt catcgaaact 60
 tgctcctgaa tccagagaaac aacgaagaat gtgtaaatct atttcagtag cctggtcatt 120
 gtgcaattca gcgactttat ttctgtgctt caagctaact tcttcattat gccactctc 180
 ttctctcgct attttttcgc tatctaattc aaaatcttcg tctgaaacgg aatcaactcc 240
 tgacgatgta ctcgacactg ataataattt catgccgatt tttctctcaa acgaatcttt 300

SEQ ID NO: 92 moltype = DNA length = 300
 FEATURE Location/Qualifiers
 source 1..300
 mol_type = genomic DNA
 organism = *Dirofilaria immitis*

SEQUENCE: 92
 gaatgaagag caaaaaaata gtcacgacca cctgcaataa aaacagcatc tccgtaaaaa 60
 tgattgaatt gattocccgaa atacgagttt atcaaatgta gaattatgca aattaattat 120
 cagcatgcag atttactgat tttatatctc tcataccgaa attaaggtga tgttttccat 180
 ttctttgttt ccacaatgct ttctttgtga atcgtttttg atcaactatt aatccgatcg 240
 aatcaatcct ccaaatatga gttttattcaa cgtaacaaaa cattgtccga gataatcaaa 300

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SEQ ID NO: 93 moltype = DNA length = 300
 FEATURE Location/Qualifiers
 source 1..300
 mol_type = genomic DNA
 organism = *Dirofilaria immitis*

SEQUENCE: 93

tggaatttc	gaaatcgaaa	ggatgaagaa	aaaggatcct	tgatctatac	attaaatc	60
accatatcaa	ctagcatggc	aagtcaaaagt	aatgttatca	tttaataaaa	aaagatgaat	120
agtaggacta	caggttatat	tgttaaaagt	cgacaaat	ggagtaattg	acagagatca	180
acgattaaat	gtaatggtag	atcttatctt	cttttttcaa	ctacgccaaa	atgaaaaata	240
caattgaatt	tgtcgaataa	gaaactaaca	ttttgaaaat	aagattgaac	atttataaat	300

SEQ ID NO: 94 moltype = DNA length = 300
 FEATURE Location/Qualifiers
 source 1..300
 mol_type = genomic DNA
 organism = *Dirofilaria immitis*

SEQUENCE: 94

ggttgatca	ttatcgacag	aactttagaa	gtttcttgat	aaggacgaaa	agaagcagca	60
ccattgctga	tctaaacaag	gaaaaaagac	cttttttggg	atattgaagt	ttttactgat	120
aggtgcgtgc	tgtgtactgt	gggcataaagt	acaagcttca	tgctccgcag	cgtgaatac	180
tgctgcctgc	atactatgca	gtaaagggtgc	gtgtcgtatt	gctcaataag	tgtataaatt	240
gtgtcttttc	ttgcatagtt	aaatatcttg	ttttcatttt	ttccgctatt	caaaaataaat	300

SEQ ID NO: 95 moltype = DNA length = 300
 FEATURE Location/Qualifiers
 source 1..300
 mol_type = genomic DNA
 organism = *Dirofilaria immitis*

SEQUENCE: 95

gttgggattt	cagactctca	ctcgggtgctg	tttcacagtg	atatctgaat	cgaagtcaca	60
agcaggatg	atgcataaac	aactaatatc	cattgcagaa	acaaggcaaa	actgagaagc	120
tcgagcaata	tagctataga	agctggtacc	acagatgaca	ttacatggta	tttccatttc	180
agcttcacaa	acattgtaaa	tagcttgctt	cgatgattca	atatctcggt	ctacgatatt	240
cttaaaagta	tttttattta	tttgaagtat	agattacatc	catgttctat	ctatcatttc	300

SEQ ID NO: 96 moltype = DNA length = 300
 FEATURE Location/Qualifiers
 source 1..300
 mol_type = genomic DNA
 organism = *Dirofilaria immitis*

SEQUENCE: 96

tgttctgaac	atctcttttt	gattatcttt	tttaattcct	ccattatttt	cgtttttttc	60
gttgtgaatt	aatattgttt	gtctttgatt	cagatgatat	tttcggatcg	taaatagatg	120
gcatcgcat	aagcgtattg	agaagcattc	aatggtgcac	tcttgcctct	tttttttttg	180
aaatctttct	cgataatcaa	ataagtgcag	gatgccaatc	attaacaatt	tcgttccact	240
ttttcagttc	ttattcttat	aacaccacat	ctcatttgca	attttgcgc	caatgatatt	300

SEQ ID NO: 97 moltype = DNA length = 300
 FEATURE Location/Qualifiers
 source 1..300
 mol_type = genomic DNA
 organism = *Dirofilaria immitis*

SEQUENCE: 97

ttttttcgag	gtcactctgg	aaaaataaat	catattttta	aaagacataa	aataaaaaat	60
atgtatatat	aagaaaattt	ttactctgaa	tttcttaaga	aaattctcga	ttctgttttc	120
cataaattcc	ggaatatggt	gtccctgaat	taagaattcg	attccttgca	caccattatt	180
tcgtctagtt	cctgtgtgaa	caatgtaacc	tggaatgaa	cacataaact	gtaatatatt	240
gagcttaaaa	taattatgag	gatgcgaaac	tgaagatatt	cataaatggt	taaaaaaaaa	300

SEQ ID NO: 98 moltype = DNA length = 300
 FEATURE Location/Qualifiers
 source 1..300
 mol_type = genomic DNA
 organism = *Dirofilaria immitis*

SEQUENCE: 98

gtccatgcat	tgcttttcgg	aagttagtgt	agattcagtg	aatattttaa	accagtctct	60
ttctaatcca	aaagagcctc	ccatttcttt	tttcagtttc	agtctctgaa	tcagagcgtg	120
taatctacca	ctccattgcc	gaaaacagct	cgatgtattt	cctgctacgt	agtggttaga	180
attggcgtat	gccacttgct	cattattcgc	gcatgaagtg	taactgtgaa	tagaatgata	240
ctactgttag	aagagaatgc	gttcacttta	tttaacatta	tactgattca	tttcttcttt	300

SEQ ID NO: 99 moltype = DNA length = 300
 FEATURE Location/Qualifiers
 source 1..300
 mol_type = genomic DNA
 organism = *Dirofilaria immitis*

SEQUENCE: 99

agtgaacgag	aaaaaacaga	agaagagata	gcacatcaag	atcgtgagaa	attaattaga	60
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caagaaaaag ctcgtcttac acaaatatat cagggttttct ttttcttgc ttcgaaagtt 120
at ttgaaatta tctcatttct ttgaatttta taagaaataa ttttaatttt ttttgaaatt 180
ttgcctattg agctctaaat ttgtaaaaaa gttttctagg atgatgttag caaagcaaaa 240
aagaaatcca aaagtgatgg taacaaacag gaagatttta tagtgaggta cgataatagc 300

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SEQ ID NO: 100      moltype = DNA length = 300
FEATURE            Location/Qualifiers
source             1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

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SEQUENCE: 100
tagacaatat catccttctt ttttttttgc tcaattttct tgctcattgc tttgatgata 60
atggtaggtg gtataatgaa acgaatagat aattgatgtt cgaaacatt tgctgttaaa 120
tttcagtaaa gaaattgacc tttttgcttt gtgttggatg tttagcttca ttttcttctt 180
gttcattgtc atattcattc tctcaaaact tcttgcttag cgatgctaata ataaatactg 240
gaagaatgcc tttgctttgt tttagttgta aatcatcacc aaggtatttt tttgcaaaat 300

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SEQ ID NO: 101      moltype = DNA length = 300
FEATURE            Location/Qualifiers
source             1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

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SEQUENCE: 101
aagatgaaac taaaaaaat tatttcgaaa aaaagaaaaa aaaattaatg aaataaaaagc 60
aaaaatgaac aaaccgtatt aattttaaac aataaacaat atcgaaatcg aaaaatggac 120
tattattgat gaactatatt ttcaaaatgt gaaagggtcaa agtttggttc aattatgata 180
aatacaattt aaaataagat taagctaaca aataagttga gcaaattgat gaaacaaaca 240
aatcagaata tattacagaa aatgatataa catgaaaata tattagacca attattttta 300

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```

SEQ ID NO: 102      moltype = DNA length = 300
FEATURE            Location/Qualifiers
source             1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

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SEQUENCE: 102
ttgaagtttt cagataaaact ttgataaaaa attgttctat gaattctcaa atttcaatta 60
gtgatactta tttcgaagggt aattatgcct gattgaatct tcaatatcaa caaaatgaaa 120
at ttttagtat gattgttaac tcatacacct ctaattaaag gtattttctt tatcccatga 180
aatgaaaatt tattaagaac ttgaaaagct acggtatgcc tttgatgcaa aagaaagatt 240
cattttcatt aaatcatgtt taaaaaaaag agcaaaagagc aaaagggtgat gaaagttttt 300

```

```

SEQ ID NO: 103      moltype = DNA length = 300
FEATURE            Location/Qualifiers
source             1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

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```

SEQUENCE: 103
ttctatacga aatatttgtc tgccataaat ctactcagga actcgataga tcaaaacata 60
agtacgcttg ctcttttatt ttcgtttgaa aaataaatag atcatttttcg cacttacatt 120
tcaaattcaa ttgctttatt catatctttc tgtttttact tactgggtatt taacagtcgt 180
tgttcacaat ttaatgatct atgaaacacc atttaattgt atttggaacta acttttcgac 240
aagcaaaaaga ttaaaattgt cttcagatac agttataaat ttacattgaa gataaatgaa 300

```

```

SEQ ID NO: 104      moltype = DNA length = 300
FEATURE            Location/Qualifiers
source             1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

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SEQUENCE: 104
taacgatctg tatatcaatg gaataatatt cagttcatgt tgtactcgat atgagataga 60
attacaattt tggaacaaga taatctcaac agctattttc aagaatagtt aaattaggat 120
accattcaaa gaaactttaa aaaatgattt ccatacatta atgctttttg tgttttcgct 180
ctcgaccaga atccaggaat tgtccattat catcaatttg attaactttt atctttattc 240
taattcttca acatttctct aattgatatt agtttcaata ttttaataag taaaaattta 300

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```

SEQ ID NO: 105      moltype = DNA length = 300
FEATURE            Location/Qualifiers
source             1..300
                  mol_type = genomic DNA
                  organism = Dirofilaria immitis

```

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SEQUENCE: 105
ataatgtgtt attgatcaaa ggatttttag ttacctacca gatggaaaaa aagcaagttt 60
acgaaaacag aagtttagcat caactttcat ccatgggttac accgtatata atccaatcga 120
ctcatacttt atgttgatct gattttatag cagataacta gttaccttgc tcagcagcag 180
ctaaatcctt tctatttgc ttaataacaga aatatttttc attaacaag aaattatact 240
cogtgtttga catttcattt taatttcgtt ccaaaaaatga aaaaagcttc gtcggaat 300

```

```

SEQ ID NO: 106      moltype = DNA length = 300
FEATURE            Location/Qualifiers

```


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source                1..300
                      mol_type = genomic DNA
                      organism = Dirofilaria immitis

SEQUENCE: 106
attatatttgt agtttttcat tttttagttc aatttttcctt tgcttatttt aaatatgcc 60
ttcttttattc agactcatag cgaatgcata tgttcattaa tttttttagt tacagttaca 120
aattctcaat ttctctttaa tcattttttt ttccaaaaat agtctgagca ctcaaccatt 180
cattcaacaa ttgcagcttt ttttattgga gccttggtcaa attatcaatt cgtttccatg 240
tttattattg aaataataaa cggtatattg gataacgaag ttcgcttagc ttctttgact 300

SEQ ID NO: 107        moltype = DNA length = 300
FEATURE              Location/Qualifiers
source                1..300
                      mol_type = genomic DNA
                      organism = Dirofilaria immitis

SEQUENCE: 107
aaaaattcag gtaatgagat cagtaatttt ttttggtcac tttgctgttt cttatcagct 60
cattgttattc catatcaaat gagcgaaagt gtgtatcaca tattggcaga gtgtaattcta 120
tgaagatttt gcgtatcaaa gtaattatga gagaactgat aattttattt taaagtagta 180
gaaaactcga attagctaa taaataatcg gttgatattc atgaaatgaa ttactaatga 240
aatggataat tgagtaataa caaatgatat tcatgaagaa aggcagggtt tttttaatag 300

SEQ ID NO: 108        moltype = DNA length = 300
FEATURE              Location/Qualifiers
source                1..300
                      mol_type = genomic DNA
                      organism = Dirofilaria immitis

SEQUENCE: 108
tatacttaaa acaagaaata caattaatgc caatagcaga gtgaaacttc tgaaaaataa 60
tgagttgaaa ctggtaaaat taacatttta ttagaaattt cagaaactta tgactcctca 120
tggcactatc acaaaatggt tgaaaaaaat tgacagctcg cgctcgattgc aaaaatcatg 180
attcctgata tttagtatcg aacatgtgac aaataatata aagacctaac cataaagcac 240
tgaaacaact cgcggaaaca aaaaattaat ttgcataaac acggaatagc atcagaaaat 300

SEQ ID NO: 109        moltype = DNA length = 300
FEATURE              Location/Qualifiers
source                1..300
                      mol_type = genomic DNA
                      organism = Dirofilaria immitis

SEQUENCE: 109
gaattttttt agaaggcttg aagtcgagaa tattagagac tatatcgaag acttaaaataa 60
tcctgggtaat cttctgtatg aatcaaaatt acctcgaaca gaaccattca gcacatcacg 120
agataattca tggaatgaaa ctagccaatc agagcgttgt aaaagaagaa agttatgaaa 180
tgaccttaaa atcaatttaa agcatgtcct cgccatataa gcgttgaaaa gttaggatag 240
aatcaattat caaaaaaata tgttaactag atcttatcaa tcaaaacatc agaaggaaaa 300

SEQ ID NO: 110        moltype = DNA length = 300
FEATURE              Location/Qualifiers
source                1..300
                      mol_type = genomic DNA
                      organism = Dirofilaria immitis

SEQUENCE: 110
atatgataat agtgaaacaa ttccatcaca ataaatatta tcgattagga gataaaataa 60
cattgatgcc tcaatttttg tcaacaatat atatttgcta ttagcatttt tattaaatcg 120
tttttatctg acttgacata aattgaaata gaaaaaattg aatctgttcc ttgttagatt 180
ttcttctaaa aattcttgaa atacaataaa tttcttaaat ttcaatatct ctacataatg 240
tattgcgaca aaaatgctaa tgattggcct attattattt cgaataattt ttaatacaaa 300

SEQ ID NO: 111        moltype = DNA length = 300
FEATURE              Location/Qualifiers
source                1..300
                      mol_type = genomic DNA
                      organism = Dirofilaria immitis

SEQUENCE: 111
agctcgaaga tcggacaaaa tttgttcagc ttgttgctt gaggccttag tctgaaaaga 60
cacttaaaag tataaacaaa ttatatcaa aaatcttat tttgcatttg cgtcttaatt 120
tttgtttttt gcaaaagttt ttccgagcaa gtttttctat cttcgaaaag attatatcaa 180
ttaaaatttc aatttaagca atcattgcct cttcgagttt ctgtttcagc aaataaatat 240
caccaccacg acgctgtcgg aagaaagaaa cgcttttccc aatttctcgt ctcaactttt 300

SEQ ID NO: 112        moltype = DNA length = 300
FEATURE              Location/Qualifiers
source                1..300
                      mol_type = genomic DNA
                      organism = Dirofilaria immitis

SEQUENCE: 112
taagaaagct gggagatttt ccaaaaacac tatttccac gatttgttgt tttctatgat 60
caattcttaa tcaaacctcg aaattctcaa attttcgatt tctatccaac ttctacatat 120
ttttttagaa aattcatatt tagcaaagct gagtgtagaa ataattcata cttgcaattc 180

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atttttctta aattttcgaa tttcttaaaa aagtatttca aattacctac caattttgat 240
tggaaaaattc gtggatgcta aaaattcaaa tcaaaatagt taaacagtat tcttaattgt 300

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SEQ ID NO: 113      moltype = DNA length = 300
FEATURE            Location/Qualifiers
source              1..300
                    mol_type = genomic DNA
                    organism = Dirofilaria immitis

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SEQUENCE: 113
aatttaaaaa acacatcgac attttgcggt acggtaatga ttgtttacag taactaaatg 60
tgtctacagg tagtaatact cgtgtacgta atgaatgagt atagtgaacc gatatttcct 120
tcactagtag gcaatattaa gaagtatttt cattttcata ttctatctaa aataaaccca 180
taaaatgggt tttgaattat tactttttca ttgttatttt ttgatcctaa attgtaaaat 240
actgtaataa tttagctaata ttctatgatt ctattcaata tgcttaaat aaattcttaa 300

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SEQ ID NO: 114      moltype = DNA length = 300
FEATURE            Location/Qualifiers
source              1..300
                    mol_type = genomic DNA
                    organism = Dirofilaria immitis

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SEQUENCE: 114
tcgtatttgt tgtatgtaat atagaaatat tgtttaaatt caatatgtag aaaaaatttc 60
tannnnnnnn nnaattaatt acatattaac tcgtatttgt tgtatgtaat atagaaatat 120
tgtttaaat caatatgtag aaaaaatttc cataataaag acgaacagca tttataatta 180
tcaatgataa gttgaaatta attcatcaat gataagttga aattaattta ttgaaataa 240
tttctttgaa attcgaatat agacgagaat tttttttttt ttgctaatac tttatcaaat 300

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SEQ ID NO: 115      moltype = DNA length = 300
FEATURE            Location/Qualifiers
source              1..300
                    mol_type = genomic DNA
                    organism = Dirofilaria immitis

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SEQUENCE: 115
tctagcaata taaattacaa gaatatgccg tccaagtatt tcagaattta ttattaattt 60
ggataaata acattgtaaa tactgcgcat tctggattat tatgcactgc ataataacat 120
gcaatttcgt ctacatatcg cgaataaacg ccaaaagatt tctcgataaa agaaaatata 180
agaattcgta aatgaattgt gtgtcagaga tatgtgttaa ttcataagtc aagatgttgt 240
aaatcgatcc atattagtaa tcatatttac gtgctcgtaa ataaaagcgg tgattcttgt 300

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SEQ ID NO: 116      moltype = DNA length = 300
FEATURE            Location/Qualifiers
source              1..300
                    mol_type = genomic DNA
                    organism = Dirofilaria immitis

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SEQUENCE: 116
atcgaaaaaa gatgatctga tgacggaagg cgaaatgtct gcagaagcta agatgacgga 60
agaaaaaagt gaagaaatga aagaagaagc tggtaaaact cagaaggaaat gtaaaactgg 120
agaatcgaaa aaagatgatc tgatgacgga gggcgaaatg tctaagaag ctaagatgtc 180
ggaagaaaaa agtgaagaaa tgaaagaaga agctgataaa actcagaagg aatgtaaaac 240
ggaagaatcg aaaaaagacg atctgacgac agaaggcgaa aaatctgaag tagatgagcc 300

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SEQ ID NO: 117      moltype = DNA length = 300
FEATURE            Location/Qualifiers
source              1..300
                    mol_type = genomic DNA
                    organism = Dirofilaria immitis

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SEQUENCE: 117
actaatgata agaaacggag ccgacgattt taggaaatga ataataacga cattgacaac 60
cattgttaga aaattgatag tactgataat aaaagctagt tatagaaaaa tgataataat 120
aataaaattg ctggtagcaa atgtctagaa gtgataataa aattaatgat agcaaatgga 180
ttagcaatga taattaaact gatgatagcg aatggattag taatgataat aaaattgatg 240
atagcaaatg actaataatg gtaataaaag ttaatgctag tgataacttg tattttaagt 300

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SEQ ID NO: 118      moltype = DNA length = 300
FEATURE            Location/Qualifiers
source              1..300
                    mol_type = genomic DNA
                    organism = Dirofilaria immitis

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SEQUENCE: 118
acagtttata gttacaatat tctccggtga ctaactgtat tttacaactt ataattatag 60
attacaaaaa atattatagt agttttataa ttacagtatt cttaagtga taactatact 120
ttacagctta cagttacagt agttttctat gtttttgaat attaatttta catggttttt 180
cctagtttca gtttcaaaat ttccagatat tttatgtgtt aaagcaaat atattcgaga 240
tataaaaagt actggtcata tcttacaatt ctcaccttc tatattggaa agaattgagt 300

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SEQ ID NO: 119      moltype = DNA length = 300
FEATURE            Location/Qualifiers
source              1..300
                    mol_type = genomic DNA

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organism = Dirofilaria immitis

SEQUENCE: 119
gtattgggac cgcgtatcgg gaaatctgaa agaagtcctt aacagtatct taaatgaata 60
attcaaatcg ttacttctta atatattaat ttatgcgtat atatgcagta catagcattg 120
cttaaatctt tatttttccg cggttaaaaa cctatgtaag ataagggagg tgattgtatc 180
tgcgccgtac tccttggttt aatctacctg cttgttgtat atcctccaca tattgttaact 240
gcagcttcac atttgcata atagtaaggg catcgttgct tccagaagag atatattatc 300

SEQ ID NO: 120      moltype = DNA length = 300
FEATURE            Location/Qualifiers
source              1..300
                    mol_type = genomic DNA
                    organism = Dirofilaria immitis

SEQUENCE: 120
gtgccccgaa tgttacaaatt aggacgaaag taaaagtagt tgactgtagg tatgacgata 60
aaggaaaaat ttgtattctta agactttaca atttctaaat attacgtggt ttatcgtgct 120
aacatcacga attccatatt cacaaaaaaa attttgtaga actccatctg gtttgatga 180
atttgctaca gttgaactgg atgatggaac gaaattgcaa acatctctta ttgttagtat 240
tttctaaatt ctgtgaaatt ttgcaacggc attcatgttt aattattaat ttggagaaag 300

SEQ ID NO: 121      moltype = DNA length = 300
FEATURE            Location/Qualifiers
source              1..300
                    mol_type = genomic DNA
                    organism = Dirofilaria immitis

SEQUENCE: 121
aaataagcaa atccgaaagt attacatata cggactaaat attgccattc attcgggagt 60
ataccattgc aaccattggg atttcatttg atcgagaaaa ctagtttttg tagtttgga 120
taaagagaaa tggagagagg aactttcatg atcaatttct ttacgtactg aaattcattt 180
ctatggatgt tctttttcta ttctattctc ctacagcaat acagtccgaa cagtcatcaa 240
ataagtctaa aaggcatgaa taatataaac atcagcaact ttttaaatga atgcttatta 300

SEQ ID NO: 122      moltype = DNA length = 300
FEATURE            Location/Qualifiers
source              1..300
                    mol_type = genomic DNA
                    organism = Dirofilaria immitis

SEQUENCE: 122
atttctataa acatctcttg cattgattaa tttaacatgt tgcaataaat atttcttact 60
tttgaatgta tcattttact gaaaaaactt caatcgagga aataagtttt aaaataaatt 120
catatttgaa ttcattgctg ttcaaaaaatt ctattactat aatacatgtc tcttggttgt 180
atcttttttt cttttgaaat aatacaatca aacggtttcc taaattttca tagacatcat 240
attttaaaaa aaaatgcatt tgaaaatttt cgaaaatcaa tgaacttaat tgatgaaaaa 300

SEQ ID NO: 123      moltype = DNA length = 300
FEATURE            Location/Qualifiers
source              1..300
                    mol_type = genomic DNA
                    organism = Dirofilaria immitis

SEQUENCE: 123
gcatgtgtat gtagtatctt tttgtaaaaca acatatctaa tctgtctgtc cctttaacat 60
tatagaatag tcagtttagtc cgctatttat tttaataaca aaatatctca cttaacttcc 120
atttctttcc taaataattt tgtttcgcta gatctttcct ataattttca aattttcaaa 180
aatgaattaa tcttttattt atatatgtgt atgtatgtgt atgtatgtat gtgtacgttg 240
catatatgta tatgtatgtg tgtatgtgtg tatatgtata tgtatatgtg tgtatgtgtg 300

SEQ ID NO: 124      moltype = DNA length = 300
FEATURE            Location/Qualifiers
source              1..300
                    mol_type = genomic DNA
                    organism = Dirofilaria immitis

SEQUENCE: 124
tatgcataat gtgcgaccag ccaataatgt cttcaaacca taattatgca gaaataaatt 60
ttttccagaa ataatttttt tttttttaca tatacttccg atctgtgaga aaatacattt 120
gaagtgaagt gtgaagcaat gctacttttt caaacaacat tgtgaaaatg gattaaaacg 180
caccaatgga gcaagagatc gtaagtttcg ttccgcatgt cctgtggcaa cgtgtaaac 240
atccgttaac gatatatgat gtaaaagccg acacacccaa attaaaatcc attataaaca 300

SEQ ID NO: 125      moltype = DNA length = 300
FEATURE            Location/Qualifiers
source              1..300
                    mol_type = genomic DNA
                    organism = Dirofilaria immitis

SEQUENCE: 125
aaatggatcg tattcacttc gtaagaactt agtgaacgaa aaatcaaacc atcacaataa 60
ctttactttt tttctttttt tactaaacac actatcctat gaaaacaaaa tgtccaaata 120
gattcatatg ataataaact gtgaagttat ccaatctatc agttctcgaa gagggaaata 180
ataaaaacat taagcaaccc accgatcttc gctgaccatc tccttcttca ttgcaagaa 240
gcaaactctg tggtgatatt tctgcaacca tctgcaaaat aaagcacgaa aaattaagga 300

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SEQ ID NO: 126      moltype = DNA length = 300
FEATURE            Location/Qualifiers
source             1..300
                   mol_type = genomic DNA
                   organism = Dirofilaria immitis

SEQUENCE: 126
tttgatatgc aatcaactaa ccaaatcaga attcaatgca ttctgataaa tttcttcaat 60
atcgtgcatc aattcgacat catattttga cagtgatgct accttttttag ccgtatttcg 120
gaaaaatatg aattcaacca gctgctgcc aaaatttaag gctgtagcaa gtccagcaac 180
aaccagccct acaactgaaa attctaaaaa ctgggttcacg tgcttatcat taataatttc 240
aacactatca ctatctccac atgaacttga tcgattataa tttagtagaa ctgaaaaaaa 300

SEQ ID NO: 127      moltype = DNA length = 300
FEATURE            Location/Qualifiers
source             1..300
                   mol_type = genomic DNA
                   organism = Dirofilaria immitis

SEQUENCE: 127
acaaattcgt tttaatattg gattacattg aaattgctga aataaagtgg aaatattgaa 60
aagcatttta caatatttgt taacaacatt atatttaaag aatatacacc ttgggtttaa 120
tggtaaaata atctcaagaa ttttcattag gttaattttt ttttatttat ttatattcac 180
aaaaaattgt aaaagaaaac aaaaacaaca ataataacgg tgacaacaac aacaataata 240
ataacaaaac tatttgttgt gattttgcag cattgatgta gtggggatct tttggagcga 300

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The invention claimed is:

1. A method of treating an animal infected with a *Dirofilaria* spp. nematode, the method comprising determining the genotype of the nematode at a polymorphic site in a nucleic acid molecule that includes SEQ ID NO: 118, wherein the polymorphic site at position 151, wherein if position 151 is G, then the animal is treated with an alternative agent, and wherein if position 151 is not G, then the animal is treated with a macrocyclic lactone.

2. The method of claim 1, wherein the alternative agent comprises one or more of an arsenic-based therapy, diethylcarbamazine, and antibiotics.

3. The method of claim 2, wherein the arsenic-based therapy is melarsomine dihydrochloride.

4. The method of claim 3, wherein the melarsomine dihydrochloride is administered to the animal intramuscularly.

5. The method of claim 2, wherein the antibiotic is tetracycline.

6. The method of claim 2, wherein the antibiotic is doxycycline.

7. The method of claim 1, wherein the *Dirofilaria* spp. nematode is *Dirofilaria immitis*.

8. The method of claim 1, including isolating the nucleic acid molecule from the nematode, and optionally purifying the nucleic acids prior to determining the genotype of the nematode.

9. The method of claim 1, wherein the genotype of the nematode is determined by DNA sequencing, hybridization-based methods including with allele specific oligonucleotides, microarray analysis, enzyme-based methods, single strand conformational polymorphism (SSCP), high resolution melt (HRM) or approaches based on PCR, RT-PCR, and qRT-PCR.

10. The method of claim 1, wherein the genotype of the nematode is determined by DNA sequencing.

11. The method of claim 1, wherein the genotype of the nematode is determined by hybridization-based methods including with allele specific oligonucleotides.

12. The method of claim 1, wherein the genotype of the nematode is determined by microarray analysis.

13. The method of claim 1, wherein the genotype of the nematode is determined by enzyme-based methods.

14. The method of claim 1, wherein the genotype of the nematode is determined by single strand conformational polymorphism (SSCP).

15. The method of claim 1, wherein the genotype of the nematode is determined by high resolution melt (HRM).

16. The method of claim 1, wherein the genotype of the nematode is determined by one or more of PCR, RT-PCR, and qRT-PCR.

* * * * *