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(54) Titre : LOCI GENETIQUES ASSOCIES A LA FERTILITE ACCRUE DANS LE MAIS

(54) Title: GENETIC LOCI ASSOCIATED WITH INCREASED FERTILITY IN MAIZE

Temperature (°F)	Relative Humidity (%)	Vip3 Homozygous	Vip3 Hemizygous	Vip Null
85	49	6.0	4.4	2.3
80	51	5.8	3.2	1.7
74	61	4.9	1.6	1.0

Final Anther Scale	
1 = exceptional anther extrusion	
2 = good anther extrusion, normal	
3 = reduced anther extrusion, below normal	
4 = sparse, scattered anthers	
5 = very sparse anthers, but more than 15 total	
6 = 15 or fewer total anthers extruded	

(57) Abrégé/Abstract:

The present invention relates to methods and compositions for identifying, selecting and/or producing a maize plant or plant part having increased fertility. A maize plant or plant part that has been identified, selected and/or produced by any of the methods of the present invention is also provided.

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(54) Title: GENETIC LOCI ASSOCIATED WITH INCREASED FERTILITY IN MAIZE

Temperature (°F)	Relative Humidity (%)	Vip3 Homozygous	Vip3 Hemizygous	Vip Null
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Fig. 1

(57) Abstract: The present invention relates to methods and compositions for identifying, selecting and/or producing a maize plant or plant part having increased fertility. A maize plant or plant part that has been identified, selected and/or produced by any of the methods of the present invention is also provided.

WO 2015/127248 A1**Declarations under Rule 4.17:**

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- *as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii))*

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GENETIC LOCI ASSOCIATED WITH INCREASED FERTILITY IN MAIZE

FIELD OF THE INVENTION

The present invention relates to compositions and methods for identifying, selecting
5 and producing maize plants having increased fertility.

BACKGROUND

Vip3 proteins have been successfully expressed in transgenic plants such as maize and cotton. For example, hybrid transgenic maize plants can express Vip3A proteins at levels
10 which are insecticidal to pest insects and which have no negative impact on the plant phenotype. Thus, the Vip3A trait protects yield and yield potential of hybrid maize plants. However, Vip3 has been observed to cause decreased male fertility in certain inbred maize plants under normal growing conditions. This phenomenon is more prominent in inbred maize plants that are homozygous for a *vip3A* transgene. The degree to which male fertility is
15 decreased is inbred specific - some inbreds exhibit little or no reduction in male fertility when homozygous for a *vip3* gene, other inbreds are somewhat sensitive to Vip3 and exhibit a significant reduction in male fertility when homozygous for a *vip3* gene, and other inbreds are highly sensitive to Vip3 and exhibit extremely low or no male fertility when homozygous for a *vip3* gene. The degree to which male fertility is decreased is also affected by
20 environmental factors, such as water availability and temperature. In Vip3-induced reductions in male fertility, drought and high temperature conditions exacerbate the the reduction in male fertility; however, cooler growth conditions have been shown to mitigate the negative effects of Vip3 expression on male fertility.

Identifying genetic loci that enhance the fertility of maize plants expressing a *vip3*
25 transgene could lead to more efficient crop production by allowing for the identification, selection and production of *vip3*-expressing inbred maize plants with increased male fertility.

SUMMARY OF THE CLAIMED INVENTION

The present invention provides maize plants having increased male fertility, as well as
30 compositions and methods for identifying, selecting and producing such plants.

In some embodiments, methods of identifying a maize plant or plant part having one or more characteristics associated with increased male fertility are provided. Such methods may comprise detecting, in a maize plant or plant part, a marker associated with increased male fertility.

In some embodiments, methods of producing a maize plant having one or more characteristics associated with increased male fertility are provided. Such methods may comprise detecting, in a maize plant part, the presence of a marker associated with increased male fertility and producing a maize plant from said maize plant part. Such methods may
5 further comprise introducing the marker into said maize plant part.

In some embodiments, breeding methods are provided. Such methods may comprise detecting, in a maize plant or plant part, the presence of a marker associated with increased male fertility (*e.g.*, in nucleic acid, for example, in an amplification product from a nucleic acid sample from the plant or plant part) and selecting said maize plant or plant part for
10 breeding. In embodiments, the method may further comprise crossing the maize plant (or an ancestor, progeny or sibling thereof) with a second maize plant that optionally lacks the marker to produce a progeny maize plant, which optionally comprises the marker.

Still further, the invention provides a method for producing a plant having one or more characteristics associated with increased male fertility, comprising: selecting from a
15 diverse maize plant population a maize plant comprising a marker associated with increased male fertility as described herein; and crossing the maize plant (or an ancestor, progeny or sibling thereof) with itself or a second maize plant to produce a progeny plant comprising the marker, thereby producing a plant having one or more characteristics associated with increased male fertility. In embodiments, the second maize plant does not comprise the
20 marker. In embodiments, the marker is detected in nucleic acid from the first maize plant and/or progeny plant (*e.g.*, in an amplification product from a nucleic acid sample from the maize plant and/or progeny).

In some embodiments, methods of reducing costs associated with breeding and/or seed production are provided. Such methods may comprise detecting, in a maize plant or
25 plant part, the presence of a marker associated with increased male fertility and selecting said maize plant or plant part for breeding.

In some embodiments, methods of predicting male fertility are provided. Such methods may comprise detecting, in a maize plant or plant part, the presence of a marker associated with increased male fertility (*e.g.*, in nucleic acid from the plant or plant part),
30 wherein the presence of the marker predicts a likelihood of increased male fertility.

In some embodiments, methods of identifying a maize plant or plant part comprising at least one allele associated with increased male fertility are provided. Such methods may comprise detecting, in a maize plant or plant part (*e.g.*, in nucleic acid from the plant or plant part), a marker associated with increased male fertility.

In some embodiments, methods of producing a maize plant or plant part having one or more characteristics associated with increased male fertility are provided. Such methods may comprise introducing a nucleic acid comprising at least one allele associated with increased male fertility into the genome of a maize plant part and producing a maize plant from said maize plant part. Such methods may further comprise detecting a marker associated with increased male fertility and/or the allele associated with increased male fertility in nucleic acid (e.g., in a nucleic acid sample) from said maize plant or plant part. In embodiments, the marker and/or allele is detected in an amplification product from a nucleic acid sample from said maize plant or plant part.

10 In some embodiments, methods of improving pollen production are provided. Such methods may comprise introducing a nucleic acid comprising at least one allele associated with increased pollen production into the genome of a maize plant part and producing a maize plant from said maize plant part. Such methods may further comprise detecting a marker associated with increased pollen production and/or the allele associated with
15 increased pollen production in nucleic acid (e.g., a nucleic acid sample) from said maize plant part. In embodiments, the marker is detected in an amplification product from a nucleic acid sample from said plant or plant part.

In some embodiments, methods of producing a maize plant or plant part having one or more characteristics associated with increased male fertility are provided. Such methods may
20 comprise introducing a genomic region associated with increased male fertility into the genome of a maize plant part and producing a maize plant from said maize plant part. Such methods may further comprise detecting a marker associated with increased male fertility and/or the genomic region associated with increased male fertility in nucleic acid (e.g., a nucleic acid sample) from said maize plant part. In embodiments, the marker is detected in
25 an amplification product from a nucleic acid sample from the maize plant or plant part.

In some embodiments, methods of improving pollen production are provided. Such methods may comprise, consist essentially of or consist of introducing a genomic region associated with increased pollen production into the genome of a maize plant part and producing a maize plant from said maize plant part. Such methods may further comprise
30 detecting a marker associated with increased pollen production and/or the genomic region associated with increased pollen production in nucleic acid (e.g., a nucleic acid sample) from said maize plant part. In embodiments, the marker is detected in an amplification product from a nucleic acid sample from the maize plant or plant part.

In some embodiments, methods of producing a maize plant or plant part having one or more characteristics associated with increased male fertility are provided. Such methods may comprise introducing a genomic region comprising one or more transgenes associated with increased male fertility into the genome of a maize plant or plant part.

5 In some embodiments, methods of improving pollen production are provided. Such methods may comprise introducing a genomic region associated with increased pollen production into the genome of a maize plant or plant part and producing a maize plant from said maize plant part.

10 In some embodiments, methods of producing a maize plant or plant part having one or more characteristics associated with increased male fertility are provided. Such methods may comprise crossing a first maize plant or plant part with a second maize plant or plant part to produce a progeny maize plant or plant part, wherein said first maize plant or plant part comprises within its genome a marker associated with increased male fertility, optionally wherein said second maize plant or plant part lacks said marker, and wherein said progeny
15 maize plant or plant part has said marker within its genome. Such methods may further comprise selecting said progeny plant based upon the presence of said marker.

In some embodiments, methods of producing a maize plant or plant part having one or more characteristics associated with increased male fertility are provided. Such methods may comprise crossing a first maize plant or plant part with a second maize plant or plant part to
20 produce a progeny maize plant or plant part, wherein said first maize plant or plant part comprises within its genome an allele associated with increased male fertility, optionally wherein said second maize plant or plant part lacks said allele, and wherein said progeny maize plant or plant part has said allele within its genome. Such methods may further comprise selecting said progeny plant based upon the presence of said allele and/or the
25 presence of a marker linked to said allele.

In some embodiments, methods of producing a maize plant or plant part having one or more characteristics associated with increased male fertility are provided. Such methods may comprise crossing a first maize plant or plant part with a second maize plant or plant part to produce a progeny maize plant or plant part, wherein said first maize plant or plant part
30 comprises within its genome a genomic region comprising one or more transgenes associated with increased male fertility, optionally wherein said second maize plant or plant part lacks said genomic region, and wherein said progeny maize plant or plant part has said genomic region within its genome. Such methods may further comprise selecting said progeny plant

based upon the presence of said genomic region and/or the presence of a marker linked to said genomic region.

In some embodiments, methods of selecting a maize plant or plant part having one or more characteristics associated with increased male fertility are provided. Such methods may
5 comprise crossing a first maize plant or plant part with a second maize plant or plant part, wherein the first maize plant or plant part comprises a marker associated with increased male fertility and optionally wherein said second maize plant or plant part lacks said marker, and selecting a progeny plant or plant part that possesses said marker.

In some embodiments, methods of selecting a maize plant or plant part having one or
10 more characteristics associated with increased male fertility are provided. Such methods may comprise crossing a first maize plant or plant part with a second maize plant or plant part, wherein the first maize plant or plant part comprises an allele associated with increased male fertility and optionally wherein said second maize plant or plant part lacks said allele, and selecting a progeny plant or plant part that possesses said allele and/or a marker linked to said
15 allele.

In some embodiments, methods of selecting a maize plant or plant part having one or more characteristics associated with increased male fertility are provided. Such methods may
comprise crossing a first maize plant or plant part with a second maize plant or plant part, wherein the first maize plant or plant part comprises a genomic region comprising one or
20 more transgenes associated with increased male fertility and optionally wherein said second maize plant or plant part lacks said genomic region, and selecting a progeny plant or plant part that possesses said genomic region and/or a marker linked to said genomic region.

In some embodiments, methods of producing a maize plant or plant part having one or more characteristics associated with increased male fertility are provided. Such methods may
25 comprise crossing a donor maize plant or plant part with a recurrent maize plant or plant part and backcrossing progeny with said recurrent maize plants or plant part for one or more generations, wherein said donor maize plant or plant part comprises within its genome a marker associated with increased male fertility, wherein said recurrent maize plant or plant part optionally lacks said marker, and wherein at least one generation of said progeny are
30 identified and/or selected for backcrossing by detecting the presence of said marker.

In some embodiments, methods of producing a maize plant or plant part having one or more characteristics associated with increased male fertility are provided. Such methods may
comprise crossing a donor maize plant or plant part with a recurrent maize plant or plant part and backcrossing progeny with said recurrent maize plants or plant part for one or more

generations, wherein said donor maize plant or plant part comprises within its genome an allele associated with increased male fertility, wherein said recurrent maize plant or plant part optionally lacks said allele, and wherein at least one generation of said progeny are identified and/or selected for backcrossing by detecting the presence of said allele and/or the presence of a marker linked to said allele.

5 In some embodiments, methods of producing a maize plant or plant part having one or more characteristics associated with increased male fertility are provided. Such methods may comprise crossing a donor maize plant or plant part with a recurrent maize plant or plant part and backcrossing progeny with said recurrent maize plants or plant part for one or more generations, wherein said donor maize plant or plant part comprises within its genome a genomic region comprising one or more transgenes associated with increased male fertility, wherein said recurrent maize plant or plant part optionally lacks said genomic, and wherein at least one generation of said progeny are identified and/or selected for backcrossing by detecting the presence of said genomic region and/or the presence of a marker linked to said genomic region.

15 In embodiments, the invention also provides methods of improving seed production from a maize plant. To illustrate, in representative embodiments, the invention provides a method of improving seed production from a maize plant, comprising: crossing a first maize plant with a second maize plant, wherein said first maize plant comprises within its genome a marker associated with increased male fertility as described herein and said second maize plant optionally lacks said marker, to produce a progeny maize plant comprising said marker; and using a progeny maize plant comprising said marker as a pollenator in a cross with itself or a second maize plant that functions as a seed parent (e.g., crossing said progeny plant comprising said marker with itself, wherein the progeny plant functions as a pollenator and as a seed parent, or crossing said progeny plant comprising with a second maize plant, wherein the progeny plant functions as a pollenator and the second maize plant that functions as a seed parent), thereby improving seed production from the cross as compared with a suitable control cross.

25 In representative embodiments of the methods of the invention, the marker, allele, haplotype and/or genomic region comprises, consists essentially of or consists of:

- (a) one or more markers located within one or more of the chromosomal intervals described in Table 1 or a marker/allele/haplotype/genomic region that maps at 10 cM or less therefrom;

- (b) one or more of the desired alleles described in Table 2, Table 8 and/or Table 10, or a marker/allele/haplotype/genomic region that maps at 10 cM or less therefrom;
- 5 (c) a haplotype comprising two or more of the desired alleles described in Table 2, Table 8 and/or Table 10, or a marker/allele/haplotype/genomic region that maps at 10 cM or less therefrom;
- (d) an allele or haplotype that is in linkage disequilibrium with one or more of the chromosomal intervals described in Table 1 or a marker/allele/haplotype/genomic region that maps at 10 cM or less therefrom;
- 10 (e) an allele or haplotype that is in linkage disequilibrium with one or more of the desired alleles described in Table 2, Table 8 and/or Table 10, or a marker/allele/haplotype/genomic region that maps at 10 cM or less therefrom;
- (f) an allele or haplotype that is in linkage disequilibrium with a haplotype comprising two or more of the desired alleles described in Table 2, Table 8 and/or Table 10, or a marker/allele/haplotype/genomic region that maps at 10 cM or less therefrom; or
- 15 (g) any combination of (a) to (f).

In further embodiments of the methods of the invention, the marker/allele/haplotype/genomic region is located within:

- 20 (a) chromosomal interval 1 as described in Table 1;
- (b) chromosomal interval 2 as described in Table 1;
- (c) one or more of chromosomal intervals 3 to 17 as described in Table 1;
- (d) one or more of chromosomal interval 18 to 45 as described in Table 1;
- (e) one or more of chromosomal intervals 46 to 12743 as described in Table 1;
- 25 (f) one or more of chromosomal intervals 12744 to 12749 as described in Table 1;
- (g) one or more of chromosomal intervals 12750 to 12755 as described in Table 1;
- (h) chromosomal interval 12756 as described in Table 1;
- (i) one or more of chromosomal intervals 12757 to 12762 as described in Table 1;
- (j) one or more of chromosomal intervals 12763 to 12768 as described in Table 1;
- 30 (k) one or more of chromosomal intervals 6 to 9371 as described in Table 1;
- (l) chromosomal interval 3 as described in Table 1;
- (m) chromosomal interval 13 as described in Table 1;
- (n) chromosomal interval 25 as described in Table 1; or
- (o) any combination of (a) to (n).

In some embodiments, the marker/allele/haplotype/genomic region comprises, consists essentially of or consists of one or more of the desired alleles:

- (a) on chromosome 5 as described in Table 8;
- (b) on chromosome 3 as described in Table 8;
- 5 (c) on chromosome 7 as described in Table 8;
- (d) on chromosome 10 as described in Table 8;
- (e) on chromosomes 3 and 5 as described in Table 8;
- (f) on chromosomes 5 and 7 as described in Table 8;
- (g) on chromosomes 3, 5 and 7 as described in Table 8;
- 10 (h) on chromosomes 5 and 10 as described in Table 8;
- (i) on chromosomes 3, 5 and 10 as described in Table 8;
- (j) any combination of (a) to (i); or
- (k) or a marker/allele/haplotype/genomic region that maps at 10 cM or less from any of (a) to (j).

15 In other representative embodiments, the marker/allele/haplotype/genomic region comprises a haplotype comprising two or more of the desired alleles:

- (a) on chromosome 5 (QTL 5.1 and/or QTL 5.2) as described in Table 8;
- (b) on chromosome 3 as described in Table 8;
- (c) on chromosome 7 as described in Table 8;
- 20 (d) on chromosome 10 as described in Table 8;
- (e) on chromosomes 3 and 5 as described in Table 8;
- (f) on chromosomes 5 and 7 as described in Table 8;
- (g) on chromosomes 3, 5 and 7 as described in Table 8;
- (h) on chromosomes 5 and 10 as described in Table 8;
- 25 (i) on chromosomes 3, 5 and 10 as described in Table 8;
- (j) any combination of (a) to (i); or
- (k) or a marker/allele/haplotype/genomic region that maps at 10 cM or less from any of (a) to (j).

In some embodiments, non-naturally occurring maize plants and plant parts comprising one or more markers, alleles and/or genomic regions associated with increased male fertility (e.g., maize plants and plant identified, selected and/or produced according to methods of the invention) are provided.

In some embodiments, progeny and plant parts derived from maize plants and plant parts comprising one or more markers, alleles and/or genomic regions associated with

increased male fertility (*e.g.*, maize plants and plant identified, selected and/or produced according to methods of the invention) are provided.

In some embodiments, isolated and/or purified markers associated with increased male fertility are provided. Such markers may comprise, consist essentially of or consist of one or more of the nucleotide sequences set forth in SEQ ID NOs: 1–350, the reverse complement thereof, or an informative or functional fragment thereof.

In some embodiments, isolated and/or purified quantitative trait loci (QTLs) associated with increased male fertility are provided. Such QTLs may comprise, consist essentially of or consist of one or more of the chromosomal segments described in Table 1.

In some embodiments, amplification products comprising one or more markers, alleles and/or genomic regions associated with increased male fertility are provided. Such amplification products may comprise, consist essentially of or consist of one or more of the nucleotide sequences set forth in SEQ ID NOs: 1 to 350, the reverse complement thereof, or an informative or functional fragment thereof.

In some embodiments, probes (*e.g.*, as described in Table 9) for detecting one or more markers, alleles and/or genomic regions associated with increased male fertility are provided. Such probes may comprise, consist essentially of, or consist of one or more of the nucleotide sequences set forth in SEQ ID NOs: 526 to 613, the reverse complement thereof, or an informative or functional fragment thereof.

The foregoing and other objects and aspects of the present invention are explained in detail in the drawings and specification set forth below.

BRIEF DESCRIPTION OF THE TABLES

Table 1 describes segments of maize chromosomes 1, 3, 4, 5, 6, 7, 8, 9 and 10.

Table 2 describes alleles of interest located on maize chromosome 5.

Table 3 describes proteins of interest encoded by maize chromosome 5, as well as the segments of chromosome 5 that encode those proteins.

Table 4 describes Vip3 proteins and the nucleic acid sequences encoding those proteins.

Table 5 shows that Vip3-induced reductions in male fertility vary across genetic backgrounds.

Table 6 shows the LOD (logarithm of the odds) scores of QTLs (quantitative trait locus) identified using F2 plants from bi-parental crosses of NP2222 (described in U.S. Patent No. 6,710,233) and NP2276 (described in U.S. Patent No. 6,706,955) and bi-parental

crosses of ID3461 (described in International Patent Application No. WO2009142752) and NP2276.

Table 7 shows the Fertility Index used to score F2 plants from bi-parental crosses of NP2222 and NP2276 and bi-parental crosses of ID3461 and NP2276.

5 **Table 8** describes QTLs associated with increased anther quantity and/or improved anther quality in maize plants expressing a Vip3 protein.

Table 9 describes exemplary nucleic acid probes and primers useful to identify the favorable alleles in the QTLs described in Table 8.

10 **Table 10** describes SNPs present in inbred maize line NP2222 versus line NP2276 across the male fertility-associated QTL intervals in Table 8. Where the alleles differ between the two lines, the NP2222 allele corresponds to the desired (favorable) allele.

Table 11 provides public lines predicted to contain favorable alleles.

BRIEF DESCRIPTION OF THE DRAWINGS

15 **Fig. 1** is a chart comparing anther quantity of Vip3-expressing NP2276 inbred lines grown under varying thermal and moisture conditions.

Fig. 2 shows that thermal stress exacerbates Vip3-induced reductions in male fertility.

DETAILED DESCRIPTION

20 The present invention provides maize plants having increased fertility, as well as compositions and methods for identifying, selecting and producing maize plants and plant parts having one or more characteristics associated with increased fertility.

Although the following terms are believed to be well understood by one of ordinary skill in the art, the following definitions are set forth to facilitate understanding of the
25 presently disclosed subject matter.

All technical and scientific terms used herein, unless otherwise defined below, are intended to have the same meaning as commonly understood by one of ordinary skill in the art. References to techniques employed herein are intended to refer to the techniques as commonly understood in the art, including variations on those techniques or substitutions of
30 equivalent techniques that would be apparent to one of skill in the art.

Unless otherwise specified, genetic loci are described herein with respect to their positions in the Maize B73 Ref Gen_v2 reference genome (available at www.maizgedb.org).

Unless otherwise specified, nucleotides are described herein using the following standard abbreviations: adenine (A), cytosine (C), thymine (T), guanine (G), uracil (U), adenine or guanine (R), cytosine or thymine/uracil (Y), adenine or cytosine (M), guanine or thymine/uracil (K), guanine or cytosine (S), adenine or thymine/uracil (W), guanine or cytosine or thymine/uracil (B), adenine or guanine or thymine/uracil (D), adenine or cytosine or thymine/uracil (H), adenine or guanine or cytosine (V) and adenine or guanine or cytosine or thymine/uracil (N).

Unless otherwise specified, amino acids are described herein using the following standard abbreviations: alanine (Ala; A), arginine (Arg; R), asparagine (Asn; N), aspartic acid (Asp; D), cysteine (Cys; C), glutamine (Gln; Q), glutamic acid (Glu; E), glycine (Gly; G), histidine (His; H), isoleucine (Ile; I), leucine (Leu; L), lysine (Lys; K), methionine (Met; M), phenylalanine (Phe; F), proline (Pro; P), serine (Ser; S), threonine (Thr; T), tryptophan (Trp; W), tyrosine (Tyr; Y), and valine (Val; V).

As used herein, the terms "a" or "an" or "the" may refer to one or more than one. For example, "a" marker can mean one marker or a plurality of markers.

As used herein, the term "and/or" refers to and encompasses any and all possible combinations of one or more of the associated listed items, as well as the lack of combinations when interpreted in the alternative ("or").

As used herein, the term "about," when used in reference to a measurable value such as an amount of mass, dose, time, temperature, and the like, is meant to encompass variations of 20%, 10%, 5%, 1%, 0.5%, or even 0.1% of the specified amount.

As used herein, the term "allele" refers to one of two or more different nucleotides or nucleotide sequences (or the absence thereof) that occur at a specific locus or set of contiguous loci. In some embodiments, the term "allele" may be used interchangeably with the term "marker."

As used herein, the terms "allele of interest," "desired allele" and "favorable allele" are used interchangeably to refer to an allele that is linked to a desired trait. An "allele of interest" may be associated with either an increase or decrease of or in a given trait, depending on the nature of the desired phenotype, and may be associated with a change in morphology, color, etc. In some embodiments of the present invention, the "allele of interest" is associated with increased male fertility and may therefore be used as a marker to identify, select and/or produce fertile maize plants; to predict whether and/or to what extent a maize plant will be fertile; to reduce the costs associated with breeding and/or seed

production programs; and/or to increase the efficiency of breeding and/or seed production programs.

As used herein, the terms "backcross" and "backcrossing" refer to the process whereby a progeny plant is crossed back to one of its parents for one or more generations (e.g., 2 or more, 3 or more, 4 or more, 5 or more, 6 or more, or 7 or more times, etc.). In a backcrossing scheme, the "donor" parent refers to the parental plant with the desired gene or locus to be introgressed. The "recipient" parent (used one or more times) or "recurrent" parent (used two or more times) refers to the parental plant into which the gene or locus is being introgressed. For example, see Ragot et al. *Marker-assisted Backcrossing: A Practical Example*, in TECHNIQUES ET UTILISATIONS DES MARQUEURS MOLECULAIRES LES COLLOQUES, Vol. 72, pp. 45-56 (1995); and Openshaw et al., *Marker-assisted Selection in Backcross Breeding*, in PROCEEDINGS OF THE SYMPOSIUM "ANALYSIS OF MOLECULAR MARKER DATA," pp. 41-43 (1994). The initial cross gives rise to the F1 generation. The term "BC1" refers to the second use of the recurrent parent, "BC2" refers to the third use of the recurrent parent, and so on. In embodiments, at least one or more generations of progeny are identified and/or selected for the presence of the desired gene or locus (e.g., in a nucleic acid sample from the progeny plant or plant part). In embodiments, two or more generations (or even all generations) of progeny are identified and/or selected for the presence of the desired gene or locus.

As used herein, the term "closely linked loci" refers to genetic loci that display an inter-locus recombination frequency of about 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1%, 0.75%, 0.5%, 0.25% or less. Since one cM equals the distance between two loci that show a 1% recombination frequency, closely linked loci on the same chromosome will reside at about 10, 9, 8, 7, 6, 5, 4, 3, 2, 1, 0.75, 0.5 or 0.25 cM or less from another. Such loci may be said to be "proximal to" one another.

As used herein, the terms "centimorgan" and "cM" refer to a unit of measure of recombination frequency. One cM is equal to a 1% chance that a marker at one genetic locus will be separated from a marker at a second locus due to crossing over in a single generation.

As used herein, the term "coding sequence" refers to a nucleic acid sequence that is transcribed into RNA such as mRNA, rRNA, tRNA, snRNA, shRNA, sense RNA or antisense RNA. The RNA may be translated to produce a polypeptide.

As used herein, the term "completely fertile" refers to a plant that is at least as fertile as a control plant (e.g., one or both of its parents, a near isogenic plant that lacks one or more markers/alleles associated with increased fertility, a near isogenic plant that lacks a *vip3*

coding sequence, etc.). In some embodiments, "completely fertile" plants release at least as many pollen grains per tassel per day in the three-day period immediately following anther extrusion as the control plant. In some embodiments, "completely fertile" plants release more pollen grains per tassel per day in the three-day period immediately following anther
5 extrusion than the control plant.

As used herein, the terms "cross" or "crossed" refer to the fusion of gametes via pollination to produce progeny (e.g., cells, seeds or plants). The term encompasses both sexual crosses (the pollination of one plant by another) and selfing (self-pollination, e.g., when the pollen and ovule are from the same plant). The term "crossing" refers to the act of
10 fusing gametes via pollination to produce progeny.

As used herein, the terms "cultivar" and "variety" refer to a group of similar plants that by structural or genetic features and/or performance can be distinguished from other varieties within the same species.

As used herein, the term "cultivated" refers to a plant that is no longer in the natural
15 state, but has been developed and domesticated by human care and for agricultural use and/or human consumption. "Cultivated" plants, as used herein, excludes native plants that comprise the subject trait of this invention as a natural trait and/or as part of its natural genetics.

As used herein, the terms "decrease," "decreases," "decreasing" and similar terms
20 refer to a reduction of at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more. In some embodiments, the reduction results in no or essentially no activity (*i.e.*, an insignificant or undetectable amount of activity).

As used herein, the terms "elite" and "elite line" refer to any line that has resulted
25 from breeding and selection for desirable agronomic performance. An elite line may be substantially homozygous. Numerous elite lines are available and known to those of skill in the art.

As used herein, the term "elite germplasm" refers to any germplasm that is derived from or is capable of giving rise to an elite plant.

As used herein, the term "event" refers to a particular transformant. In a typical
30 transgenic breeding program, a transformation construct responsible for a trait is introduced into the genome via a transformation method. Numerous independent transformants (events) are usually generated for each construct. These events are evaluated to select those with superior performance.

As used herein, with respect to nucleic acids, the term "exogenous" refers to a nucleic acid that is not in the natural genetic background of the cell/organism in which it resides. In some embodiments, the exogenous nucleic acid comprises one or more nucleic acid sequences that are not found in the natural genetic background of the cell/organism. In some
5 embodiments, the exogenous nucleic acid comprises one or more additional copies of a nucleic acid that is endogenous to the cell/organism.

As used herein, the term "expression cassette" refers to a nucleotide capable of directing expression of a particular nucleic acid sequence in a host cell (*e.g.*, a maize cell). In some embodiments, the expression cassette comprises, consists essentially of or consists of
10 one or more promoter sequences (*e.g.*, one or more constitutive/inducible promoter sequences, one or more tissue- and/or organ-specific promoter sequences and/or one or more developmental stage-specific promoter sequences) operably linked to a nucleic acid of interest, which is operably linked to a termination sequence. Expression cassettes often
15 comprise sequences required for proper translation of the nucleic acid sequence of interest in the host cell. The expression cassette may be chimeric in that at least one of its components is heterologous with respect to at least one of its other components. The expression cassette may be one that is naturally occurring but that has been obtained in a recombinant form useful for heterologous expression. Typically, however, the expression cassette is
20 heterologous with respect to the host (*i.e.*, the particular nucleic acid sequence of the expression cassette does not occur naturally in the host cell and must have been introduced into the host cell or an ancestor of the host cell by a transformation event).

As used herein with respect to nucleic acids, the term "fragment" refers to a nucleic acid that is reduced in length relative to a reference nucleic acid and that comprises, consists essentially of and/or consists of a nucleotide sequence of contiguous nucleotides identical or
25 almost identical (*e.g.*, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical) to a corresponding portion of the reference nucleic acid. Such a nucleic acid fragment may be, where appropriate, included in a larger polynucleotide of which it is a constituent. In some
30 embodiments, the nucleic acid fragment comprises, consists essentially of or consists of at least about 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75,
80, 85, 90, 95, 100, 125, 150, 175, 200, 225, 250, 300, 350, 400, 450, 500, or more
consecutive nucleotides. In some embodiments, the nucleic acid fragment comprises, consists essentially of or consists of less than about 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25,
30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200, 225, 250, 300,
350, 400, 450 or 500 consecutive nucleotides.

As used herein with respect to polypeptides, the term "fragment" refers to a polypeptide that is reduced in length relative to a reference polypeptide and that comprises, consists essentially of and/or consists of an amino acid sequence of contiguous amino acids identical or almost identical (*e.g.*, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical) to a corresponding portion of the reference polypeptide. Such a polypeptide fragment may be, where appropriate, included in a larger polypeptide of which it is a constituent. In some embodiments, the polypeptide fragment comprises, consists essentially of or consists of at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200, 225, 250, 300, 350, 400, 450, 500, or more consecutive amino acids. In some embodiments, the polypeptide fragment comprises, consists essentially of or consists of less than about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200, 225, 250, 300, 350, 400, 450 or 500 consecutive amino acids.

As used herein with respect to nucleic acids, the term "functional fragment" refers to nucleic acid that encodes a functional fragment of a polypeptide.

As used herein with respect to polypeptides, the term "functional fragment" refers to polypeptide fragment that retains at least about 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more of at least one biological activity of the full-length polypeptide (*e.g.*, the ability to convert all-*trans*- β -carotene into 9-*cis*- β -carotene). In some embodiments, the functional fragment actually has a higher level of at least one biological activity of the full-length polypeptide.

As used herein, the terms "fertile" and "functionally fertile" are used interchangeably and refer to a plant that is fertile enough for use in a breeding and/or seed production program. In some embodiments, "functionally fertile" plants are plants that release at least about 100,000; 150,000; 200,000; 250,000; 300,000; 350,000; 400,000 or 450,000 pollen grains per tassel per day in the three-day period immediately following anther extrusion.

As used herein, the term "gene product" refers to a material resulting from expression of a nucleic acid. In some embodiments, the gene product is an RNA molecule (*e.g.*, an mRNA molecule or an antisense RNA molecule). In some embodiments, the gene product is a polypeptide.

As used herein, the term "genetic map" refers to a description of genetic linkage relationships among loci on one or more chromosomes within a given species, generally depicted in a diagrammatic or tabular form. For each genetic map, distances between loci are measured by the recombination frequencies between them. Recombinations between loci can

be detected using a variety of markers. A genetic map is a product of the mapping population, types of markers used, and the polymorphic potential of each marker between different populations. The order and genetic distances between loci can differ from one genetic map to another.

- 5 As used herein, the term "genetic marker" refers to one or more nucleotides associated with a phenotype, trait or trait form of interest. In some embodiments, a marker may be associated with an allele or alleles of interest and may be indicative of the presence or absence of the allele or alleles of interest in a cell or organism. In some embodiments, the marker may comprise, consist essentially of, or consist of an allele or alleles of interest. A
- 10 marker may be, but is not limited to, an allele, a haplotype, a restriction fragment length polymorphism (RFLP), a simple sequence repeat (SSR), random amplified polymorphic DNA (RAPD), cleaved amplified polymorphic sequences (CAPS) (Rafalski and Tingey, *Trends in Genetics* 9:275 (1993)), an amplified fragment length polymorphism (AFLP) (Vos et al., *Nucleic Acids Res.* 23:4407 (1995)), a single nucleotide polymorphism (SNP)
- 15 (Brookes, *Gene* 234:177 (1993)), a sequence-characterized amplified region (SCAR) (Paran and Michelmore, *Theor. Appl. Genet.* 85:985 (1993)), a sequence-tagged site (STS) (Onozaki et al., *Euphytica* 138:255 (2004)), a single-stranded conformation polymorphism (SSCP) (Orita et al., *Proc. Natl. Acad. Sci. USA* 86:2766 (1989)), an inter-simple sequence repeat (ISSR) (Blair et al., *Theor. Appl. Genet.* 98:780 (1999)), an inter-retrotransposon amplified
- 20 polymorphism (IRAP), a retrotransposon-microsatellite amplified polymorphism (REMAP) (Kalendar et al., *Theor. Appl. Genet.* 98:704 (1999)) or an RNA cleavage product (such as a Lynx tag). A marker may be present in genomic or expressed nucleic acids (e.g., ESTs). Some of the markers described herein are also referred to as hybridization markers when located on an indel region. This is because the insertion region is, by definition, a
- 25 polymorphism vis-à-vis a plant without the insertion. Thus, the marker need only indicate whether the indel region is present or absent. Any suitable marker detection technology may be used to identify such a hybridization marker, e.g., SNP technology is used in the examples provided herein. A large number of maize genetic markers are known in the art, and are published or available from various sources, such as the Maize GDB internet resource and the
- 30 Arizona Genomics Institute internet resource run by the University of Arizona.

As will be understood by those skilled in the art, "genetic markers" may comprise "dominant" and/or "codominant" markers. "Codominant markers" reveal the presence of two or more alleles (two per diploid individual). "Dominant markers" reveal the presence of only a single allele. The presence of the dominant marker phenotype (e.g., a band of DNA) is an

indication that one allele is present in either the homozygous or heterozygous condition. In the case of populations where individuals are predominantly homozygous and loci are predominantly dimorphic, dominant and codominant markers can be equally valuable. As populations become more heterozygous and multiallelic, codominant markers often become
5 more informative of the genotype than dominant markers.

As used herein, the term "genotype" refers to the genetic constitution of an individual (or group of individuals) at one or more genetic loci, as contrasted with the observable and/or detectable and/or manifested trait (the phenotype). Genotype is defined by the allele(s) of one or more known loci that the individual has inherited from its parents. The term genotype
10 can be used to refer to an individual's genetic constitution at a single locus, at multiple loci, or more generally, the term genotype can be used to refer to an individual's genetic make-up for all the genes in its genome. Genotypes can be indirectly characterized, e.g., using markers and/or directly characterized by nucleic acid sequencing.

As used herein, the term "germplasm" refers to genetic material of or from an
15 individual plant, a group of plants (e.g., a plant line, variety or family), or a clone derived from a plant line, variety, species, or culture. The genetic material can be part of a cell, tissue or organism, or can be isolated from a cell, tissue or organism.

As used herein, the term "haplotype" refers to a combination of alleles (two or more) at a plurality of genetic loci. Typically, the genetic loci that define a haplotype are physically
20 and genetically linked (i.e., the alleles that make up a haplotype are generally located on the same chromosome segment). Thus, in some embodiments, the term "haplotype" refers to a plurality of alleles within a single chromosomal segment or to a plurality of alleles within two or more chromosomal segments residing on the same chromosome.

As used herein, the terms "haplotype of interest" and "desired haplotype" are used
25 interchangeably to refer to a haplotype that is linked to a desired trait. A "haplotype of interest" may be associated with either an increase or decrease of or in a given trait, depending on the nature of the trait, and may be associated with a change in morphology, color, etc. In some embodiments of the present invention, the "haplotype of interest" is associated with increased male fertility and may therefore be used as a marker to identify,
30 select and/or produce fertile maize plants; to predict whether and/or to what extent a maize plant will be fertile; to reduce the costs associated with breeding and/or seed production programs; and/or to increase the efficiency of breeding and/or seed production programs.

As used herein, the term "hemizygous" refers to a genetic status in a diploid cell in which there is only one copy of a gene instead of the typical two copies (i.e., the gene has no

counterpart on a homologous chromosome). For example, in mammals, the genes on the X chromosome are hemizygous in males. As another illustration, a heterologous transgene can be present in a hemizygous state.

As used herein, the term "heterologous" refers to a nucleotide/polypeptide that
5 originates from a foreign species, or, if from the same species, is substantially modified from its native form in composition and/or genomic locus by deliberate human intervention.

As used herein, the term "heterotic group" refers to a set of genotypes that display similar heterotic response when crossed with genetically distinct groups of genotypes (*i.e.*, when crossed with genotypes from a different heterotic group). Hallauer et al., *Corn breeding, in CORN AND CORN IMPROVEMENT* p. 463-564 (1998). Inbred lines are classified
10 into heterotic groups, and are further subdivided into families within a heterotic group, based on several criteria such as pedigree, molecular marker-based associations, and performance in hybrid combinations. Smith et al., *Theor. Appl. Gen.* 80:833 (1990). The "Stiff Stalk" heterotic group represents a major heterotic group in the northern U.S. and Canadian corn
15 growing regions; it is sometimes referred to as the "Iowa Stiff Stalk Synthetic" or "BSSS" heterotic group. The "non-Stiff Stalk" heterotic group represents a major heterotic group in the northern U.S. and Canadian corn growing regions; it is sometimes referred to as the "Lancaster" or "Lancaster Sure Crop" heterotic group.

As used herein, the term "heterozygous" refers to a genetic status wherein different
20 alleles reside at corresponding loci on homologous chromosomes.

As used herein, the term "homozygous" refers to a genetic status wherein identical alleles reside at corresponding loci on homologous chromosomes.

As used herein, the term "hybrid" refers to a plant or plant part produced when at least two genetically dissimilar parents are crossed. Without limitation, examples of mating
25 schemes include single crosses, modified single crosses, double modified single crosses, three-way crosses, modified three-way crosses, and double crosses, wherein at least one parent in a modified cross is the progeny of a cross between sister lines.

As used herein, the term "inbred" refers to a substantially homozygous plant or variety. The term may refer to a plant or variety that is substantially homozygous throughout
30 the entire genome or that is substantially homozygous with respect to a portion of the genome that is of particular interest. Without limitation, examples of breeding methods to derive inbreds include pedigree breeding, recurrent selection, single-seed descent, backcrossing, and doubled haploids.

As used herein, the terms "increase," "increases," "increasing" and similar terms refer to an augmentation of at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, 125%, 150%, 175%, 200%, 300% or more.

5 As used herein, the term "increased fertility" refers to an improvement in one or more fertility traits as compared to one or more controls (*e.g.*, a native plant/germplasm of the same species, one or both parents, a near isogenic plant that lacks one or more markers/alleles associated with increased fertility, a near isogenic plant that lacks a *vip3* coding sequence, etc.). Exemplary fertility traits include, but are not limited to, pollen count, pollen
10 morphology, pollen production per anther, anther count, anther morphology, anthers per tassel, tassel count, tassel morphology, tassels per plant, silk count, silk morphology, silk production per plant, kernel count, kernel morphology, kernel production per ear, prevalence of kernel abortion, kernel production per plant and kernel viability. Thus, a plant that exhibits increased pollen production, increased pollen production per anther, improved pollen
15 morphology, increased anther production, increased anther production per tassel, improved anther morphology, increased tassel production, improved tassel morphology, increased silk production, improved silk morphology, increased silk production per plant, increased kernel count, improved kernel morphology, increased kernel production per ear, decreased prevalence of kernel abortion, increased kernel production per plant, increased kernel
20 viability, increased fertility under stress conditions (*e.g.*, drought conditions), increased fertility under elevated daytime temperatures and/or increased fertility under elevated nighttime temperatures as compared to a control plant (*e.g.*, a native plant/germplasm of the same species, one or both parents, a near isogenic plant that lacks one or more markers/alleles associated with increased fertility, a near isogenic plant that lacks a *vip3* coding sequence, etc.) displays increased fertility. When used in reference to a plant part (*e.g.*, a germplasm),
25 the term "increased fertility" refers to an improvement in one or more fertility traits in a plant that arises from that plant part.

As used herein, the term "increased female fertility" refers to an improvement in one or more female fertility traits as compared to one or more controls (*e.g.*, a native
30 plant/germplasm of the same species, one or both parents, a near isogenic plant that lacks one or more markers/alleles associated with increased fertility, a near isogenic plant that lacks a *vip3* coding sequence, etc.). Exemplary female fertility traits include, but are not limited to, silk count, silk morphology, silk production per plant, kernel count, kernel morphology, kernel production per ear, prevalence of kernel abortion, kernel production per plant and

kernel viability. Thus, a plant that exhibits increased silk production, improved silk morphology, increased silk production per plant, increased kernel count, improved kernel morphology, increased kernel production per ear, decreased prevalence of kernel abortion, increased kernel production per plant, increased kernel viability, increased female fertility
 5 under stress conditions (*e.g.*, drought conditions), increased female fertility under elevated daytime temperatures and/or increased female fertility under elevated nighttime temperatures as compared to a control plant (*e.g.*, a native plant/germplasm of the same species, one or both parents, a near isogenic plant that lacks one or more markers/alleles associated with increased fertility, a near isogenic plant that lacks a *vip3* coding sequence, etc.) displays
 10 increased female fertility. When used in reference to a plant part (*e.g.*, a germplasm), the term "increased female fertility" refers to an improvement in one or more female fertility traits in a plant that arises from that plant part.

As used herein, the term "increased male fertility" refers to an improvement in one or more male fertility traits as compared to one or more controls (*e.g.*, a native plant/germplasm
 15 of the same species; one or both parents, a near isogenic plant that lacks one or more markers/alleles associated with increased fertility, a near isogenic plant that lacks a *vip3* coding sequence, etc.). Exemplary male fertility traits include, but are not limited to, pollen count, pollen morphology, pollen production per anther, anther count, anther morphology, anthers per tassel, tassel count, tassel morphology and tassels per plant. Thus, a plant that
 20 exhibits increased pollen production, increased pollen production per anther, improved pollen morphology, increased anther production, increased anther production per tassel, improved anther morphology, increased tassel production, improved tassel morphology, increased male fertility under stress conditions (*e.g.*, drought conditions), increased male fertility under elevated daytime temperatures and/or increased male fertility under elevated nighttime
 25 temperatures as compared to a control plant (*e.g.*, a native plant/germplasm of the same species, one or both parents, a near isogenic plant that lacks one or more markers/alleles associated with increased fertility, a near isogenic plant that lacks a *vip3* coding sequence, etc.). displays increased male fertility. When used in reference to a plant part (*e.g.*, a germplasm), the term "increased male fertility" refers to an improvement in one or more male
 30 fertility traits in a plant that arises from that plant part.

As used herein, the term "indel" refers to an insertion or deletion in a pair of nucleotide sequences, wherein a first sequence may be referred to as having an insertion relative to a second sequence or the second sequence may be referred to as having a deletion relative to the first sequence.

As used herein, the term "infertile" refers to a plant that is insufficiently fertile for use in a breeding program. In some embodiments, "infertile" plants are plants that release fewer than 25,000; 50,000; 75,000 or 100,000 pollen grains per tassel per day in the three-day period immediately following anther extrusion. "Infertile" plants may produce and/or release
5 viable pollen grains. Indeed, in some embodiments, "infertile" plants produce and release viable pollen grains, but do so at a rate that is insufficient for effective use in a breeding and/or seed production program.

As used herein, the term "informative fragment" refers to a nucleotide sequence comprising a fragment of a larger nucleotide sequence, wherein the fragment allows for the
10 identification of one or more alleles within the larger nucleotide sequence. For example, an informative fragment of the nucleotide sequence of SEQ ID NO: 1 comprises a fragment of the nucleotide sequence of SEQ ID NO: 1 and allows for the identification of one or more alleles of interest located within the portion of the nucleotide sequence corresponding to that fragment of SEQ ID NO: 1.

As used herein, the terms "introgression," "introgressing" and "introgressed" refer to both the natural and artificial transmission of a desired allele or combination of desired alleles of a genetic locus or genetic loci from one genetic background to another. For example, a desired allele at a specified locus can be transmitted to at least one progeny via a sexual cross between two parents of the same species, where at least one of the parents has the desired
20 allele in its genome. Alternatively, for example, transmission of an allele can occur by recombination between two donor genomes, e.g., in a fused protoplast, where at least one of the donor protoplasts has the desired allele in its genome. The desired allele may be a selected allele of a marker, a QTL, a transgene, or the like. Offspring comprising the desired allele can be repeatedly backcrossed to a line having a desired genetic background and
25 selected for the desired allele, with the result being that the desired allele becomes fixed in the desired genetic background. For example, a marker associated with increased fertility may be introgressed from a donor into a recurrent parent that is not functionally fertile. The resulting offspring could then be repeatedly backcrossed and selected until the progeny possess the enhanced fertility allele in the recurrent parent background.

As used herein with respect to nucleotides and polypeptides, the term "isolated" refers
30 to a nucleotide or polypeptide that is substantially free of cellular material, viral material, culture medium (when produced by recombinant DNA techniques), or chemical precursors or other chemicals (when chemically synthesized). An "isolated fragment" is a fragment of a nucleotide or polypeptide that is not naturally occurring as a fragment and would not be

found in the natural state. "Isolated" does not mean that the preparation is technically pure (homogeneous), but rather that it is sufficiently pure to provide the nucleotide or polypeptide in a form in which it can be used for the intended purpose. In certain embodiments, the composition comprising the nucleotide or polypeptide is at least about 50%, 55%, 60%, 65%,
 5 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% or more pure.

As used herein with respect to cells, the term "isolated" refers to a cell that is separated from other components with which it is normally associated in its natural state. For example, an isolated plant cell may be a plant cell in culture medium and/or a plant cell in a suitable carrier. "Isolated" does not mean that the preparation is technically pure
 10 (homogeneous), but rather that it is sufficiently pure to provide the cell in a form in which it can be used for the intended purpose. In certain embodiments, the composition comprising the cell is at least about 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% or more pure.

As used herein, the term "linkage" refers to the degree to which a marker is associated
 15 with a given allele and/or phenotypic trait (*e.g.*, increased male fertility). The more closely a marker is linked to an allele/phenotype, the better an indicator that marker becomes. The degree of linkage between a marker and a phenotypic trait may be measured and expressed as the statistical probability of cosegregation of the marker and phenotypic trait. The linkage relationship between a marker and an allele/phenotype may be given as a "probability" or
 20 "adjusted probability." Linkage can be expressed as a desired limit or range. For example, in some embodiments, two genetic markers are deemed to be linked if they are separated by less than about 50, 40, 30, 25, 20, 15, 10, 5, 4, 3, 2, or 1 cM. In representative embodiments, two genetic markers are linked if they are separated by 10cM or less.

As used herein, the term "linkage disequilibrium" refers to a non-random segregation
 25 of genetic loci or traits (or both). Linkage disequilibrium implies that the relevant loci are within sufficient physical proximity along a length of a chromosome so that they segregate together with greater than random (*i.e.*, non-random) frequency. Markers/alleles that show linkage disequilibrium are considered linked. Linked markers/alleles co-segregate more than 50% of the time. In other words, markers/alleles that co-segregate have a recombination
 30 frequency of less than 50%. Linkage disequilibrium is most commonly assessed using the measure r^2 , which is calculated using the formula described by Hill and Robertson, *Theor. Appl. Genet.* 38:226 (1968). When $r^2=1$, complete linkage disequilibrium exists between the markers/alleles, meaning that the markers have not been separated by recombination and have the same allele frequency. Values for r^2 above 1/3 generally indicate sufficiently strong

linkage disequilibrium to be useful for mapping. Ardlie et al., *Nature Reviews Genetics* 3:299 (2002). Hence, in some embodiments, markers/alleles are said to be in linkage disequilibrium when r^2 values between pairwise marker loci are greater than or equal to about 0.33, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, or 1.0.

5 As used herein, the term "linkage equilibrium" describes a situation where markers/alleles independently segregate (*i.e.*, sort among progeny randomly). Markers that show linkage equilibrium are considered unlinked (whether or not they lie on the same chromosome).

As used herein, the term "linkage group" refers to a group of genes associated together by linkage relationships.

As used herein, the term "locus" refers to a position on a chromosome. Loci may encompass one or more nucleotides.

As used here, the terms "logarithm of odds" and "LOD score" refer to the likelihood that two genetic loci are linked. LOD scores are most commonly assessed using the measure Z , which is equal to the logarithm of the ratio of the likelihood that the genetic loci are linked and 0.5 times the likelihood that the two genetic loci are independently sorted. Positive LOD scores are indicative of linkage, whereas negative LOD scores are indicative of independent assortment. LOD scores of 2.5 and higher generally sufficiently strong linkage to be useful for mapping. Hence, in some embodiments, markers/alleles are said to be linked when the

15 Z , which is equal to the logarithm of the ratio of the likelihood that the genetic loci are linked and 0.5 times the likelihood that the two genetic loci are independently sorted. Positive LOD scores are indicative of linkage, whereas negative LOD scores are indicative of independent assortment. LOD scores of 2.5 and higher generally sufficiently strong linkage to be useful for mapping. Hence, in some embodiments, markers/alleles are said to be linked when the

20 LOD score is greater than or equal to about 2, 2.5, 3, 3.5, 4, 4.5, 5, 5.5, 6, 6.5, 7, 7.5, 8, 8.5, 9, 9.5, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more.

As used herein, the term "maize" refers to *Zea mays* L. subsp. *mays*. In some embodiments, the maize plant or plant part is from the group *Zea mays* L. subsp. *mays* Identata, sometimes referred to as dent corn. In some embodiments, the maize plant or plant part is from the group *Zea mays* L. subsp. *mays* Indurata, sometimes referred to as flint corn. In some embodiments, the maize plant or plant part is from the group *Zea mays* L. subsp. *mays* Saccharata, sometimes referred to as sweet corn. In some embodiments, the maize plant or plant part is from the group *Zea mays* L. subsp. *mays* Amylacea, sometimes referred to as flour corn. In some embodiments, the maize plant or plant part is from the group *Zea mays* L. subsp. *mays* Everta, sometimes referred to as pop corn. Maize plants that can be identified selected and/or produced with methods and compositions of the present invention include hybrids, inbreds, partial inbreds, members of defined populations and members of undefined populations.

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As used herein, the terms "male fertile" and "male fertility" refer to the ability of a plant to produced and release viable, functional pollen grains.

As used herein, the terms "male sterile" and "male sterility" refer to the inability of a plant to produce and/or release viable, functional pollen grains. Male sterility generally
5 occurs as a result of failure of formation or development of functional stamens, microspores or gametes. Typically there are three types of male sterility: 1) "pollen sterility" in which male sterile individuals differ from normal only in the absence or extreme scarcity of functional pollen grains; 2) "structural or staminal male sterility" in which male flowers or stamen are malformed and non-functional or completely absent; and 3) "functional male
10 sterility" in which perfectly good and viable pollen is trapped in indehiscent anther and thus prevented from functioning.

As used herein, the term "marker" refers to a detectable characteristic that can be used to discriminate between organisms. Examples of such characteristics may include genetic composition (e.g., genetic marker), gene expression levels, protein composition, protein
15 levels, oil composition, oil levels, carbohydrate composition, carbohydrate levels, fatty acid composition, fatty acid levels, amino acid composition, amino acid levels, biopolymers, pharmaceutical, starch composition, starch levels, fermentable starch, fermentation yield, fermentation efficiency, energy yield, secondary compounds, metabolites, morphological characteristics, and agronomic characteristics.

A marker is "associated with" a trait when it is linked to it and when the presence of the marker is an indicator of whether and/or to what extent the desired trait or trait form will occur in a plant/plant part comprising the marker. Similarly, a marker is "associated with" an allele when it is linked to it and when the presence of the marker is an indicator of whether the allele is present in a plant/plant part comprising the marker. For example, "a marker
25 associated with increased male fertility" refers to a marker whose presence or absence can be used to predict whether and/or to what extent a plant/plant part will display increased male fertility.

Markers corresponding to genetic polymorphisms between members of a population can be detected by methods well-established in the art. These include, e.g., nucleic acid
30 sequencing, hybridization methods, amplification methods (e.g., PCR-based sequence specific amplification methods), detection of restriction fragment length polymorphisms (RFLP), detection of isozyme markers, detection of polynucleotide polymorphisms by allele specific hybridization (ASH), detection of amplified variable sequences of the plant genome, detection of self-sustained sequence replication, detection of simple sequence repeats (SSRs),

detection of single nucleotide polymorphisms (SNPs), and/or detection of amplified fragment length polymorphisms (AFLPs). Well established methods are also known for the detection of expressed sequence tags (ESTs) and SSR markers derived from EST sequences and randomly amplified polymorphic DNA (RAPD).

5 As used herein, the terms "marker allele" and "allele of a marker locus" refer to one of a plurality of polymorphic nucleotides or nucleotide sequences found at a marker locus in a population that is polymorphic for the marker locus.

As used herein, the term "marker locus" refers to a specific chromosome location in the genome of an organism where a specific marker can be found. A marker locus can be
10 used to track the presence of a second linked locus, e.g., a linked locus that encodes or contributes to expression of a phenotypic trait. For example, a marker locus can be used to monitor segregation of alleles at a locus, such as a QTL or single gene, that are genetically or physically linked to the marker locus.

As used herein, the terms "marker probe" and "probe" refer to a molecule that can be
15 used to detect the presence of one or more particular alleles, haplotypes and/or molecules of interest. In some embodiments, a "marker probe" is a nucleic acid sequence that is complementary to all of or a portion of an allele of interest. Marker probes (as described in Table 9) comprising 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25,
26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50
20 or more contiguous nucleotides may be used for nucleic acid hybridization. In some embodiments, the marker probe comprises at least about 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200 or more contiguous nucleotides. In some embodiments, the marker probe may be used to distinguish (*i.e.*, genotype) the particular allele that is present at a marker locus.

25 As used herein, the terms "marker-assisted selection" and "MAS" refer to a process by which phenotypes are indirectly selected based on marker genotypes. MAS can optionally be supplemented by direct phenotyping of the trait of interest. For example, when MAS is used for breeding, phenotyping can be done at one or more points in the process to confirm that the individuals or their progeny express the phenotype of interest.

30 As used herein, the term "marker-assisted counter-selection" refers to a process by which marker genotypes are used to identify plants that will not be selected, allowing them to be removed from a breeding program or planting.

As used herein, the terms "MIR162 plant" and "MIR162 plant part" refer to maize plants/plant parts that comprise the MIR162 event as described in U.S. Patent No. 8,232,456.

The MIR162 plant or MIR162 plant part can be hemizygous or homozygous for the MIR162 event.

As used herein, the term "molecular marker" may be used to refer to a genetic marker, as defined above, or an encoded product thereof (e.g., a protein) used as a point of reference when identifying a linked locus. A molecular marker can be derived from genomic nucleotide sequences or from expressed nucleotide sequences (e.g., from a spliced RNA, a cDNA, etc.). The term also refers to nucleotide sequences complementary to or flanking the marker sequences, such as nucleotide sequences used as probes (as described in Table 9) and/or primers capable of amplifying the marker sequence. Nucleotide sequences are "complementary" when they specifically hybridize in solution, e.g., according to Watson-Crick base pairing rules.

As used herein, the terms "molecule of interest" and "desired molecule" are used interchangeably to refer to a haplotype that is linked to a desired trait. A "molecule of interest" may be associated with either an increase or decrease of or in a given trait, depending on the nature of the desired phenotype, and may be associated with a change in morphology, color, etc. In some embodiments of the present invention, the "molecule of interest" is associated with increased male fertility and may therefore be used as a marker to identify, select and/or produce fertile maize plants; to predict whether and/or to what extent a maize plant will be fertile; to reduce the costs associated with breeding and/or seed production programs; and/or to increase the efficiency of breeding and/or seed production programs.

As used herein with respect to nucleotides, the term "native" refers to a nucleic acid sequence that is naturally present in the genome of a cell or plant.

As used herein with respect to polypeptides, the term "native" refers to an amino acid sequence that is naturally present in the proteome of a cell or plant.

As used herein, the terms "near isogenic line" (NIL) and "near isogenic plant" refer to maize lines/plants that are genetically identical except for one or a few genetic loci. Such lines/plants can be created by crossing a donor line, containing a gene or trait of interest, with a recurrent parent to produce a heterozygous F1, and then repeatedly back-crossing the offspring to the recurrent parent (BC1, BC2, etc), retaining the donor gene or trait in each successive generation. Marker assisted selection (MAS) can be used to increase the efficiency of NIL development by screening individuals for the presence of the target locus (gene) in each generation and the absence of extraneous donor DNA throughout the rest of the genome to speed up the return to recurrent parent type.

As used herein, the term "nonnaturally occurring" refers to a plant or plant part that does not naturally exist in nature. A nonnaturally occurring plant or plant part may be produced by any method known in the art, including, but not limited to, transforming a plant or plant part, transfecting a plant or plant part, and crossing a naturally occurring plant or plant part with a nonnaturally occurring plant or plant part. In some embodiments, the nonnaturally occurring plant or plant part comprises one or more exogenous nucleotide sequences. In some embodiments, the nonnaturally occurring plant or plant part comprises one or more nonnaturally occurring copies of a naturally occurring nucleotide sequence (*i.e.*, additional copies of a gene that naturally occurs in plants/plant parts of that species that may be, for example in a nonnatural location in the genome).

As used herein, the terms "nucleic acid," "nucleic acid sequence," "nucleotide sequence" and "polynucleotide" refer to deoxyribonucleotide, ribonucleotide and deoxyribonucleotide-ribonucleotide polymers in either single- or double-stranded form and, unless otherwise limited, encompasses analogues having the essential nature of natural polynucleotides in that they hybridize to single-stranded nucleic acids in a manner similar to naturally occurring polynucleotides. Thus, deoxyribopolynucleotides and ribopolynucleotides that have been chemically, enzymatically or metabolically modified for stability or for other reasons and deoxyribopolynucleotides and ribopolynucleotides comprising unusual bases (*e.g.*, inosine and/or tritylated bases) are "nucleic acids" "nucleic acid sequences" "nucleotide sequences" and "polynucleotides" as those terms are used herein.

As used herein, the term "nucleotide" refers to a monomeric unit from which DNA or RNA polymers are constructed and that consists of a purine or pyrimidine base, a pentose, and a phosphoric acid group. Nucleotides (usually found in their 5'-monophosphate form) are referred to by their single letter designation as follows: "A" for adenylate or deoxyadenylate (for RNA or DNA, respectively), "C" for cytidylate or deoxycytidylate, "G" for guanylate or deoxyguanylate, "U" for uridylate, "T" for deoxythymidylate, "R" for purines (A or G), "Y" for pyrimidines (C or T), "K" for G or T, "H" for A or C or T, "I" for inosine, and "N" for any nucleotide.

As used herein, the term "nucleotide sequence identity" refers to the presence of identical nucleotides at corresponding positions of two polynucleotides. Polynucleotides have "identical" sequences if the sequence of nucleotides in the two polynucleotides is the same when aligned for maximum correspondence (*e.g.*, in a comparison window). Sequence comparison between two or more polynucleotides is generally performed by comparing portions of the two sequences over a comparison window to identify and compare local

regions of sequence similarity. The comparison window is generally from about 20 to 200 contiguous nucleotides. The "percentage of sequence identity" for polynucleotides, such as about 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 98, 99 or 100 percent sequence identity, can be determined by comparing two optimally aligned sequences over a comparison window,

5 wherein the portion of the polynucleotide sequence in the comparison window can include additions or deletions (i.e., gaps) as compared to the reference sequence for optimal alignment of the two sequences. The percentage is calculated by: (a) determining the number of positions at which the identical nucleic acid base occurs in both sequences; (b) dividing the number of matched positions by the total number of positions in the window of comparison;

10 and (c) multiplying the result by 100. Optimal alignment of sequences for comparison can also be conducted by computerized implementations of known algorithms, or by visual inspection. Readily available sequence comparison and multiple sequence alignment algorithms are, respectively, the Basic Local Alignment Search Tool (BLAST) and ClustalW programs, both available on the internet. Other suitable programs include, but are not limited

15 to, GAP, BestFit, Plot Similarity, and FASTA, which are part of the Accelrys GCG Package available from Accelrys, Inc. of San Diego, California, United States of America. In some embodiments, a percentage of sequence identity refers to sequence identity over the full length of one of the sequences being compared. In some embodiments, a calculation to determine a percentage of sequence identity does not include in the calculation any

20 nucleotide positions in which either of the compared nucleic acids includes an "N" (i.e., where any nucleotide could be present at that position).

As used herein with respect to nucleic acids, the term "operably linked" refers to a functional linkage between two or more nucleic acids. For example, a promoter sequence may be described as being "operably linked" to a heterologous nucleic acid sequence because

25 the promoter sequences initiates and/or mediates transcription of the heterologous nucleic acid sequence. In some embodiments, the operably linked nucleic acid sequences are contiguous and/or are in the same reading frame.

As used herein, the terms "phenotype," "phenotypic trait" or "trait" refer to one or more traits of an organism. The phenotype can be observable to the naked eye, or by any

30 other means of evaluation known in the art, e.g., microscopy, biochemical analysis, or an electromechanical assay. In some cases, a phenotype is directly controlled by a single gene or genetic locus, i.e., a "single gene trait." In other cases, a phenotype is the result of several genes.

As used herein, the term "plant" may refer to any suitable plant, including, but not limited to, spermatophytes (*e.g.*, angiosperms and gymnosperms) and embryophytes (*e.g.*, bryophytes, ferns and fern allies). In some embodiments, the plant is a monocotyledonous (monocot) plant such as a rice, maize, wheat, barley, sorghum, millet, oat, triticale, rye, 5 buckwheat, fonio, quinoa, sugar cane, bamboo, banana, ginger, onion, lily, daffodil, iris, amaryllis, orchid, canna, bluebell, tulip, garlic, secale, einkorn, spelt, emmer, durum, kamut, grass (*e.g.*, gramma grass), teff, milo, flax, *Tripsacum sp.*, or teosinte plant. In some 10 embodiments, the plant is a dicotyledonous (dicot) plant such as a blackberry, raspberry, strawberry, barberry, bearberry, blueberry, coffee berry, cranberry, crowberry, currant, elderberry, gooseberry, goji berry, honeyberry, lemon, lime, lingonberry, mangosteen, orange, pepper, persimmon, pomegranate, prune, cotton, clover, acai, plum, peach, nectarin, 15 cherry, guava, almond, pecan, walnut, amaranth, apple, sweet pea, pear, potato, soybean, sugar beet, sunflower, sweet potato, tamarind, tea, tobacco or tomato plant.

As used herein, the term "plant cell" refers to a cell existing in, taken from and/or 15 derived from a plant (*e.g.*, derived from a plant cell/tissue culture). Thus, the term "plant cell" may refer to an isolated plant cell, a plant cell in a culture, a plant cell in an isolated tissue/organ and/or a plant cell in a whole plant.

As used herein, the term "plant part" refers to at least a fragment of a whole plant or to a cell culture or tissue culture derived from a plant. Thus, the term "plant part" may refer to 20 plant cells, plant tissues and plant organs, as well as cell/tissue cultures derived from plant cells, plant tissues and plant cultures. Embodiments of the present invention may comprise and/or make use of any suitable plant part, including, but not limited to, anthers, branches, buds, calli, clumps, cobs, cotyledons, ears, embryos, filaments, flowers, fruits, husks, kernels, leaves, lodicules, ovaries, palea, panicles, pedicels, pods, pollen, protoplasts, roots, root tips, 25 seeds, silks, stalks, stems, stigma, styles, and tassels. In some embodiments, the plant part is a plant germplasm.

As used herein, the term "polymorphism" refers to a variation in the nucleotide sequence at a locus, where said variation is too common to be due merely to a spontaneous mutation. A polymorphism generally has a frequency of at least about 1% in a population. A 30 polymorphism can be a single nucleotide polymorphism (SNP), or an insertion/deletion polymorphism, also referred to herein as an "indel." Additionally, the variation can be in a transcriptional profile or a methylation pattern. The polymorphic site or sites of a nucleotide sequence can be determined by comparing the nucleotide sequences at one or more loci in two or more germplasm entries.

As used herein, the terms "polypeptide," "peptide" and "protein" refer to a polymer of amino acid residues. The terms encompass amino acid polymers in which one or more amino acid residue is an artificial chemical analogue of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers.

5 As used herein, the term "population" refers to a genetically heterogeneous collection of plants sharing a common genetic derivation.

As used herein, the term "progeny" refers to plants generated from the vegetative or sexual reproduction of one or more parent plants. Progeny plants may be obtained by cloning or selfing a single parent plant, or by crossing two parental plants. In some embodiments, the
10 progeny plants comprise the markers, alleles, haplotypes and/or genomic regions of the invention. Depending upon the context, it is not always advantageous that the progeny comprise the marker/allele/haplotype/genomic region(s) of the invention associated with increased male fertility (*e.g.*, in hybrid production). Thus, in some embodiments, the progeny of the invention may not comprise the marker/allele/haplotype/genomic region(s) of the
15 invention associated with increased male fertility.

As used herein, the terms "promoter" and "promoter sequence" refer to nucleic acid sequences involved in the regulation of transcription initiation. A "plant promoter" is a promoter capable of initiating transcription in plant cells. Exemplary plant promoters include, but are not limited to, those that are obtained from plants, plant viruses and bacteria
20 that comprise genes expressed in plant cells such *Agrobacterium* or *Rhizobium*. A "tissue-specific promoter" is a promoter that preferentially initiates transcription in a certain tissues. A "stress-inducible promoter" is a promoter that preferentially initiates transcription under certain environmental conditions. A "developmental stage-specific promoter" is a promoter that preferentially initiates transcription during certain developmental stages.

25 As used herein, the term "quantitative trait locus" (QTL) refers to a genetic locus that comprises and/or is associated with one or more genes underlying a quantitative trait.

As used herein, the term "recessive allele" refers to an allele whose phenotypic effect is not expressed in a heterozygote.

As used herein, the term "recombinant" refers to a molecule (*e.g.*, DNA, RNA,
30 protein, etc.) that results from human manipulation, however indirect, of a nucleic acid molecule.

As used herein, the term "reference sequence" refers to a defined nucleotide sequence used as a basis for nucleotide sequence comparison. The reference sequence for a marker, for example, is obtained by genotyping a number of lines at the locus or loci of interest, aligning

the nucleotide sequences in a sequence alignment program, and then obtaining the consensus sequence of the alignment. Hence, a reference sequence identifies the polymorphisms in alleles at a locus. A reference sequence may not be a copy of an actual nucleic acid sequence from any particular organism; however, it is useful for designing primers and probes (as described in Table 9) for actual polymorphisms in the locus or loci.

As used herein, the term "regulatory element" refers to a nucleotide sequence involved in controlling the expression of a nucleic acid sequence of interest. Regulatory elements comprise a promoter operably linked to the nucleic acid sequence of interest and termination signals. They also typically encompass sequences required for proper translation of the nucleotide sequence.

As used herein, the terms "selectively hybridize" and "specifically hybridize" refer to the hybridization of a nucleic acid sequence to a specified nucleic acid target sequence, wherein the nucleic acid sequence preferentially hybridizes to the specified nucleic acid target sequence (e.g., at least about a two-fold difference as compared to its hybridization with non-target nucleic acid sequences) to the substantial exclusion of non-target nucleic acids.

As used herein, the term "stringent hybridization conditions" refers to conditions under which a nucleic acid will selectively hybridize to a target nucleic acid sequence. An extensive guide to the hybridization of nucleic acids is found in Tijssen, *Laboratory Techniques in Biochemistry and Molecular Biology-Hybridization with Nucleic Acid Probes* part I chapter 2 "Overview of principles of hybridization and the strategy of nucleic acid probe assays" Elsevier, New York (1993). In some embodiments, stringent hybridization conditions comprise 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1x SSC, 0.1% SDS at 65°C. In some embodiments, stringent hybridization conditions comprise a wash stringency of 50% formamide with 5x Denhardt's solution, 0.5% SDS and 1x SSPE at 42°C. Typically, under "stringent conditions" a probe will hybridize to its target subsequence, but to no other sequences.

As used herein, "T_m" refers to the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Very stringent conditions are selected to be equal to the T_m for a particular probe. An example of stringent hybridization conditions for hybridization of complementary nucleic acids which have more than 100 complementary residues on a filter in a Southern or northern blot is 50% formamide with 1 mg of heparin at 42°C, with the hybridization being carried out overnight. An example of highly stringent wash conditions is 0.1 5M NaCl at 72°C for about 15 minutes.

An example of stringent wash conditions is a 0.2x SSC wash at 65°C for 15 minutes (*see*, Sambrook, *infra*, for a description of SSC buffer). Often, a high stringency wash is preceded by a low stringency wash to remove background probe signal. An example medium stringency wash for a duplex of, e.g., more than 100 nucleotides, is 1x SSC at 45°C for 15 minutes. An example low stringency wash for a duplex of, e.g., more than 100 nucleotides, is 4-6x SSC at 40°C for 15 minutes. For short probes (e.g., about 10 to 50 nucleotides), stringent conditions typically involve salt concentrations of less than about 1.0 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3, and the temperature is typically at least about 30°C. Stringent conditions can also be achieved with the addition of destabilizing agents such as formamide. In general, a signal to noise ratio of 2x (or higher) than that observed for an unrelated probe in the particular hybridization assay indicates detection of a specific hybridization. Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the proteins that they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code.

The following are examples of sets of hybridization/wash conditions that may be used to clone homologous nucleotide sequences that are substantially identical to reference nucleotide sequences of the present invention: 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 2X SSC, 0.1% SDS at 50°C; 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 1X SSC, 0.1% SDS at 50°C; 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.5X SSC, 0.1% SDS at 50°C; 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 50°C; 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 65°C.

A further indication that two nucleic acid sequences or proteins are substantially identical is that the protein encoded by the first nucleic acid is immunologically cross reactive with, or specifically binds to, the protein encoded by the second nucleic acid. Thus, a protein is typically substantially identical to a second protein, for example, where the two proteins differ only by conservative substitutions.

As used herein, the term "substantially fertile" refers to a plant whose fertility is substantially the same as that of a control plant (e.g., one or both of its parents, a near isogenic plant that lacks one or more markers/alleles associated with increased fertility, a near isogenic plant that lacks a *vip3* coding sequence, etc.). In some embodiments, substantially

fertile plants are plants that release pollen grains at a per tassel per day rate that is at least about 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90% or 95% of that of the control in the three-day period immediately following anther extrusion. In some embodiments, "substantially fertile" plants are plants that release at least about 500,000; 600,000; 700,000; 800,000;
 5 900,000; or 1,000,000 pollen grains per tassel per day in the three-day period immediately following anther extrusion.

As used herein, the phrase "TAQMAN[®] Assay" refers to real-time sequence detection using PCR based on the TAQMAN[®] Assay sold by Applied Biosystems, Inc. of Foster City, California, United States of America. For an identified marker, a TAQMAN[®] Assay can be
 10 developed for application in a breeding program.

As used herein, the terms "transformation", "transfection" and "transduction" refer to the introduction of an exogenous/heterologous nucleic acid (RNA and/or DNA) into a host cell. A cell has been "transformed," "transfected" or "transduced" with an exogenous/heterologous nucleic acid when such nucleic acid has been introduced or
 15 delivered into the cell.

As used herein, the terms "transgenic" and "recombinant" refer to an organism (*e.g.*, a bacterium or plant) that comprises one or more exogenous nucleic acids. Generally, the exogenous nucleic acid is stably integrated within the genome such that at least a portion of the exogenous nucleic acid is passed on to successive generations. The exogenous nucleic
 20 acid may be integrated into the genome alone or as part of a recombinant expression cassette. "Transgenic" may be used to designate any plant or plant part the genotype of which has been altered by the presence of an exogenous nucleic acid, including those transgenics initially so altered and those created by sexual crosses or asexual propagation from the initial transgenic. As used herein, the term "transgenic" does not encompass the alteration of the genome
 25 (chromosomal or extra-chromosomal) by conventional plant breeding methods or by naturally occurring events such as random cross-fertilization, non-recombinant viral infection, non-recombinant bacterial transformation, non-recombinant transposition or spontaneous mutation.

Transformation of a cell may be stable or transient. Thus, in some embodiments, a
 30 plant cell of the invention is stably transformed with a nucleotide sequence encoding a synthetic miRNA precursor molecule of the invention. In other embodiments, a plant of the invention is transiently transformed with a nucleotide sequence encoding a synthetic miRNA precursor molecule of the invention.

"Transient transformation" in the context of a polynucleotide means that a polynucleotide is introduced into the cell and does not integrate into the genome of the cell.

"Stable transformation" or "stably transformed," "stably introducing," or "stably introduced" as used herein means that a nucleic acid is introduced into a cell and integrates
 5 into the genome of the cell. As such, the integrated nucleic acid is capable of being inherited by the progeny thereof, more particularly, by the progeny of multiple successive generations. "Genome" as used herein also includes the nuclear and the plastid genome, and therefore includes integration of the nucleic acid into, for example, the chloroplast genome. Stable transformation as used herein can also refer to a transgene that is maintained
 10 extrachromasomally, for example, as a minichromosome.

As used herein, the term "transgene" refers to an exogenous nucleic acid. Transgenes may be single- or double-stranded.

As used herein with respect to plants and plant parts, the term "transgenic" refers to a plant or plant part that comprises one or more exogenous nucleic acids.

15 As used herein, the term "unfavorable allele" refers to a marker allele that segregates with an unfavorable plant phenotype, therefore providing the benefit of identifying plants that can be removed from a breeding program or planting.

As used herein, the term "vector" refers to a nucleic acid molecule for the cloning of and/or transfer of a nucleic acid into a cell. A vector may be a replicon to which another
 20 nucleotide sequence may be attached to allow for replication of the attached nucleotide sequence. A "replicon" can be any genetic element (*e.g.*, plasmid, phage, cosmid, chromosome, viral genome) that functions as an autonomous unit of nucleic acid replication *in vivo* (*i.e.*, is capable of replication under its own control). The term "vector" includes both viral and nonviral (*e.g.*, plasmid) nucleic acid molecules for introducing a nucleic acid into a
 25 cell *in vitro*, *ex vivo*, and/or *in vivo*. A large number of vectors known in the art may be used to manipulate nucleic acids, incorporate response elements and promoters into genes, etc. For example, the insertion of nucleic acid fragments corresponding to response elements and promoters into a suitable vector can be accomplished by ligating the appropriate nucleic acid fragments into a chosen vector that has complementary cohesive termini. Alternatively, the
 30 ends of the nucleic acid molecules may be enzymatically modified or any site may be produced by ligating nucleotide sequences (linkers) to the nucleic acid termini. Such vectors may be engineered to contain sequences encoding selectable markers that provide for the selection of cells that contain the vector and/or have incorporated the nucleic acid of the vector into the cellular genome. Such markers allow for the identification and/or selection of

cells that incorporate and express the proteins encoded by the marker. A "recombinant" vector refers to a viral or non-viral vector that comprises one or more heterologous nucleotide sequences (*i.e.*, transgenes). Vectors may be introduced into cells by any suitable method known in the art, including, but not limited to, transfection, electroporation, microinjection, transduction, cell fusion, DEAE dextran, calcium phosphate precipitation, lipofection (lysosome fusion), and use of a gene gun or nucleic acid vector transporter.

As used herein, the term "Vip3 protein" refers to a vegetative insecticidal protein (VIP) that is a member of the Vip3 class of proteins and includes, but is not limited to, Vip3A(a), Vip3A(b), Vip3A(c), Vip3B, Vip3C(a), Vip3C(b) and Vip3Z proteins and their homologues. Homologues of the aforementioned members of the Vip3 class of proteins include, but are not limited to, proteins that are cross-reactive with antibodies that immunologically recognize one or more of the aforementioned member of the Vip3 class of proteins, proteins that are cross-reactive with receptors (*e.g.*, on a nematode pest or insect gut) affected by one or more of the aforementioned member of the Vip3 class of proteins, proteins having an amino acid sequence that is at least about 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99% or more similar or identical to one or more of the aforementioned member of the Vip3 class of proteins, and proteins having a toxic core region, the amino acid sequence of which is at least about 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99% or more similar or identical to the toxic core region of one or more of the aforementioned member of the Vip3 class of proteins. Homologues of the aforementioned members of the Vip3 class of proteins may exhibit pesticidal activity (*e.g.*, nematocidal and/or insecticidal) when expressed in a transgenic maize plant or plant part. Examples of Vip3 proteins (and corresponding GenBank accession numbers and/or U.S. patent publication numbers) are described in Table 4.

Markers can be used in a variety of plant breeding applications. *See, e.g.*, Staub et al., *Hortscience* 31: 729 (1996); Tanksley, *Plant Molecular Biology Reporter* 1: 3 (1983). One of the main areas of interest is to increase the efficiency of backcrossing and introgressing genes using marker-assisted selection (MAS). In general, MAS takes advantage of genetic markers that have been identified as having a significant likelihood of co-segregation with a desired trait. Such markers are presumed to be in/near the gene(s) that give rise to the desired phenotype, and their presence indicates that the plant will possess the desired trait. Plants which possess the marker are expected to transfer the desired phenotype to their progeny.

A marker that demonstrates linkage with a locus affecting a desired phenotypic trait provides a useful tool for the selection of the trait in a plant population. This is particularly true where the phenotype is hard to assay or occurs at a late stage in plant development. Since DNA marker assays are less laborious and take up less physical space than field
5 phenotyping, much larger populations can be assayed, increasing the chances of finding a recombinant with the target segment from the donor line moved to the recipient line. The closer the linkage, the more useful the marker, as recombination is less likely to occur between the marker and the gene causing or imparting the trait. Having flanking markers decreases the chances that false positive selection will occur. The ideal situation is to have a
10 marker in the gene itself, so that recombination cannot occur between the marker and the gene. Such a marker is called a "perfect marker."

When a gene is introgressed by MAS, it is not only the gene that is introduced but also the flanking regions. Gepts, *Crop Sci.* 42:1780 (2002). This is referred to as "linkage drag." In the case where the donor plant is highly unrelated to the recipient plant, these
15 flanking regions carry additional genes that may code for agronomically undesirable traits. This "linkage drag" may also result in reduced yield or other negative agronomic characteristics even after multiple cycles of backcrossing into the elite maize line. This is also sometimes referred to as "yield drag." The size of the flanking region can be decreased by additional backcrossing, although this is not always successful, as breeders do not have
20 control over the size of the region or the recombination breakpoints. Young et al., *Genetics* 120:579 (1998). In classical breeding, it is usually only by chance that recombinations which contribute to a reduction in the size of the donor segment are selected. Tanksley et al., *Biotechnology* 7: 257 (1989). Even after 20 backcrosses, one may expect to find a sizeable piece of the donor chromosome still linked to the gene being selected. With markers,
25 however, it is possible to select those rare individuals that have experienced recombination near the gene of interest. In 150 backcross plants, there is a 95% chance that at least one plant will have experienced a crossover within 1 cM of the gene, based on a single meiosis map distance. Markers allow for unequivocal identification of those individuals. With one additional backcross of 300 plants, there would be a 95% chance of a crossover within 1 cM
30 single meiosis map distance of the other side of the gene, generating a segment around the target gene of less than 2 cM based on a single meiosis map distance. This can be accomplished in two generations with markers, while it would have required on average 100 generations without markers. See Tanksley et al., *supra*. When the exact location of a gene is known, flanking markers surrounding the gene can be utilized to select for recombinations in

different population sizes. For example, in smaller population sizes, recombinations may be expected further away from the gene, so more distal flanking markers would be required to detect the recombination.

The availability of integrated linkage maps of the maize genome containing
 5 increasing densities of public maize markers has facilitated maize genetic mapping and MAS. See, e.g. the IBM2 Neighbors maps, which are available online on the MaizeGDB website.

Of all the molecular marker types, SNPs are the most abundant and have the potential to provide the highest genetic map resolution. Bhatramakki et al., *Plant Molec. Biol.* 48:539 (2002). SNPs can be assayed in a so-called "ultra-high-throughput" fashion because they do
 10 not require large amounts of nucleic acid and automation of the assay is straight-forward. SNPs also have the benefit of being relatively low-cost systems. These three factors together make SNPs highly attractive for use in MAS. Several methods are available for SNP genotyping, including but not limited to, hybridization, primer extension, oligonucleotide ligation, nuclease cleavage, minisequencing and coded spheres. Such methods have been
 15 reviewed in various publications: Gut, *Hum. Mutat.* 17:475 (2001); Shi, *Clin. Chem.* 47:164 (2001); Kwok, *Pharmacogenomics* 1:95 (2000); Bhatramakki and Rafalski, *Discovery and application of single nucleotide polymorphism markers in plants*, in PLANT GENOTYPING: THE DNA FINGERPRINTING OF PLANTS, CABI Publishing, Wallingford (2001). A wide range of commercially available technologies utilize these and other methods to interrogate SNPs,
 20 including Masscode™ (Qiagen, Germantown, MD), Invader® (Hologic, Madison, WI), SnapShot® (Applied Biosystems, Foster City, CA), Taqman® (Applied Biosystems, Foster City, CA) and Beadarrays™ (Illumina, San Diego, CA).

A number of SNPs together within a sequence, or across linked sequences, can be used to describe a haplotype for any particular genotype. Ching et al., *BMC Genet.* 3:19
 25 (2002); Gupta et al., (2001), Rafalski, *Plant Sci.* 162:329 (2002b). Haplotypes can be more informative than single SNPs and can be more descriptive of any particular genotype. For example, a single SNP may be allele "T" for a specific donor line or variety, but the allele "T" might also occur in the maize breeding population being utilized for recurrent parents lacking the favorable allele. In this case, a combination of alleles at linked SNPs may be more
 30 informative. Once a unique haplotype has been assigned to a donor chromosomal region, that haplotype can be used in that population or any subset thereof to determine whether an individual has a particular gene. The use of automated high throughput marker detection platforms known to those of ordinary skill in the art makes this process highly efficient and effective.

The present invention provides markers associated with increased fertility (*e.g.*, increased male fertility). Analysis of these markers can be used to identify, select and/or produce fertile maize plants, to identify infertile maize plants, to predict whether and/or to what extent a maize plant will be fertile, to increase the efficiency of and/or reduce the cost of breeding and/or seed production programs, etc.

Markers of the present invention may comprise, consist essentially of or consist of a single allele or a combination of alleles at one or more genetic loci. For example, the marker may comprise a marker allele located at a first marker locus, a marker allele at a second marker locus, a marker allele at a third marker locus, a fourth marker at a fourth marker locus, etc.

In some embodiments, the marker is located within one or more of the chromosomal segments described in Table 1 as if each interval and all possible combinations thereof were individually set forth. For example, the marker may be located within one or more of chromosomal segments 46 to 12473 (*e.g.*, within chromosomal segment 7514).

In some embodiments, the marker comprises, consists essentially of or consists of an allele of interest located within one or more of the chromosomal segments described in Table 1. For example, in some embodiments, the marker comprises, consists essentially of or consists of an allele of interest located within one or more of chromosomal segments 46 to 12473 (*e.g.*, an allele of interest located within chromosomal segment 7514).

In some embodiments, the marker comprises, consists essentially of or consists of a haplotype comprising, consisting essentially of, or consisting of two or more alleles of interest located within one or more of the chromosomal segments described in Table 1. For example, in some embodiments, the marker comprises, consists essentially of or consists of a haplotype comprising, consisting essentially of, or consisting of two or more alleles of interest located within one or more of chromosomal segments 46 to 12473 (*e.g.*, a haplotype comprising two or more alleles of interest located within chromosomal segment 7514).

In some embodiments, the marker comprises, consists essentially of or consists of a haplotype comprising, consisting essentially of, or consisting of one or more alleles of interest located within a first chromosomal segment, one or more alleles of interest located within a second chromosomal segment different from the first chromosomal segment, one or more alleles of interest located within a third chromosomal segment different from the first and second chromosomal segments, etc., wherein each of the chromosomal segments comprises one or more of the chromosomal segments described in Table 1. For example, in

some embodiments, the marker comprises, consists essentially of or consists of a haplotype comprising, consisting essentially of, or consisting of:

- 1) one or more alleles of interest located within one or more of chromosomal segments 46 to 12473 (*e.g.*, one or more alleles of interest located within chromosomal segment 7514) and one or more alleles of interest located within chromosomal segment 1;
- 2) one or more alleles of interest located within one or more of chromosomal segments 46 to 12473 (*e.g.*, one or more alleles of interest located within chromosomal segment 7514) and one or more alleles of interest located on chromosome 2;
- 3) one or more alleles of interest located within one or more of chromosomal segments 46 to 12473 (*e.g.*, one or more alleles of interest located within chromosomal segment 7514) and one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (*e.g.*, one or more alleles of interest located within chromosomal segment 3);
- 4) one or more alleles of interest located within one or more of chromosomal segments 46 to 12473 (*e.g.*, one or more alleles of interest located within chromosomal segment 7514) and one or more alleles of interest located within one or more of chromosomal segments 18 to 45 (*e.g.*, one or more alleles of interest located within chromosomal segment 25);
- 5) one or more alleles of interest located within one or more of chromosomal segments 46 to 12473 (*e.g.*, one or more alleles of interest located within chromosomal segment 7514) and one or more alleles of interest located within one or more of chromosomal segments 12744 to 12749 (*e.g.*, one or more alleles of interest located within chromosomal segment 12747);
- 6) one or more alleles of interest located within one or more of chromosomal segments 46 to 12473 (*e.g.*, one or more alleles of interest located within chromosomal segment 7514) and one or more alleles of interest located within one or more of chromosomal segments 12750 to 12755 (*e.g.*, one or more alleles of interest located within chromosomal segment 12753);
- 7) one or more alleles of interest located within one or more of chromosomal segments 46 to 12473 (*e.g.*, one or more alleles of interest located within chromosomal segment 7514) and one or more alleles of interest located within chromosomal segment 12756;
- 8) one or more alleles of interest located within one or more of chromosomal segments 46 to 12473 (*e.g.*, one or more alleles of interest located within chromosomal segment 7514) and one or more alleles of interest located within one or more of chromosomal

segments 12757 to 12762 (e.g., one or more alleles of interest located within chromosomal segment 12760 and/or chromosomal segment 12761);

- 9) one or more alleles of interest located within one or more of chromosomal segments 46 to 12473 (e.g., one or more alleles of interest located within chromosomal segment 7514) and one or more alleles of interest located within one or more of chromosomal segments 12763 to 12768 (e.g., one or more alleles of interest located within chromosomal segment 12768);
- 10) one or more alleles of interest located within one or more of chromosomal segments 46 to 12473 (e.g., one or more alleles of interest located within chromosomal segment 7514), one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (e.g., one or more alleles of interest located within chromosomal segment 3), one or more alleles of interest located within one or more of chromosomal segments 18 to 45 (e.g., one or more alleles of interest located within chromosomal segment 25) and one or more alleles of interest located within one or more of chromosomal segments 12763 to 12768 (e.g., one or more alleles of interest located within chromosomal segment 12768);
- 11) one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (e.g., one or more alleles of interest located within chromosomal segment 3) and one or more alleles of interest located within chromosomal segment 1;
- 12) one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (e.g., one or more alleles of interest located within chromosomal segment 3) and one or more alleles of interest located on chromosome 2;
- 13) one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (e.g., one or more alleles of interest located within chromosomal segment 3) and one or more alleles of interest located within one or more of chromosomal segments 18 to 45 (e.g., one or more alleles of interest located within chromosomal segment 25);
- 14) one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (e.g., one or more alleles of interest located within chromosomal segment 3) and one or more alleles of interest located within one or more of chromosomal segments 12744 to 12749 (e.g., one or more alleles of interest located within chromosomal segment 12747);
- 15) one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (e.g., one or more alleles of interest located within chromosomal segment 3) and

one or more alleles of interest located within one or more of chromosomal segments 12750 to 12755 (e.g., one or more alleles of interest located within chromosomal segment 12753);

- 16) one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (e.g., one or more alleles of interest located within chromosomal segment 3) and one or more alleles of interest located within chromosomal segment 12756;
- 17) one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (e.g., one or more alleles of interest located within chromosomal segment 3) and one or more alleles of interest located within one or more of chromosomal segments 12757 to 12762 (e.g., one or more alleles of interest located within chromosomal segment 12760 and/or chromosomal segment 12761);
- 18) one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (e.g., one or more alleles of interest located within chromosomal segment 3) and one or more alleles of interest located within one or more of chromosomal segments 12763 to 12768 (e.g., one or more alleles of interest located within chromosomal segment 12768);
- 19) one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (e.g., one or more alleles of interest located within chromosomal segment 3), one or more alleles of interest located within one or more of chromosomal segments 12750 to 12755 (e.g., one or more alleles of interest located within chromosomal segment 12753) and one or more alleles of interest located within chromosomal segment 12756.

In embodiments, the marker comprises one or more of the desired alleles described in Table 8. For example, in some embodiments, the marker comprises at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 or more, or all 18 of the desired alleles described in Table 8.

In embodiments, the marker comprises one or more of the favorable (desired) alleles:

- (a) on chromosome 5 (QTL 5.1 and/or QTL 5.2) as described in Table 8;
- (b) on chromosome 3 as described in Table 8;
- (c) on chromosome 7 as described in Table 8;
- (d) on chromosome 10 as described in Table 8;
- (e) on chromosomes 3 and 5 as described in Table 8;
- (f) on chromosomes 5 and 7 as described in Table 8;
- (g) on chromosomes 3, 5 and 7 as described in Table 8;

- (h) on chromosomes 5 and 10 as described in Table 8;
- (i) on chromosomes 3, 5 and 10 as described in Table 8; or
- (j) any combination of (a) to (i).

In embodiments, the marker comprises one or more of the favorable (desired) alleles
 5 described in Table 10.

In some embodiments, the marker comprises, consists essentially of or consists of one or more marker alleles linked to one or more of the markers, chromosomal segments, alleles and/or haplotypes described herein. In some embodiments, the marker allele and the marker(s), segment(s), allele(s) and/or haplotype(s) described herein are separated by less
 10 than about 50, 40, 30, 25, 20, 15, 10, 5, 4, 3, 2, or 1 cM. In some embodiments, the pairwise r^2 value(s) of the marker allele and the marker(s)/segment(s)/allele(s)/haplotype(s) described herein is/are greater than or equal to about 0.33, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, or 1.0. In some embodiments, the LOD score for the marker allele and the marker(s)/segment(s)/allele(s)/haplotype(s) described herein is greater than or equal to about
 15 0.5, 1, 1.5, 2, 2.5, 3, 3.5, 4, 4.5, 5, 5.5, 6, 6.5, 7, 7.5, 8, 8.5, 9, 9.5, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more. Linked markers may be determined, for example, by using resources available on the MaizeGDB website (www.maizegdb.org).

In some embodiments, the marker comprises, consists essentially of or consists of a marker allele located within about 25cM, 20 cM, 15 cM, 10 cM, 5 cM or 1 cM or less (the
 20 term “within” including the end point of the specified region) of any one of the markers, chromosomal segments, alleles and/or haplotypes described herein. For example, in some embodiments, the marker allele comprises, consists essentially of or consists of one or more markers located within about 25 cM, 10cM, 5 cM, 1cM or less of chromosomal segment 7514.

25 In some embodiments, the marker is not in the natural genetic background of the maize plant (*e.g.*, is not naturally occurring in the maize line or variety, and has been introduced therein by human intervention).

Markers of the present invention may associated with any suitable trait, including, but not limited to, increased pollen production per plant, increased pollen production per tassel,
 30 increased pollen production per anther, improved pollen morphology, increased anther production per plant, increased anther production per tassel, improved anther morphology, increased tassel production per plant, improved tassel morphology, increased fertility (*e.g.*, increased male fertility) under stress conditions (*e.g.*, drought conditions), increased fertility (*e.g.*, increased male fertility) under elevated daytime temperatures, increased fertility (*e.g.*,

increased male fertility) under elevated nighttime temperatures and/or increased fertility (e.g., increased male fertility) under conditions comprising a large differential between daytime temperatures and nighttime temperatures.

Markers of the present invention may be analyzed using any suitable marker probe, including, but not limited to, the marker probes described herein.

Markers of the present invention may be detected in any suitable amplification product, including, but not limited to, the amplification products described herein.

Markers of the present invention may be analyzed using any suitable technique(s), including, but not limited to, PCR-based detection methods (e.g., TAQMAN[®] Assays), polymorphism detection techniques (*see, e.g.*, U.S. Patent Nos. 5,468,613, 5,217,863; 5,210,015; 5,876,930; 6,030,787; 6,004,744; 6,013,431; 5,595,890; 5,762,876; 5,945,283; 5,468,613; 6,090,558; 5,800,944; 5,616,464; 7,312,039; 7,238,476; 7,297,485; 7,282,355; 7,270,981 and 7,250,252), probe ligation techniques (*see, e.g.*, U.S. Patent No. 5,800,944), microarray techniques (*see, e.g.*, U.S. Patent Nos. 6,799,122; 6,913,879 and 6,996,476; *see also* Borevitz et al., GENOME RES. 13:513-523 (2003); Cui et al., BIOINFORMATICS 21:3852-3858 (2005)), probe linking methods (e.g., U.S. Patent No. 5,616,464), single base extension methods (*see, e.g.*, U.S. Patent Nos. 6,004,744; 6,013,431; 5,595,890; 5,762,876 and 5,945,283), fluorescent tagging methods (e.g., U.S. Patent Nos. 5,210,015; 5,876,930 and 6,030,787) and direct sequencing (*see, e.g.*, Service, SCIENCE 2006 311:1544-1546(2006)).

The present invention also provides nonnaturally occurring plants and plant parts comprising one or more markers associated with increased fertility (e.g., increased male fertility).

The present invention extends to products harvested from nonnaturally occurring plants of the present invention, including, but not limited to, plant cells and harvestable plant parts including but not limited to seeds, leaves, fruits, flowers, stems, rhizomes, tubers and bulbs.

In some embodiments, the harvested product can be a plant cell or plant part capable of producing a plant having increased fertility (e.g., increased male fertility).

The present invention also extends to products derived from nonnaturally occurring plants and plant parts of the present invention, including, but not limited to, dry pellets and powders, oils, fats, fatty acids, starches and proteins.

Markers and nonnaturally occurring plants and plant parts of the present invention may comprise any suitable allele(s), haplotype(s) and/or molecule(s) of interest.

In some embodiments, the allele of interest comprises, consists essentially of or consists of one or more nucleic acid sequences derived from NP2222 maize germplasm. For example, the alleles of interest may comprise, consist essentially of or consist of one or more of the chromosomal segments described in Table 1, wherein the chromosomal segment is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the corresponding segment(s) of NP2222 maize germplasm. In some such embodiments, the allele of interest comprises, consists essentially of or consists of one or more of chromosomal segments 3 to 12768, (*e.g.*, chromosomal segments 3, 13, 25, 506, 7514, 7546, 12747, 12753, 12760–12761 and/or 12767–12768) of NP2222 maize germplasm.

In some embodiments, the allele of interest comprises, consists essentially of or consists of one or more nucleic acid sequences derived from NP2660 maize germplasm. For example, the alleles of interest may comprise, consist essentially of or consist of one or more of the chromosomal segments described in Table 1, wherein the chromosomal segment is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the corresponding segment(s) of NP2660 maize germplasm. In some such embodiments, the allele of interest comprises, consists essentially of or consists of one or more of chromosomal segments 3 to 12743 and/or one or more of chromosomal segments 12757 to 12768, (*e.g.*, chromosomal segments 3, 13, 25, 506, 7514, 7546, 12747, 12753, 12760–12761 and/or 12767–12768) of NP2660 maize germplasm.

In some embodiments, the allele of interest comprises, consists essentially of or consists of one or more nucleic acid sequences derived from NP2276 maize germplasm. For example, the alleles of interest may comprise, consist essentially of or consist of one or more of the chromosomal segments described in Table 1, wherein the chromosomal segment is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the corresponding segment(s) of NP2276 maize germplasm. In some such embodiments, the allele of interest comprises, consists essentially of or consists of chromosomal segment 1, one or more of chromosomal segments 46 to 12743 and/or one or more of chromosomal segments 12757 to 12768, (*e.g.*, chromosomal segments 13, 506, 7514, 7546 and/or 12760–12761) of NP2276 maize germplasm.

In some embodiments, the allele of interest comprises, consists essentially of or consists of one or more nucleic acid sequences derived from ID3461 maize germplasm. For example, the alleles of interest may comprise, consist essentially of or consist of one or more of the chromosomal segments described in Table 1, wherein the chromosomal segment is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to

the corresponding segment(s) of ID3461 maize germplasm. In some such embodiments, the allele of interest comprises, consists essentially of or consists of one or more of chromosomal segments 1 to 17 (*e.g.*, chromosomal segments 1 and/or 13) of ID3461 maize germplasm.

In embodiments, the allele of interest comprises, consists essentially of or consists of
5 one or more nucleic acid sequences derived from a line in Table 11.

In some embodiments, the allele of interest comprises, consists essentially of or consists of at least one of SEQ ID NOs: 1 to 350 (as described in Table 3).

In some embodiments, the allele of interest comprises, consists essentially of or consists of at least one nucleotide sequence that is at least about 75%, 80%, 85%, 90%, 95%,
10 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of SEQ ID NOs: 1 to 350 (as described in Table 3).

In some embodiments, the allele of interest comprises, consists essentially of or consists of at least one nucleotide sequence that specifically hybridizes to the nucleotide sequence of one or more of SEQ ID NOs: 1 to 350 (as described in Table 3) under stringent
15 hybridization conditions.

In some embodiments, the allele of interest comprises, consists essentially of or consists of at least one nucleotide sequence that encodes the amino acid sequence set forth in one or more of SEQ ID NOs: 351 to 525 (as described in Table 3).

In some embodiments, the allele of interest comprises, consists essentially of or
20 consists of at least one nucleotide sequence that encodes an amino acid sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the amino acid sequence set forth in one or more of SEQ ID NOs: 351 to 525 (as described in Table 3).

In some embodiments, the allele of interest comprises, consists essentially of or
25 consists of at least one of SEQ ID NOs: 526 to 613 (as described in Table 9).

In some embodiments, the allele of interest comprises, consists essentially of or consists of at least one nucleotide sequence that is at least about 75%, 80%, 85%, 90%, 95%,
96%, 97%, 98%, 99%, 99.5% or more identical to one or more of SEQ ID NOs: 526 to 613
(as described in Table 9).

In some embodiments, the allele of interest comprises, consists essentially of or
30 consists of at least one nucleotide sequence that specifically hybridizes to the nucleotide sequence of one or more of SEQ ID NOs: 526 to 613 (as described in Table 9) under stringent hybridization conditions.

In some embodiments, the allele of interest comprises, consists essentially of or consists of one or more of the desired alleles described in Table 2. For example, in some embodiments, the marker comprises, consists essentially of or consists of at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90,
 5 95, 100, 110, 120, 130, 140 or more of the desired alleles described in Table 2.

In embodiments, the allele of interest comprises one or more of the desired alleles described in Table 8. For example, in some embodiments, the marker comprises at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 or more, or all 18 of the desired alleles described in Table 8.

10 In embodiments, the allele of interest comprises one or more of the desired alleles:

- (a) on chromosome 5 (QTL 5.1 and/or QTL 5.2) as described in Table 8;
- (b) on chromosome 3 as described in Table 8;
- (c) on chromosome 7 as described in Table 8;
- (d) on chromosome 10 as described in Table 8;
- 15 (e) on chromosomes 3 and 5 as described in Table 8;
- (f) on chromosomes 5 and 7 as described in Table 8;
- (g) on chromosomes 3, 5 and 7 as described in Table 8;
- (h) on chromosomes 5 and 10 as described in Table 8;
- (i) on chromosomes 3, 5 and 10 as described in Table 8; or
- 20 (j) any combination of (a) to (i).

In embodiments, the allele of interest comprises one or more of the desired alleles described in Table 10. For example, in some embodiments, the marker comprises at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25 or more of the desired alleles described in Table 10.

25 In some embodiments, the allele of interest comprises, consists essentially of or consists of the reverse complement of one of the alleles of interest described herein.

In some embodiments, the allele of interest comprises, consists essentially of or consists of an informative fragment of one of the alleles of interest described herein.

In some embodiments, the allele of comprises, consists essentially of or consists of an
 30 informative fragment of the reverse complement of one of the alleles of interest described herein.

In some embodiments, the allele of interest is not in the natural genetic background of the maize plant (e.g., is not naturally occurring in the maize line or variety, and has been introduced therein by human intervention).

In some embodiments, the haplotype of interest comprises, consists essentially of or consists of nucleic acid sequences derived from NP2222 maize germplasm. For example, the haplotype of interest may comprise, consist essentially of or consist of one or more (or two or more) of the chromosomal segments described in Table 1, wherein the chromosomal segment
 5 is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the corresponding segment(s) of NP2222 maize germplasm. In some such embodiments, the haplotype of interest comprises one or more nucleic acid sequences is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of chromosomal segments 3 to 12768, (e.g., chromosomal segments 3, 13, 25, 506, 7514, 7546,
 10 12747, 12753, 12760–12761 and/or 12767–12768) of NP2222 maize germplasm.

In some embodiments, the haplotype of interest comprises, consists essentially of or consists of nucleic acid sequences derived from NP2660 maize germplasm. For example, the haplotype of interest may comprise, consist essentially of or consist of one or more (or two or more) of the chromosomal segments described in Table 1, wherein the chromosomal segment
 15 is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the corresponding segment(s) of NP2660 maize germplasm. In some such embodiments, the haplotype of interest comprises one or more nucleic acid sequences is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of chromosomal segments 3 to 12743 and/or one or more of chromosomal segments 12757 to
 20 12768, (e.g., chromosomal segments 3, 13, 25, 506, 7514, 7546, 12747, 12753, 12760–12761 and/or 12767–12768) of NP2660 maize germplasm.

In some embodiments, the haplotype of interest comprises, consists essentially of or consists of nucleic acid sequences derived from NP2276 maize germplasm. For example, the haplotype of interest may comprise, consist essentially of or consist of one or more (or two or
 25 more) of the chromosomal segments described in Table 1, wherein the chromosomal segment is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the corresponding segment(s) of NP2276 maize germplasm. In some such embodiments, the haplotype of interest comprises one or more nucleic acid sequences is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to chromosomal
 30 segment 1, one or more of chromosomal segments 46 to 12743 and/or one or more of chromosomal segments 12757 to 12768, (e.g., chromosomal segments 13, 506, 7514, 7546 and/or 12760–12761) of NP2276 maize germplasm.

In some embodiments, the haplotype of interest comprises, consists essentially of, or consists of nucleic acid sequences derived from ID3461 maize germplasm. For example, the

haplotype of interest may comprise, consist essentially of or consist of one or more (or two or more) of the chromosomal segments described in Table 1, wherein the chromosomal segment is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the corresponding segment(s) of ID3461 maize germplasm. In some such embodiments, the haplotype of interest comprises one or more nucleic acid sequences is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of chromosomal segments 1 to 17 (*e.g.*, chromosomal segments 1 and/or 13) of ID3461 maize germplasm.

In embodiments, the haplotype of interest comprises, consists essentially of or consists of one or more nucleic acid sequences derived from a line in Table 11.

In some embodiments, the haplotype of interest comprises one or more of the nucleic acid sequences set forth in SEQ ID NOs: 1 to 350 (as described in Table 3).

In some embodiments, the haplotype of interest comprises one or more (or two or more) nucleotide sequences that is/are at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of SEQ ID NOs: 1 to 350 (as described in Table 3).

In some embodiments, the haplotype of interest comprises one or more (or two or more) nucleotide sequences that specifically hybridize to the nucleotide sequence of one or more of SEQ ID NOs: 1 to 350 (as described in Table 3) under stringent hybridization conditions.

In some embodiments, the haplotype of interest comprises one or more (or two or more) nucleotide sequences encoding the amino acid sequence set forth in one or more of SEQ ID NOs: 351 to 525 (as described in Table 3).

In some embodiments, the haplotype of interest comprises one or more (or two or more) nucleotide sequences encoding an amino acid sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the amino acid sequence set forth in one or more of SEQ ID NOs: 351 to 525 (as described in Table 3).

In some embodiments, the haplotype of interest comprises one or more (or two or more) of the nucleic acid sequences set forth in SEQ ID NOs: 526 to 613 (as described in Table 9).

In some embodiments, the haplotype of interest comprises one or more (or two or more) nucleotide sequences that is/are at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of SEQ ID NOs: 526 to 613 (as described in Table 9).

In some embodiments, the haplotype of interest comprises one or more (or two or more) nucleotide sequences that specifically hybridize to the nucleotide sequence of one or more of SEQ ID NOs: 526 to 613 (as described in Table 9) under stringent hybridization conditions.

5 In some embodiments, the haplotype of interest comprises one or more of the desired alleles described in Table 2. For example, in some embodiments, the haplotype of interest comprises, consists essentially of or consists of at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140 or more of the desired alleles described in Table 2.

10 In embodiments, the haplotype of interest comprises one or more of the desired alleles described in Table 8. For example, in some embodiments, the haplotype of interest comprises at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 or more, or all 18 of the desired alleles described in Table 8.

In embodiments, the haplotype of interest comprises one or more (or two or more) of the desired allele(s):

- 15 (a) on chromosome 5 (QTL 5.1 and/or QTL 5.2) as described in Table 8;
- (b) on chromosome 3 as described in Table 8;
- (c) on chromosome 7 as described in Table 8;
- (d) on chromosome 10 as described in Table 8;
- 20 (e) on chromosomes 3 and 5 as described in Table 8;
- (f) on chromosomes 5 and 7 as described in Table 8;
- (g) on chromosomes 3, 5 and 7 as described in Table 8;
- (h) on chromosomes 5 and 10 as described in Table 8;
- (i) on chromosomes 3, 5 and 10 as described in Table 8; or
- 25 (j) any combination of (a) to (i).

In embodiments, the haplotype of interest comprises one or more (or two or more) of the desired alleles described in Table 10. For example, in some embodiments, the haplotype of interest comprises at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25 or more of the desired alleles described in Table 10.

30 In some embodiments, the haplotype of interest comprises the reverse complement of one or more (or two or more) of the alleles of interest described herein. For example, in some embodiments, at least one allele of interest in a haplotype of interest is present as described herein, whilst at least one other allele of interest in the haplotype of interest is present as the reverse complement of the allele(s) described herein.

In some embodiments, the haplotype of interest comprises an informative fragment of one or more (or two or more) of the alleles of interest described herein. For example, in some embodiments, at least one allele of interest in a haplotype of interest is present as described herein, whilst at least one other allele of interest in the haplotype of interest is present as an

5 informative fragment of the allele(s) described herein.

In some embodiments, the haplotype of interest comprises an informative fragment of the reverse complement of one or more (or two or more) of the alleles of interest described herein. For example, in some embodiments, at least one allele of interest in a haplotype of interest is present as described herein, whilst at least one other allele of interest in the

10 haplotype of interest is present as an informative fragment of the reverse complement of the allele(s) described herein.

In some embodiments, the molecule of interest comprises, consists essentially of or consists of at least one of SEQ ID NOs: 351 to 525 (as described in Table 3).

In some embodiments, the molecule of interest comprises, consists essentially of or

15 consists of at least one amino acid sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of SEQ ID NOs: 351 to 525 (as described in Table 3).

In some embodiments, the molecule of interest is not in the natural proteome of the maize plant (*e.g.*, is not naturally occurring in the maize line or variety, and has been

20 introduced therein by human intervention).

In some embodiments, the allele/haplotype/molecule of interest is associated with increased pollen production per plant, increased pollen production per tassel, increased pollen production per anther, improved pollen morphology, increased anther production per plant, increased anther production per tassel, improved anther morphology, increased tassel

25 production per plant, improved tassel morphology, increased fertility (*e.g.*, increased male fertility) under stress conditions (*e.g.*, drought conditions), increased fertility (*e.g.*, increased male fertility) under elevated daytime temperatures, increased fertility (*e.g.*, increased male fertility) under elevated nighttime temperatures and/or increased fertility (*e.g.*, increased male fertility) under conditions comprising a large differential between daytime temperatures and

30 nighttime temperatures.

Markers and nonnaturally occurring plants and plant parts of the present invention may comprise any suitable number of alleles, haplotypes and/or molecules of interest as described herein.

In some embodiments, the marker/nonnaturally occurring plant or plant part comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140 or more alleles, haplotypes and/or molecules of interest associated with increased fertility (e.g., increased male fertility) as

5 described herein. For example, in some such embodiments, the marker/nonnaturally occurring plant or plant part comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140 or more alleles, haplotypes, molecules of interest (as described herein) associated with increased pollen production, increased pollen production per tassel, increased pollen production per

10 anther, improved pollen morphology, increased anther production per plant, increased anther production per tassel, improved anther morphology, increased tassel production per plant, improved tassel morphology, increased fertility (e.g., increased male fertility) under stress conditions (e.g., drought conditions), increased fertility (e.g., increased male fertility) under elevated daytime temperatures, increased fertility (e.g., increased male fertility) under

15 elevated nighttime temperatures and/or increased fertility (e.g., increased male fertility) under conditions comprising a large differential between daytime temperatures and nighttime temperatures.

Nonnaturally occurring plants of the present invention may comprise any suitable insecticidal protein, including, but not limited to Vip3 proteins.

20 In some embodiments, the nonnaturally occurring plant or plant part comprises one or more nucleic acids encoding a Vip3 protein. For example, in some embodiments, the nonnaturally occurring plant or plant part comprises the maize MIR162 event, optionally in a hemizygous or homozygous state. In embodiments, the nonnaturally occurring plant or plant part is an inbred line (e.g., a male inbred line) or a double haploid line. In embodiments, the

25 nonnaturally occurring plant or plant part is from an elite maize line. In embodiments, the nonnaturally occurring plant or plant part is from a cultivated plant or plant part. In some embodiments, the nonnaturally occurring plant or plant part comprises one or more Vip nucleotide sequences of as set forth by the Accession Numbers provided in Table 4.

Table 4. Examples of Vip3 proteins.

Name	GenBank Accession No.	GenBank Accession No.	Publication(s)
Vip3Aa1	L48811	AAC37036	International Patent Pub. No. WO2013015993
Vip3Aa2	L48812	AAC37037	International Patent Pub. No. WO2013015993
Vip3Aa3			U.S. Patent No. 6,137,033; International Patent Pub. No. WO2013015993
Vip3Aa4		AAR81079	U.S. Patent No. 6,656,908; International Patent Pub. No. WO2013015993
Vip3Aa5		AAR81080	U.S. Patent No. 6,656,908; International Patent Pub. No. WO2013015993
Vip3Aa6		AAR81081	U.S. Patent No. 6,656,908; International Patent Pub. No. WO2013015993
Vip3Aa7	AY044227	AAK95326	International Patent Pub. No. WO2013015993
Vip3Aa8	AF399667	AAK97481	International Patent Pub. No. WO2013015993
Vip3Aa9	Y17158	CAA76665	International Patent Pub. No. WO2013015993
Vip3Aa10	AF373030	AAN60738	International Patent Pub. No. WO2013015993
Vip3Aa11	AY489126	AAR36859	International Patent Pub. No. WO2013015993
Vip3Aa12	AF500478	AAM22456	International Patent Pub. No. WO2013015993
Vip3Aa13	AY074706	AAL69542	International Patent Pub. No. WO2013015993
Vip3Aa14	AF548629	AAQ12340	International Patent Pub. No. WO2013015993
Vip3Aa15	AY295778	AAF51131	International Patent Pub. No. WO2013015993
Vip3Aa16	AY739665	AAW65132	International Patent Pub. No. WO2013015993
Vip3Aa17			U.S. Patent No. 6,603,063
Vip3Aa18	AY945939	AAX49395	International Patent Pub. No. WO2013015993
Vip3Aa19	DQ241674	ABB72459	International Patent Pub. No. WO2013015993
Vip3Aa19	DQ539887	ABG20428	International Patent Pub. No. WO2013015993
Vip3Aa20	DQ539888	ABG20429	International Patent Pub. No. WO2013015993
Vip3Aa21	DQ426899	ABD84410	International Patent Pub. No. WO2013015993
Vip3Aa22	DQ016968	AAV41427	International Patent Pub. No. WO2013015993
Vip3Aa23	DQ016969	AAV41428	International Patent Pub. No. WO2013015993
Vip3Aa24	EF432794	ABO20895	International Patent Pub. No. WO2013015993
Vip3Aa25	EF608501	ABR22260	International Patent Pub. No. WO2013015993
Vip3Aa26	EU294496	ABX90027	International Patent Pub. No. WO2013015993
Vip3Aa27	EU332167	ABY51679	International Patent Pub. No. WO2013015993
Vip3Aa28	FJ494817	ACR15110	International Patent Pub. No. WO2013015993
Vip3Aa29	FJ626674	ACV04598	International Patent Pub. No. WO2013015993
Vip3Aa30	FJ626675	ACV04599	International Patent Pub. No. WO2013015993
Vip3Aa31	FJ626676	ACV04600	International Patent Pub. No. WO2013015993
Vip3Aa32	FJ626677	ACV04601	International Patent Pub. No. WO2013015993
Vip3Aa33	GU073128	ACY38212	International Patent Pub. No. WO2013015993
Vip3Aa34	GU073129	ACY38213	International Patent Pub. No. WO2013015993
Vip3Aa35	GU733921	ADE06071	International Patent Pub. No. WO2013015993
Vip3Aa36	GU951510	ADF43020	International Patent Pub. No. WO2013015993
Vip3Aa37	HM1132041	ADJ18213	International Patent Pub. No. WO2013015993
Vip3Aa38	HM117632	AEH31411	International Patent Pub. No. WO2013015993
Vip3Aa39	HM117631	AEH31410	International Patent Pub. No. WO2013015993
Vip3Aa40	HM132042	ADJ18214	International Patent Pub. No. WO2013015993
Vip3Aa41	HM132043	ADJ18215	International Patent Pub. No. WO2013015993
Vip3Aa42	HQ587048	ADQ73634	International Patent Pub. No. WO2013015993
Vip3Aa43	HQ594534	ADY76643	International Patent Pub. No. WO2013015993
Vip3Aa44	HQ650163	ADW66453	International Patent Pub. No. WO2013015993
Vip3Ab1		AAR40284	U.S. Patent No. 6,603,063; International Patent Pub. No. WO2013015993
Vip3Ab2	DQ054848	AAV88247	International Patent Publication No. WO2013015993
Vip3Ac1			International Patent Pub. No. WO2013015993
Vip3Ad1			U.S. Patent Pub. No. 2004/0128716; International Patent Pub. No. WO2013015993
Vip3Ad2	AJ872071	CAI43276	International Patent Pub. No. WO2013015993
Vip3Ac1	AJ872072	CAI43277	International Patent Pub. No. WO2013015993
Vip3Af1	AJ872070	CAI43275	International Patent Pub. No. WO2013015993
Vip3Af2		ADN08753	International Patent Pub. No. WO2013015993
Vip3Af3	HM117634	AEH31413	International Patent Pub. No. WO2013015993
Vip3Af4			International Patent Pub. No. WO2013015993
Vip3Af5			International Patent Pub. No. WO2013015993
Vip3Ag1		ADN08758	International Patent Pub. No. WO2013015993
Vip3Ag2	FJ556803	ACL97352	International Patent Pub. No. WO2013015993
Vip3Ag3	HM117633	AEH31412	International Patent Pub. No. WO2013015993
Vip3Ag4	HQ414237	ADZ46177	International Patent Pub. No. WO2013015993
Vip3Ag5	HQ542193	ADY76642	International Patent Pub. No. WO2013015993
Vip3Ah1	DQ832323	ABH10614	International Patent Pub. No. WO2013015993
Vip3Be1	AY823271	AAV70653	International Patent Pub. No. WO2013015993
Vip3Bb1		ADN08760	International Patent Pub. No. WO2013015993
Vip3Bb2	EF439819	ABO30520	International Patent Pub. No. WO2013015993
Vip3B-like	HM016910	ADI48120	International Patent Pub. No. WO2013015993

In some embodiments, the nonnaturally occurring plant or plant part comprises at least one nucleotide sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of the Vip nucleotide sequences of as set forth by the accession numbers provided in Table 4.

5 In some embodiments, the nonnaturally occurring plant or plant part comprises at least one nucleotide sequence that specifically hybridizes to the nucleotide sequence of one or more of Vip nucleotide sequences of as set forth by the accession numbers provided in Table 4 under stringent hybridization conditions.

10 In some embodiments, the nonnaturally occurring plant or plant part comprises at least one nucleotide sequence that encodes the amino acid sequence set forth in one or more of Vip nucleotide sequences of as set forth by the accession numbers provided in Table 4.

In some embodiments, the nonnaturally occurring plant or plant part comprises at least one nucleotide sequence that encodes an amino acid sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the amino acid
15 sequence set forth in one or more of Vip nucleotide sequences of as set forth by the accession numbers provided in Table 4.

The present invention also provides nonnaturally occurring nucleic acids. As used herein with respect to nucleic acids, the term “nonnaturally occurring” refers to nucleic acids that do not naturally exist in nature. In some embodiments, a nonnaturally occurring nucleic
20 acid does not naturally exist in nature because it is not in the genetic background of the cell/organism in which it naturally resides. That is, the nonnaturally occurring nucleic acid is substantially modified by deliberate human intervention from its native form in composition (e.g., comprised in a heterologous/recombinant expression cassette with one or more heterologous promoter sequences, intron sequences and/or termination sequences) and/or is
25 located at a non-native genomic locus. Thus, nonnaturally occurring plants, and plant parts of the present invention may comprise one more exogenous or heterologous nucleotide sequences and/or one or more nonnaturally occurring copies of a naturally occurring nucleotide sequence (*i.e.*, extraneous copies of a gene that naturally occurs in that species). In some embodiments, the nonnaturally occurring nucleic acid molecules of the invention may
30 comprise any suitable variation(s) from their closest naturally occurring counterparts. For example, nonnaturally occurring nucleic acid molecules of the present invention may comprise an otherwise naturally occurring nucleotide sequence having one or more point mutations, insertions or deletions relative to the naturally occurring nucleotide sequence.

Nonnaturally occurring nucleic acids of the present invention may comprise any suitable marker/allele of interest, including, but not limited to, those described herein.

In some embodiments, the nonnaturally occurring nucleic acid comprises, consists essentially of or consists of one or more of the chromosomal segments described in Table 1.

5 For example, the nonnaturally occurring nucleic acid may comprise, consist essentially of or consist of one or more of chromosomal segments 46 to 12473 (*e.g.*, within chromosomal segment 7514).

In some embodiments, the nonnaturally occurring nucleic acid comprises, consists essentially of or consists of one or more nucleic acid sequences derived from NP2222 maize
10 germplasm. For example, the nonnaturally occurring nucleic acid may comprise, consist essentially of or consist of one or more of the chromosomal segments described in Table 1, wherein the chromosomal segment is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the corresponding segment(s) of NP2222 maize germplasm. In some such embodiments, the nonnaturally occurring nucleic acid comprises,
15 consists essentially of or consists of one or more of chromosomal segments 3 to 12768, (*e.g.*, chromosomal segments 3, 13, 25, 506, 7514, 7546, 12747, 12753, 12760–12761 and/or 12767–12768) of NP2222 maize germplasm, the reverse complement thereof, an informative fragment thereof, or an informative fragment of the reverse complement thereof.

In some embodiments, the nonnaturally occurring nucleic acid comprises, consists
20 essentially of or consists of one or more nucleic acid sequences derived from NP2660 maize germplasm. For example, the nonnaturally occurring nucleic acid may comprise, consist essentially of or consist of one or more of the chromosomal segments described in Table 1, wherein the chromosomal segment is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the corresponding segment(s) of NP2660 maize
25 germplasm. In some such embodiments, the nonnaturally occurring nucleic acid comprises, consists essentially of or consists of one or more of chromosomal segments 3 to 12743 and/or one or more of chromosomal segments 12757 to 12768, (*e.g.*, chromosomal segments 3, 13, 25, 506, 7514, 7546, 12747, 12753, 12760–12761 and/or 12767–12768) of NP2660 maize germplasm, the reverse complement thereof, an informative fragment thereof, or an
30 informative fragment of the reverse complement thereof.

In some embodiments, the nonnaturally occurring nucleic acid comprises, consists essentially of or consists of one or more nucleic acid sequences derived from NP2276 maize germplasm. For example, the nonnaturally occurring nucleic acid may comprise, consist essentially of or consist of one or more of the chromosomal segments described in Table 1,

wherein the chromosomal segment is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the corresponding segment(s) of NP2276 maize germplasm. In some such embodiments, the nonnaturally occurring nucleic acid comprises, consists essentially of or consists of chromosomal segment 1, one or more of chromosomal segments 46 to 12743 and/or one or more of chromosomal segments 12757 to 12768, (e.g., chromosomal segments 13, 506, 7514, 7546 and/or 12760–12761) of NP2276 maize germplasm, the reverse complement thereof, an informative fragment thereof, or an informative fragment of the reverse complement thereof.

In some embodiments, the nonnaturally occurring nucleic acid comprises, consists essentially of or consists of one or more nucleic acid sequences derived from ID3461 maize germplasm. For example, the nonnaturally occurring nucleic acid may comprise, consist essentially of or consist of one or more of the chromosomal segments described in Table 1, wherein the chromosomal segment is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the corresponding segment(s) of ID3461 maize germplasm. In some such embodiments, the nonnaturally occurring nucleic acid comprises, consists essentially of or consists of one or more of chromosomal segments 1 to 17 (e.g., chromosomal segments 1 and/or 13) of ID3461 maize germplasm, the reverse complement thereof, an informative fragment thereof, or an informative fragment of the reverse complement thereof.

In embodiments, the nonnaturally occurring nucleic acid comprises, consists essentially of or consists of one or more nucleic acid sequences derived from a line in Table 11.

In some embodiments, the nonnaturally occurring nucleic acid comprises, consists essentially of or consists of one or more nucleotide sequences that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of the nucleotide sequences set forth in SEQ ID NOs: 1 to 350 and Vip polypeptides (as described in Tables 3 and 4), the reverse complement thereof, an informative fragment thereof, or an informative fragment of the reverse complement thereof.

In some embodiments, the nonnaturally occurring nucleic acid comprises, consists essentially of or consists of at least one nucleotide sequence that encodes an amino acid sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the amino acid sequence set forth in one or more of SEQ ID NOs: 351 to 525 (as described in Table 3).

In some embodiments, the nonnaturally occurring nucleic acid comprises one or more of the desired alleles described in Table 2. For example, in some embodiments, the isolated nucleic acid sequence comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140 or more of the desired alleles described in Table 2.

In embodiments, the nonnaturally occurring nucleic acid comprises one or more of the desired alleles described in Table 8. For example, in some embodiments, the nonnaturally occurring nucleic acid comprises at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 or more, or all 18 of the desired alleles described in Table 8.

In embodiments, the nonnaturally occurring nucleic acid comprises one or more of the desired alleles:

- (a) on chromosome 5 (QTL 5.1 and/or QTL 5.2) as described in Table 8;
- (b) on chromosome 3 as described in Table 8;
- (c) on chromosome 7 as described in Table 8;
- (d) on chromosome 10 as described in Table 8;
- (e) on chromosomes 3 and 5 as described in Table 8;
- (f) on chromosomes 5 and 7 as described in Table 8;
- (g) on chromosomes 3, 5 and 7 as described in Table 8;
- (h) on chromosomes 5 and 10 as described in Table 8;
- (i) on chromosomes 3, 5 and 10 as described in Table 8; or
- (j) any combination of (a) to (i).

In embodiments, the nonnaturally occurring nucleic acid comprises one or more of the desired alleles described in Table 10. For example, in some embodiments, the nonnaturally occurring nucleic acid comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25 or more of the desired alleles described in Table 10.

In some embodiments, the nonnaturally occurring nucleic acid comprises codons specific for expression in plants.

In some embodiments, the nonnaturally occurring nucleic acid is an isolated nucleic acid.

In some embodiments, the nonnaturally occurring nucleic acid comprises one or more detectable moieties, such as digoxigenin, fluorescein, acridine-ester, biotin, alkaline phosphatase, horseradish peroxidase, β -glucuronidase, β -galactosidase, luciferase, ferritin or a radioactive isotope. *See, e.g.*, Prober et al. SCIENCE 238:336-340 (1987); European Patent Nos. 144914 and 119448; and U.S. Patent Nos. 4,582,789 and 4,563,417.

Nonnaturally occurring nucleic acids of the present invention may comprise any suitable transgene(s), including, but not limited to, transgenes that encode gene products that provide herbicide-resistance, pest-resistance (e.g., a *vip3* transgene) and/or disease-resistance.

In some embodiments, the nonnaturally occurring nucleic acid comprises one or more
 5 transgenes encoding a gene product that provides resistance to one or more herbicides. For example, the nonnaturally occurring nucleic acid may comprise a transgene that encodes a gene product that provides glyphosate-, sulfonylurea-, imidazolinone-, dicamba-, glufosinate-, phenoxy propionic acid-, cyclohexime-, triazine-, benzonitrile-, and/or broxynil-resistance.

10 In some embodiments, the nonnaturally occurring nucleic acid comprises one or more transgenes encoding a gene product that provides resistance to one or more pests. For example, the nonnaturally occurring nucleic acid may comprise a transgene that encodes a gene product that provides bacterial-, fungal, gastropod-, insect-, nematode-, oomycete-, phytoplasma-, protozoa-, and/or viral-resistance.

15 In some embodiments, the nonnaturally occurring nucleic acid comprises one or more transgenes encoding a gene product that provides resistance to one or more diseases.

Nonnaturally occurring nucleic acids of the present invention may comprise any suitable number of nucleic acids. In some embodiments, the nonnaturally occurring nucleic acid is 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29,
 20 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 450, 500 or more nucleotides in length. In some embodiments, the nonnaturally occurring nucleic acid is less than about 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 450 or 500
 25 nucleotides in length. In some embodiments, the nonnaturally occurring nucleic acid is about 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 450 or 500 nucleotides in length.

The present invention also provides expression cassettes comprising one or more
 30 nonnaturally occurring nucleic acids of the present invention. In some embodiments, the expression cassette comprises a nucleic acid encoding a polypeptide that confers at least one property (e.g., resistance to a selection agent) that can be used to detect, identify or select transformed plant cells and tissues.

The present invention also provides vectors comprising one or more nonnaturally occurring nucleic acids and/or expression cassettes of the present invention.

The present invention also extends to compositions comprising nonnaturally occurring nucleic acids, expression cassettes and/or vectors of the present invention.

5 The present invention extends to uses of nonnaturally occurring nucleic acids, expression cassettes and vectors of the present invention, including, but not limited to, methods of identifying, selecting and/or producing fertile maize plants; predicting whether and/or to what extent a maize plant will be fertile; reducing the costs associated with breeding and/or seed production programs; and/or to increasing the efficiency of breeding and/or seed
10 production programs.

The present invention also provides primers for amplifying nucleic acid sequences comprising one or more markers associated with increased fertility (*e.g.*, one or more markers of the present invention).

15 Primers of the present invention may comprise any nucleic acid sequence useful for amplifying one or more markers associated with increased fertility (*e.g.*, one or more markers of the present invention).

In some embodiments, the primer comprises nucleic acid sequences useful for amplifying one or more of the chromosomal segments described in Table 1. For example, in some embodiments, the primer pair comprises nucleotide sequences useful for amplifying
20 one or more of chromosomal segments 46 to 12473 (*e.g.*, chromosomal segment 7514).

The present invention extends to compositions comprising primers of the present invention. In some embodiments, the composition comprises a pair of primers, wherein each of the primers is a primer of the present invention.

25 The present invention also provides amplification products comprising one or more markers/alleles associated with increased fertility (*e.g.*, one or more markers/alleles associated with increased male fertility).

Amplification products of the present invention may be derived from any suitable chromosomal segment(s).

30 In some embodiments, the amplification product is derived from one or more of the chromosomal segments described in Table 1. For example, in some embodiments, the amplification product is derived from one or more of chromosomal segments 46 to 12473 (*e.g.*, chromosomal segment 7514).

Amplification products of the present invention may comprise any suitable allele(s) of interest.

In some embodiments, the amplification product comprises, consists essentially of or consists of one or more nucleic acid sequences derived from NP2222 maize germplasm. For example, the amplification product may comprise, consist essentially of or consist of one or more of the chromosomal segments described in Table 1 (e.g., chromosomal segments 3, 13, 25, 506, 7514, 7546, 12747, 12753, 12760–12761 and/or 12767–12768), wherein the chromosomal segment is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the corresponding segment(s) of NP2222 maize germplasm.

In some embodiments, the amplification product comprises, consists essentially of or consists of one or more nucleic acid sequences derived from NP2660 maize germplasm. For example, the amplification product may comprise, consist essentially of or consist of one or more of the chromosomal segments described in Table 1 (e.g., chromosomal segments 3, 13, 25, 506, 7514, 7546, 12747, 12753, 12760–12761 and/or 12767–12768), wherein the chromosomal segment is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the corresponding segment(s) of NP2660 maize germplasm.

In some embodiments, the amplification product comprises, consists essentially of or consists of one or more nucleic acid sequences derived from NP2276 maize germplasm. For example, the amplification product may comprise, consist essentially of or consist of one or more of the chromosomal segments described in Table 1 (e.g., chromosomal segments 1, 182, 184, 10230, 10259 and/or 10276–10277), wherein the chromosomal segment is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the corresponding segment(s) of NP2276 maize germplasm.

In some embodiments, the amplification product comprises, consists essentially of or consists of one or more nucleic acid sequences derived from ID3461 maize germplasm. For example, the amplification product may comprise, consist essentially of or consist of one or more of chromosomal segments 1 to 17 described in Table 1 (e.g., chromosomal segments 1 and/or 13), wherein the chromosomal segment is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the corresponding segment(s) of ID3461 maize germplasm.

In embodiments, the amplification product comprises, consists essentially of or consists of one or more nucleic acid sequences derived from a line in Table 11.

In some embodiments, the amplification product comprises, consists essentially of or consists of at least one nucleotide sequence of SEQ ID NOs: 1 to 350, the reverse complement thereof, an informative fragment thereof, or an informative fragment of the reverse complement thereof.

In some embodiments, the amplification product comprises, consists essentially of or consists of at least one nucleotide sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of SEQ ID NOs: 1 to 350, the reverse complement thereof, an informative fragment thereof or an informative fragment of the reverse complement thereof.

In some embodiments, the amplification product comprises, consists essentially of or consists of at least one nucleotide sequence that specifically hybridizes to the nucleotide sequence of one or more of SEQ ID NOs: 1 to 350, the reverse complement thereof, an informative fragment thereof or an informative fragment of the reverse complement thereof under stringent hybridization conditions.

In some embodiments, the amplification product comprises, consists essentially of or consists of at least one nucleotide sequence that encodes the amino acid sequence set forth in one or more of SEQ ID NOs: 351 to 525 (as described in Table 3).

In some embodiments, the amplification product comprises, consists essentially of or consists of at least one nucleotide sequence that encodes an amino acid sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the amino acid sequence set forth in one or more of SEQ ID NOs: 351 to 525 (as described in Table 3).

In some embodiments, the amplification product comprises, consists essentially of or consists of at least one of SEQ ID NOs: 526 to 613 (as described in Table 9), the reverse complement thereof, an informative fragment thereof or an informative fragment of the reverse complement thereof.

In some embodiments, the amplification product comprises, consists essentially of or consists of at least one nucleotide sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of SEQ ID NOs: 526 to 613 (as described in Table 9), the reverse complement thereof, an informative fragment thereof or an informative fragment of the reverse complement thereof.

In some embodiments, amplification product comprises, consists essentially of or consists of at least one nucleotide sequence that specifically hybridizes to the nucleotide sequence of one or more of SEQ ID NOs: 526 to 613 (as described in Table 9), the reverse complement thereof, an informative fragment thereof or an informative fragment of the reverse complement thereof under stringent hybridization conditions.

In some embodiments, the amplification product comprises, consists essentially of or consists of one or more of the desired alleles described in Table 2 or the reverse complement

thereof. For example, in some embodiments, the amplification product comprises, consists essentially of or consists of at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140 or more of the desired alleles described in Table 2.

5 In embodiments, the amplification product comprises one or more of the desired alleles described in Table 8. For example, in some embodiments, the amplification product comprises at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 or more, or all 18 of the desired alleles described in Table 8.

In embodiments, the amplification product comprises one or more of the desired
10 alleles:

- (a) on chromosome 5 (QTL 5.1 and/or QTL 5.2) as described in Table 8;
- (b) on chromosome 3 as described in Table 8;
- (c) on chromosome 7 as described in Table 8;
- (d) on chromosome 10 as described in Table 8;
- 15 (e) on chromosomes 3 and 5 as described in Table 8;
- (f) on chromosomes 5 and 7 as described in Table 8;
- (g) on chromosomes 3, 5 and 7 as described in Table 8;
- (h) on chromosomes 5 and 10 as described in Table 8;
- (i) on chromosomes 3, 5 and 10 as described in Table 8; or
- 20 (j) any combination of (a) to (i).

In some embodiments, the amplification product comprises one or more of the desired alleles described in Table 10. For example, in some embodiments, the amplification product comprises at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25 or more of the desired alleles described in Table 10.

25 In some embodiments, the amplification product comprises one or more detectable moieties, such as digoxigenin, fluorescein, acridine-ester, biotin, alkaline phosphatase, horseradish peroxidase, β -glucuronidase, β -galactosidase, luciferase, ferritin or a radioactive isotope. *See, e.g.*, Prober et al. SCIENCE 238:336-340 (1987); European Patent Nos. 144914 and 119448; and U.S. Patent Nos. 4,582,789 and 4,563,417.

30 Amplification products of the present invention may be derived using any suitable primers.

Amplification products of the present invention may be generated using any suitable technique(s), including, but not limited to, polymerase chain reaction (PCR) (*e.g.*, Mullis et al. COLD SPRING HARBOR SYMP. QUANT. BIOL. 51:263-273 (1986); European Patent

Nos.50,424; 84,796; 258,017; 237,362 and 201,184; U.S. Patent Nos. 4,683,202; 4,582,788 and 4,683,194).

The present invention also provides isolated and purified marker probes (as described in Table 9).

5 Marker probes (as described in Table 9) of the present invention may be directed against any suitable allele(s), haplotype(s) and/or molecule(s) of interest.

10 In some embodiments, the marker probe is directed against a chromosomal segment of NP2222 maize germplasm. For example, the marker probe may be directed against one or more of chromosomal segments 3 to 12768 as described in Table 1, (e.g., chromosomal segments 3, 13, 25, 506, 7514, 7546, 12747, 12753, 12760-12761 and/or 12767-12768) of NP2222 maize germplasm, the reverse complement thereof, an informative fragment thereof or an informative fragment of the reverse complement thereof.

15 In some embodiments, the marker probe is directed against a chromosomal segment of NP2660 maize germplasm. For example, the marker probe may be directed against one or more of chromosomal segments 3 to 12743 and/or one or more of chromosomal segments 12757 to 12768, (as described in Table 1; e.g., chromosomal segments 3, 13, 25, 506, 7514, 7546, 12747, 12753, 12760-12761 and/or 12767-12768) of NP2660 maize germplasm, the reverse complement thereof, an informative fragment thereof or an informative fragment of the reverse complement thereof.

20 In some embodiments, the marker probe is directed against a chromosomal segment of NP2276 maize germplasm. For example, the marker probe may be directed against chromosomal segment 1 as described in Table 1, one or more of chromosomal segments 46 to 12743 and/or one or more of chromosomal segments 12757 to 12768, (e.g., chromosomal segments 13, 506, 7514, 7546 and/or 12760-12761) of NP2276 maize germplasm, the reverse complement thereof, an informative fragment thereof or an informative fragment of the reverse complement thereof. In some embodiments, the marker probe is directed against a chromosomal segment of ID3461 maize germplasm. For example, the marker probe may be directed against one or more of chromosomal segments 1 to 17 of Table 1 (e.g., chromosomal segments 1 and/or 13) of ID3461 maize germplasm, the reverse complement thereof, an informative fragment thereof or an informative fragment of the reverse complement thereof.

30 In embodiments, the marker probe is directed against a chromosomal segment of a line in Table 11, for example, the marker probe may be directed against one or more of the chromosomal segments described in Table 1, the reverse complement thereof, an informative fragment thereof or an informative fragment of the reverse complement thereof.

In some embodiments, the marker probe is directed against a nucleotide sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of the nucleotide sequences set forth in SEQ ID NOs: 1 to 350 as described in Table 3 and in the VIP accession numbers described in Table 4, the reverse complement thereof, or an informative fragment thereof.

In some embodiments, the marker probe is directed against one or more nucleotide sequences that encode an amino acid sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of the amino acid sequences set forth in SEQ ID NOs: 351 to 525 (as described in Table 3), the reverse complement thereof, or an informative fragment thereof.

In some embodiments, the marker probe is directed against a nucleotide sequence that comprises one or more of the desired alleles described in Table 2. For example, in some embodiments, the marker probe is directed against a nucleotide sequence that comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140 or more of the desired alleles described in Table 2.

In embodiments, the marker probe is directed against a nucleotide sequence that comprises one or more of the desired alleles described in Table 8. For example, in some embodiments, the marker probe is directed against a nucleotide sequence that comprises at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 or more, or all 18 of the desired alleles described in Table 8 (*see, e.g.*, the exemplary probes described in Table 9).

In embodiments, the marker probe is directed against a nucleotide sequence that comprises one or more of the desired alleles:

- (a) on chromosome 5 (QTL 5.1 and/or QTL 5.2) as described in Table 8;
- (b) on chromosome 3 as described in Table 8;
- (c) on chromosome 7 as described in Table 8;
- (d) on chromosome 10 as described in Table 8;
- (e) on chromosomes 3 and 5 as described in Table 8;
- (f) on chromosomes 5 and 7 as described in Table 8;
- (g) on chromosomes 3, 5 and 7 as described in Table 8;
- (h) on chromosomes 5 and 10 as described in Table 8;
- (i) on chromosomes 3, 5 and 10 as described in Table 8; or
- (j) any combination of (a) to (i).

In some embodiments, the marker probe is directed against a nucleotide sequence that comprises one or more of the desired alleles described in Table 10. For example, in some

embodiments, the marker probe is directed against a nucleotide sequence that comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25 or more of the desired alleles described in Table 10.

In some embodiments, the marker probe is directed against an amino acid sequence
5 that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of the amino acid sequences set forth in SEQ ID NOs: 351 to 525 (as described in Table 3) or an informative fragment thereof.

In some embodiments, the marker probe comprises, consists essentially of or consists of an amino acid sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%,
10 99%, 99.5% or more identical to a chromosomal segment of NP2222, the reverse complement thereof, an informative fragment thereof or an informative fragment of the reverse complement thereof. In some such embodiments, the chromosomal segment comprises, consists essentially of or consists of one or more of chromosomal segments 3 to 12768, as described in Table 1 (e.g., chromosomal segments 3, 13, 25, 506, 7514, 7546,
15 12747, 12753, 12760–12761 and/or 12767–12768).

In some embodiments, the marker probe comprises, consists essentially of or consists of an amino acid sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to a chromosomal segment of NP2660, the reverse complement thereof, an informative fragment thereof or an informative fragment of the
20 reverse complement thereof. In some such embodiments, the chromosomal segment comprises, consists essentially of or consists of one or more of chromosomal segments 3 to 12743 and/or one or more of chromosomal segments 12757 to 12768, as described in Table 1 (e.g., chromosomal segments 3, 13, 25, 506, 7514, 7546, 12747, 12753, 12760–12761 and/or 12767–12768).

In some embodiments, the marker probe comprises, consists essentially of or consists of an amino acid sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to a chromosomal segment of NP2276, the reverse complement thereof, an informative fragment thereof or an informative fragment of the reverse complement thereof. In some such embodiments, the chromosomal segment
30 comprises, consists essentially of or consists of chromosomal segment 1, one or more of chromosomal segments 46 to 12743 and/or one or more of chromosomal segments 12757 to 12768, as described in Table 1 (e.g., chromosomal segments 13, 506, 7514, 7546 and/or 12760–12761

In some embodiments, the marker probe comprises, consists essentially of or consists of an amino acid sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to a chromosomal segment of ID3461, the reverse complement thereof, an informative fragment thereof or an informative fragment of the reverse complement thereof. In some such embodiments, the chromosomal segment comprises, consists essentially of or consists of one or more of chromosomal segments 1 to 17 as described in Table 1 (*e.g.*, chromosomal segments 1 and/or 13).

For example, the marker probe may be directed against one or more of chromosomal segments 1 to 17 as described in Table 1 (*e.g.*, chromosomal segments 1 and/or 13) of ID3461 maize germplasm, the reverse complement thereof, an informative fragment thereof or an informative fragment of the reverse complement thereof.

In embodiments, the marker probe is directed against one or more chromosomal segments of a line in Table 11.

In some embodiments, the marker probe comprises, consists essentially of or consists of an amino acid sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of SEQ ID NOs: 1 to 350, the reverse complement thereof, an informative fragment thereof or an informative fragment of the reverse complement thereof.

In some embodiments, the marker probe comprises, consists essentially of or consists of a nucleotide sequence that encodes an amino acid sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the amino acid sequence set forth in one or more of SEQ ID NOs: 351 to 525 (as described in Table 3).

In some embodiments, the marker probe comprises, consists essentially of or consists of an amino acid sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of SEQ ID NOs: 526 to 613 (as described in Table 9), the reverse complement thereof, an informative fragment thereof or an informative fragment of the reverse complement thereof.

In some embodiments, the marker probe comprises one or more detectable moieties, such as digoxigenin, fluorescein, acridine-ester, biotin, alkaline phosphatase, horseradish peroxidase, β -glucuronidase, β -galactosidase, luciferase, ferritin or a radioactive isotope. *See, e.g.*, Prober et al. SCIENCE 238:336-340 (1987); European Patent Nos. 144914 and 119448; and U.S. Patent Nos. 4,582,789 and 4,563,417.

The present invention also provides methods of identifying, selecting and/or producing maize plants and plant parts having increased fertility or one or more

characteristics associated with increased fertility (*e.g.*, one or more characteristics associated with increased male fertility); methods of predicting fertility (*e.g.*, male fertility) in maize plants and plant parts; breeding methods; methods of reducing the costs associated with a breeding and/or seed production program; and methods of improving seed or pollen

5 production in a maize plant (*e.g.*, increasing pollen count per anther, tassel and/or plant).

The methods of the invention can be practiced using one or more of any of the markers, alleles, haplotypes, molecules of interest and/or nonnaturally occurring nucleic acids described herein.

10 Methods of identifying maize plants and plant parts having increased fertility or one or more characteristics associated with increased fertility may comprise, consist essentially of or consist of detecting one or more markers associated with increased fertility (*e.g.*, one or more markers of the present invention as described herein) in a maize plant or plant part (*e.g.*, a maize germplasm or an amplification product from a maize germplasm).

15 Methods of selecting maize plants and plant parts having increased fertility or one or more characteristics associated with increased fertility may comprise, consist essentially of or consist of detecting one or more markers associated with increased fertility (*e.g.*, one or more markers of the present invention as described herein) in a maize plant or plant part (*e.g.*, a maize germplasm or an amplification product from a maize germplasm) and selecting said maize plant or plant part based upon the presence of said marker(s).

20 Methods of predicting fertility (*e.g.*, male fertility) in maize plants and plant parts may comprise, consist essentially of or consist of detecting the presence of one or more markers associated with increased fertility (*e.g.*, one or more markers of the present invention) in a maize plant or plant part (*e.g.*, a maize germplasm or an amplification product from a maize germplasm). In some embodiments, the presence of said marker(s) in the genome of said
 25 maize plant or plant part is associated with an increase of at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, 110%, 120%, 130%, 140%, 150%, 160%, 170%, 180%, 190%, 200%, 225%, 250%, 275%, 300% or more in the ratio of functionally fertile plants to infertile plants. For example, in some embodiments, the presence of said marker(s) in the genome of a maize plant or plant
 30 part indicates that said maize plant or plant part will likely exhibit increased pollen production, increased pollen production per anther, improved pollen morphology, increased anther production, increased anther production per tassel, improved anther morphology, increased tassel production, improved tassel morphology, increased silk production, improved silk morphology, increased silk production per plant, increased kernel count,

improved kernel morphology, increased kernel production per ear, decreased prevalence of kernel abortion, increased kernel production per plant, increased kernel viability, increased fertility under stress conditions (*e.g.*, drought conditions), increased fertility under elevated daytime temperatures and/or increased fertility under elevated nighttime temperatures as compared to a control plant (*e.g.*, one or both of its parents, a near isogenic line lacking a Vip3 protein coding sequence, etc.).

In embodiments of the methods described herein, a plant or part thereof (or an ancestor or progeny plant or part thereof) is phenotyped to confirm the fertility state (*e.g.*, the state of male fertility) or the presence of characteristics associated with fertility.

Breeding methods of the present invention may comprise, consist essentially of or consist of:

- (a) detecting one or more markers associated with increased fertility (*e.g.*, one or more markers of the present invention) in a maize plant or plant part (*e.g.*, a maize germplasm or an amplification product from a maize germplasm) and selecting said maize plant or plant part for inclusion in a breeding program based upon the presence of said marker(s); and/or
- (b) detecting the absence of one or more markers associated with increased fertility (*e.g.*, one or more markers of the present invention) in a maize plant or plant part (*e.g.*, a maize germplasm or an amplification product from a maize germplasm) and excluding said maize plant or plant part from a breeding program based upon the absence of said marker(s).

In embodiments of the method of (a), the method further comprises crossing the maize plant (or an ancestor, progeny or sibling thereof) with a second maize plant that optionally lacks the marker to produce a progeny maize plant, which optionally comprises the marker. Those skilled in the art will appreciate that in the case of an inbred line, the term “crossing the maize plant” or “crossing the selected maize plant” can refer to an identical or essentially (*e.g.*, at least 95% genetically identical) parent, sibling or progeny plant.

Optionally, the method further comprises phenotyping the maize plant or plant part (or an ancestor or progeny plant or part thereof) to confirm the fertility state (*e.g.*, the state of male fertility) or the presence of characteristics associated with fertility.

Maize plants and plant parts selected for inclusion in the breeding program may be used to produce one or more generations of fertile progeny. In some embodiments, each generation of progeny plants comprises substantially and/or completely fertile maize plants and plant parts.

The invention also encompasses methods for producing a plant having one or more characteristics associated with increased male fertility. In embodiments, the method comprises: selecting from a diverse maize plant population a maize plant comprising a marker, allele, haplotype, genomic region, and the like associated with increased male fertility as described herein; and crossing the maize plant (or an ancestor, progeny or sibling thereof) with itself or a second maize plant to produce a progeny plant comprising the marker/allele/haplotype/genomic region, thereby producing a plant having one or more characteristics associated with increased male fertility. In embodiments, the second maize plant does not comprise the marker/allele/haplotype/genomic region. In embodiments, the marker/allele/haplotype/genomic region is detected in nucleic acid from the first maize plant and/or progeny plant (*e.g.*, in an amplification product from a nucleic acid sample from the maize plant and/or progeny). Optionally, the method further comprises phenotyping the maize plant or plant part (or an ancestor or progeny plant or part thereof) to confirm the fertility state (*e.g.*, the state of male fertility) or the presence of characteristics associated with fertility.

In embodiments, methods of increasing seed production or reducing the costs associated with a breeding and/or seed production program comprise, consisting essentially of, or consisting of:

- (a) detecting one or more markers associated with increased fertility (*e.g.*, one or more markers of the present invention) in a maize plant or plant part (*e.g.*, a maize germplasm or an amplification product from a maize germplasm) and selecting said maize plant or plant part for inclusion in the breeding and/or seed production program based upon the presence of said marker(s); and/or
- (b) detecting the absence of one or more markers associated with increased fertility (*e.g.*, one or more markers of the present invention) in a maize plant or plant part (*e.g.*, a maize germplasm or an amplification product from a maize germplasm) and excluding said maize plant or plant part from the breeding and/or seed production program based upon the absence of said marker(s).

Optionally, the method further comprises phenotyping the maize plant or plant part (or an ancestor or progeny plant or part thereof) to confirm the fertility state (*e.g.*, the state of male fertility) or the presence of characteristics associated with fertility.

Maize plants and plant parts selected for inclusion in the breeding and/or seed production program may be used to produce one or more generations of fertile progeny. In

some embodiments, each generation of progeny plants comprises substantially and/or completely fertile maize plants and plant parts.

Methods of producing maize plants and plant parts having increased fertility or one or more characteristics associated with increased fertility may comprise, consist essentially of or

5 consist of:

- (a) detecting one or more markers associated with increased fertility (*e.g.*, one or more markers of the present invention) in a maize plant or plant part (*e.g.*, a maize germplasm or an amplification product from a maize germplasm) and producing a maize plant from said maize plant or plant part;
- 10 (b) introducing a nucleic acid comprising one or more alleles associated with increased fertility (*e.g.*, one or more alleles associated with increased male fertility) into the genome of a maize plant or plant part and producing a maize plant from said maize plant or plant part;
- 15 (c) introducing a nucleic acid comprising one or more alleles associated with increased fertility (*e.g.*, one or more alleles associated with increased male fertility) into the genome of a maize plant or plant part, detecting said allele(s) in said maize plant or plant part (by detecting said allele(s) or an informative fragment thereof in an amplification product from said maize plant or plant part, for example) and producing a maize plant from said maize plant or plant part;
- 20 (d) introducing a nucleic acid comprising one or more alleles associated with increased fertility (*e.g.*, one or more alleles associated with increased male fertility) into the genome of a maize plant part or plant part, detecting one or more markers linked to said allele(s) in said maize plant part or plant part (by detecting said marker(s) or an informative fragment thereof in an amplification product from said maize plant or
- 25 plant part, for example) and producing a maize plant from said maize plant or plant part;
- (e) introducing a genomic region comprising one or more transgenes associated with increased fertility (*e.g.*, one or more transgenes associated with increased male fertility) into the genome of a maize plant or plant part and producing a maize plant
- 30 from said maize plant or plant part;
- (f) introducing a genomic region comprising one or more transgenes associated with increased fertility (*e.g.*, one or more transgenes associated with increased male fertility) into the genome of a maize plant or plant part, detecting said genomic region in said maize plant or plant part (by detecting said transgene(s) or an informative

fragment thereof in an amplification product from said maize plant or plant part, for example) and producing a maize plant from said maize plant or plant part; and/or

(g) introducing a genomic region comprising one or more transgenes associated with increased fertility (*e.g.*, one or more transgenes associated with increased male

5 fertility) into the genome of a maize plant part or plant part, detecting one or more markers linked to said genomic region in said maize plant part or plant part (by detecting said marker(s) or an informative fragment thereof in an amplification product from said maize plant or plant part, for example) and producing a maize plant from said maize plant or plant part.

10 Optionally, the method further comprises phenotyping the maize plant or plant part (or an ancestor or progeny plant or part thereof) to confirm the fertility state (*e.g.*, the state of male fertility) or the presence of characteristics associated with fertility.

Methods of improving pollen production in a maize plant (*e.g.*, increasing pollen count per anther, tassel and/or plant) may comprise, consist essentially of or consist of:

15 (a) introducing a nucleic acid comprising one or more alleles associated with increased fertility (*e.g.*, one or more alleles associated with increased male fertility) into the genome of a maize plant and, optionally, detecting said allele(s) in said maize plant (by detecting said allele(s) or an informative fragment thereof in an amplification product from said maize plant, for example).

20 (b) introducing a nucleic acid comprising one or more alleles associated with increased fertility (*e.g.*, one or more alleles associated with increased male fertility) into the genome of a maize plant and, optionally, detecting one or more markers linked to said allele(s) in said maize plant (by detecting said marker(s) or an informative fragment thereof in an amplification product from said maize plant part, for example);

25 (c) introducing a nucleic acid comprising one or more alleles associated with increased fertility (*e.g.*, one or more alleles associated with increased male fertility) into the genome of a maize plant part and producing a maize plant from said maize plant part;

(d) introducing a nucleic acid comprising one or more alleles associated with increased fertility (*e.g.*, one or more alleles associated with increased male fertility) into the
30 genome of a maize plant or plant part, detecting said allele(s) in said maize plant or plant part (by detecting said allele(s) or an informative fragment thereof in an amplification product from said maize plant or plant part, for example) and producing a maize plant from said maize plant or plant part;

- (e) introducing a nucleic acid comprising one or more alleles associated with increased fertility (*e.g.*, one or more alleles associated with increased male fertility) into the genome of a maize plant or plant part, detecting one or more markers linked to said allele(s) in said maize plant or plant part (by detecting said marker(s) or an informative fragment thereof in an amplification product from said maize plant or plant part, for example) and producing a maize plant from said maize plant or plant part;
- (f) introducing a genomic region comprising one or more transgenes associated with increased fertility (*e.g.*, one or more transgenes associated with increased male fertility) into the genome of a maize plant or plant part and producing a maize plant from said maize plant or plant part;
- (g) introducing a genomic region comprising one or more transgenes associated with increased fertility (*e.g.*, one or more transgenes associated with increased male fertility) into the genome of a maize plant or plant part, detecting said genomic region in said maize plant or plant part (by detecting said transgene(s) or an informative fragment thereof in an amplification product from said maize plant or plant part, for example) and producing a maize plant from said maize plant or plant part; and/or
- (h) introducing a genomic region comprising one or more transgenes associated with increased fertility (*e.g.*, one or more transgenes associated with increased male fertility) into the genome of a maize plant part or plant part, detecting one or more markers linked to said genomic region in said maize plant part or plant part (by detecting said marker(s) or an informative fragment thereof in an amplification product from said maize plant or plant part, for example) and producing a maize plant from said maize plant or plant part.
- Optionally, the method further comprises phenotyping the maize plant or plant part (or an ancestor or progeny plant or part thereof) to confirm the fertility state (*e.g.*, the state of male fertility) or the presence of characteristics associated with fertility.

The invention further contemplates a method of improving seed production from a maize plant, comprising: crossing a first maize plant with a second maize plant, wherein the first maize plant comprises within its genome a marker associated with increased male fertility, and wherein said marker is located within one or more of the chromosomal intervals described in Table 1, to produce a progeny maize plant comprising said marker; and using a progeny maize plant comprising said marker as a pollinator (male) in a cross with itself or a second maize plant that functions as a seed parent (female), thereby improving seed

production from the cross as compared with a suitable control cross (*e.g.*, a selfing or cross with the progeny plant lacking the marker associated with increased fertility). In embodiments, the second maize plant lacks the marker. In exemplary embodiments, the method reduces the ratio of pollinator parent to seed parent maize plants required for seed
 5 production by at least about 25% as compared with a suitable control cross. In embodiments, the method increases the number of seeds produced per pollinator parent plant and/or seed parent plant by at least about 25%.

Optionally, the method further comprises phenotyping the first maize plant and/or the progeny plant (or an ancestor or progeny plant or part thereof) to confirm the fertility state
 10 (*e.g.*, the state of male fertility) or the presence of characteristics associated with fertility.

Markers for use with the methods of the invention can include any one or more suitable markers as described herein.

Markers associated with increased fertility (*e.g.*, male fertility) may be detected using any suitable marker probe as described herein.

15 In some embodiments, the marker is detected using a probe designed to detect an allele of interest located within one or more of the chromosomal segments described in Table 1. For example, in some embodiments, the marker is detected using a probe designed to detect an allele of interest located within one or more of chromosomal segments 46 to 12473 (*e.g.*, within chromosomal segment 7514).

20 In some embodiments, the marker is detected using a probe designed to detect two or more alleles located within one or more of the chromosomal segments described in Table 1. For example, in some embodiments, the marker is detected using a probe designed to detect two or more alleles located within one or more of chromosomal segments 46 to 12473 (*e.g.*, a haplotype comprising two or more alleles of interest located within chromosomal segment
 25 7514).

In some embodiments, the marker is detected using a probe designed to detect alleles located in distinct chromosomal segments, wherein each of the distinct chromosomal segments comprises one or more of the chromosomal segments described in Table 1. For example, in some embodiments, the marker is detected using probes designed to detect:

30 1) one or more alleles of interest located within one or more of chromosomal segments 46 to 12473 (*e.g.*, one or more alleles of interest located within chromosomal segment 7514) and one or more alleles of interest located within chromosomal segment 1;

- 2) one or more alleles of interest located within one or more of chromosomal segments 46 to 12473 (e.g., one or more alleles of interest located within chromosomal segment 7514) and one or more alleles of interest located on chromosome 2;
- 3) one or more alleles of interest located within one or more of chromosomal segments 46 to 12473 (e.g., one or more alleles of interest located within chromosomal segment 7514) and one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (e.g., one or more alleles of interest located within chromosomal segment 3);
- 4) one or more alleles of interest located within one or more of chromosomal segments 46 to 12473 (e.g., one or more alleles of interest located within chromosomal segment 7514) and one or more alleles of interest located within one or more of chromosomal segments 18 to 45 (e.g., one or more alleles of interest located within chromosomal segment 25);
- 5) one or more alleles of interest located within one or more of chromosomal segments 46 to 12473 (e.g., one or more alleles of interest located within chromosomal segment 7514) and one or more alleles of interest located within one or more of chromosomal segments 12744 to 12749 (e.g., one or more alleles of interest located within chromosomal segment 12747);
- 6) one or more alleles of interest located within one or more of chromosomal segments 46 to 12473 (e.g., one or more alleles of interest located within chromosomal segment 7514) and one or more alleles of interest located within one or more of chromosomal segments 12750 to 12755 (e.g., one or more alleles of interest located within chromosomal segment 12753);
- 7) one or more alleles of interest located within one or more of chromosomal segments 46 to 12473 (e.g., one or more alleles of interest located within chromosomal segment 7514) and one or more alleles of interest located within chromosomal segment 12756;
- 8) one or more alleles of interest located within one or more of chromosomal segments 46 to 12473 (e.g., one or more alleles of interest located within chromosomal segment 7514) and one or more alleles of interest located within one or more of chromosomal segments 12757 to 12762 (e.g., one or more alleles of interest located within chromosomal segment 12760 and/or chromosomal segment 12761);
- 9) one or more alleles of interest located within one or more of chromosomal segments 46 to 12473 (e.g., one or more alleles of interest located within chromosomal segment 7514) and one or more alleles of interest located within one or more of chromosomal

segments 12763 to 12768 (e.g., one or more alleles of interest located within chromosomal segment 12768);

- 10) one or more alleles of interest located within one or more of chromosomal segments 46 to 12473 (e.g., one or more alleles of interest located within chromosomal segment 7514), one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (e.g., one or more alleles of interest located within chromosomal segment 3), one or more alleles of interest located within one or more of chromosomal segments 18 to 45 (e.g., one or more alleles of interest located within chromosomal segment 25) and one or more alleles of interest located within one or more of chromosomal segments 12763 to 12768 (e.g., one or more alleles of interest located within chromosomal segment 12768);
- 11) one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (e.g., one or more alleles of interest located within chromosomal segment 3) and one or more alleles of interest located within chromosomal segment 1;
- 12) one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (e.g., one or more alleles of interest located within chromosomal segment 3) and one or more alleles of interest located on chromosome 2;
- 13) one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (e.g., one or more alleles of interest located within chromosomal segment 3) and one or more alleles of interest located within one or more of chromosomal segments 18 to 45 (e.g., one or more alleles of interest located within chromosomal segment 25);
- 14) one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (e.g., one or more alleles of interest located within chromosomal segment 3) and one or more alleles of interest located within one or more of chromosomal segments 12744 to 12749 (e.g., one or more alleles of interest located within chromosomal segment 12747);
- 15) one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (e.g., one or more alleles of interest located within chromosomal segment 3) and one or more alleles of interest located within one or more of chromosomal segments 12750 to 12755 (e.g., one or more alleles of interest located within chromosomal segment 12753);

- 16) one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (*e.g.*, one or more alleles of interest located within chromosomal segment 3) and one or more alleles of interest located within chromosomal segment 12756;
- 17) one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (*e.g.*, one or more alleles of interest located within chromosomal segment 3) and one or more alleles of interest located within one or more of chromosomal segments 12757 to 12762 (*e.g.*, one or more alleles of interest located within chromosomal segment 12760 and/or chromosomal segment 12761);
- 18) one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (*e.g.*, one or more alleles of interest located within chromosomal segment 3) and one or more alleles of interest located within one or more of chromosomal segments 12763 to 12768 (*e.g.*, one or more alleles of interest located within chromosomal segment 12768);
- 19) one or more alleles of interest located on chromosome 2, one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (*e.g.*, one or more alleles of interest located within chromosomal segment 3), one or more alleles of interest located within one or more of chromosomal segments 10266 to 10271 (*e.g.*, one or more alleles of interest located within chromosomal segment 10269) and one or more alleles of interest located within chromosomal segment 12756.
- In some embodiments, the marker is detected using a probe designed to detect one or more chromosomal segments derived from NP2222 maize germplasm (*e.g.*, NP2222AC maize germplasm), wherein said one or more chromosomal segments comprises, consists essentially of or consists of one or more of the chromosomal segments described in Table 1. For example, in some embodiments, the marker is detected using a probe designed to detect one or more of chromosomal segments 3 to 12768, (*e.g.*, chromosomal segments 3, 13, 25, 506, 7514, 7546, 12747, 12753, 12760–12761 and/or 12767–12768) derived from NP2222 maize germplasm.

In some embodiments, the marker is detected using a probe designed to detect one or more chromosomal segments derived from NP2660 maize germplasm (*e.g.*, NP2660AC NIL-2343, NP2660AC NIL-3338 or NP2660AC NIL-3367 maize germplasm), wherein said one or more chromosomal segments comprises, consists essentially of or consists of one or more of the chromosomal segments described in Table 1. For example, in some embodiments, the marker is detected using a probe designed to detect one or more of chromosomal segments 3 to 12743 and/or one or more of chromosomal segments 12757 to 12768, (*e.g.*, chromosomal

segments 3, 13, 25, 506, 7514, 7546, 12747, 12753, 12760–12761 and/or 12767–12768) derived from NP2660 maize germplasm.

In some embodiments, the marker is detected using a probe designed to detect one or more chromosomal segments derived from NP2276 maize germplasm (e.g., NP2276AC NIL
5 maize germplasm), wherein said one or more chromosomal segments comprises, consists essentially of or consists of one or more of the chromosomal segments described in Table 1. For example, in some embodiments, the marker is detected using a probe designed to detect chromosomal segment 1, one or more of chromosomal segments 46 to 12743 and/or one or more of chromosomal segments 12757 to 12768, (e.g., chromosomal segments 13, 506, 7514,
10 7546 and/or 12760–12761) derived from NP2276 maize germplasm.

In some embodiments, the marker is detected using a probe designed to detect one or more chromosomal segments derived from ID3461 maize germplasm, wherein said one or more chromosomal segments comprises, consists essentially of or consists of one or more of the chromosomal segments described in Table 1. For example, in some embodiments, the
15 marker is detected using a probe designed to detect one or more of chromosomal segments 1 to 17 (e.g., chromosomal segments 1 and/or 13) derived from ID3461 maize germplasm.

In embodiments, the marker is detected using a probe designed to detect one or more chromosomal segments derived from a line in Table 11.

In some embodiments, the marker is detected using a probe designed to detect at least
20 one of SEQ ID NOs: 1 to 350 (as described in Table 3).

In some embodiments, the marker is detected using a probe designed to detect any nucleotide sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of SEQ ID NOs: 1 to 350 (as described in Table 3).

In some embodiments, the marker is detected using a probe designed to detect any
25 nucleotide sequence that specifically hybridizes to the nucleotide sequence of one or more of SEQ ID NOs: 1 to 350 (as described in Table 3) under stringent hybridization conditions. In some embodiments, the marker is detected using a probe designed to detect any nucleotide sequence that encodes the amino acid sequence set forth in one or more of SEQ ID NOs: 351 to 525 (as described in Table 3).

30 In some embodiments the marker is detected using a probe designed to detect any nucleotide sequence that encodes an amino acid sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the amino acid sequence set forth in one or more of SEQ ID NOs: 351 to 525 (as described in Table 3).

In some embodiments, the marker is detected using a probe designed to detect at least one of SEQ ID NOs: 526 to 613 (as described in Table 9).

In some embodiments, the marker is detected using a probe designed to detect any nucleotide sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%,
5 99.5% or more identical to one or more of SEQ ID NOs: 526 to 613 (as described in Table 9).

In some embodiments, the marker is detected using a probe designed to detect any nucleotide sequence that specifically hybridizes to the nucleotide sequence of one or more of SEQ ID NOs: 526 to 613 (as described in Table 9) under stringent hybridization conditions.

In some embodiments, the marker is detected using a probe designed to detect one or
10 more of the desired alleles described in Table 2. For example, in some embodiments, the marker is detected using a probe designed to detect 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140 or more of the desired alleles described in Table 2.

In embodiments, the marker is detected using a probe designed to detect one or more
15 of the desired alleles described in Table 8. For example, in some embodiments, the marker is detected using a probe designed to detect at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 or more, or all 18 of the desired alleles described in Table 8 (*see, e.g.*, the exemplary probes described in Table 9).

In embodiments, the marker is detected using a probe designed to detect one or more
20 of the desired alleles:

- (a) on chromosome 5 (QTL 5.1 and/or QTL 5.2) as described in Table 8;
- (b) on chromosome 3 as described in Table 8;
- (c) on chromosome 7 as described in Table 8;
- (d) on chromosome 10 as described in Table 8;
- 25 (e) on chromosomes 3 and 5 as described in Table 8;
- (f) on chromosomes 5 and 7 as described in Table 8;
- (g) on chromosomes 3, 5 and 7 as described in Table 8;
- (h) on chromosomes 5 and 10 as described in Table 8;
- (i) on chromosomes 3, 5 and 10 as described in Table 8; or
- 30 (j) any combination of (a) to (i).

In some embodiments, the marker is detected using a probe designed to detect one or more of the desired alleles described in Table 10. For example, in some embodiments, the

marker is detected using a probe designed to detect 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25 or more of the desired alleles described in Table 10.

In some embodiments, the marker is detected using a probe designed to detect the reverse complement of one of a marker as described herein.

5 In some embodiments, the marker is detected using a probe designed to detect an informative fragment of one of the markers as described herein.

In some embodiments, the marker is detected using a probe designed to detect a marker linked to one or more of the markers described herein. That is, the marker may be detected using a probe designed to detect a marker that is in linkage disequilibrium with any
10 of the markers described herein.

In some embodiments, the marker is detected using a probe designed to detect a marker located within about 20 cM, 15 cM, 10 cM, 5 cM or 1 cM or less of any one of the markers described herein. For example, in some embodiments, the marker is detected using a probe designed to detect one or more markers located within about 5 cM, 1 cM or less of
15 chromosomal segment 7514.

Markers associated with increased fertility may be detected in any suitable plant part, including, but not limited to, amplification products derived from maize germplasm.

Markers associated with increased fertility may be detected in any suitable amplification product, for example, an amplification product as described herein.

20 In some embodiments, the marker is detected in an amplification product comprising, consisting essentially of, or consisting of one or more of the chromosomal segments described in Table 1. For example, in some embodiments, the marker may be detected in an amplification product comprising, consisting essentially of, or consisting of:

- (a) chromosomal segment 1;
- 25 (b) one or more of chromosomal segments 3 to 17 (*e.g.*, within chromosomal segment 3);
- (c) one or more of chromosomal segments 18 to 45 (*e.g.*, within chromosomal segment 25);
- (d) one or more of chromosomal segments 46 to 12473 (*e.g.*, within chromosomal segment 7514);
- 30 (e) one or more of chromosomal segments 12744 to 12749 (*e.g.*, within chromosomal segment 12747);
- (f) one or more of chromosomal segments 12750 to 12755 (*e.g.*, within chromosomal segment 12753);
- (g) one or more of chromosomal segment 12756;

- (h) one or more of chromosomal segments 12757 to 12762 (*e.g.*, within chromosomal segment 12760 and/or chromosomal segment 12761); or
- (i) one or more of chromosomal segments 12763 to 12768 (*e.g.*, within chromosomal segment 12768).

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In some embodiments, the marker is detected in an amplification product comprising, consisting essentially of, or consisting of at least one of SEQ ID NOs: 1 to 350 (as described in Table 3).

10 In some embodiments, the marker is detected in an amplification product comprising, consisting essentially of, or consisting of a nucleotide sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of SEQ ID NOs: 1 to 350 (as described in Table 3).

15 In some embodiments, the marker is detected in an amplification product comprising, consisting essentially of, or consisting of a nucleotide sequence that specifically hybridizes to the nucleotide sequence of one or more of SEQ ID NOs: 1 to 350 (as described in Table 3) under stringent hybridization conditions.

In some embodiments, the marker is detected in an amplification product comprising, consisting essentially of, or consisting of a nucleotide sequence that encodes the amino acid sequence set forth in one or more of SEQ ID NOs: 351 to 525 (as described in Table 3).

20 In some embodiments, the marker is detected in an amplification product comprising, consisting essentially of, or consisting of a nucleotide sequence that encodes an amino acid sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the amino acid sequence set forth in one or more of SEQ ID NOs: 351 to 525 (as described in Table 3).

25 In some embodiments, the marker is detected using a probe designed to detect at least one of SEQ ID NOs: 526 to 613 (as described in Table 9).

In some embodiments, the marker is detected in an amplification product comprising, consisting essentially of, or consisting of a nucleotide sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of SEQ ID NOs: 526 to 613 (as described in Table 9).

30 In some embodiments, the marker is detected in an amplification product comprising, consisting essentially of, or consisting of a nucleotide sequence that specifically hybridizes to the nucleotide sequence of one or more of SEQ ID NOs: 526 to 613 (as described in Table 9) under stringent hybridization conditions.

In some embodiments, the marker is detected in an amplification product comprising one or more of the desired alleles described in Table 2. For example, in some embodiments, the marker is detected in an amplification product comprising 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130,

5 140 or more of the desired alleles described in Table 2.

In embodiments, the marker is detected in an amplification product comprising one or more of the desired alleles described in Table 8. For example, in some embodiments, the marker is detected in an amplification product comprising at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 or more, or all 18 of the desired alleles described in Table 8

10 (*see, e.g.*, the exemplary amplification primers and probes described in Table 9).

In embodiments, the marker is detected in an amplification product comprising one or more of the desired alleles:

- (a) on chromosome 5 (QTL 5.1 and/or QTL 5.2) as described in Table 8;
- (b) on chromosome 3 as described in Table 8;
- 15 (c) on chromosome 7 as described in Table 8;
- (d) on chromosome 10 as described in Table 8;
- (e) on chromosomes 3 and 5 as described in Table 8;
- (f) on chromosomes 5 and 7 as described in Table 8;
- (g) on chromosomes 3, 5 and 7 as described in Table 8;
- 20 (h) on chromosomes 5 and 10 as described in Table 8;
- (i) on chromosomes 3, 5 and 10 as described in Table 8; or
- (j) any combination of (a) to (i).

In some embodiments, the marker is detected in an amplification product comprising one or more of the desired alleles described in Table 10. For example, in some embodiments,

25 the marker is detected in an amplification product comprising 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25 or more of the desired alleles described in Table 10.

Alleles may be introduced into maize plants and plant parts using any suitable method, including, but not limited to, crossing, transfection, transduction, protoplast transformation or fusion, double haploid technique, embryo rescue, or by any other nucleic acid transfer system. In some embodiments, one or more alleles associated with increased

30 fertility is/are introduced into the genome of a maize plant or plant part through a breeding program comprising MAS using one or more of the markers described herein.

Thus, in some embodiments, methods of producing maize plants and plant parts having increased fertility (*e.g.*, increased male fertility) or one or more characteristics

associated with increased fertility and/or maize plants and plant parts comprising one or more alleles associated with increased fertility and methods of improving pollen production may comprise:

- 5 (a) crossing a first maize plant or plant part with a second maize plant or plant part, wherein the first maize plant or plant part comprises within its genome one or more alleles associated with increased fertility (*e.g.*, one or more alleles associated with increased male fertility);
- 10 (b) crossing a first maize plant or plant part with a second maize plant or plant part, wherein the first maize plant or plant part comprises within its genome one or more haplotypes associated with increased fertility (*e.g.*, one or more alleles associated with increased male fertility);
- 15 (c) detecting the presence of one or more alleles associated with increased fertility (*e.g.*, one or more alleles associated with increased male fertility) in a first maize plant or plant part (by detecting said allele(s) or an informative fragment thereof in an amplification product from said maize plant or plant part, for example) and crossing the first maize plant or plant part with a second maize plant or plant part lacking said allele(s);
- 20 (d) detecting the presence of one or more haplotypes associated with increased fertility (*e.g.*, one or more haplotypes associated with increased male fertility) in a first maize plant or plant part (by detecting said haplotype(s) or an informative fragment thereof in an amplification product from said maize plant or plant part, for example) and crossing the first maize plant or plant part with a second maize plant or plant part lacking said allele(s);
- 25 (e) detecting the presence of one or more transgenes associated with increased fertility (*e.g.*, one or more transgenes associated with increased male fertility) in a first maize plant or plant part (by detecting said transgene(s) or an informative fragment thereof in an amplification product from said maize plant or plant part, for example) and crossing the first maize plant or plant part with a second maize plant or plant part lacking said marker(s);
- 30 (f) detecting the presence of a genomic region comprising one or more transgenes associated with increased fertility (*e.g.*, one or more transgenes associated with increased male fertility) in a first maize plant or plant part (by detecting said genomic region or an informative fragment thereof in an amplification product from

- said maize plant or plant part, for example) and crossing the first maize plant or plant part with a second maize plant or plant part lacking said genomic region;
- (g) detecting the presence of one or more markers associated with increased fertility (e.g., one or more markers associated with increased male fertility) in a first maize plant or plant part (by detecting said marker(s) or an informative fragment thereof in an amplification product from said maize plant or plant part, for example) and crossing the first maize plant or plant part with a second maize plant or plant part lacking said marker(s);
- (h) crossing a first maize plant or plant part comprising one or more alleles associated with increased fertility (e.g., one or more alleles associated with increased male fertility) with a second maize plant or plant part that lacks said allele(s) and backcrossing for one or more generations progeny comprising said allele(s) with said second maize plant or plant part;
- (i) detecting the presence of one or more alleles associated with increased fertility (e.g., one or more alleles associated with increased male fertility) in a first maize plant or plant part (by detecting said allele(s) or an informative fragment thereof in an amplification product from said maize plant or plant part, for example), crossing the first maize plant or plant part with a second maize plant or plant part lacking said allele(s), and backcrossing for one or more generations progeny comprising said allele(s) with said second maize plant or plant part;
- (j) detecting the presence of one or more haplotypes associated with increased fertility (e.g., one or more haplotypes associated with increased male fertility) in a first maize plant or plant part (by detecting said haplotype(s) or an informative fragment thereof in an amplification product from said maize plant or plant part, for example), crossing the first maize plant or plant part with a second maize plant or plant part lacking said haplotype(s), and backcrossing for one or more generations progeny comprising said haplotype(s) with said second maize plant or plant part;
- (k) detecting the presence of one or more transgenes associated with increased fertility (e.g., one or more transgenes associated with increased male fertility) in a first maize plant or plant part (by detecting said transgene(s) or an informative fragment thereof in an amplification product from said maize plant or plant part, for example), crossing the first maize plant or plant part with a second maize plant or plant part lacking said transgene(s), and backcrossing for one or more generations

progeny comprising said transgene(s) with said second maize plant or plant part;
and/or

- (l) detecting the presence of a genomic region comprising one or more transgenes associated with increased fertility (*e.g.*, one or more transgenes associated with increased male fertility) in a first maize plant or plant part (by detecting said genomic region or an informative fragment thereof in an amplification product from said maize plant or plant part, for example), crossing the first maize plant or plant part with a second maize plant or plant part lacking said genomic region, and backcrossing for one or more generations progeny comprising said genomic region with said second maize plant or plant part; and/or
- (m) detecting the presence of one or more markers associated with increased fertility (*e.g.*, one or more markers associated with increased male fertility) in a first maize plant or plant part (by detecting said marker(s) or an informative fragment thereof in an amplification product from said maize plant or plant part, for example), crossing the first maize plant or plant part with a second maize plant or plant part lacking said marker(s), and backcrossing for one or more generations progeny comprising said marker(s) with said second maize plant or plant part.

Optionally, the method further comprises phenotyping the maize plant or plant part (or an ancestor or progeny plant or part thereof) to confirm the fertility state (*e.g.*, the state of male fertility) or the presence of characteristics associated with fertility.

Any suitable allele(s) may be introduced into the maize plant or plant part, including, but not limited to, any one or more of the alleles described.

In some embodiments, a nucleic acid comprising, consisting essentially of, or consisting of one or more of the chromosomal segments described in Table 1 is introduced into the maize plant or plant part. For example, in some embodiments, one or more of chromosomal segments 46 to 12473 (*e.g.*, chromosomal segment 7514) is introduced into the maize plant or plant part.

In some embodiments, one or more haplotypes associated with increased fertility (*e.g.*, increased male fertility) is introduced into the maize plant or plant part. The haplotype can include any of one or more of the haplotypes as described herein. In some such embodiments, the haplotype comprises, consists essentially of or consists of two or more alleles of interest located within one or more of the chromosomal segments described in Table 1 (*e.g.*, a haplotype comprising two or more alleles of interest located within chromosomal segment 7514). In some such embodiments, the haplotype comprises, consists

essentially of or consists of one or more alleles of interest located within a first chromosomal segment and one or more alleles of interest located within a second chromosomal segment different from the first chromosomal segment, wherein each of the first and second chromosomal segments comprises one or more of the chromosomal segments described in

5 Table 1. For example, the haplotype may comprise, consist essentially of or consist of:

- 1) one or more alleles of interest located within one or more of chromosomal segments 46 to 12473 (*e.g.*, one or more alleles of interest located within chromosomal segment 7514) and one or more alleles of interest located within chromosomal segment 1;
- 10 2) one or more alleles of interest located within one or more of chromosomal segments 46 to 12473 (*e.g.*, one or more alleles of interest located within chromosomal segment 7514) and one or more alleles of interest located on chromosome 2;
- 15 3) one or more alleles of interest located within one or more of chromosomal segments 46 to 12473 (*e.g.*, one or more alleles of interest located within chromosomal segment 7514) and one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (*e.g.*, one or more alleles of interest located within chromosomal segment 3);
- 20 4) one or more alleles of interest located within one or more of chromosomal segments 46 to 12473 (*e.g.*, one or more alleles of interest located within chromosomal segment 7514) and one or more alleles of interest located within one or more of chromosomal segments 18 to 45 (*e.g.*, one or more alleles of interest located within chromosomal segment 25);
- 25 5) one or more alleles of interest located within one or more of chromosomal segments 46 to 12473 (*e.g.*, one or more alleles of interest located within chromosomal segment 7514) and one or more alleles of interest located within one or more of chromosomal segments 12744 to 12749 (*e.g.*, one or more alleles of interest located within chromosomal segment 12747);
- 30 6) one or more alleles of interest located within one or more of chromosomal segments 46 to 12473 (*e.g.*, one or more alleles of interest located within chromosomal segment 7514) and one or more alleles of interest located within one or more of chromosomal segments 12750 to 12755 (*e.g.*, one or more alleles of interest located within chromosomal segment 12753);
- 7) one or more alleles of interest located within one or more of chromosomal segments 46 to 12473 (*e.g.*, one or more alleles of interest located within chromosomal segment 7514) and one or more alleles of interest located within chromosomal segment 12756;

- 8) one or more alleles of interest located within one or more of chromosomal segments 46 to 12473 (*e.g.*, one or more alleles of interest located within chromosomal segment 7514) and one or more alleles of interest located within one or more of chromosomal segments 12757 to 12762 (*e.g.*, one or more alleles of interest located within chromosomal segment 12760 and/or chromosomal segment 12761);
- 9) one or more alleles of interest located within one or more of chromosomal segments 46 to 12473 (*e.g.*, one or more alleles of interest located within chromosomal segment 7514) and one or more alleles of interest located within one or more of chromosomal segments 12763 to 12768 (*e.g.*, one or more alleles of interest located within chromosomal segment 12768);
- 10) one or more alleles of interest located within one or more of chromosomal segments 46 to 12473 (*e.g.*, one or more alleles of interest located within chromosomal segment 7514), one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (*e.g.*, one or more alleles of interest located within chromosomal segment 3), one or more alleles of interest located within one or more of chromosomal segments 18 to 45 (*e.g.*, one or more alleles of interest located within chromosomal segment 25) and one or more alleles of interest located within one or more of chromosomal segments 12763 to 12768 (*e.g.*, one or more alleles of interest located within chromosomal segment 12768);
- 11) one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (*e.g.*, one or more alleles of interest located within chromosomal segment 3) and one or more alleles of interest located within chromosomal segment 1;
- 12) one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (*e.g.*, one or more alleles of interest located within chromosomal segment 3) and one or more alleles of interest located on chromosome 2;
- 13) one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (*e.g.*, one or more alleles of interest located within chromosomal segment 3) and one or more alleles of interest located within one or more of chromosomal segments 18 to 45 (*e.g.*, one or more alleles of interest located within chromosomal segment 25);
- 14) one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (*e.g.*, one or more alleles of interest located within chromosomal segment 3) and one or more alleles of interest located within one or more of chromosomal segments

12744 to 12749 (e.g., one or more alleles of interest located within chromosomal segment 12747);

15) one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (e.g., one or more alleles of interest located within chromosomal segment 3) and one or more alleles of interest located within one or more of chromosomal segments 12750 to 12755 (e.g., one or more alleles of interest located within chromosomal segment 12753);

16) one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (e.g., one or more alleles of interest located within chromosomal segment 3) and one or more alleles of interest located within chromosomal segment 12756);

17) one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (e.g., one or more alleles of interest located within chromosomal segment 3) and one or more alleles of interest located within one or more of chromosomal segments 12757 to 12762 (e.g., one or more alleles of interest located within chromosomal segment 12760 and/or chromosomal segment 12761);

18) one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (e.g., one or more alleles of interest located within chromosomal segment 3) and one or more alleles of interest located within one or more of chromosomal segments 12763 to 12768 (e.g., one or more alleles of interest located within chromosomal segment 12768);

19) one or more alleles of interest located on chromosome 2, one or more alleles of interest located within one or more of chromosomal segments 3 to 17 (e.g., one or more alleles of interest located within chromosomal segment 3), one or more alleles of interest located within one or more of chromosomal segments 10266 to 10271 (e.g., one or more alleles of interest located within chromosomal segment 10269) and one or more alleles of interest located within chromosomal segment 12756.

In some embodiments, a nucleic acid comprising, consisting essentially of, or consisting of one or more chromosomal segments derived from NP2222 maize germplasm is introduced into the maize plant or plant part, wherein said one or more chromosomal segments comprises, consists essentially of or consists of one or more of the chromosomal segments described in Table 1. For example, in some embodiments, one or more of chromosomal segments 3 to 12768, (e.g., chromosomal segments 3, 13, 25, 506, 7514, 7546,

12747, 12753, 12760–12761 and/or 12767–12768) derived from NP2222 maize germplasm is introduced into the maize plant or plant part.

In some embodiments, a nucleic acid comprising, consisting essentially of, or consisting of one or more chromosomal segments derived from NP2660 maize germplasm is introduced into the maize plant or plant part, wherein said one or more chromosomal segments comprises, consists essentially of or consists of one or more of the chromosomal segments described in Table 1. For example, in some embodiments, one or more of chromosomal segments 3 to 12743 and/or one or more of chromosomal segments 12757 to 12768, (e.g., chromosomal segments 3, 13, 25, 506, 7514, 7546, 12747, 12753, 12760–12761 and/or 12767–12768) derived from NP2660 maize germplasm is introduced into the maize plant or plant part.

In some embodiments, a nucleic acid comprising, consisting essentially of, or consisting of one or more chromosomal segments derived from NP2276 maize germplasm is introduced into the maize plant or plant part, wherein said one or more chromosomal segments comprises, consists essentially of or consists of one or more of the chromosomal segments described in Table 1. For example, in some embodiments, chromosomal segment 1, one or more of chromosomal segments 46 to 12743 and/or one or more of chromosomal segments 12757 to 12768, (e.g., chromosomal segments 13, 506, 7514, 7546 and/or 12760–12761) derived from NP2276 maize germplasm is introduced into the maize plant or plant part.

In some embodiments, a nucleic acid comprising, consisting essentially of, or consisting of one or more chromosomal segments derived from ID3461 maize germplasm is introduced into the maize plant or plant part, wherein said one or more chromosomal segments comprises, consists essentially of or consists of one or more of the chromosomal segments described in Table 1. For example, in some embodiments, one or more of chromosomal segments 1 to 17 (e.g., chromosomal segments 1 and/or 13) derived from ID3461 maize germplasm is introduced into the maize plant or plant part.

In some embodiments, a nucleic acid comprising, consisting essentially of, or consisting of one or more chromosomal segments derived from a maize line in Table 11 is introduced into the maize plant or plant part, wherein said one or more chromosomal segments comprises, consists essentially of or consists of one or more of the chromosomal segments described in Table 1.

In some embodiments, one or more genes associated with increased fertility (e.g., increased male fertility) is introduced into the maize plant or plant part.

In some embodiments, a nucleic acid comprising, consisting essentially of, or consisting of at least one of the nucleotide sequences of SEQ ID NOs: 1 to 350 (as described in Table 3) is introduced into the maize plant or plant part.

In some embodiments, a nucleic acid comprising, consisting essentially of, or
 5 consisting of at least one nucleotide sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of SEQ ID NOs: 1 to 350 (as described in Table 3) is introduced into the maize plant or plant part.

In some embodiments, a nucleic acid comprising, consisting essentially of, or consisting of at least one nucleotide sequence that specifically hybridizes to the nucleotide
 10 sequence of one or more of SEQ ID NOs: 1 to 350 (as described in Table 3) under stringent hybridization conditions is introduced into the maize plant or plant part.

In some embodiments, a nucleic acid comprising, consisting essentially of, or consisting of at least one nucleotide sequence that encodes the amino acid sequence set forth in one or more of SEQ ID NOs: 351 to 525 (as described in Table 3) is introduced into the
 15 maize plant or plant part.

In some embodiments, a nucleic acid comprising, consisting essentially of, or consisting of at least one nucleotide sequence that encodes an amino acid sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to the amino acid sequence set forth in one or more of SEQ ID NOs: 351 to 525 (as described in
 20 Table 3) is introduced into the maize plant or plant part.

In some embodiments, a nucleic acid comprising, consisting essentially of, or consisting of one or more of the desired alleles described in Table 2 is introduced into the maize plant or plant part.

In embodiments, a nucleic acid comprising, consisting essentially of, or consisting of
 25 one or more of the desired alleles described in Table 8 is introduced into the maize plant or plant part.

In embodiments, a nucleic acid is introduced into a maize plant or plant part, the nucleic acid comprising, consisting essentially of, or consisting of one or more of the desired alleles:

- 30
- (a) on chromosome 5 (QTL 5.1 and/or QTL 5.2) as described in Table 8;
 - (b) on chromosome 3 as described in Table 8;
 - (c) on chromosome 7 as described in Table 8;
 - (d) on chromosome 10 as described in Table 8;
 - (e) on chromosomes 3 and 5 as described in Table 8;

- (f) on chromosomes 5 and 7 as described in Table 8;
- (g) on chromosomes 3, 5 and 7 as described in Table 8;
- (h) on chromosomes 5 and 10 as described in Table 8;
- (i) on chromosomes 3, 5 and 10 as described in Table 8; or
- (j) any combination of (a) to (i).

In some embodiments, a nucleic acid comprising one or more of the desired alleles described in Table 10 is introduced into the maize plant or plant part.

In some embodiments, a nucleic acid comprising, consisting essentially of, or consisting of the reverse complement of one of the nucleic acids described herein is introduced into the maize plant or plant part.

In some embodiments, the nucleic acid introduced into the maize plant or plant part is not in the natural genetic background of the maize plant (*e.g.*, is not naturally occurring in the maize line or variety, and has been introduced therein by human intervention).

In the methods of the invention described herein, the marker, allele and/or haplotype, and the like, is detected in nucleic acid (*e.g.*, a nucleic acid sample) from plant or plant part. In embodiments, the marker, allele and/or haplotype, and the like, is detected in an amplification product from a nucleic acid sample from the plant or plant part.

The methods of the invention can be used for forward breeding or for introgressing one or more genetic loci associated with increased fertility into a new genetic background (*e.g.*, to introgress the trait into an elite inbred maize line).

Methods of the present invention may be used to increase the efficiency of a breeding and/or seed production program (*e.g.*, seed production from a double haploid or inbred line) by reducing the number of male plants required for breeding and/or seed production, reducing the ratio of male to female plants required for breeding and/or seed production, reducing the costs associated with breeding and/or seed production (*e.g.*, the cost(s) of land and seedbed preparation, planting, fertilizer application, weed control, harvesting and/or testing), increasing pollen production (*e.g.*, pollen production per anther/tassel/plant), improving pollen morphology, increasing pollen viability, increasing anther production (*e.g.*, anther production per tassel/plant), improving anther morphology, increasing anther viability, increasing tassel production (*e.g.*, tassel production per plant), improving tassel morphology, increasing tassel viability, increasing silk production (*e.g.*, silk production per ear/plant), improving silk morphology, increasing silk viability, increasing seed production (*e.g.*, seed production per ear/plant), improving seed morphology, decreasing the prevalence of kernel abortion, increasing seed viability, increasing male fertility under stress conditions (*e.g.*,

drought conditions), increasing fertility (*e.g.*, male fertility) under elevated daytime temperatures and/or increasing fertility (*e.g.*, male fertility) under elevated nighttime temperatures.

In some embodiments, methods of the present invention increase the efficiency of a breeding and/or seed production program by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, 110%, 120%, 130%, 140%, 150%, 160%, 170%, 180%, 190%, 200%, 225%, 250%, 275%, 300% or more as compared to a control breeding/seed production program (*e.g.*, a breeding/seed production program using the same maize varieties in the absence of marker-assisted selection with markers of the present invention).

In some embodiments, methods of the present invention reduce the number of male plants required for a breeding and/or seed production program by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more as compared to a control breeding program (*e.g.*, a breeding program using the same maize varieties in the absence of marker-assisted selection with markers of the present invention).

In some embodiments, methods of the present invention reduce the ratio of male to female plants required for a breeding and/or seed production program by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more as compared to a control breeding program (*e.g.*, a breeding program using the same maize varieties in the absence of marker-assisted selection with markers of the present invention).

In some embodiments, methods of the present invention reduce one or more of the costs associated with a breeding and/or seed production program (*e.g.*, the cost(s) of land and seedbed preparation, planting, fertilizer application, weed control, harvesting and/or testing) by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more as compared to a control breeding/seed production program (*e.g.*, a breeding/seed production program using the same maize varieties in the absence of marker-assisted selection with markers of the present invention). In embodiments, the seed production program produces seed from a double haploid or inbred line).

In some embodiments, methods of the present invention reduce the overall cost associated of a breeding and/or seed production program by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%,

96%, 97%, 98%, 99% or more as compared to a control breeding/seed production program (e.g., a breeding/seed production program using the same maize varieties in the absence of marker-assisted selection with markers of the present invention). In embodiments, the seed production program produces seed from a double haploid or inbred line).

5 In some embodiments, methods of the present invention increase the number of pollen grains produced per plant in a breeding and/or seed production program by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, 110%, 120%, 130%, 140%, 150%, 160%, 170%, 180%, 190%, 200%, 225%, 250%, 275%, 300% or more as compared to a control breeding/seed production
10 program (e.g., a breeding/seed production program using the same maize varieties in the absence of marker-assisted selection with markers of the present invention).

In some embodiments, methods of the present invention increase the number of anthers produced per plant in a breeding and/or seed production program by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%,
15 85%, 90%, 95%, 100%, 110%, 120%, 130%, 140%, 150%, 160%, 170%, 180%, 190%, 200%, 225%, 250%, 275%, 300% or more as compared to a control breeding/seed production program (e.g., a breeding/seed production program using the same maize varieties in the absence of marker-assisted selection with markers of the present invention).

In some embodiments, methods of the present invention increase the number of
20 tassels produced per plant in a breeding and/or seed production program by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, 110%, 120%, 130%, 140%, 150%, 160%, 170%, 180%, 190%, 200%, 225%, 250%, 275%, 300% or more as compared to a control breeding/seed production program (e.g., a breeding/seed production program using the same maize varieties in the
25 absence of marker-assisted selection with markers of the present invention).

In some embodiments, methods of the present invention increase the number of seeds produced per plant in a breeding and/or seed production program by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, 110%, 120%, 130%, 140%, 150%, 160%, 170%, 180%, 190%, 200%, 225%,
30 250%, 275%, 300% or more as compared to a control breeding/seed production program (e.g., a breeding/seed production program using the same maize varieties in the absence of marker-assisted selection with markers of the present invention).

In some embodiments, methods of the present invention increase the number of seeds produced per male plant in a breeding and/or seed production program by at least about 5%,

10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%,
 90%, 95%, 100%, 110%, 120%, 130%, 140%, 150%, 160%, 170%, 180%, 190%, 200%,
 225%, 250%, 275%, 300% or more as compared to a control breeding/seed production
 program (e.g., a breeding/seed production program using the same maize varieties in the
 5 absence of marker-assisted selection with markers of the present invention).

In some embodiments, methods of the present invention increase the number of seeds
 produced per female plant in a breeding and/or seed production program by at least about 5%,
 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%,
 90%, 95%, 100%, 110%, 120%, 130%, 140%, 150%, 160%, 170%, 180%, 190%, 200%,
 10 225%, 250%, 275%, 300% or more as compared to a control breeding/seed production
 program (e.g., a breeding/seed production program using the same maize varieties in the
 absence of marker-assisted selection with markers of the present invention).

Methods of the present invention can be practiced with and/or used to identify, breed,
 select and/or produce any suitable maize plant or plant part.

15 In some embodiments, the maize plant or plant part (e.g., the donor and/or the
 recipient plant or plant part) is a member of the Stiff Stalk heterotic group.

In some embodiments, the maize plant or plant part (e.g., the donor and/or the
 recipient plant or plant part) is a member of the non-Stiff Stalk heterotic group.

20 In some embodiments, the maize plant or plant part (e.g., the donor and/or the
 recipient plant or plant part) is a member of the Iodent heterotic group.

In some embodiments, the maize plant or plant part (e.g., the donor and/or the
 recipient plant or plant part) is a B14, B37, B73, OH43 or Iodent maize plant or plant part. In
 embodiments, the donor plant or plant part is from the B14 group. In embodiments, the
 recipient plant or plant part is from the B37 or B73 group.

25 In some embodiments, the maize plant or plant part (e.g., the donor and/or the
 recipient plant or plant part) is an NP2391, NP2460, NP2222, NP2660, NP2276 or ID3461
 maize plant or plant part.

In some embodiments, the maize plant or plant part (e.g., the donor and/or the
 recipient plant or plant part) is from a line described in Table 11.

30 In some embodiments, the maize plant or plant part (e.g., the donor and/or the
 recipient plant or plant part) is derived from a B14, B37, B73, OH43 or Iodent maize plant or
 plant part.

In some embodiments, the maize plant or plant part (*e.g.*, the donor and/or the recipient plant or plant part) is derived from an NP2391, NP2460, NP2222, NP2660, NP2276 or ID3461 maize plant or plant part.

5 In some embodiments, the maize plant or plant part (*e.g.*, the donor and/or the recipient plant or plant part) is derived from a line in Table 11.

In some embodiments, the maize plant or plant part (*e.g.*, the donor and/or the recipient plant or plant part) is of a nonnaturally occurring maize line or variety. In representative embodiments, the nonnaturally occurring plant or plant part (*e.g.*, the donor and/or the recipient plant or plant part) is from a cultivated plant or plant part.

10 In some embodiments, the maize plant or plant part (*e.g.*, the donor and/or the recipient plant or plant part) is an inbred maize plant or plant part.

In some embodiments, the maize plant or plant part (*e.g.*, the donor and/or the recipient plant or plant part) is a double haploid maize plant or plant part.

15 In some embodiments, an inbred or double haploid or inbred maize plant or plant part (*e.g.*, the donor and/or the recipient plant or plant part) is a male inbred or double haploid plant or plant part (*e.g.*, is used as a pollinator in a cross or to self).

In some embodiments, the maize plant or plant part (*e.g.*, the donor and/or the recipient plant or plant part) is of an elite variety of maize. For example, in some embodiments, the maize plant or plant part is NP2222, NP2660, NP2276, NP2391 or
20 NP2460.

In embodiments, the maize plant or plant part (*e.g.*, the recipient plant or plant part) has a decrease in male fertility when hemizygous and/or homozygous for a *vip3* gene (for example, a *vip3a* gene, as illustrated by maize event MIR162). In embodiments, the maize plant or plant part is not functionally fertile or is even male sterile when hemizygous and/or
25 homozygous for a *vip3* gene.

In some embodiments, the genome of the maize plant or plant part is at least about 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to an elite variety of maize. For example, in some embodiments, the genome of the maize plant or plant part is at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%,
30 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to that of NP2222, NP2660, NP2276, NP2391 and/or NP2460.

In some embodiments, the maize plant or plant part is the progeny of a cross between an elite variety of maize and a variety of maize that comprises an allele associated with increased fertility. For example, in some embodiments, the genome of the elite variety of

maize is at least about 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 99% or 100% identical to that of NP2222, NP2660, NP2276, NP2391 and/or NP2460 or an elite line described in Table 11; and the genome of the variety comprising an allele associated with increased fertility is at least about 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 99% or 100% identical to that of NP2222, NP2660, NP2276, ID3461 or a line described in Table 11.

In some embodiments, the maize plant or plant part is the progeny of an introgression wherein the recurrent parent is an elite variety of maize and the donor comprises an allele associated with increased fertility. For example, in some embodiments, the genome of the recurrent parent is at least about 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 99% or 100% identical to that of NP2222, NP2660, NP2276, NP2391 and/or NP2460 or a line described in Table 11; and the genome of the donor is at least about 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 99% or 100% identical to that of NP2222, NP2660, NP2276, ID3461 or a line described in Table 11.

In some embodiments, the maize plant or plant part is the progeny of a cross between a first elite variety of maize (e.g., a tester line) and the progeny of a cross between a second elite variety of maize (e.g., a recurrent parent) and a variety of maize that comprises an allele associated with increased fertility (e.g., a donor). For example, in some embodiments, the genome of the first elite variety of maize is at least about 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 99% or 100% identical to that of NP2222, NP2660, NP2276, NP2391 and/or NP2460 or a line described in Table 11; the genome of the second elite variety of maize is at least about 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 99% or 100% identical to that of NP2222, NP2660, NP2276, NP2391 and/or NP2460 or a line described in Table 11; and the genome of the variety comprising an allele associated with increased fertility is at least about 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 99% or 100% identical to that of NP2222, NP2660, NP2276, ID3461 or a line described in Table 11.

In some embodiments, the maize plant or plant part is the progeny of a cross between a first elite variety of maize and the progeny of an introgression wherein the recurrent parent is a second elite variety of maize and the donor comprises an allele associated with increased fertility. For example, in some embodiments, the genome of the first elite variety of maize is at least about 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 99% or 100% identical to that of NP2222, NP2660, NP2276, NP2391 and/or NP2460 or a line described in Table 11; the genome of the recurrent parent is at least about 50%, 55%, 60%, 65%, 70%,

75%, 80%, 85%, 90%, 95%, 97%, 99% or 100% identical to that of NP2222, NP2660, NP2276, NP2391 and/or NP2460 or a line described in Table 11; and the genome of the donor is at least about 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 99% or 100% identical to that of NP2222, NP2660, NP2276 or ID3461 or a line described in Table

5 11.

In some embodiments, the maize plant or plant part comprises one or more transgenes that encode a gene product that provides resistance to one or more herbicides (*e.g.*, glyphosate, sulfonylurea, imidazolinione, dicamba, glufosinate, phenoxy proprionic acid, cyclohexime, triazine, benzonitrile and/or broxynil).

10 In some embodiments, the maize plant or plant part comprises one or more transgenes that encode a gene product that provides resistance to one or more pests (*e.g.*, one or more bacteria, one or more fungi, one or more gastropods, one or more insects, one or more nematodes, one or more oomycetes, one or more phytoplasmas, one or more protozoa and/or one or more viruses).

15 In some embodiments, the maize plant or plant part comprises one or more transgenes that encode a gene product that provides resistance to one or more diseases.

In some embodiments, the maize plant or plant part expresses one or more Vip3 proteins, for example, comprises a *vip3* transgene in a hemizygous or homozygous state.

20 In some embodiments, the maize plant or plant part expresses one or more nucleic acids encoding a Vip3 protein (*e.g.*, a Vip3A protein). Then maize plant or plant part can be hemizygous or homozygous for the nucleic acid(s) encoding the Vip3 protein(s). For example, in embodiments, the plant or plant part is hemizygous or homozygous for maize event MIR162. In some embodiments, the maize plant or plant part comprises one or more Vip nucleotide sequences as set forth by the accession numbers in Table 4.

25 In some embodiments, the maize plant or plant part expresses at least one nucleotide sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of Vip nucleotide sequences as set forth by the accession numbers in Table 4.

30 In some embodiments, the maize plant or plant part expresses at least one nucleotide sequence that specifically hybridizes to the nucleotide sequence of one or more of SEQ ID NOs: 536 to 601 (as described in Table 4) under stringent hybridization conditions.

In some embodiments, the maize plant or plant part expresses at least one nucleotide sequence that encodes one or more of the Vip amino acid sequences as set forth by the accession numbers in Table 4.

In some embodiments, the maize plant or plant part expresses at least one nucleotide sequence that encodes an amino acid sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identical to one or more of the Vip amino acid sequences as set forth by the accession numbers in Table 4.

5 The present invention extends to plants identified, selected and/or produced according to methods of the present invention.

 The present invention also extends to products harvested from plants identified, selected and/or produced according to methods of the present invention, including, but not limited to, plant cells and harvestable plant parts including but not limited to seeds, leaves,
10 fruits, flowers, stems.

 In some embodiments, the harvested product is a plant cell or plant part capable of producing a plant having increased fertility (*e.g.*, increased male fertility).

 The present invention also extends to products derived from plants produced according to methods of the present invention, including, but not limited to, dry pellets and
15 powders, oils, fats, fatty acids, starches and proteins.

EXAMPLES

 The following examples are not intended to be a detailed catalog of all the different ways in which the present invention may be implemented or of all the features that may be
20 added to the present invention. Persons skilled in the art will appreciate that numerous variations and additions to the various embodiments may be made without departing from the present invention. Hence, the following descriptions are intended to illustrate some particular embodiments of the invention, and not to exhaustively specify all permutations, combinations and variations thereof.

Example 1

Development of Mapping Populations

 Following the initial discovery of genetic variation in Vip3-induced reductions in male fertility, trials were conducted to characterize which inbred maize lines were most
25 affected and which inbred maize lines were least affected by Vip3-induced reduction in male fertility.

 A number of maize inbred lines homozygous for Vip3A (event MIR162) were evaluated. It was observed that male fertility was reduced in each of the Vip3A-homozygous inbred lines tested, albeit to varying degrees. *See* Table 9 below. Under normal growth conditions, some inbred lines (*e.g.*, line NP2222) exhibited minimal reduction in male

fertility, while others (*e.g.*, some ID3461 lines) exhibited a significant reduction in male fertility. Indeed, several of the Vip3A-homozygous inbred lines (*e.g.*, some NP2660 and NP2276 lines) proved to be infertile. The average reduction in male fertility was approximately 50 %.

5

Table 5. Vip3A-induced reductions in male fertility vary across genetic backgrounds.

Inbred Line	Pollen Count of Donor Parent Used to Introduce Vip3A into Inbred Line	Male Fertile?
B14 line 1	good	yes
B37 line 1	very poor	no
B37 line 2	very good	no
B73 line 1	marginal	no
B73 line 2	poor	no
OH43 line 1	very good	yes
Iodent line 1	acceptable	no
Iodent line 2	acceptable	yes
Iodent line 3	very poor	yes

It was observed that the effect of Vip3A expression was mitigated in Vip3A-hemizygous inbred lines. Inbred lines that were male infertile when homozygous for Vip3A were male fertile when hemizygous for Vip3A. Likewise, fertile inbred lines that exhibited a significant reduction in male fertility when homozygous for Vip3A were substantially or completely male fertile when hemizygous for Vip3A.

It was observed that an increase in environmental stress exacerbated the Vip3A-induced reductions in male fertility. In particular, it was observed that Vip3A-induced reductions in male fertility were more prominent in inbred lines grown under drought and/or high temperature conditions (*e.g.*, high daytime temperatures and/or high nighttime temperatures). *See Fig. 1.* Vip3A-induced reductions in male fertility were also prominent in inbred lines grown under conditions comprising a large differential between daytime and nighttime temperatures. *See Fig. 2.*

Based upon the foregoing observations, bi-parental F2 mapping populations were developed by crossing male fertile Vip3A-expressing inbred lines (NP2222 and ID3461) with a male infertile Vip3A-expressing inbred line (NP2276) in a reciprocal manner. Because the infertile line could not be used as a male when homozygous for Vip3A, the F1 crosses in those cases were made by crossing pollen from the corresponding Vip3A-hemizygous line onto silks from male fertile inbred lines that were homozygous for Vip3A to derive the F1 plants, and then selecting the homozygous F1 plants for making the F2 seed. All F1 plants

resulting from the initial crosses were sufficiently male fertile for self-pollination to make F2 seed.

Example 2

5 **Molecular Marker Analysis and Identification** **of QTLs Associated with Increased Male Fertility**

Using NP2276 genetics crossed with NP2222 or ID3461 as described in Example 1, QTLs associated with male fertility were identified. No cytoplasmic effect was found.

10 F2 plants derived from the F2 seeds described in Example 1 were field-grown at Syngenta® winter nursery sites in Puerto Rico. Each F2 population consisted of ~500 plants. Each plant was phenotyped and/or scored for male fertility as described in Example 3. Each plant was tested for zygosity of the *vip3A* transgene (null, hemizygous, homozygous) and confirmed to be expressing the *vip3A* transgene at a suitable level. Each F2 plant was also genotyped using ~200 SNP markers that represented polymorphisms between the parents and

15 with the markers spaced across the genome. QTL Cartographer software was used for analysis to identify QTLs responsive to the phenotype of interest (increased male fertility).

The LOD scores for four of the QTLs identified in this study are set forth in Table 6 below. As shown therein, a QTL identified on chromosome 5 exhibited a strong association with increased male fertility.

20

Table 6. LOD scores of QTLs identified using F2 plants from bi-parental crosses of NP2222 and NP2276 and bi-parental crosses of ID3461 and NP2276

Chrom	NP2276/ NP2222	NP2222/ NP2276	NP2222/ NP2276 comb	NP2276/ ID3461	ID3461/ NP2276	XO/ID comb
3	NS	5.8	8.2	7.9	NS	6.2
4	NS	7.4	7.7	(3.6)	NS	(3.6)
5	11.1	8.3	19.9	14.3	13.0	23.1
10	NS	10.9	8.9	6.2	12.3	26.8

LOD significance threshold = 2.5.

Example 3**Phenotyping for Increased Male Fertility**

To phenotype for increased male fertility, each F2 plant tassel was scored in the field for anther quality/ quantity and pollen quantity. Those scores were combined into a single 1 to 9 Fertility Index score (see Table 7 below; a score of 1 representing the best fertility and 9 representing infertility). Because pollen quantity is a more relevant measure of male fertility, it was weighted more in the derived Fertility Index. Fertility Index scores were determined on a daily basis starting the day after a plant began to extrude anthers. On the first sign of anther extrusion, the tassel was bagged for scoring on the next two consecutive days. The highest fertility score was used in the final data analysis. Inclement weather sometimes required skipping a day, but two days of data were always collected on each plant. Anther quality was scored on a 1 to 3 scale with 1 being normal anther extrusion pattern, 2 being irregular and/or reduced anther extrusion, and 3 being no anther extrusion (complete male sterility). Pollen quantity was scored on a relative 1 to 4 scale with 1 being high pollen production and 4 being zero pollen production over the 24 hour period. Segregating Vip3A parent plants grown in the same field were used as controls to calibrate the pollen quantity determinations.

Table 7. Fertility Index used to score F2 plants from bi-parental crosses of NP2222 and NP2276 and bi-parental crosses of ID3461 and NP2276.

Anther Score	Pollen Score	Fertility Index
1	1	1
2	1	
3	1	
1	2	2
2	2	3
3	2	
1	3	4
2	3	5
3	3	6
1	4	7
2	4	8
3	4	9

Example 4**Fine Mapping of a QTL on Chromosome 5**

Inbred line NP2276 is normally highly male fertile, but is male infertile when homozygous for Vip3A. Given this large Vip3A-induced reduction in male fertility, it was
 5 decided to fine map the QTL found to have the largest effect in the F2 mapping studies (a QTL on chromosome 5) to define a smaller interval that could be used for conversion of other genetics with this fertility QTL.

Near isogenic lines (NILs) comprising an NP2222-homozygous QTL on chromosome 3 in the NP2276 genetic background were used to fine map the QTL on chromosome 5.

10 F1 materials from the NP2276 x NP2222 crosses described in Example 1 were backcrossed with NP2276 three times and selfed multiple times with selection for maintenance of NP2222 genetics at a QTL on chromosome 3 and maintenance of both NP2222 and NP2276 genetics at a QTL on chromosome 5. The remainder of the genome outside of those two QTLs was selected for NP2276 genetics as much as possible. The QTLs
 15 on chromosome 4 and 10 were allowed to segregate back to NP2276 genetics along with the rest of the genome.

The finished NILs were grown under normal field conditions at Syngenta® winter nursery sites in Puerto Rico. NILs comprising NP2222 genetics at the QTL on chromosome 3 and the QTL on chromosome 5 exhibited relatively high male fertility, similar to null
 20 segregates of NP2276. NILs comprising NP2222 genetics at the QTL on chromosome 3 and NP2276 genetics at the QTL on chromosome 5 were male infertile. Following multiple rounds of fine mapping, the QTL on chromosome 5 was iteratively reduced to a 12.13 MB region bounded by and including positions 72,696,160 and 84,824,203 (chromosomal segment 190, as described in Table 1).

25 In greenhouse studies wherein pollen production was quantitated, NILs comprising NP2222 genetics at the QTL on chromosome 3 and this smaller QTL on chromosome 5 exhibited male fertility at ~80% of that measured for wild-type or null segregates of NP2276.

Example 5**Identification and Fine Mapping of QTLs Associated with Increased Male Fertility**

30 QTLs associated with increased male fertility were identified and mapped using the techniques described above with respect to Examples 1–4.

Examples of the QTLs identified are provided in Table 8.

Attorney Docket No.: 9207-115WO

Table 8. QTLs associated with increased anther quantity and/or improved anther quality.

QTL	Chr.	cM	Left Marker	Position	Favorable Allele	Right Marker	Position	Favorable Allele	Phenotype	LOD score	% phenotypic variation explained
3	3	151.6	1	174825991	G	2	195514453	A	Anther Quality	3.2	7.1
4-1	4	92.5	3	25326309	G	4	26400247	G	Anther Quality/ Anther Quantity	2.61	7.06
4-2	4	216.3	5	233629032	A	6	232968070	A	Anther Quality/ Anther Quantity	Quality-20.8 Quantity-20.3	Quality-32.1 Quantity-32.8
5-1	5	94.9	7	181522829	A	8	77920728	G	Anther Quality/ Anther Quantity	Quality-90.1 Quantity-84.85	Quality-56.9 Quantity-55.7
5-2	5	147.6	9	84824103	T	10	169454950	T	Anther Quality/ Anther Quantity	Quality-24.3 Quantity-23.3	Quality-48.3 Quantity-47.9
6	6	189.3	11	165317744	T	12	165632140	G	Anther Quality	Quality-5.2 Quantity-6.1	Quality-7.8 Quantity-8.8
7	7	92.2	13	33157904	G	14	52027945	A	Anther Quality/ Anther Quantity	Quality-21.0 Quantity-20.2	Quality-32.6 Quantity-20.2
9	9	176.8	15	128947590	A	16	147896266	C	Anther Quality/ Anther Quantity	Quality-9.9 Quantity-9.6	Quality-14.4 Quantity-14.7
10	10	192.5	17	142092409	G	18	145273700	G	Anther Quality	3.25	6.85

LOD significance threshold = 2.5.

Table 9. Design sequences, probes and primers useful to identify the favorable alleles in the QTLs described in Table 8

Chr	QTL	Marker	Favorable Allele	Design (SEQ ID)	Probe (SEQ ID)	Probe (SEQ ID)	Primer (SEQ ID)	Primer (SEQ ID)
3	3	1	G	536	537	538	539	540
3	3	2	A	526	528	530	527	529
4	4-1	3	G	541	542	543	544	545
4	4-1	4	G	546	547	548	549	550
4	4-2	5	A	551	552	553	554	555
4	4-2	6	A	556	557	558	559	560
5	5-1	7	A	561	562	563	564	565
5	5-1	8	G	566	567	568	569	570
5	5-2	9	T	531	532	534	535	533
5	5-2	10	T	571	572	573	574	575
6	6	11	T	576	577	578	579	580
6	6	12	G	581	582	583		
7	7	13	G	584	585	586	587	588
7	7	14	A	589	590	591	592	593
9	9	15	A	594	595	596	597	598
9	9	16	C	599	600	601	602	603
10	10	17	G	604	605	606	607	608
10	10	18	G	609	610	611	612	613

Inbred line B14 line 1 (see Table 8 above) was observed to comprise alleles associated with increased male fertility at QTLs on chromosomes 2, 3, 4, 5, 7, 8, 9 and 10.

Inbred lines B37 line 2 and B73 line 2 (see Table 8 above) were observed to comprise alleles associated with increased male fertility at a QTL on chromosomes 5, 7 and 9.

The predominant QTL identified in this study, which was centered around position 81,265,937 on chromosome 5, was finely mapped using a variety of markers and techniques. Following multiple rounds of fine mapping, the QTL was iteratively reduced to a 1.431 MB region bounded by and including positions 80,804,587 and 82,325,587 (chromosomal

segment 7514, as described in Table 1). As shown in Table 3, that chromosomal segment encodes a number of proteins.

Example 6

Alleles Associated with QTL Intervals

A comparison was made of the SNPs present in inbred maize line NP2222 versus line NP2276 across the male fertility-associated QTL intervals in Table 8 above. The results are shown in Table 10. Where the alleles differ between the two lines, the NP2222 allele corresponds to the favorable allele.

The design of assay methods, including the design of suitable primers and probes, to detect the presence or absence of the favorable alleles identified in Table 10 in other maize plants and plant parts is readily apparent to those skilled in the art. For example, one can evaluate a sequence extending 5' and/or 3' from the indicated position of each SNP (e.g., 25, 50, 100, 150, 200, 250 nucleotides or more in the 5' and/or 3' direction) and use any of a variety of known software programs to design appropriate amplification primers and probes to detect the presence or absence of the favorable allele present in NP2222 in an amplification assay.

Table 10. Additional Polymorphisms in Fertility QTLs

QTL	Chromosome	Nucleotide Position	Favorable
3	Chr3	176,322,027	C
3	Chr3	184,155,559	C
3	Chr3	184,215,519	A
3	Chr3	184,672,762	G
3	Chr3	185,229,529	A
3	Chr3	186,563,317	A
3	Chr3	187,045,835	A
3	Chr3	188,335,251	A
3	Chr3	189,901,375	G
3	Chr3	191,195,919	A
3	Chr3	193,847,182	A
4.1	Chr4	25,639,678	G
4.1	Chr4	25,988,159	A
4.1	Chr4	26,373,200	A
4.2	Chr4	232,928,019	G
4.2	Chr4	232,940,724	G
4.2	Chr4	233,005,187	G
4.2	Chr4	233,204,685	A

4 2	Chr4	233,268,189	C
5 1	Chr5	78,301,966	A
5 1	Chr5	81,454,989	A
5 1	Chr5	82,952,810	A
5 1	Chr5	83,278,003	A
5 1 AND 5 2	Chr5	86,074,618	C
5 1 AND 5 2	Chr5	92,369,931	A
5 1 AND 5 2	Chr5	99,818,185	A
5 1 AND 5 2	Chr5	107,477,545	G
5 1 AND 5 2	Chr5	113,579,713	A
5 1 AND 5 2	Chr5	120,984,518	A
5 1 AND 5 2	Chr5	131,435,275	G
5 1 AND 5 2	Chr5	141,169,239	G
5 1 AND 5 2	Chr5	149,998,432	A
5 1 AND 5 2	Chr5	163,409,720	G
5 1 AND 5 2	Chr5	168,858,119	A
5 1	Chr5	170,069,183	A
5 1	Chr5	175,459,402	G
5 1	Chr5	178,321,558	A
6	Chr6	165,353,049	C
6	Chr6	165,632,314	C
6	Chr6	165,348,117	C
7	Chr7	34,171,694	C
7	Chr7	33,520,778	A
7	Chr7	34,141,494	G
9	Chr9	129,905,275	A
9	Chr9	131,727,013	A
9	Chr9	138,019,524	A
9	Chr9	138,312,159	C
9	Chr9	138,685,900	G
9	Chr9	141,476,864	G
9	Chr9	142,462,911	A
9	Chr9	135,855,445	A
9	Chr9	144,740,620	G
10	Chr10	142,596,522	A
10	Chr10	143,063,299	G
10	Chr10	143,394,664	G
10	Chr10	143,663,216	C
10	Chr10	144,109,193	A
10	Chr10	144,314,228	C
10	Chr10	144,741,863	G

Example 7**Other Publicly Available Sources of Favorable Alleles**

Using linear regression analysis and pairwise genetic distances, the following public lines in Table 11 from the Ames Germplasm collection are predicted to contain the favorable alleles identified in Table 8 above.

Table 11. Public lines predicted to contain favorable alleles.

QTL	Public Lines Predicted to Have Favorable Allele	Probability Favorable Allele Present	Other Lines with Global Similarity
3	A659	65%	A73, A660, EP29, W22
4-1	V102	86.8%	W8304, W8555
4-2	B103	99.8%	OC4, PHG50, PHP76
5-1	NC372, N192, A680	99.7%	PB80, TX714, NC372, B73, GEMS-0101, W8304
5-2	NC372, N192, A680	99.7%	PB80, TX714, NC372, B73, GEMS-0101, W8304
6	B104, NC268, NC306, NC310, NC372	99.8%	B121, B110, NC306, NC268A, NC312, NC308, NC326, PB80, TX714
7	ND253, LH52	99.8%, 99.2%	ND264, S117, MO17, MO17T, SeagullSeventeen
9	Pa762	97%	R218, R219, VEN981, SAN349a-1, OH43T, OH43
10	DE1	96.2%	DE2, PHP02, MS81, MS75

Example 8**Producing Vip3A-Expressing Maize Plants with Increased Male Fertility**

Chromosomal segment 13 (as described in Table 1) is introgressed from NP2222 into a Vip3A-homozygous inbred line (e.g., a MIR162 inbred line). The introgressed maize line exhibits increased male fertility as compared to its recurrent parent. In particular, the introgressed maize line exhibits increased pollen production, increased anther production and improved anther morphology under normal growth conditions or environmental stress conditions (e.g., drought and/or high temperature stress conditions). The beneficial effects of the introgressed chromosomal segment are more pronounced in plants grown under high temperature conditions (e.g., high daytime and/or nighttime temperatures).

Example 9**Producing Vip3A-Expressing Maize Plants with Increased Male Fertility**

Chromosomal segment 13 (as described in Table 1) is introgressed from NP2660 into aVip3A-homozygous inbred line (*e.g.*, a MIR162 inbred line). The introgressed maize line exhibits increased male fertility as compared to its recurrent parent. In particular, the introgressed maize line exhibits increased pollen production, increased anther production and improved anther morphology under normal growth conditions or environmental stress conditions (*e.g.*, drought and/or high temperature stress conditions). The beneficial effects of the introgressed chromosomal segment are more pronounced in plants grown under high temperature conditions (*e.g.*, high daytime and/or nighttime temperatures).

Example 10**Producing Vip3A-Expressing Maize Plants with Increased Male Fertility**

Chromosomal segment 43 (as described in Table 1) is introgressed from NP2222 into aVip3A-homozygous inbred line (*e.g.*, a MIR162 inbred line). The introgressed maize line exhibits increased male fertility as compared to its recurrent parent. In particular, the introgressed maize line exhibits increased pollen production, increased anther production and improved anther morphology under normal growth conditions or environmental stress conditions (*e.g.*, drought and/or high temperature stress conditions). The beneficial effects of the introgressed chromosomal segment are more pronounced in plants grown under high temperature conditions (*e.g.*, high daytime and/or nighttime temperatures).

Example 11**Producing Vip3A-Expressing Maize Plants with Increased Male Fertility**

Chromosomal segment 43 (as described in Table 1) is introgressed from NP2660 into aVip3A-homozygous inbred line (*e.g.*, a MIR162 inbred line). The introgressed maize line exhibits increased male fertility as compared to its recurrent parent. In particular, the introgressed maize line exhibits increased pollen production, increased anther production and improved anther morphology under normal growth conditions or environmental stress conditions (*e.g.*, drought and/or high temperature stress conditions). The beneficial effects of the introgressed chromosomal segment are more pronounced in plants grown under high temperature conditions (*e.g.*, high daytime and/or nighttime temperatures).

Example 12**Producing Vip3A-Expressing Maize Plants with Increased Male Fertility**

Chromosomal segment 7514 (as described in Table 1) is introgressed from NP2222 into aVip3A-homozygous inbred line (*e.g.*, a MIR162 inbred line). The introgressed maize line exhibits increased male fertility as compared to its recurrent parent. In particular, the introgressed maize line exhibits increased pollen production, increased anther production and improved anther morphology under normal growth conditions or environmental stress conditions (*e.g.*, drought and/or high temperature stress conditions). The beneficial effects of the introgressed chromosomal segment are more pronounced in plants grown under high temperature conditions (*e.g.*, high daytime and/or nighttime temperatures).

Example 13**Producing Vip3A-Expressing Maize Plants with Increased Male Fertility**

Chromosomal segment 7514 (as described in Table 1) is introgressed from NP2660 into aVip3A-homozygous inbred line (*e.g.*, a MIR162 inbred line). The introgressed maize line exhibits increased male fertility as compared to its recurrent parent. In particular, the introgressed maize line exhibits increased pollen production, increased anther production and improved anther morphology under normal growth conditions or environmental stress conditions (*e.g.*, drought and/or high temperature stress conditions). The beneficial effects of the introgressed chromosomal segment are more pronounced in plants grown under high temperature conditions (*e.g.*, high daytime and/or nighttime temperatures).

Example 14**Producing Vip3A-Expressing Maize Plants with Increased Male Fertility**

Chromosomal segment 7514 (as described in Table 1) is introgressed from NP2276 into aVip3A-homozygous inbred line (*e.g.*, a MIR162 inbred line). The introgressed maize line exhibits increased male fertility as compared to its recurrent parent. In particular, the introgressed maize line exhibits increased pollen production, increased anther production and improved anther morphology under normal growth conditions or environmental stress conditions (*e.g.*, drought and/or high temperature stress conditions). The beneficial effects of the introgressed chromosomal segment are more pronounced in plants grown under high temperature conditions (*e.g.*, high daytime and/or nighttime temperatures).

Example 15**Producing Vip3A-Expressing Maize Plants with Increased Male Fertility**

Chromosomal segment 12747 (as described in Table 1) is introgressed from NP2222 into aVip3A-homozygous inbred line (*e.g.*, a MIR162 inbred line). The introgressed maize line exhibits increased male fertility as compared to its recurrent parent. In particular, the introgressed maize line exhibits increased pollen production, increased anther production and improved anther morphology under normal growth conditions or environmental stress conditions (*e.g.*, drought and/or high temperature stress conditions). The beneficial effects of the introgressed chromosomal segment are more pronounced in plants grown under high temperature conditions (*e.g.*, high daytime and/or nighttime temperatures).

Example 16**Producing Vip3A-Expressing Maize Plants with Increased Male Fertility**

Chromosomal segment 12747 (as described in Table 1) is introgressed from NP2660 into aVip3A-homozygous inbred line (*e.g.*, a MIR162 inbred line). The introgressed maize line exhibits increased male fertility as compared to its recurrent parent. In particular, the introgressed maize line exhibits increased pollen production, increased anther production and improved anther morphology under normal growth conditions or environmental stress conditions (*e.g.*, drought and/or high temperature stress conditions). The beneficial effects of the introgressed chromosomal segment are more pronounced in plants grown under high temperature conditions (*e.g.*, high daytime and/or nighttime temperatures).

Example 17**Producing Vip3A-Expressing Maize Plants with Increased Male Fertility**

Chromosomal segment 12753 (as described in Table 1) is introgressed from NP2222 into aVip3A-homozygous inbred line (*e.g.*, a MIR162 inbred line). The introgressed maize line exhibits increased male fertility as compared to its recurrent parent. In particular, the introgressed maize line exhibits increased pollen production, increased anther production and improved anther morphology under normal growth conditions or environmental stress conditions (*e.g.*, drought and/or high temperature stress conditions). The beneficial effects of the introgressed chromosomal segment are more pronounced in plants grown under high temperature conditions (*e.g.*, high daytime and/or nighttime temperatures).

Example 18**Producing Vip3A-Expressing Maize Plants with Increased Male Fertility**

Chromosomal segment 12753 (as described in Table 1) is introgressed from NP2660 into aVip3A-homozygous inbred line (*e.g.*, a MIR162 inbred line). The introgressed maize line exhibits increased male fertility as compared to its recurrent parent. In particular, the introgressed maize line exhibits increased pollen production, increased anther production and improved anther morphology under normal growth conditions or environmental stress conditions (*e.g.*, drought and/or high temperature stress conditions). The beneficial effects of the introgressed chromosomal segment are more pronounced in plants grown under high temperature conditions (*e.g.*, high daytime and/or nighttime temperatures).

Example 19**Producing Vip3A-Expressing Maize Plants with Increased Male Fertility**

Chromosomal segment 12760 (as described in Table 1) is introgressed from NP2222 into aVip3A-homozygous inbred line (*e.g.*, a MIR162 inbred line). The introgressed maize line exhibits increased male fertility as compared to its recurrent parent. In particular, the introgressed maize line exhibits increased pollen production, increased anther production and improved anther morphology under normal growth conditions or environmental stress conditions (*e.g.*, drought and/or high temperature stress conditions). The beneficial effects of the introgressed chromosomal segment are more pronounced in plants grown under high temperature conditions (*e.g.*, high daytime and/or nighttime temperatures).

Example 20**Producing Vip3A-Expressing Maize Plants with Increased Male Fertility**

Chromosomal segment 12760 (as described in Table 1) is introgressed from NP2660 into aVip3A-homozygous inbred line (*e.g.*, a MIR162 inbred line). The introgressed maize line exhibits increased male fertility as compared to its recurrent parent. In particular, the introgressed maize line exhibits increased pollen production, increased anther production and improved anther morphology under normal growth conditions or environmental stress conditions (*e.g.*, drought and/or high temperature stress conditions). The beneficial effects of the introgressed chromosomal segment are more pronounced in plants grown under high temperature conditions (*e.g.*, high daytime and/or nighttime temperatures).

Example 21**Producing Vip3A-Expressing Maize Plants with Increased Male Fertility**

Chromosomal segment 12760 (as described in Table 1) is introgressed from NP2276 into aVip3A-homozygous inbred line (e.g., a MIR162 inbred line). The introgressed maize line exhibits increased male fertility as compared to its recurrent parent. In particular, the introgressed maize line exhibits increased pollen production, increased anther production and improved anther morphology under normal growth conditions or environmental stress conditions (e.g., drought and/or high temperature stress conditions). The beneficial effects of the introgressed chromosomal segment are more pronounced in plants grown under high temperature conditions (e.g., high daytime and/or nighttime temperatures).

Table 1. Examples of chromosomal segments associated with increased fertility in maize.

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
1	1	39248635	198733255	28	4	25326309	232968070
2	2			29	4	25326309	233629032
3	3	7411453	168481421	30	4	25326309	238991842
4	3	7411453	174825991	31	4	26400247	182010511
5	3	7411453	184816495	32	4	26400247	216707012
6	3	7411453	195514453	33	4	26400247	232968070
7	3	7411453	213804184	34	4	26400247	233629032
8	3	168481421	174825991	35	4	26400247	238991842
9	3	168481421	184816495	36	4	182010511	216707012
10	3	168481421	195514453	37	4	182010511	232968070
11	3	168481421	213804184	38	4	182010511	233629032
12	3	174825991	184816495	39	4	182010511	238991842
13	3	174825991	195514453	40	4	216707012	232968070
14	3	174825991	213804184	41	4	216707012	233629032
15	3	184816495	195514453	42	4	216707012	238991842
16	3	184816495	213804184	43	4	232968070	233629032
17	3	195514453	213804184	44	4	232968070	238991842
18	4	9852206	25326309	45	4	233629032	238991842
19	4	9852206	26400247	46	5	72696160	73132763
20	4	9852206	182010511	47	5	72696160	74614332
21	4	9852206	216707012	48	5	72696160	78022476
22	4	9852206	232968070	49	5	72696160	78023096
23	4	9852206	233629032	50	5	72696160	78131652
24	4	9852206	238991842	51	5	72696160	78131784
25	4	25326309	26400247	52	5	72696160	78310499
26	4	25326309	182010511	53	5	72696160	78381593
27	4	25326309	216707012	54	5	72696160	78389884

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
55	5	72696160	78520683	99	5	72696160	80411639
56	5	72696160	78765635	100	5	72696160	80446855
57	5	72696160	78780292	101	5	72696160	80492790
58	5	72696160	78813114	102	5	72696160	80670554
59	5	72696160	78814710	103	5	72696160	80674679
60	5	72696160	78814976	104	5	72696160	80720509
61	5	72696160	78815306	105	5	72696160	80800856
62	5	72696160	78821393	106	5	72696160	80804587
63	5	72696160	78826528	107	5	72696160	80807409
64	5	72696160	78826538	108	5	72696160	80835734
65	5	72696160	78826612	109	5	72696160	80835734
66	5	72696160	78918620	110	5	72696160	80971764
67	5	72696160	78918850	111	5	72696160	80972258
68	5	72696160	79056960	112	5	72696160	80974450
69	5	72696160	79163631	113	5	72696160	81047638
70	5	72696160	79176557	114	5	72696160	81082921
71	5	72696160	79188028	115	5	72696160	81157909
72	5	72696160	79201760	116	5	72696160	81265937
73	5	72696160	79230005	117	5	72696160	81267485
74	5	72696160	79230318	118	5	72696160	81267499
75	5	72696160	79505592	119	5	72696160	81274512
76	5	72696160	79510072	120	5	72696160	81763618
77	5	72696160	79538012	121	5	72696160	81797217
78	5	72696160	79538048	122	5	72696160	81800186
79	5	72696160	79538367	123	5	72696160	81806213
80	5	72696160	79669824	124	5	72696160	81854583
81	5	72696160	79682242	125	5	72696160	81859374
82	5	72696160	79699261	126	5	72696160	81861368
83	5	72696160	79710673	127	5	72696160	81863686
84	5	72696160	79861902	128	5	72696160	81916850
85	5	72696160	79867710	129	5	72696160	81954891
86	5	72696160	79867868	130	5	72696160	81985250
87	5	72696160	79867873	131	5	72696160	82083752
88	5	72696160	79961961	132	5	72696160	82101253
89	5	72696160	80086268	133	5	72696160	82143124
90	5	72696160	80190673	134	5	72696160	82236318
91	5	72696160	80190777	135	5	72696160	82325587
92	5	72696160	80192546	136	5	72696160	82427210
93	5	72696160	80195395	137	5	72696160	82431853
94	5	72696160	80199923	138	5	72696160	82446714
95	5	72696160	80241911	139	5	72696160	82446794
96	5	72696160	80282785	140	5	72696160	82551111
97	5	72696160	80345337	141	5	72696160	82552090
98	5	72696160	80389787	142	5	72696160	82555641

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
143	5	72696160	82555670	187	5	72696160	84799488
144	5	72696160	82556511	188	5	72696160	84801081
145	5	72696160	82559047	189	5	72696160	84824103
146	5	72696160	82561335	190	5	72696160	84824203
147	5	72696160	82610100	191	5	72696160	84824816
148	5	72696160	82676822	192	5	72696160	84825422
149	5	72696160	82676901	193	5	72696160	84825763
150	5	72696160	82883691	194	5	72696160	84825942
151	5	72696160	82954942	195	5	72696160	84936441
152	5	72696160	82971688	196	5	72696160	84936493
153	5	72696160	83023965	197	5	72696160	84943705
154	5	72696160	83094205	198	5	72696160	169454950
155	5	72696160	83146355	199	5	72696160	181522829
156	5	72696160	83280630	200	5	72696160	204759879
157	5	72696160	83281412	201	5	72696160	209874191
158	5	72696160	83400242	202	5	73132763	74614332
159	5	72696160	83405797	203	5	74614332	78022476
160	5	72696160	83437132	204	5	74614332	78023096
161	5	72696160	83522252	205	5	74614332	78131652
162	5	72696160	83560095	206	5	74614332	78131784
163	5	72696160	83560204	207	5	74614332	78310499
164	5	72696160	83572400	208	5	74614332	78381593
165	5	72696160	83607661	209	5	74614332	78389884
166	5	72696160	83745342	210	5	74614332	78520683
167	5	72696160	83861275	211	5	74614332	78765635
168	5	72696160	83861633	212	5	74614332	78780292
169	5	72696160	83865653	213	5	74614332	78813114
170	5	72696160	83865914	214	5	74614332	78814710
171	5	72696160	83865920	215	5	74614332	78814976
172	5	72696160	83868010	216	5	74614332	78815306
173	5	72696160	84019752	217	5	74614332	78821393
174	5	72696160	84065912	218	5	74614332	78826528
175	5	72696160	84086632	219	5	74614332	78826538
176	5	72696160	84089603	220	5	74614332	78826612
177	5	72696160	84104814	221	5	74614332	78918620
178	5	72696160	84105175	222	5	74614332	78918850
179	5	72696160	84251635	223	5	74614332	79056960
180	5	72696160	84252180	224	5	74614332	79163631
181	5	72696160	84253030	225	5	74614332	79176557
182	5	72696160	84254208	226	5	74614332	79188028
183	5	72696160	84314930	227	5	74614332	79201760
184	5	72696160	84340523	228	5	74614332	79230005
185	5	72696160	84516340	229	5	74614332	79230318
186	5	72696160	84706916	230	5	74614332	79505592

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
231	5	74614332	79510072	275	5	74614332	81763618
232	5	74614332	79538012	276	5	74614332	81797217
233	5	74614332	79538048	277	5	74614332	81800186
234	5	74614332	79538367	278	5	74614332	81806213
235	5	74614332	79669824	279	5	74614332	81854583
236	5	74614332	79682242	280	5	74614332	81859374
237	5	74614332	79699261	281	5	74614332	81861368
238	5	74614332	79710673	282	5	74614332	81863686
239	5	74614332	79861902	283	5	74614332	81916850
240	5	74614332	79867710	284	5	74614332	81954891
241	5	74614332	79867868	285	5	74614332	81985250
242	5	74614332	79867873	286	5	74614332	82083752
243	5	74614332	79961961	287	5	74614332	82101253
244	5	74614332	80086268	288	5	74614332	82143124
245	5	74614332	80190673	289	5	74614332	82236318
246	5	74614332	80190777	290	5	74614332	82325587
247	5	74614332	80192546	291	5	74614332	82427210
248	5	74614332	80195395	292	5	74614332	82431853
249	5	74614332	80199923	293	5	74614332	82446714
250	5	74614332	80241911	294	5	74614332	82446794
251	5	74614332	80282785	295	5	74614332	82551111
252	5	74614332	80345337	296	5	74614332	82552090
253	5	74614332	80389787	297	5	74614332	82555641
254	5	74614332	80411639	298	5	74614332	82555670
255	5	74614332	80446855	299	5	74614332	82556511
256	5	74614332	80492790	300	5	74614332	82559047
257	5	74614332	80670554	301	5	74614332	82561533
258	5	74614332	80674679	302	5	74614332	82610100
259	5	74614332	80720509	303	5	74614332	82676822
260	5	74614332	80800856	304	5	74614332	82676901
261	5	74614332	80804587	305	5	74614332	82883691
262	5	74614332	80807409	306	5	74614332	82954942
263	5	74614332	80835734	307	5	74614332	82971688
264	5	74614332	80835734	308	5	74614332	83023965
265	5	74614332	80971764	309	5	74614332	83094205
266	5	74614332	80972258	310	5	74614332	83146355
267	5	74614332	80974450	311	5	74614332	83280630
268	5	74614332	81047638	312	5	74614332	83281412
269	5	74614332	81082921	313	5	74614332	83400242
270	5	74614332	81157909	314	5	74614332	83405797
271	5	74614332	81265937	315	5	74614332	83437132
272	5	74614332	81267485	316	5	74614332	83522252
273	5	74614332	81267499	317	5	74614332	83560095
274	5	74614332	81274512	318	5	74614332	83560204

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
319	5	74614332	83572400	363	5	74614332	78389884
320	5	74614332	83607661	364	5	74614332	78520683
321	5	74614332	83745342	365	5	74614332	78765635
322	5	74614332	83861275	366	5	74614332	78780292
323	5	74614332	83861633	367	5	74614332	78813114
324	5	74614332	83865653	368	5	74614332	78814710
325	5	74614332	83865914	369	5	74614332	78814976
326	5	74614332	83865920	370	5	74614332	78815306
327	5	74614332	83868010	371	5	74614332	78821393
328	5	74614332	84019752	372	5	74614332	78826528
329	5	74614332	84065912	373	5	74614332	78826538
330	5	74614332	84086632	374	5	74614332	78826612
331	5	74614332	84089603	375	5	74614332	78918620
332	5	74614332	84104814	376	5	74614332	78918850
333	5	74614332	84105175	377	5	74614332	79056960
334	5	74614332	84251635	378	5	74614332	79163631
335	5	74614332	84252180	379	5	74614332	79176557
336	5	74614332	84253030	380	5	74614332	79188028
337	5	74614332	84254208	381	5	74614332	79201760
338	5	74614332	84314930	382	5	74614332	79230005
339	5	74614332	84340523	383	5	74614332	79230318
340	5	74614332	84516340	384	5	74614332	79505592
341	5	74614332	84706916	385	5	74614332	79510072
342	5	74614332	84799488	386	5	74614332	79538012
343	5	74614332	84801081	387	5	74614332	79538048
344	5	74614332	84824103	388	5	74614332	79538367
345	5	74614332	84824203	389	5	74614332	79669824
346	5	74614332	84824816	390	5	74614332	79682242
347	5	74614332	84825422	391	5	74614332	79699261
348	5	74614332	84825763	392	5	74614332	79710673
349	5	74614332	84825942	393	5	74614332	79861902
350	5	74614332	84936441	394	5	74614332	79867710
351	5	74614332	84936493	395	5	74614332	79867868
352	5	74614332	84943705	396	5	74614332	79867873
353	5	74614332	169454950	397	5	74614332	79961961
354	5	74614332	181522829	398	5	74614332	80086268
355	5	74614332	204759879	399	5	74614332	80190673
356	5	74614332	209874191	400	5	74614332	80190777
357	5	74614332	78022476	401	5	74614332	80192546
358	5	74614332	78023096	402	5	74614332	80195395
359	5	74614332	78131652	403	5	74614332	80199923
360	5	74614332	78131784	404	5	74614332	80241911
361	5	74614332	78310499	405	5	74614332	80282785
362	5	74614332	78381593	406	5	74614332	80345337

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
407	5	74614332	80389787	451	5	74614332	82555641
408	5	74614332	80411639	452	5	74614332	82555670
409	5	74614332	80446855	453	5	74614332	82555611
410	5	74614332	80492790	454	5	74614332	82559047
411	5	74614332	80670554	455	5	74614332	82561535
412	5	74614332	80674679	456	5	74614332	82610100
413	5	74614332	80720509	457	5	74614332	82676822
414	5	74614332	80800856	458	5	74614332	82676901
415	5	74614332	80804587	459	5	74614332	82883691
416	5	74614332	80807409	460	5	74614332	82954942
417	5	74614332	80835734	461	5	74614332	82971688
418	5	74614332	80835734	462	5	74614332	83023965
419	5	74614332	80971764	463	5	74614332	83094205
420	5	74614332	80972258	464	5	74614332	83146355
421	5	74614332	80974450	465	5	74614332	83280630
422	5	74614332	81047638	466	5	74614332	83281412
423	5	74614332	81082021	467	5	74614332	83400242
424	5	74614332	81157909	468	5	74614332	83405797
425	5	74614332	81265937	469	5	74614332	83437132
426	5	74614332	81267485	470	5	74614332	83522252
427	5	74614332	81267499	471	5	74614332	83560095
428	5	74614332	81274512	472	5	74614332	83560204
429	5	74614332	81763618	473	5	74614332	83572400
430	5	74614332	81797217	474	5	74614332	83607661
431	5	74614332	81800186	475	5	74614332	83745342
432	5	74614332	81806213	476	5	74614332	83861275
433	5	74614332	81854583	477	5	74614332	83861633
434	5	74614332	81859374	478	5	74614332	83865653
435	5	74614332	81861368	479	5	74614332	83865914
436	5	74614332	81863686	480	5	74614332	83865920
437	5	74614332	81916850	481	5	74614332	83868010
438	5	74614332	81954891	482	5	74614332	84019752
439	5	74614332	81985250	483	5	74614332	84065912
440	5	74614332	82083752	484	5	74614332	84086632
441	5	74614332	82101253	485	5	74614332	84089603
442	5	74614332	82143124	486	5	74614332	84104814
443	5	74614332	82236318	487	5	74614332	84105175
444	5	74614332	82325587	488	5	74614332	84251635
445	5	74614332	82427210	489	5	74614332	84252180
446	5	74614332	82431853	490	5	74614332	84253030
447	5	74614332	82446714	491	5	74614332	84254208
448	5	74614332	82446794	492	5	74614332	84314930
449	5	74614332	82551111	493	5	74614332	84340523
450	5	74614332	82552090	494	5	74614332	84516340

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
495	5	74614332	84706916	539	5	77920728	79510072
496	5	74614332	84799488	540	5	77920728	79538012
497	5	74614332	84801081	541	5	77920728	79538048
498	5	74614332	84824103	542	5	77920728	79538367
499	5	74614332	84824203	543	5	77920728	79669824
500	5	74614332	84824816	544	5	77920728	79682242
501	5	74614332	84825422	545	5	77920728	79699261
502	5	74614332	84825763	546	5	77920728	79710673
503	5	74614332	84825942	547	5	77920728	79861902
504	5	74614332	84936441	548	5	77920728	79867710
505	5	74614332	84936493	549	5	77920728	79867868
506	5	74614332	84943705	550	5	77920728	79867873
507	5	74614332	169454950	551	5	77920728	79961061
508	5	74614332	181522829	552	5	77920728	80086268
509	5	74614332	204759879	553	5	77920728	80190673
510	5	74614332	209874191	554	5	77920728	80190777
511	5	77920728	78022476	555	5	77920728	80192546
512	5	77920728	78023096	556	5	77920728	80195395
513	5	77920728	78131652	557	5	77920728	80199923
514	5	77920728	78131784	558	5	77920728	80241911
515	5	77920728	78310499	559	5	77920728	80282785
516	5	77920728	78381593	560	5	77920728	80345337
517	5	77920728	78389884	561	5	77920728	80389787
518	5	77920728	78520683	562	5	77920728	80411639
519	5	77920728	78765635	563	5	77920728	80446855
520	5	77920728	78780292	564	5	77920728	80492790
521	5	77920728	78813114	565	5	77920728	80670554
522	5	77920728	78814710	566	5	77920728	80674679
523	5	77920728	78814976	567	5	77920728	80720509
524	5	77920728	78815306	568	5	77920728	80800856
525	5	77920728	78821393	569	5	77920728	80804587
526	5	77920728	78826528	570	5	77920728	80807409
527	5	77920728	78826538	571	5	77920728	80835734
528	5	77920728	78826612	572	5	77920728	80835734
529	5	77920728	78918620	573	5	77920728	80971764
530	5	77920728	78918850	574	5	77920728	80972258
531	5	77920728	79056960	575	5	77920728	80974450
532	5	77920728	79163631	576	5	77920728	81047638
533	5	77920728	79176557	577	5	77920728	81082921
534	5	77920728	79188028	578	5	77920728	81157909
535	5	77920728	79201760	579	5	77920728	81265937
536	5	77920728	79230005	580	5	77920728	81265937
537	5	77920728	79230318	581	5	77920728	81267485
538	5	77920728	79505592	582	5	77920728	81267499

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
583	5	77920728	81274512	627	5	77920728	83560204
584	5	77920728	81763618	628	5	77920728	83572400
585	5	77920728	81797217	629	5	77920728	83607661
586	5	77920728	81800186	630	5	77920728	83745342
587	5	77920728	81806213	631	5	77920728	83861275
588	5	77920728	81854583	632	5	77920728	83861633
589	5	77920728	81859374	633	5	77920728	83865653
590	5	77920728	81861368	634	5	77920728	83865914
591	5	77920728	81863686	635	5	77920728	83865920
592	5	77920728	81916850	636	5	77920728	83868010
593	5	77920728	81954891	637	5	77920728	84019752
594	5	77920728	81985250	638	5	77920728	84065912
595	5	77920728	82083752	639	5	77920728	84086632
596	5	77920728	82101253	640	5	77920728	84089603
597	5	77920728	82143124	641	5	77920728	84104814
598	5	77920728	82236318	642	5	77920728	84105175
599	5	77920728	82325587	643	5	77920728	84251635
600	5	77920728	82427210	644	5	77920728	84252180
601	5	77920728	82431853	645	5	77920728	84253030
602	5	77920728	82446714	646	5	77920728	84254208
603	5	77920728	82446794	647	5	77920728	84314930
604	5	77920728	82551111	648	5	77920728	84340523
605	5	77920728	82552090	649	5	77920728	84516340
606	5	77920728	82555641	650	5	77920728	84706916
607	5	77920728	82555670	651	5	77920728	84799488
608	5	77920728	82556511	652	5	77920728	84801081
609	5	77920728	82559047	653	5	77920728	84824103
610	5	77920728	82561535	654	5	77920728	84824103
611	5	77920728	82610100	655	5	77920728	84824203
612	5	77920728	82676822	656	5	77920728	84824816
613	5	77920728	82676901	657	5	77920728	84825422
614	5	77920728	82883691	658	5	77920728	84825763
615	5	77920728	82954942	659	5	77920728	84825942
616	5	77920728	82971688	660	5	77920728	84936441
617	5	77920728	83023965	661	5	77920728	84936493
618	5	77920728	83094205	662	5	77920728	84943705
619	5	77920728	83146355	663	5	77920728	169454950
620	5	77920728	83280630	664	5	77920728	181522829
621	5	77920728	83281412	665	5	77920728	204759879
622	5	77920728	83400242	666	5	77920728	209874191
623	5	77920728	83405797	667	5	78022476	78023096
624	5	77920728	83437132	668	5	78022476	78131652
625	5	77920728	83522252	669	5	78022476	78131784
626	5	77920728	83560095	670	5	78022476	78310499

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
671	5	78022476	78381593	715	5	78022476	80345337
672	5	78022476	78389884	716	5	78022476	80389787
673	5	78022476	78520683	717	5	78022476	80411639
674	5	78022476	78765635	718	5	78022476	80446855
675	5	78022476	78780292	719	5	78022476	80492790
676	5	78022476	78813114	720	5	78022476	80670554
677	5	78022476	78814710	721	5	78022476	80674679
678	5	78022476	78814976	722	5	78022476	80720509
679	5	78022476	78815306	723	5	78022476	80800856
680	5	78022476	78821393	724	5	78022476	80804587
681	5	78022476	78826528	725	5	78022476	80807409
682	5	78022476	78826538	726	5	78022476	80835734
683	5	78022476	78826612	727	5	78022476	80835734
684	5	78022476	78918620	728	5	78022476	80971764
685	5	78022476	78918850	729	5	78022476	80972258
686	5	78022476	79056960	730	5	78022476	80974450
687	5	78022476	79163631	731	5	78022476	81047638
688	5	78022476	79176557	732	5	78022476	81082921
689	5	78022476	79188028	733	5	78022476	81157909
690	5	78022476	79201760	734	5	78022476	81265937
691	5	78022476	79230005	735	5	78022476	81265937
692	5	78022476	79230318	736	5	78022476	81267485
693	5	78022476	79505592	737	5	78022476	81267499
694	5	78022476	79510072	738	5	78022476	81274512
695	5	78022476	79538012	739	5	78022476	81763618
696	5	78022476	79538048	740	5	78022476	81797217
697	5	78022476	79538367	741	5	78022476	81800186
698	5	78022476	79669824	742	5	78022476	81806213
699	5	78022476	79682242	743	5	78022476	81854583
700	5	78022476	79699261	744	5	78022476	81859374
701	5	78022476	79710673	745	5	78022476	81861368
702	5	78022476	79861902	746	5	78022476	81863686
703	5	78022476	79867710	747	5	78022476	81916850
704	5	78022476	79867868	748	5	78022476	81954891
705	5	78022476	79867873	749	5	78022476	81985250
706	5	78022476	79961961	750	5	78022476	82083752
707	5	78022476	80086268	751	5	78022476	82101253
708	5	78022476	80190673	752	5	78022476	82143124
709	5	78022476	80190777	753	5	78022476	82236318
710	5	78022476	80192546	754	5	78022476	82325587
711	5	78022476	80195395	755	5	78022476	82427210
712	5	78022476	80199923	756	5	78022476	82431853
713	5	78022476	80241911	757	5	78022476	82446714
714	5	78022476	80282785	758	5	78022476	82446794

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
759	5	78022476	82551111	803	5	78022476	84340523
760	5	78022476	82552090	804	5	78022476	84516340
761	5	78022476	82555641	805	5	78022476	84706916
762	5	78022476	82555670	806	5	78022476	84799488
763	5	78022476	82556511	807	5	78022476	84801081
764	5	78022476	82559047	808	5	78022476	84824103
765	5	78022476	82561535	809	5	78022476	84824203
766	5	78022476	82610100	810	5	78022476	84824816
767	5	78022476	82676822	811	5	78022476	84825422
768	5	78022476	82676901	812	5	78022476	84825763
769	5	78022476	82883691	813	5	78022476	84825942
770	5	78022476	82954942	814	5	78022476	84936441
771	5	78022476	82971688	815	5	78022476	84936493
772	5	78022476	83023965	816	5	78022476	84943705
773	5	78022476	83094205	817	5	78022476	169454950
774	5	78022476	83146355	818	5	78022476	181522829
775	5	78022476	83280630	819	5	78022476	204739879
776	5	78022476	83281412	820	5	78022476	209874191
777	5	78022476	83400242	821	5	78129898	78131652
778	5	78022476	83405797	822	5	78129898	78131784
779	5	78022476	83437132	823	5	78129898	78310499
780	5	78022476	83522252	824	5	78129898	78381593
781	5	78022476	83560095	825	5	78129898	78389884
782	5	78022476	83560204	826	5	78129898	78520683
783	5	78022476	83572400	827	5	78129898	78765635
784	5	78022476	83607661	828	5	78129898	78780292
785	5	78022476	83745342	829	5	78129898	78813114
786	5	78022476	83861275	830	5	78129898	78814710
787	5	78022476	83861633	831	5	78129898	78814976
788	5	78022476	83865653	832	5	78129898	78815306
789	5	78022476	83865914	833	5	78129898	78821393
790	5	78022476	83865920	834	5	78129898	78826528
791	5	78022476	83868010	835	5	78129898	78826538
792	5	78022476	84019752	836	5	78129898	78826612
793	5	78022476	84065912	837	5	78129898	78918620
794	5	78022476	84086632	838	5	78129898	78918850
795	5	78022476	84089603	839	5	78129898	79056960
796	5	78022476	84104814	840	5	78129898	79163631
797	5	78022476	84105175	841	5	78129898	79176557
798	5	78022476	84251635	842	5	78129898	79188028
799	5	78022476	84252180	843	5	78129898	79201760
800	5	78022476	84253030	844	5	78129898	79230005
801	5	78022476	84254208	845	5	78129898	79230318
802	5	78022476	84314930	846	5	78129898	79505592

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
847	5	78129898	79510072	891	5	78129898	81763618
848	5	78129898	79538012	892	5	78129898	81797217
849	5	78129898	79538048	893	5	78129898	81800186
850	5	78129898	79538367	894	5	78129898	81806213
851	5	78129898	79669824	895	5	78129898	81854583
852	5	78129898	79682242	896	5	78129898	81859374
853	5	78129898	79699261	897	5	78129898	81861368
854	5	78129898	79710673	898	5	78129898	81863686
855	5	78129898	79861902	899	5	78129898	81916850
856	5	78129898	79867710	900	5	78129898	81954891
857	5	78129898	79867868	901	5	78129898	81985250
858	5	78129898	79867873	902	5	78129898	82083752
859	5	78129898	79961961	903	5	78129898	82101253
860	5	78129898	80086268	904	5	78129898	82143124
861	5	78129898	80190673	905	5	78129898	82236318
862	5	78129898	80190777	906	5	78129898	82325587
863	5	78129898	80192546	907	5	78129898	82427210
864	5	78129898	80195395	908	5	78129898	82431853
865	5	78129898	80199923	909	5	78129898	82446714
866	5	78129898	80241911	910	5	78129898	82446794
867	5	78129898	80282785	911	5	78129898	82551111
868	5	78129898	80345337	912	5	78129898	82552090
869	5	78129898	80389787	913	5	78129898	82555670
870	5	78129898	80411639	914	5	78129898	82555670
871	5	78129898	80446855	915	5	78129898	82556511
872	5	78129898	80492790	916	5	78129898	82559047
873	5	78129898	80670554	917	5	78129898	82561535
874	5	78129898	80674679	918	5	78129898	82610100
875	5	78129898	80720509	919	5	78129898	82676822
876	5	78129898	80800856	920	5	78129898	82676901
877	5	78129898	80804587	921	5	78129898	82883691
878	5	78129898	80807409	922	5	78129898	82954942
879	5	78129898	80835734	923	5	78129898	82971688
880	5	78129898	80971764	924	5	78129898	83023965
881	5	78129898	80972258	925	5	78129898	83094205
882	5	78129898	80974450	926	5	78129898	83146355
883	5	78129898	81047638	927	5	78129898	83280630
884	5	78129898	81082921	928	5	78129898	83281412
885	5	78129898	81157909	929	5	78129898	83400242
886	5	78129898	81265937	930	5	78129898	83405797
887	5	78129898	81265937	931	5	78129898	83437132
888	5	78129898	81267485	932	5	78129898	83522252
889	5	78129898	81267499	933	5	78129898	83560095
890	5	78129898	81274512	934	5	78129898	83560204

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
935	5	78129898	83572400	979	5	78255163	78780292
936	5	78129898	83607661	980	5	78255163	78813114
937	5	78129898	83745342	981	5	78255163	78814710
938	5	78129898	83861275	982	5	78255163	78814976
939	5	78129898	83861633	983	5	78255163	78815306
940	5	78129898	83865653	984	5	78255163	78821393
941	5	78129898	83865914	985	5	78255163	78826528
942	5	78129898	83865920	986	5	78255163	78826538
943	5	78129898	83868010	987	5	78255163	78826612
944	5	78129898	84019752	988	5	78255163	78918620
945	5	78129898	84065912	989	5	78255163	78918850
946	5	78129898	84086632	990	5	78255163	79056960
947	5	78129898	84089603	991	5	78255163	79163631
948	5	78129898	84104814	992	5	78255163	79176557
949	5	78129898	84105175	993	5	78255163	79188028
950	5	78129898	84251635	994	5	78255163	79201760
951	5	78129898	84252180	995	5	78255163	79230005
952	5	78129898	84253030	996	5	78255163	79230318
953	5	78129898	84254208	997	5	78255163	79505592
954	5	78129898	84314930	998	5	78255163	79510072
955	5	78129898	84340523	999	5	78255163	79538012
956	5	78129898	84516340	1000	5	78255163	79538048
957	5	78129898	84706916	1001	5	78255163	79538367
958	5	78129898	84799488	1002	5	78255163	79669824
959	5	78129898	84801081	1003	5	78255163	79682242
960	5	78129898	84824103	1004	5	78255163	79699261
961	5	78129898	84824203	1005	5	78255163	79710673
962	5	78129898	84824816	1006	5	78255163	79861902
963	5	78129898	84825422	1007	5	78255163	79867710
964	5	78129898	84825763	1008	5	78255163	79867868
965	5	78129898	84825942	1009	5	78255163	79867873
966	5	78129898	84843411	1010	5	78255163	79961961
967	5	78129898	84936441	1011	5	78255163	80086268
968	5	78129898	84936493	1012	5	78255163	80190673
969	5	78129898	84943705	1013	5	78255163	80190777
970	5	78129898	169454950	1014	5	78255163	80192546
971	5	78129898	181522829	1015	5	78255163	80195395
972	5	78129898	204759879	1016	5	78255163	80199923
973	5	78129898	209874191	1017	5	78255163	80241911
974	5	78255163	78310499	1018	5	78255163	80282785
975	5	78255163	78381593	1019	5	78255163	80345337
976	5	78255163	78389884	1020	5	78255163	80389787
977	5	78255163	78520683	1021	5	78255163	80411639
978	5	78255163	78765635	1022	5	78255163	80446855

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
1023	5	78255163	80492790	1067	5	78255163	82559047
1024	5	78255163	80670554	1068	5	78255163	82561535
1025	5	78255163	80674679	1069	5	78255163	82610100
1026	5	78255163	80720509	1070	5	78255163	82676822
1027	5	78255163	80800856	1071	5	78255163	82676901
1028	5	78255163	80804587	1072	5	78255163	82883691
1029	5	78255163	80807409	1073	5	78255163	82954942
1030	5	78255163	80835734	1074	5	78255163	82971688
1031	5	78255163	80971764	1075	5	78255163	83023965
1032	5	78255163	80972258	1076	5	78255163	83094205
1033	5	78255163	80974450	1077	5	78255163	83146355
1034	5	78255163	81047638	1078	5	78255163	83280630
1035	5	78255163	81082921	1079	5	78255163	83281412
1036	5	78255163	81157909	1080	5	78255163	83400242
1037	5	78255163	81265937	1081	5	78255163	83405797
1038	5	78255163	81265937	1082	5	78255163	83437132
1039	5	78255163	81267485	1083	5	78255163	83522252
1040	5	78255163	81267499	1084	5	78255163	83560095
1041	5	78255163	81274512	1085	5	78255163	83560204
1042	5	78255163	81763618	1086	5	78255163	83572400
1043	5	78255163	81797217	1087	5	78255163	83607661
1044	5	78255163	81800186	1088	5	78255163	83745342
1045	5	78255163	81806213	1089	5	78255163	83861275
1046	5	78255163	81854583	1090	5	78255163	83861633
1047	5	78255163	81859374	1091	5	78255163	83865653
1048	5	78255163	81861368	1092	5	78255163	83865914
1049	5	78255163	81863686	1093	5	78255163	83865920
1050	5	78255163	81916850	1094	5	78255163	83868010
1051	5	78255163	81954891	1095	5	78255163	84019752
1052	5	78255163	81985250	1096	5	78255163	84065912
1053	5	78255163	82083752	1097	5	78255163	84086632
1054	5	78255163	82101253	1098	5	78255163	84089603
1055	5	78255163	82143124	1099	5	78255163	84104814
1056	5	78255163	82236318	1100	5	78255163	84105175
1057	5	78255163	82325587	1101	5	78255163	84251635
1058	5	78255163	82427210	1102	5	78255163	84252180
1059	5	78255163	82431853	1103	5	78255163	84253030
1060	5	78255163	82446714	1104	5	78255163	84254208
1061	5	78255163	82446794	1105	5	78255163	84314930
1062	5	78255163	82551111	1106	5	78255163	84340523
1063	5	78255163	82552090	1107	5	78255163	84516340
1064	5	78255163	82555641	1108	5	78255163	84706916
1065	5	78255163	82555670	1109	5	78255163	84799488
1066	5	78255163	82556511	1110	5	78255163	84801081

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
1111	5	78255163	84824103	1155	5	78380304	79699261
1112	5	78255163	84824203	1156	5	78380304	79710673
1113	5	78255163	84824816	1157	5	78380304	79861902
1114	5	78255163	84825422	1158	5	78380304	79867710
1115	5	78255163	84825763	1159	5	78380304	79867868
1116	5	78255163	84825942	1160	5	78380304	79867873
1117	5	78255163	84843411	1161	5	78380304	79961961
1118	5	78255163	84936441	1162	5	78380304	80086268
1119	5	78255163	84936493	1163	5	78380304	80190673
1120	5	78255163	84943705	1164	5	78380304	80190777
1121	5	78255163	169454950	1165	5	78380304	80192546
1122	5	78255163	181522829	1166	5	78380304	80195395
1123	5	78255163	204759879	1167	5	78380304	80199923
1124	5	78255163	209874191	1168	5	78380304	80241911
1125	5	78380304	78381593	1169	5	78380304	80282785
1126	5	78380304	78389884	1170	5	78380304	80345337
1127	5	78380304	78520683	1171	5	78380304	80389787
1128	5	78380304	78765635	1172	5	78380304	80411639
1129	5	78380304	78780292	1173	5	78380304	80446855
1130	5	78380304	78813114	1174	5	78380304	80492790
1131	5	78380304	78814710	1175	5	78380304	80670554
1132	5	78380304	78814976	1176	5	78380304	80674679
1133	5	78380304	78815306	1177	5	78380304	80720509
1134	5	78380304	78821393	1178	5	78380304	80800856
1135	5	78380304	78826528	1179	5	78380304	80804587
1136	5	78380304	78826538	1180	5	78380304	80807409
1137	5	78380304	78826612	1181	5	78380304	80835734
1138	5	78380304	78918620	1182	5	78380304	80971764
1139	5	78380304	78918850	1183	5	78380304	80972258
1140	5	78380304	79056960	1184	5	78380304	80974450
1141	5	78380304	79163631	1185	5	78380304	81047638
1142	5	78380304	79176557	1186	5	78380304	81082921
1143	5	78380304	79188028	1187	5	78380304	81157909
1144	5	78380304	79201760	1188	5	78380304	81265937
1145	5	78380304	79230005	1189	5	78380304	81265937
1146	5	78380304	79230318	1190	5	78380304	81267485
1147	5	78380304	79505592	1191	5	78380304	81267499
1148	5	78380304	79510072	1192	5	78380304	81274512
1149	5	78380304	79538012	1193	5	78380304	81763618
1150	5	78380304	79538048	1194	5	78380304	81797217
1151	5	78380304	79538048	1195	5	78380304	81800186
1152	5	78380304	79538367	1196	5	78380304	81806213
1153	5	78380304	79669824	1197	5	78380304	81854583
1154	5	78380304	79682242	1198	5	78380304	81859374

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
1199	5	78380304	81861368	1243	5	78380304	83865914
1200	5	78380304	81863686	1244	5	78380304	83865920
1201	5	78380304	81916850	1245	5	78380304	83868010
1202	5	78380304	81954891	1246	5	78380304	84019752
1203	5	78380304	81985250	1247	5	78380304	84065912
1204	5	78380304	82083752	1248	5	78380304	84086632
1205	5	78380304	82101253	1249	5	78380304	84089603
1206	5	78380304	82143124	1250	5	78380304	84104814
1207	5	78380304	82236318	1251	5	78380304	84105175
1208	5	78380304	82325587	1252	5	78380304	84251635
1209	5	78380304	82427210	1253	5	78380304	84252180
1210	5	78380304	82431853	1254	5	78380304	84253030
1211	5	78380304	82446714	1255	5	78380304	84254208
1212	5	78380304	82446794	1256	5	78380304	84314930
1213	5	78380304	82551111	1257	5	78380304	84340523
1214	5	78380304	82552090	1258	5	78380304	84516340
1215	5	78380304	82555641	1259	5	78380304	84706916
1216	5	78380304	82555670	1260	5	78380304	84799488
1217	5	78380304	82556511	1261	5	78380304	84801081
1218	5	78380304	82559047	1262	5	78380304	84824103
1219	5	78380304	82561535	1263	5	78380304	84824203
1220	5	78380304	82610100	1264	5	78380304	84824816
1221	5	78380304	82676822	1265	5	78380304	84825422
1222	5	78380304	82676901	1266	5	78380304	84825763
1223	5	78380304	82883691	1267	5	78380304	84825942
1224	5	78380304	82954942	1268	5	78380304	84843411
1225	5	78380304	82971688	1269	5	78380304	84936441
1226	5	78380304	83023965	1270	5	78380304	84936493
1227	5	78380304	83094205	1271	5	78380304	84943705
1228	5	78380304	83146355	1272	5	78380304	169454950
1229	5	78380304	83280630	1273	5	78380304	181522829
1230	5	78380304	83281412	1274	5	78380304	204759879
1231	5	78380304	83400242	1275	5	78380304	209874191
1232	5	78380304	83405797	1276	5	78381834	78389884
1233	5	78380304	83437132	1277	5	78381834	78520683
1234	5	78380304	83522252	1278	5	78381834	78765635
1235	5	78380304	83560095	1279	5	78381834	78780292
1236	5	78380304	83560204	1280	5	78381834	78813114
1237	5	78380304	83572400	1281	5	78381834	78814710
1238	5	78380304	83607661	1282	5	78381834	78814976
1239	5	78380304	83745342	1283	5	78381834	78815306
1240	5	78380304	83861275	1284	5	78381834	78821393
1241	5	78380304	83861633	1285	5	78381834	78826528
1242	5	78380304	83865653	1286	5	78381834	78826538

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
1287	5	78381834	78826612	1331	5	78381834	80971764
1288	5	78381834	78918620	1332	5	78381834	80972258
1289	5	78381834	78918850	1333	5	78381834	80974450
1290	5	78381834	79056960	1334	5	78381834	81047638
1291	5	78381834	79163631	1335	5	78381834	81082921
1292	5	78381834	79176557	1336	5	78381834	81157909
1293	5	78381834	79188028	1337	5	78381834	81265937
1294	5	78381834	79201760	1338	5	78381834	81265937
1295	5	78381834	79230005	1339	5	78381834	81267485
1296	5	78381834	79230318	1340	5	78381834	81267499
1297	5	78381834	79505592	1341	5	78381834	81274512
1298	5	78381834	79510072	1342	5	78381834	81763618
1299	5	78381834	79538012	1343	5	78381834	81797217
1300	5	78381834	79538048	1344	5	78381834	81800186
1301	5	78381834	79538367	1345	5	78381834	81806213
1302	5	78381834	79669824	1346	5	78381834	81854583
1303	5	78381834	79682242	1347	5	78381834	81859374
1304	5	78381834	79699261	1348	5	78381834	81861368
1305	5	78381834	79710673	1349	5	78381834	81863686
1306	5	78381834	79861902	1350	5	78381834	81916830
1307	5	78381834	79867710	1351	5	78381834	81954891
1308	5	78381834	79867868	1352	5	78381834	81985250
1309	5	78381834	79867873	1353	5	78381834	82083752
1310	5	78381834	79961961	1354	5	78381834	82101253
1311	5	78381834	80086268	1355	5	78381834	82143124
1312	5	78381834	80190673	1356	5	78381834	82236318
1313	5	78381834	80190777	1357	5	78381834	82325587
1314	5	78381834	80192546	1358	5	78381834	82427210
1315	5	78381834	80195395	1359	5	78381834	82431853
1316	5	78381834	80199923	1360	5	78381834	82446714
1317	5	78381834	80241911	1361	5	78381834	82446794
1318	5	78381834	80282785	1362	5	78381834	82551111
1319	5	78381834	80345337	1363	5	78381834	82552090
1320	5	78381834	80389787	1364	5	78381834	82555641
1321	5	78381834	80411639	1365	5	78381834	82555670
1322	5	78381834	80446855	1366	5	78381834	82556511
1323	5	78381834	80492790	1367	5	78381834	82559047
1324	5	78381834	80670554	1368	5	78381834	82561535
1325	5	78381834	80674679	1369	5	78381834	82610100
1326	5	78381834	80720509	1370	5	78381834	82676822
1327	5	78381834	80800856	1371	5	78381834	82676901
1328	5	78381834	80804587	1372	5	78381834	82883691
1329	5	78381834	80807409	1373	5	78381834	82954942
1330	5	78381834	80835734	1374	5	78381834	82971688

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
1375	5	78381834	83023965	1419	5	78381834	84936493
1376	5	78381834	83094205	1420	5	78381834	84943705
1377	5	78381834	83146355	1421	5	78381834	169454950
1378	5	78381834	83280630	1422	5	78381834	181522829
1379	5	78381834	83281412	1423	5	78381834	204759879
1380	5	78381834	83400242	1424	5	78381834	209874191
1381	5	78381834	83405797	1425	5	78519893	78520683
1382	5	78381834	83437132	1426	5	78519893	78765635
1383	5	78381834	83522252	1427	5	78519893	78780292
1384	5	78381834	83560095	1428	5	78519893	78813114
1385	5	78381834	83560204	1429	5	78519893	78814710
1386	5	78381834	83572400	1430	5	78519893	78814976
1387	5	78381834	83607661	1431	5	78519893	78815306
1388	5	78381834	83745342	1432	5	78519893	78821393
1389	5	78381834	83861275	1433	5	78519893	78826528
1390	5	78381834	83861633	1434	5	78519893	78826538
1391	5	78381834	83865653	1435	5	78519893	78826612
1392	5	78381834	83865914	1436	5	78519893	78918620
1393	5	78381834	83865920	1437	5	78519893	78918850
1394	5	78381834	83868010	1438	5	78519893	79056960
1395	5	78381834	84019752	1439	5	78519893	79163631
1396	5	78381834	84065912	1440	5	78519893	79176557
1397	5	78381834	84086632	1441	5	78519893	79188028
1398	5	78381834	84089603	1442	5	78519893	79201760
1399	5	78381834	84104814	1443	5	78519893	79230005
1400	5	78381834	84105175	1444	5	78519893	79230318
1401	5	78381834	84251635	1445	5	78519893	79505592
1402	5	78381834	84252180	1446	5	78519893	79510072
1403	5	78381834	84253030	1447	5	78519893	79538012
1404	5	78381834	84254208	1448	5	78519893	79538048
1405	5	78381834	84314930	1449	5	78519893	79538367
1406	5	78381834	84340523	1450	5	78519893	79669824
1407	5	78381834	84516340	1451	5	78519893	79682242
1408	5	78381834	84706916	1452	5	78519893	79699261
1409	5	78381834	84799488	1453	5	78519893	79710673
1410	5	78381834	84801081	1454	5	78519893	79861902
1411	5	78381834	84824103	1455	5	78519893	79867710
1412	5	78381834	84824203	1456	5	78519893	79867868
1413	5	78381834	84824816	1457	5	78519893	79867873
1414	5	78381834	84825422	1458	5	78519893	79961961
1415	5	78381834	84825763	1459	5	78519893	80086268
1416	5	78381834	84825942	1460	5	78519893	80190673
1417	5	78381834	84843411	1461	5	78519893	80190777
1418	5	78381834	84936441	1462	5	78519893	80192546

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
1463	5	78519893	80195395	1507	5	78519893	82431853
1464	5	78519893	80199923	1508	5	78519893	82446714
1465	5	78519893	80241911	1509	5	78519893	82446794
1466	5	78519893	80282785	1510	5	78519893	82551111
1467	5	78519893	80345337	1511	5	78519893	82552090
1468	5	78519893	80389787	1512	5	78519893	82555641
1469	5	78519893	80411639	1513	5	78519893	82555670
1470	5	78519893	80446855	1514	5	78519893	82556511
1471	5	78519893	80492790	1515	5	78519893	82559047
1472	5	78519893	80670554	1516	5	78519893	82561535
1473	5	78519893	80674679	1517	5	78519893	82610100
1474	5	78519893	80720509	1518	5	78519893	82676822
1475	5	78519893	80800856	1519	5	78519893	82676901
1476	5	78519893	80804587	1520	5	78519893	82883691
1477	5	78519893	80807409	1521	5	78519893	82954942
1478	5	78519893	80835734	1522	5	78519893	82971688
1479	5	78519893	80971764	1523	5	78519893	83023965
1480	5	78519893	80972258	1524	5	78519893	83094205
1481	5	78519893	80974450	1525	5	78519893	83146355
1482	5	78519893	81047638	1526	5	78519893	83280630
1483	5	78519893	81082921	1527	5	78519893	83281412
1484	5	78519893	81157909	1528	5	78519893	83400242
1485	5	78519893	81265937	1529	5	78519893	83405797
1486	5	78519893	81265937	1530	5	78519893	83437132
1487	5	78519893	81267485	1531	5	78519893	83522252
1488	5	78519893	81267499	1532	5	78519893	83560095
1489	5	78519893	81274512	1533	5	78519893	83560204
1490	5	78519893	81763618	1534	5	78519893	83572400
1491	5	78519893	81797217	1535	5	78519893	83607661
1492	5	78519893	81800186	1536	5	78519893	83745342
1493	5	78519893	81806213	1537	5	78519893	83861275
1494	5	78519893	81854583	1538	5	78519893	83861633
1495	5	78519893	81859374	1539	5	78519893	83865653
1496	5	78519893	81861368	1540	5	78519893	83865914
1497	5	78519893	81863686	1541	5	78519893	83865920
1498	5	78519893	81916850	1542	5	78519893	83868010
1499	5	78519893	81954891	1543	5	78519893	84019752
1500	5	78519893	81985250	1544	5	78519893	84065912
1501	5	78519893	82083752	1545	5	78519893	84086632
1502	5	78519893	82101253	1546	5	78519893	84089603
1503	5	78519893	82143124	1547	5	78519893	84104814
1504	5	78519893	82236318	1548	5	78519893	84105175
1505	5	78519893	82325587	1549	5	78519893	84251635
1506	5	78519893	82427210	1550	5	78519893	84252180

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
1551	5	78519893	84253030	1595	5	78758856	79538048
1552	5	78519893	84254208	1596	5	78758856	79538367
1553	5	78519893	84314930	1597	5	78758856	79669824
1554	5	78519893	84340523	1598	5	78758856	79682242
1555	5	78519893	84516340	1599	5	78758856	79699261
1556	5	78519893	84706916	1600	5	78758856	79710673
1557	5	78519893	84799488	1601	5	78758856	79861902
1558	5	78519893	84801081	1602	5	78758856	79867710
1559	5	78519893	84824103	1603	5	78758856	79867868
1560	5	78519893	84824203	1604	5	78758856	79867873
1561	5	78519893	84824816	1605	5	78758856	79961961
1562	5	78519893	84825422	1606	5	78758856	80086268
1563	5	78519893	84825763	1607	5	78758856	80190673
1564	5	78519893	84825942	1608	5	78758856	80190777
1565	5	78519893	84843411	1609	5	78758856	80192546
1566	5	78519893	84936441	1610	5	78758856	80195395
1567	5	78519893	84936493	1611	5	78758856	80199923
1568	5	78519893	84943705	1612	5	78758856	80241911
1569	5	78519893	169454950	1613	5	78758856	80282785
1570	5	78519893	181522829	1614	5	78758856	80345337
1571	5	78519893	204759879	1615	5	78758856	80389787
1572	5	78519893	209874191	1616	5	78758856	80411639
1573	5	78758856	78765635	1617	5	78758856	80446855
1574	5	78758856	78780292	1618	5	78758856	80492790
1575	5	78758856	78813114	1619	5	78758856	80670554
1576	5	78758856	78814710	1620	5	78758856	80674679
1577	5	78758856	78814976	1621	5	78758856	80720509
1578	5	78758856	78815306	1622	5	78758856	80800856
1579	5	78758856	78821393	1623	5	78758856	80804587
1580	5	78758856	78826528	1624	5	78758856	80807409
1581	5	78758856	78826538	1625	5	78758856	80835734
1582	5	78758856	78826612	1626	5	78758856	80971764
1583	5	78758856	78918620	1627	5	78758856	80972258
1584	5	78758856	78918850	1628	5	78758856	80974450
1585	5	78758856	79056960	1629	5	78758856	81047638
1586	5	78758856	79163631	1630	5	78758856	81082921
1587	5	78758856	79176557	1631	5	78758856	81157909
1588	5	78758856	79188028	1632	5	78758856	81265937
1589	5	78758856	79201760	1633	5	78758856	81265937
1590	5	78758856	79230005	1634	5	78758856	81267485
1591	5	78758856	79230318	1635	5	78758856	81267499
1592	5	78758856	79505592	1636	5	78758856	81274512
1593	5	78758856	79510072	1637	5	78758856	81763618
1594	5	78758856	79538012	1638	5	78758856	81797217

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
1639	5	78758856	81800186	1683	5	78758856	83745342
1640	5	78758856	81806213	1684	5	78758856	83861275
1641	5	78758856	81854583	1685	5	78758856	83861633
1642	5	78758856	81859374	1686	5	78758856	83865653
1643	5	78758856	81861368	1687	5	78758856	83865914
1644	5	78758856	81863686	1688	5	78758856	83865920
1645	5	78758856	81916850	1689	5	78758856	838668010
1646	5	78758856	81954891	1690	5	78758856	84019752
1647	5	78758856	81985250	1691	5	78758856	84065912
1648	5	78758856	82083752	1692	5	78758856	84086632
1649	5	78758856	82101253	1693	5	78758856	84089603
1650	5	78758856	82143124	1694	5	78758856	84104814
1651	5	78758856	82236318	1695	5	78758856	84105175
1652	5	78758856	82325587	1696	5	78758856	84251635
1653	5	78758856	82427210	1697	5	78758856	84252180
1654	5	78758856	82431853	1698	5	78758856	84253030
1655	5	78758856	82446714	1699	5	78758856	84254208
1656	5	78758856	82446794	1700	5	78758856	84314930
1657	5	78758856	82551111	1701	5	78758856	84340523
1658	5	78758856	82552090	1702	5	78758856	84516340
1659	5	78758856	82555641	1703	5	78758856	84706916
1660	5	78758856	82555670	1704	5	78758856	84799488
1661	5	78758856	82556511	1705	5	78758856	84801081
1662	5	78758856	82559047	1706	5	78758856	84824103
1663	5	78758856	82561535	1707	5	78758856	84824203
1664	5	78758856	82610100	1708	5	78758856	84824816
1665	5	78758856	82676822	1709	5	78758856	84825422
1666	5	78758856	82676901	1710	5	78758856	84825763
1667	5	78758856	82883691	1711	5	78758856	84825942
1668	5	78758856	82954942	1712	5	78758856	84843411
1669	5	78758856	82971688	1713	5	78758856	84936441
1670	5	78758856	83023965	1714	5	78758856	84936493
1671	5	78758856	83094205	1715	5	78758856	84943705
1672	5	78758856	83146355	1716	5	78758856	169454950
1673	5	78758856	83280630	1717	5	78758856	181522829
1674	5	78758856	83281412	1718	5	78758856	204759879
1675	5	78758856	83400242	1719	5	78758856	209874191
1676	5	78758856	83405797	1720	5	78772058	78780292
1677	5	78758856	83437132	1721	5	78772058	78813114
1678	5	78758856	83522252	1722	5	78772058	78814710
1679	5	78758856	83560095	1723	5	78772058	78814976
1680	5	78758856	83560204	1724	5	78772058	78815306
1681	5	78758856	83572400	1725	5	78772058	78821393
1682	5	78758856	83607661	1726	5	78772058	78826528

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
1727	5	78772058	78826538	1771	5	78772058	80835734
1728	5	78772058	78826612	1772	5	78772058	80971764
1729	5	78772058	78918620	1773	5	78772058	80972258
1730	5	78772058	78918850	1774	5	78772058	80974450
1731	5	78772058	79056960	1775	5	78772058	81047638
1732	5	78772058	79163631	1776	5	78772058	81082921
1733	5	78772058	79176557	1777	5	78772058	81157909
1734	5	78772058	79188028	1778	5	78772058	81265937
1735	5	78772058	79201760	1779	5	78772058	81265937
1736	5	78772058	79230005	1780	5	78772058	81267485
1737	5	78772058	79230318	1781	5	78772058	81267499
1738	5	78772058	79505592	1782	5	78772058	81274512
1739	5	78772058	79510072	1783	5	78772058	81763618
1740	5	78772058	79538012	1784	5	78772058	81797217
1741	5	78772058	79538048	1785	5	78772058	81800186
1742	5	78772058	79538367	1786	5	78772058	81806213
1743	5	78772058	79669824	1787	5	78772058	81854583
1744	5	78772058	79682242	1788	5	78772058	81859374
1745	5	78772058	79699261	1789	5	78772058	81861368
1746	5	78772058	79710673	1790	5	78772058	81863686
1747	5	78772058	79861902	1791	5	78772058	81916850
1748	5	78772058	79867710	1792	5	78772058	81954891
1749	5	78772058	79867868	1793	5	78772058	81985250
1750	5	78772058	79867873	1794	5	78772058	82083752
1751	5	78772058	79961961	1795	5	78772058	82101253
1752	5	78772058	80086268	1796	5	78772058	82143124
1753	5	78772058	80190673	1797	5	78772058	82236318
1754	5	78772058	80190777	1798	5	78772058	82325587
1755	5	78772058	80192546	1799	5	78772058	82427210
1756	5	78772058	80195395	1800	5	78772058	82431853
1757	5	78772058	80199923	1801	5	78772058	82446714
1758	5	78772058	80241911	1802	5	78772058	82446794
1759	5	78772058	80282785	1803	5	78772058	82551111
1760	5	78772058	80345337	1804	5	78772058	82552090
1761	5	78772058	80389787	1805	5	78772058	82555641
1762	5	78772058	80411639	1806	5	78772058	82555670
1763	5	78772058	80446855	1807	5	78772058	82556511
1764	5	78772058	80492790	1808	5	78772058	82559047
1765	5	78772058	80670554	1809	5	78772058	82561535
1766	5	78772058	80674679	1810	5	78772058	82610100
1767	5	78772058	80720509	1811	5	78772058	82676822
1768	5	78772058	80800856	1812	5	78772058	82676901
1769	5	78772058	80804587	1813	5	78772058	82883691
1770	5	78772058	80807409	1814	5	78772058	82954942

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
1815	5	78772058	82971688	1859	5	78772058	84936441
1816	5	78772058	83023965	1860	5	78772058	84936493
1817	5	78772058	83094205	1861	5	78772058	84943705
1818	5	78772058	83146355	1862	5	78772058	169454950
1819	5	78772058	83280630	1863	5	78772058	181522829
1820	5	78772058	83281412	1864	5	78772058	204759879
1821	5	78772058	83400242	1865	5	78772058	209874191
1822	5	78772058	83405797	1866	5	78804756	78813114
1823	5	78772058	83437132	1867	5	78804756	78814710
1824	5	78772058	83522252	1868	5	78804756	78814976
1825	5	78772058	83560095	1869	5	78804756	78815306
1826	5	78772058	83560204	1870	5	78804756	78821393
1827	5	78772058	83572400	1871	5	78804756	78826528
1828	5	78772058	83607661	1872	5	78804756	78826538
1829	5	78772058	83745342	1873	5	78804756	78826612
1830	5	78772058	83861275	1874	5	78804756	78918620
1831	5	78772058	83861633	1875	5	78804756	78918850
1832	5	78772058	83865653	1876	5	78804756	79056960
1833	5	78772058	83865914	1877	5	78804756	79163631
1834	5	78772058	83865920	1878	5	78804756	79176557
1835	5	78772058	83868010	1879	5	78804756	79188028
1836	5	78772058	84019752	1880	5	78804756	79201760
1837	5	78772058	84065912	1881	5	78804756	79230005
1838	5	78772058	84086632	1882	5	78804756	79230318
1839	5	78772058	84089603	1883	5	78804756	79505592
1840	5	78772058	84104814	1884	5	78804756	79510072
1841	5	78772058	84105175	1885	5	78804756	79538012
1842	5	78772058	84251635	1886	5	78804756	79538048
1843	5	78772058	84252180	1887	5	78804756	79538367
1844	5	78772058	84253030	1888	5	78804756	79669824
1845	5	78772058	84254208	1889	5	78804756	79682242
1846	5	78772058	84314930	1890	5	78804756	79699261
1847	5	78772058	84340523	1891	5	78804756	79710673
1848	5	78772058	84516340	1892	5	78804756	79861902
1849	5	78772058	84706916	1893	5	78804756	79867710
1850	5	78772058	84799488	1894	5	78804756	79867868
1851	5	78772058	84801081	1895	5	78804756	79867873
1852	5	78772058	84824103	1896	5	78804756	79961961
1853	5	78772058	84824203	1897	5	78804756	80086268
1854	5	78772058	84824816	1898	5	78804756	80190673
1855	5	78772058	84825422	1899	5	78804756	80190777
1856	5	78772058	84825763	1900	5	78804756	80192546
1857	5	78772058	84825942	1901	5	78804756	80195395
1858	5	78772058	84843411	1902	5	78804756	80199923

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
1903	5	78804756	80241911	1947	5	78804756	82446794
1904	5	78804756	80282785	1948	5	78804756	82551111
1905	5	78804756	80345337	1949	5	78804756	82552090
1906	5	78804756	80389787	1950	5	78804756	82555641
1907	5	78804756	80411639	1951	5	78804756	82555670
1908	5	78804756	80446855	1952	5	78804756	82556511
1909	5	78804756	80492790	1953	5	78804756	82559047
1910	5	78804756	80670554	1954	5	78804756	82561535
1911	5	78804756	80674679	1955	5	78804756	82610100
1912	5	78804756	80720509	1956	5	78804756	82676822
1913	5	78804756	80800856	1957	5	78804756	82676901
1914	5	78804756	80804587	1958	5	78804756	82883691
1915	5	78804756	80807409	1959	5	78804756	82954942
1916	5	78804756	80835734	1960	5	78804756	82971688
1917	5	78804756	80971764	1961	5	78804756	83023965
1918	5	78804756	80972258	1962	5	78804756	83094205
1919	5	78804756	80974450	1963	5	78804756	83146355
1920	5	78804756	81047638	1964	5	78804756	83280630
1921	5	78804756	81082921	1965	5	78804756	83281412
1922	5	78804756	81157909	1966	5	78804756	83400242
1923	5	78804756	81265937	1967	5	78804756	83405797
1924	5	78804756	81265937	1968	5	78804756	83437132
1925	5	78804756	81267485	1969	5	78804756	83522252
1926	5	78804756	81267499	1970	5	78804756	83560095
1927	5	78804756	81274512	1971	5	78804756	83560204
1928	5	78804756	81763618	1972	5	78804756	83572400
1929	5	78804756	81797217	1973	5	78804756	83607661
1930	5	78804756	81800186	1974	5	78804756	83745342
1931	5	78804756	81806213	1975	5	78804756	83861275
1932	5	78804756	81854583	1976	5	78804756	83861633
1933	5	78804756	81859374	1977	5	78804756	83865653
1934	5	78804756	81861368	1978	5	78804756	83865914
1935	5	78804756	81863686	1979	5	78804756	83865920
1936	5	78804756	81916850	1980	5	78804756	83868010
1937	5	78804756	81954891	1981	5	78804756	84019752
1938	5	78804756	81985250	1982	5	78804756	84065912
1939	5	78804756	82083752	1983	5	78804756	84086632
1940	5	78804756	82101253	1984	5	78804756	84089603
1941	5	78804756	82143124	1985	5	78804756	84104814
1942	5	78804756	82236318	1986	5	78804756	84105175
1943	5	78804756	82325587	1987	5	78804756	84251635
1944	5	78804756	82427210	1988	5	78804756	84252180
1945	5	78804756	82431853	1989	5	78804756	84253030
1946	5	78804756	82446714	1990	5	78804756	84254208

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
1991	5	78804756	84314930	2035	5	78805059	79699261
1992	5	78804756	84340523	2036	5	78805059	79710673
1993	5	78804756	84516340	2037	5	78805059	79861902
1994	5	78804756	84706916	2038	5	78805059	79867710
1995	5	78804756	84799488	2039	5	78805059	79867868
1996	5	78804756	84801081	2040	5	78805059	79867873
1997	5	78804756	84824103	2041	5	78805059	79961961
1998	5	78804756	84824203	2042	5	78805059	80086268
1999	5	78804756	84824816	2043	5	78805059	80190673
2000	5	78804756	84825422	2044	5	78805059	80190777
2001	5	78804756	84825763	2045	5	78805059	80192546
2002	5	78804756	84825942	2046	5	78805059	80195395
2003	5	78804756	84843411	2047	5	78805059	80199923
2004	5	78804756	84936441	2048	5	78805059	80241911
2005	5	78804756	84936493	2049	5	78805059	80282785
2006	5	78804756	84943705	2050	5	78805059	80345337
2007	5	78804756	169454950	2051	5	78805059	80389787
2008	5	78804756	181522829	2052	5	78805059	80411639
2009	5	78804756	204759879	2053	5	78805059	80446855
2010	5	78804756	209874191	2054	5	78805059	80492790
2011	5	78805059	78813114	2055	5	78805059	80670554
2012	5	78805059	78814710	2056	5	78805059	80674679
2013	5	78805059	78814976	2057	5	78805059	80720509
2014	5	78805059	78815306	2058	5	78805059	80800856
2015	5	78805059	78821393	2059	5	78805059	80804587
2016	5	78805059	78826528	2060	5	78805059	80807409
2017	5	78805059	78826538	2061	5	78805059	80835734
2018	5	78805059	78826612	2062	5	78805059	80971764
2019	5	78805059	78918620	2063	5	78805059	80972258
2020	5	78805059	78918850	2064	5	78805059	80974450
2021	5	78805059	79056960	2065	5	78805059	81047638
2022	5	78805059	79163631	2066	5	78805059	81082921
2023	5	78805059	79176557	2067	5	78805059	81157909
2024	5	78805059	79188028	2068	5	78805059	81265937
2025	5	78805059	79201760	2069	5	78805059	81265937
2026	5	78805059	79230005	2070	5	78805059	81267485
2027	5	78805059	79230318	2071	5	78805059	81267499
2028	5	78805059	79505592	2072	5	78805059	81274512
2029	5	78805059	79510072	2073	5	78805059	81763618
2030	5	78805059	79538012	2074	5	78805059	81797217
2031	5	78805059	79538048	2075	5	78805059	81800186
2032	5	78805059	79538367	2076	5	78805059	81806213
2033	5	78805059	79669824	2077	5	78805059	81854583
2034	5	78805059	79682242	2078	5	78805059	81859374

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
2079	5	78805059	81861368	2123	5	78805059	83865914
2080	5	78805059	81863686	2124	5	78805059	83865920
2081	5	78805059	81916850	2125	5	78805059	83868010
2082	5	78805059	81954891	2126	5	78805059	84019752
2083	5	78805059	81985250	2127	5	78805059	84065912
2084	5	78805059	82083752	2128	5	78805059	84086632
2085	5	78805059	82101253	2129	5	78805059	84089603
2086	5	78805059	82143124	2130	5	78805059	84104814
2087	5	78805059	82236318	2131	5	78805059	84105175
2088	5	78805059	82325587	2132	5	78805059	84251635
2089	5	78805059	82427210	2133	5	78805059	84252180
2090	5	78805059	82431853	2134	5	78805059	84253030
2091	5	78805059	82446714	2135	5	78805059	84254208
2092	5	78805059	82446794	2136	5	78805059	84314930
2093	5	78805059	82551111	2137	5	78805059	84340523
2094	5	78805059	82552090	2138	5	78805059	84516340
2095	5	78805059	82555641	2139	5	78805059	84706916
2096	5	78805059	82555670	2140	5	78805059	84799488
2097	5	78805059	82556511	2141	5	78805059	84801081
2098	5	78805059	82559047	2142	5	78805059	84824103
2099	5	78805059	82561535	2143	5	78805059	84824203
2100	5	78805059	82610100	2144	5	78805059	84824816
2101	5	78805059	82676822	2145	5	78805059	84825422
2102	5	78805059	82676901	2146	5	78805059	84825763
2103	5	78805059	82883691	2147	5	78805059	84825942
2104	5	78805059	82954942	2148	5	78805059	84843411
2105	5	78805059	82971688	2149	5	78805059	84936441
2106	5	78805059	83023965	2150	5	78805059	84936493
2107	5	78805059	83094205	2151	5	78805059	84943705
2108	5	78805059	83146355	2152	5	78805059	169454950
2109	5	78805059	83280630	2153	5	78805059	181522829
2110	5	78805059	83281412	2154	5	78805059	204759879
2111	5	78805059	83400242	2155	5	78805059	209874191
2112	5	78805059	83405797	2156	5	78814424	78814710
2113	5	78805059	83437132	2157	5	78814424	78814976
2114	5	78805059	83522252	2158	5	78814424	78815306
2115	5	78805059	83560095	2159	5	78814424	78821393
2116	5	78805059	83560204	2160	5	78814424	78826528
2117	5	78805059	83572400	2161	5	78814424	78826538
2118	5	78805059	83607661	2162	5	78814424	78826612
2119	5	78805059	83745342	2163	5	78814424	78918620
2120	5	78805059	83861275	2164	5	78814424	78918850
2121	5	78805059	83861633	2165	5	78814424	79056960
2122	5	78805059	83865653	2166	5	78814424	79163631

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
2167	5	78814424	79176557	2211	5	78814424	81157909
2168	5	78814424	79188028	2212	5	78814424	81265937
2169	5	78814424	79201760	2213	5	78814424	81265937
2170	5	78814424	79230005	2214	5	78814424	81267485
2171	5	78814424	79230318	2215	5	78814424	81267499
2172	5	78814424	79505592	2216	5	78814424	81274512
2173	5	78814424	79510072	2217	5	78814424	81763618
2174	5	78814424	79538012	2218	5	78814424	81797217
2175	5	78814424	79538048	2219	5	78814424	81800186
2176	5	78814424	79538367	2220	5	78814424	81806213
2177	5	78814424	79669824	2221	5	78814424	81854583
2178	5	78814424	79682242	2222	5	78814424	81859374
2179	5	78814424	79699261	2223	5	78814424	81861368
2180	5	78814424	79710673	2224	5	78814424	81863686
2181	5	78814424	79861902	2225	5	78814424	81916850
2182	5	78814424	79867710	2226	5	78814424	81954891
2183	5	78814424	79867868	2227	5	78814424	81985250
2184	5	78814424	79867873	2228	5	78814424	82083752
2185	5	78814424	79961961	2229	5	78814424	82101253
2186	5	78814424	80086268	2230	5	78814424	82143124
2187	5	78814424	80190673	2231	5	78814424	82236318
2188	5	78814424	80190777	2232	5	78814424	82325587
2189	5	78814424	80192546	2233	5	78814424	82427210
2190	5	78814424	80195395	2234	5	78814424	82431853
2191	5	78814424	80199923	2235	5	78814424	82446714
2192	5	78814424	80241911	2236	5	78814424	82446794
2193	5	78814424	80282785	2237	5	78814424	82551111
2194	5	78814424	80345337	2238	5	78814424	82552090
2195	5	78814424	80389787	2239	5	78814424	82555641
2196	5	78814424	80411639	2240	5	78814424	82555670
2197	5	78814424	80446855	2241	5	78814424	82556511
2198	5	78814424	80492790	2242	5	78814424	82559047
2199	5	78814424	80670554	2243	5	78814424	82561535
2200	5	78814424	80674679	2244	5	78814424	82610100
2201	5	78814424	80720509	2245	5	78814424	82676822
2202	5	78814424	80800856	2246	5	78814424	82676901
2203	5	78814424	80804587	2247	5	78814424	82883691
2204	5	78814424	80807409	2248	5	78814424	82954942
2205	5	78814424	80835734	2249	5	78814424	82971688
2206	5	78814424	80971764	2250	5	78814424	83023965
2207	5	78814424	80972258	2251	5	78814424	83094205
2208	5	78814424	80974450	2252	5	78814424	83146355
2209	5	78814424	81047638	2253	5	78814424	83280630
2210	5	78814424	81082921	2254	5	78814424	83281412

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
2255	5	78814424	83400242	2299	5	78814424	209874191
2256	5	78814424	83405797	2300	5	78819803	78821393
2257	5	78814424	83437132	2301	5	78819803	78826528
2258	5	78814424	83522252	2302	5	78819803	78826538
2259	5	78814424	83560095	2303	5	78819803	78826612
2260	5	78814424	83560204	2304	5	78819803	78918620
2261	5	78814424	83572400	2305	5	78819803	78918850
2262	5	78814424	83607661	2306	5	78819803	79056960
2263	5	78814424	83745342	2307	5	78819803	79163631
2264	5	78814424	83861275	2308	5	78819803	79176557
2265	5	78814424	83861633	2309	5	78819803	79188028
2266	5	78814424	83865653	2310	5	78819803	79201760
2267	5	78814424	83865914	2311	5	78819803	79230005
2268	5	78814424	83865920	2312	5	78819803	79230318
2269	5	78814424	83868010	2313	5	78819803	79305592
2270	5	78814424	84019752	2314	5	78819803	79510072
2271	5	78814424	84065912	2315	5	78819803	79538012
2272	5	78814424	84086632	2316	5	78819803	79538048
2273	5	78814424	84089603	2317	5	78819803	79538367
2274	5	78814424	84104814	2318	5	78819803	79669824
2275	5	78814424	84105175	2319	5	78819803	79682242
2276	5	78814424	84251635	2320	5	78819803	79699261
2277	5	78814424	84252180	2321	5	78819803	79710673
2278	5	78814424	84253030	2322	5	78819803	79861902
2279	5	78814424	84254208	2323	5	78819803	79867710
2280	5	78814424	84314930	2324	5	78819803	79867868
2281	5	78814424	84340523	2325	5	78819803	79867873
2282	5	78814424	84516340	2326	5	78819803	79961961
2283	5	78814424	84706916	2327	5	78819803	80086268
2284	5	78814424	84799488	2328	5	78819803	80190673
2285	5	78814424	84801081	2329	5	78819803	80190777
2286	5	78814424	84824103	2330	5	78819803	80192546
2287	5	78814424	84824203	2331	5	78819803	80195395
2288	5	78814424	84824816	2332	5	78819803	80199923
2289	5	78814424	84825422	2333	5	78819803	80241911
2290	5	78814424	84825763	2334	5	78819803	80282785
2291	5	78814424	84825942	2335	5	78819803	80345337
2292	5	78814424	84843411	2336	5	78819803	80389787
2293	5	78814424	84936441	2337	5	78819803	80411639
2294	5	78814424	84936493	2338	5	78819803	80446855
2295	5	78814424	84943705	2339	5	78819803	80492790
2296	5	78814424	169454950	2340	5	78819803	80670554
2297	5	78814424	181522829	2341	5	78819803	80674679
2298	5	78814424	204759879	2342	5	78819803	80720509

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
2343	5	78819803	80800856	2387	5	78819803	82676901
2344	5	78819803	80804587	2388	5	78819803	82883691
2345	5	78819803	80807409	2389	5	78819803	82954942
2346	5	78819803	80835734	2390	5	78819803	82971688
2347	5	78819803	80971764	2391	5	78819803	83023965
2348	5	78819803	80972258	2392	5	78819803	83094205
2349	5	78819803	80974450	2393	5	78819803	83146355
2350	5	78819803	81047638	2394	5	78819803	83280630
2351	5	78819803	81082921	2395	5	78819803	83281412
2352	5	78819803	81157909	2396	5	78819803	83400242
2353	5	78819803	81265937	2397	5	78819803	83405797
2354	5	78819803	81265937	2398	5	78819803	83437132
2355	5	78819803	81267485	2399	5	78819803	83522252
2356	5	78819803	81267499	2400	5	78819803	83560095
2357	5	78819803	81274512	2401	5	78819803	83560204
2358	5	78819803	81763618	2402	5	78819803	83572400
2359	5	78819803	81797217	2403	5	78819803	83607661
2360	5	78819803	81800186	2404	5	78819803	83745342
2361	5	78819803	81806213	2405	5	78819803	83861275
2362	5	78819803	81854583	2406	5	78819803	83861633
2363	5	78819803	81859374	2407	5	78819803	83865653
2364	5	78819803	81861368	2408	5	78819803	83865914
2365	5	78819803	81863686	2409	5	78819803	83865920
2366	5	78819803	81916850	2410	5	78819803	83868010
2367	5	78819803	81954891	2411	5	78819803	84019752
2368	5	78819803	81985250	2412	5	78819803	84065912
2369	5	78819803	82083752	2413	5	78819803	84086632
2370	5	78819803	82101253	2414	5	78819803	84089603
2371	5	78819803	82143124	2415	5	78819803	84104814
2372	5	78819803	82236318	2416	5	78819803	84105175
2373	5	78819803	82325587	2417	5	78819803	84251635
2374	5	78819803	82427210	2418	5	78819803	84252180
2375	5	78819803	82431853	2419	5	78819803	84253030
2376	5	78819803	82446714	2420	5	78819803	84254208
2377	5	78819803	82446794	2421	5	78819803	84314930
2378	5	78819803	82551111	2422	5	78819803	84340523
2379	5	78819803	82552090	2423	5	78819803	84516340
2380	5	78819803	82555641	2424	5	78819803	84706916
2381	5	78819803	82555670	2425	5	78819803	84799488
2382	5	78819803	82556511	2426	5	78819803	84801081
2383	5	78819803	82559047	2427	5	78819803	84824103
2384	5	78819803	82561535	2428	5	78819803	84824203
2385	5	78819803	82610100	2429	5	78819803	84824816
2386	5	78819803	82676822	2430	5	78819803	84825422

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
2431	5	78819803	84825763	2475	5	78820119	80282785
2432	5	78819803	84825942	2476	5	78820119	80345337
2433	5	78819803	84843411	2477	5	78820119	80389787
2434	5	78819803	84936441	2478	5	78820119	80411639
2435	5	78819803	84936493	2479	5	78820119	80446855
2436	5	78819803	84943705	2480	5	78820119	80492790
2437	5	78819803	169454950	2481	5	78820119	80670554
2438	5	78819803	181522829	2482	5	78820119	80674679
2439	5	78819803	204759879	2483	5	78820119	80720509
2440	5	78819803	209874191	2484	5	78820119	80800856
2441	5	78820119	78821393	2485	5	78820119	80804587
2442	5	78820119	78826528	2486	5	78820119	80807409
2443	5	78820119	78826538	2487	5	78820119	80835734
2444	5	78820119	78826612	2488	5	78820119	80971764
2445	5	78820119	78918620	2489	5	78820119	80972258
2446	5	78820119	78918850	2490	5	78820119	80974450
2447	5	78820119	79056960	2491	5	78820119	81047638
2448	5	78820119	79163631	2492	5	78820119	81082921
2449	5	78820119	79176557	2493	5	78820119	81157909
2450	5	78820119	79188028	2494	5	78820119	81265937
2451	5	78820119	79201760	2495	5	78820119	81265937
2452	5	78820119	79230005	2496	5	78820119	81267485
2453	5	78820119	79230318	2497	5	78820119	81267499
2454	5	78820119	79505592	2498	5	78820119	81274512
2455	5	78820119	79510072	2499	5	78820119	81763618
2456	5	78820119	79538012	2500	5	78820119	81797217
2457	5	78820119	79538048	2501	5	78820119	81800186
2458	5	78820119	79538367	2502	5	78820119	81806213
2459	5	78820119	79669824	2503	5	78820119	81854583
2460	5	78820119	79682242	2504	5	78820119	81859374
2461	5	78820119	79699261	2505	5	78820119	81861368
2462	5	78820119	79710673	2506	5	78820119	81863686
2463	5	78820119	79861902	2507	5	78820119	81916850
2464	5	78820119	79867710	2508	5	78820119	81954891
2465	5	78820119	79867868	2509	5	78820119	81985250
2466	5	78820119	79867873	2510	5	78820119	82083752
2467	5	78820119	79961961	2511	5	78820119	82101253
2468	5	78820119	80086268	2512	5	78820119	82143124
2469	5	78820119	80190673	2513	5	78820119	82236318
2470	5	78820119	80190777	2514	5	78820119	82325587
2471	5	78820119	80192546	2515	5	78820119	82427210
2472	5	78820119	80195395	2516	5	78820119	82431853
2473	5	78820119	80199923	2517	5	78820119	82446714
2474	5	78820119	80241911	2518	5	78820119	82446794

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
2519	5	78820119	82551111	2563	5	78820119	84340523
2520	5	78820119	82552090	2564	5	78820119	84516340
2521	5	78820119	82555641	2565	5	78820119	84706916
2522	5	78820119	82555670	2566	5	78820119	84799488
2523	5	78820119	82556511	2567	5	78820119	84801081
2524	5	78820119	82559047	2568	5	78820119	84824103
2525	5	78820119	82561535	2569	5	78820119	84824203
2526	5	78820119	82610100	2570	5	78820119	84824816
2527	5	78820119	82676822	2571	5	78820119	84825422
2528	5	78820119	82676901	2572	5	78820119	84825763
2529	5	78820119	82883691	2573	5	78820119	84825942
2530	5	78820119	82954942	2574	5	78820119	84843411
2531	5	78820119	82971688	2575	5	78820119	84936441
2532	5	78820119	83023965	2576	5	78820119	84936493
2533	5	78820119	83094205	2577	5	78820119	84943705
2534	5	78820119	83146355	2578	5	78820119	169454950
2535	5	78820119	83280630	2579	5	78820119	181522829
2536	5	78820119	83281412	2580	5	78820119	204759879
2537	5	78820119	83400242	2581	5	78820119	209874191
2538	5	78820119	83405797	2582	5	78904639	78918620
2539	5	78820119	83437132	2583	5	78904639	78918850
2540	5	78820119	83522252	2584	5	78904639	79056960
2541	5	78820119	83560095	2585	5	78904639	79163631
2542	5	78820119	83560204	2586	5	78904639	79176557
2543	5	78820119	83572400	2587	5	78904639	79188028
2544	5	78820119	83607661	2588	5	78904639	79201760
2545	5	78820119	83745342	2589	5	78904639	79230005
2546	5	78820119	83861275	2590	5	78904639	79230318
2547	5	78820119	83861633	2591	5	78904639	79505592
2548	5	78820119	83865653	2592	5	78904639	79510072
2549	5	78820119	83865914	2593	5	78904639	79538012
2550	5	78820119	83865920	2594	5	78904639	79538048
2551	5	78820119	83868010	2595	5	78904639	79538367
2552	5	78820119	84019752	2596	5	78904639	79669824
2553	5	78820119	84065912	2597	5	78904639	79682242
2554	5	78820119	84086632	2598	5	78904639	79699261
2555	5	78820119	84089603	2599	5	78904639	79710673
2556	5	78820119	84104814	2600	5	78904639	79861902
2557	5	78820119	84105175	2601	5	78904639	79867710
2558	5	78820119	84251635	2602	5	78904639	79867868
2559	5	78820119	84252180	2603	5	78904639	79867873
2560	5	78820119	84253030	2604	5	78904639	79961961
2561	5	78820119	84254208	2605	5	78904639	80086268
2562	5	78820119	84314930	2606	5	78904639	80190673

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
2607	5	78904639	80190777	2651	5	78904639	82325587
2608	5	78904639	80192546	2652	5	78904639	82427210
2609	5	78904639	80195395	2653	5	78904639	82431853
2610	5	78904639	80199923	2654	5	78904639	82446714
2611	5	78904639	80241911	2655	5	78904639	82446794
2612	5	78904639	80282785	2656	5	78904639	82551111
2613	5	78904639	80345337	2657	5	78904639	82552090
2614	5	78904639	80389787	2658	5	78904639	82555641
2615	5	78904639	80411639	2659	5	78904639	82555670
2616	5	78904639	80446855	2660	5	78904639	82556511
2617	5	78904639	80492790	2661	5	78904639	82559047
2618	5	78904639	80670554	2662	5	78904639	82561535
2619	5	78904639	80674679	2663	5	78904639	82610100
2620	5	78904639	80720509	2664	5	78904639	82676822
2621	5	78904639	80800856	2665	5	78904639	82676901
2622	5	78904639	80804587	2666	5	78904639	82883691
2623	5	78904639	80807409	2667	5	78904639	82954942
2624	5	78904639	80835734	2668	5	78904639	82971688
2625	5	78904639	80971764	2669	5	78904639	83023965
2626	5	78904639	80972258	2670	5	78904639	83094205
2627	5	78904639	80974450	2671	5	78904639	83146355
2628	5	78904639	81047638	2672	5	78904639	83280630
2629	5	78904639	81082921	2673	5	78904639	83281412
2630	5	78904639	81157909	2674	5	78904639	83400242
2631	5	78904639	81265937	2675	5	78904639	83405797
2632	5	78904639	81265937	2676	5	78904639	83437132
2633	5	78904639	81267485	2677	5	78904639	83522252
2634	5	78904639	81267499	2678	5	78904639	83560095
2635	5	78904639	81274512	2679	5	78904639	83560204
2636	5	78904639	81763618	2680	5	78904639	83572400
2637	5	78904639	81797217	2681	5	78904639	83607661
2638	5	78904639	81800186	2682	5	78904639	83745342
2639	5	78904639	81806213	2683	5	78904639	83861275
2640	5	78904639	81854583	2684	5	78904639	83861633
2641	5	78904639	81859374	2685	5	78904639	83865653
2642	5	78904639	81861368	2686	5	78904639	83865914
2643	5	78904639	81863686	2687	5	78904639	83865920
2644	5	78904639	81916850	2688	5	78904639	83868010
2645	5	78904639	81954891	2689	5	78904639	84019752
2646	5	78904639	81985250	2690	5	78904639	84065912
2647	5	78904639	82083752	2691	5	78904639	84086632
2648	5	78904639	82101253	2692	5	78904639	84089603
2649	5	78904639	82143124	2693	5	78904639	84104814
2650	5	78904639	82236318	2694	5	78904639	84105175

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
2695	5	78904639	84251635	2739	5	78918620	79867873
2696	5	78904639	84252180	2740	5	78918620	79961961
2697	5	78904639	84253030	2741	5	78918620	80086268
2698	5	78904639	84254208	2742	5	78918620	80190673
2699	5	78904639	84314930	2743	5	78918620	80190777
2700	5	78904639	84340523	2744	5	78918620	80192546
2701	5	78904639	84516340	2745	5	78918620	80195395
2702	5	78904639	84706916	2746	5	78918620	80199923
2703	5	78904639	84799488	2747	5	78918620	80241911
2704	5	78904639	84801081	2748	5	78918620	80282785
2705	5	78904639	84824103	2749	5	78918620	80345337
2706	5	78904639	84824203	2750	5	78918620	80389787
2707	5	78904639	84824816	2751	5	78918620	80411639
2708	5	78904639	84825422	2752	5	78918620	80446855
2709	5	78904639	84825763	2753	5	78918620	80492790
2710	5	78904639	84825942	2754	5	78918620	80670554
2711	5	78904639	84843411	2755	5	78918620	80674679
2712	5	78904639	84936441	2756	5	78918620	80720509
2713	5	78904639	84936493	2757	5	78918620	80800856
2714	5	78904639	84943705	2758	5	78918620	80804587
2715	5	78904639	169454950	2759	5	78918620	80807409
2716	5	78904639	181522829	2760	5	78918620	80835734
2717	5	78904639	204759879	2761	5	78918620	80971764
2718	5	78904639	209874191	2762	5	78918620	80972258
2719	5	78918620	78918850	2763	5	78918620	80974450
2720	5	78918620	79056960	2764	5	78918620	81047638
2721	5	78918620	79163631	2765	5	78918620	81082921
2722	5	78918620	79176557	2766	5	78918620	81157909
2723	5	78918620	79188028	2767	5	78918620	81265937
2724	5	78918620	79201760	2768	5	78918620	81265937
2725	5	78918620	79230005	2769	5	78918620	81267485
2726	5	78918620	79230318	2770	5	78918620	81267499
2727	5	78918620	79505592	2771	5	78918620	81274512
2728	5	78918620	79510072	2772	5	78918620	81763618
2729	5	78918620	79538012	2773	5	78918620	81797217
2730	5	78918620	79538048	2774	5	78918620	81800186
2731	5	78918620	79538367	2775	5	78918620	81806213
2732	5	78918620	79669824	2776	5	78918620	81854583
2733	5	78918620	79682242	2777	5	78918620	81859374
2734	5	78918620	79699261	2778	5	78918620	81861368
2735	5	78918620	79710673	2779	5	78918620	81863686
2736	5	78918620	79861902	2780	5	78918620	81916850
2737	5	78918620	79867710	2781	5	78918620	81954891
2738	5	78918620	79867868	2782	5	78918620	81985250

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
2783	5	78918620	82083752	2827	5	78918620	84086632
2784	5	78918620	82101253	2828	5	78918620	84089603
2785	5	78918620	82143124	2829	5	78918620	84104814
2786	5	78918620	82236318	2830	5	78918620	84105175
2787	5	78918620	82325587	2831	5	78918620	84251635
2788	5	78918620	82427210	2832	5	78918620	84252180
2789	5	78918620	82431853	2833	5	78918620	84253030
2790	5	78918620	82446714	2834	5	78918620	84254208
2791	5	78918620	82446794	2835	5	78918620	84314930
2792	5	78918620	82551111	2836	5	78918620	84340523
2793	5	78918620	82552090	2837	5	78918620	84516340
2794	5	78918620	82555641	2838	5	78918620	84706916
2795	5	78918620	82555670	2839	5	78918620	84799488
2796	5	78918620	82556511	2840	5	78918620	84801081
2797	5	78918620	82559047	2841	5	78918620	84824103
2798	5	78918620	82561535	2842	5	78918620	84824203
2799	5	78918620	82610100	2843	5	78918620	84824816
2800	5	78918620	82676822	2844	5	78918620	84825422
2801	5	78918620	82676901	2845	5	78918620	84825763
2802	5	78918620	82883691	2846	5	78918620	84825942
2803	5	78918620	82954942	2847	5	78918620	84843411
2804	5	78918620	82971688	2848	5	78918620	84936441
2805	5	78918620	83023965	2849	5	78918620	84936493
2806	5	78918620	83094205	2850	5	78918620	84943705
2807	5	78918620	83146355	2851	5	78918620	169454950
2808	5	78918620	83280630	2852	5	78918620	181522829
2809	5	78918620	83281412	2853	5	78918620	204759879
2810	5	78918620	83400242	2854	5	78918620	209874191
2811	5	78918620	83405797	2855	5	79055654	78918620
2812	5	78918620	83437132	2856	5	79055654	79056960
2813	5	78918620	83522252	2857	5	79055654	79163631
2814	5	78918620	83560095	2858	5	79055654	79176557
2815	5	78918620	83560204	2859	5	79055654	79188028
2816	5	78918620	83572400	2860	5	79055654	79201760
2817	5	78918620	83607661	2861	5	79055654	79230005
2818	5	78918620	83745342	2862	5	79055654	79230318
2819	5	78918620	83861275	2863	5	79055654	79505592
2820	5	78918620	83861633	2864	5	79055654	79510072
2821	5	78918620	83865653	2865	5	79055654	79538012
2822	5	78918620	83865914	2866	5	79055654	79538048
2823	5	78918620	83865920	2867	5	79055654	79538367
2824	5	78918620	83868010	2868	5	79055654	79669824
2825	5	78918620	84019752	2869	5	79055654	79682242
2826	5	78918620	84065912	2870	5	79055654	79699261

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
2871	5	79055654	79710673	2915	5	79055654	81863686
2872	5	79055654	79861902	2916	5	79055654	81916850
2873	5	79055654	79867710	2917	5	79055654	81954891
2874	5	79055654	79867868	2918	5	79055654	81985250
2875	5	79055654	79867873	2919	5	79055654	82083752
2876	5	79055654	79961961	2920	5	79055654	82101253
2877	5	79055654	80086268	2921	5	79055654	82143124
2878	5	79055654	80190673	2922	5	79055654	82236318
2879	5	79055654	80190777	2923	5	79055654	82325587
2880	5	79055654	80192546	2924	5	79055654	82427210
2881	5	79055654	80195395	2925	5	79055654	82431853
2882	5	79055654	80199923	2926	5	79055654	82446714
2883	5	79055654	80241911	2927	5	79055654	82446794
2884	5	79055654	80282785	2928	5	79055654	82551111
2885	5	79055654	80345337	2929	5	79055654	82552090
2886	5	79055654	80389787	2930	5	79055654	82555641
2887	5	79055654	80411639	2931	5	79055654	82555670
2888	5	79055654	80446855	2932	5	79055654	82556311
2889	5	79055654	80492790	2933	5	79055654	82559047
2890	5	79055654	80670554	2934	5	79055654	82561535
2891	5	79055654	80674679	2935	5	79055654	82610100
2892	5	79055654	80720509	2936	5	79055654	82676822
2893	5	79055654	80800856	2937	5	79055654	82676901
2894	5	79055654	80804587	2938	5	79055654	82883691
2895	5	79055654	80807409	2939	5	79055654	82954942
2896	5	79055654	80835734	2940	5	79055654	82971688
2897	5	79055654	80971764	2941	5	79055654	83023965
2898	5	79055654	80972258	2942	5	79055654	83094205
2899	5	79055654	80974450	2943	5	79055654	83146355
2900	5	79055654	81047638	2944	5	79055654	83280630
2901	5	79055654	81082921	2945	5	79055654	83281412
2902	5	79055654	81157909	2946	5	79055654	83400242
2903	5	79055654	81265937	2947	5	79055654	83405797
2904	5	79055654	81265937	2948	5	79055654	83437132
2905	5	79055654	81267485	2949	5	79055654	83522252
2906	5	79055654	81267499	2950	5	79055654	83560095
2907	5	79055654	81274512	2951	5	79055654	83560204
2908	5	79055654	81763618	2952	5	79055654	83572400
2909	5	79055654	81797217	2953	5	79055654	83607661
2910	5	79055654	81800186	2954	5	79055654	83745342
2911	5	79055654	81806213	2955	5	79055654	83861275
2912	5	79055654	81854583	2956	5	79055654	83861633
2913	5	79055654	81859374	2957	5	79055654	83865653
2914	5	79055654	81861368	2958	5	79055654	83865914

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
2959	5	79055654	83865920	3003	5	79162381	79682242
2960	5	79055654	83868010	3004	5	79162381	79699261
2961	5	79055654	84019752	3005	5	79162381	79710673
2962	5	79055654	84065912	3006	5	79162381	79861902
2963	5	79055654	84086632	3007	5	79162381	79867710
2964	5	79055654	84089603	3008	5	79162381	79867868
2965	5	79055654	84104814	3009	5	79162381	79867873
2966	5	79055654	84105175	3010	5	79162381	79961961
2967	5	79055654	84251635	3011	5	79162381	80086268
2968	5	79055654	84252180	3012	5	79162381	80190673
2969	5	79055654	84253030	3013	5	79162381	80190777
2970	5	79055654	84254208	3014	5	79162381	80192346
2971	5	79055654	84314930	3015	5	79162381	80195395
2972	5	79055654	84340523	3016	5	79162381	80199923
2973	5	79055654	84516340	3017	5	79162381	80241911
2974	5	79055654	84706916	3018	5	79162381	80282785
2975	5	79055654	84799488	3019	5	79162381	80345337
2976	5	79055654	84801081	3020	5	79162381	80389787
2977	5	79055654	84824103	3021	5	79162381	80411639
2978	5	79055654	84824203	3022	5	79162381	80446855
2979	5	79055654	84824816	3023	5	79162381	80492790
2980	5	79055654	84825422	3024	5	79162381	80570554
2981	5	79055654	84825763	3025	5	79162381	80674679
2982	5	79055654	84825942	3026	5	79162381	80720509
2983	5	79055654	84843411	3027	5	79162381	80800856
2984	5	79055654	84936441	3028	5	79162381	80804587
2985	5	79055654	84936493	3029	5	79162381	80807409
2986	5	79055654	84943705	3030	5	79162381	80835734
2987	5	79055654	169454950	3031	5	79162381	80971764
2988	5	79055654	181522829	3032	5	79162381	80972258
2989	5	79055654	204759879	3033	5	79162381	80974450
2990	5	79055654	209874191	3034	5	79162381	81047638
2991	5	79162381	79163631	3035	5	79162381	81082921
2992	5	79162381	79176557	3036	5	79162381	81157909
2993	5	79162381	79188028	3037	5	79162381	81265937
2994	5	79162381	79201760	3038	5	79162381	81265937
2995	5	79162381	79230005	3039	5	79162381	81267485
2996	5	79162381	79230318	3040	5	79162381	81267499
2997	5	79162381	79505592	3041	5	79162381	81274512
2998	5	79162381	79510072	3042	5	79162381	81763618
2999	5	79162381	79538012	3043	5	79162381	81797217
3000	5	79162381	79538048	3044	5	79162381	81800186
3001	5	79162381	79538367	3045	5	79162381	81806213
3002	5	79162381	79669824	3046	5	79162381	81854583

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
3047	5	79162381	81859374	3091	5	79162381	83863653
3048	5	79162381	81861368	3092	5	79162381	83865914
3049	5	79162381	81863686	3093	5	79162381	83865920
3050	5	79162381	81916850	3094	5	79162381	83868010
3051	5	79162381	81954891	3095	5	79162381	84019752
3052	5	79162381	81985250	3096	5	79162381	84065912
3053	5	79162381	82083752	3097	5	79162381	84086632
3054	5	79162381	82101253	3098	5	79162381	84089603
3055	5	79162381	82143124	3099	5	79162381	84104814
3056	5	79162381	82236318	3100	5	79162381	84105175
3057	5	79162381	82325587	3101	5	79162381	84251635
3058	5	79162381	82427210	3102	5	79162381	84252180
3059	5	79162381	82431853	3103	5	79162381	84253030
3060	5	79162381	82446714	3104	5	79162381	84254208
3061	5	79162381	82446794	3105	5	79162381	84314930
3062	5	79162381	82551111	3106	5	79162381	84340523
3063	5	79162381	82552090	3107	5	79162381	84516340
3064	5	79162381	82555641	3108	5	79162381	84706916
3065	5	79162381	82555670	3109	5	79162381	84799488
3066	5	79162381	82556511	3110	5	79162381	84801081
3067	5	79162381	82559047	3111	5	79162381	84824103
3068	5	79162381	82561535	3112	5	79162381	84824203
3069	5	79162381	82610100	3113	5	79162381	84824816
3070	5	79162381	82676822	3114	5	79162381	84825422
3071	5	79162381	82676901	3115	5	79162381	84825763
3072	5	79162381	82883691	3116	5	79162381	84825942
3073	5	79162381	82954942	3117	5	79162381	84843411
3074	5	79162381	82971688	3118	5	79162381	84936441
3075	5	79162381	83023965	3119	5	79162381	84936493
3076	5	79162381	83094205	3120	5	79162381	84943705
3077	5	79162381	83146355	3121	5	79162381	169454950
3078	5	79162381	83280630	3122	5	79162381	181522829
3079	5	79162381	83281412	3123	5	79162381	204759879
3080	5	79162381	83400242	3124	5	79162381	209874191
3081	5	79162381	83405797	3125	5	79175814	79176557
3082	5	79162381	83437132	3126	5	79175814	79188028
3083	5	79162381	83522252	3127	5	79175814	79201760
3084	5	79162381	83560095	3128	5	79175814	79230005
3085	5	79162381	83560204	3129	5	79175814	79230318
3086	5	79162381	83572400	3130	5	79175814	79505592
3087	5	79162381	83607661	3131	5	79175814	79510072
3088	5	79162381	83745342	3132	5	79175814	79538012
3089	5	79162381	83861275	3133	5	79175814	79538048
3090	5	79162381	83861633	3134	5	79175814	79538367

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
3135	5	79175814	79669824	3179	5	79175814	81854583
3136	5	79175814	79582242	3180	5	79175814	81859374
3137	5	79175814	79699261	3181	5	79175814	81861368
3138	5	79175814	79710673	3182	5	79175814	81863686
3139	5	79175814	79861902	3183	5	79175814	81916850
3140	5	79175814	79867710	3184	5	79175814	81954891
3141	5	79175814	79867868	3185	5	79175814	81985250
3142	5	79175814	79867873	3186	5	79175814	82083752
3143	5	79175814	79961961	3187	5	79175814	82101253
3144	5	79175814	80086268	3188	5	79175814	82143124
3145	5	79175814	80190673	3189	5	79175814	82236318
3146	5	79175814	80190777	3190	5	79175814	82325587
3147	5	79175814	80192546	3191	5	79175814	82427210
3148	5	79175814	80195395	3192	5	79175814	82431853
3149	5	79175814	80199923	3193	5	79175814	82446714
3150	5	79175814	80241911	3194	5	79175814	82446794
3151	5	79175814	80282785	3195	5	79175814	82551111
3152	5	79175814	80345337	3196	5	79175814	82552090
3153	5	79175814	80389787	3197	5	79175814	82555641
3154	5	79175814	80411639	3198	5	79175814	82555670
3155	5	79175814	80446855	3199	5	79175814	82556511
3156	5	79175814	80492790	3200	5	79175814	82559047
3157	5	79175814	80670554	3201	5	79175814	82561535
3158	5	79175814	80674679	3202	5	79175814	82610100
3159	5	79175814	80720509	3203	5	79175814	82676822
3160	5	79175814	80800856	3204	5	79175814	82676901
3161	5	79175814	80804587	3205	5	79175814	82883691
3162	5	79175814	80807409	3206	5	79175814	82954942
3163	5	79175814	80835734	3207	5	79175814	82971688
3164	5	79175814	80971764	3208	5	79175814	83023965
3165	5	79175814	80972258	3209	5	79175814	83094205
3166	5	79175814	80974450	3210	5	79175814	83146355
3167	5	79175814	81047638	3211	5	79175814	83280630
3168	5	79175814	81082921	3212	5	79175814	83281412
3169	5	79175814	81157909	3213	5	79175814	83400242
3170	5	79175814	81265937	3214	5	79175814	83405797
3171	5	79175814	81265937	3215	5	79175814	83437132
3172	5	79175814	81267485	3216	5	79175814	83522252
3173	5	79175814	81267499	3217	5	79175814	83560095
3174	5	79175814	81274512	3218	5	79175814	83560204
3175	5	79175814	81763618	3219	5	79175814	83572400
3176	5	79175814	81797217	3220	5	79175814	83607661
3177	5	79175814	81800186	3221	5	79175814	83745342
3178	5	79175814	81806213	3222	5	79175814	83861275

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
3223	5	79175814	83861633	3267	5	79183135	79669824
3224	5	79175814	83865653	3268	5	79183135	79682242
3225	5	79175814	83865914	3269	5	79183135	79699261
3226	5	79175814	83865920	3270	5	79183135	79710673
3227	5	79175814	83868010	3271	5	79183135	79861902
3228	5	79175814	84019752	3272	5	79183135	79867710
3229	5	79175814	84065912	3273	5	79183135	79867868
3230	5	79175814	84086632	3274	5	79183135	79867873
3231	5	79175814	84089603	3275	5	79183135	79961961
3232	5	79175814	84104814	3276	5	79183135	80086268
3233	5	79175814	84105175	3277	5	79183135	80190673
3234	5	79175814	84251635	3278	5	79183135	80190777
3235	5	79175814	84252180	3279	5	79183135	80192546
3236	5	79175814	84253030	3280	5	79183135	80195395
3237	5	79175814	84254208	3281	5	79183135	80199923
3238	5	79175814	84314930	3282	5	79183135	80241911
3239	5	79175814	84340523	3283	5	79183135	80282785
3240	5	79175814	84516340	3284	5	79183135	80345337
3241	5	79175814	84706916	3285	5	79183135	80389787
3242	5	79175814	84799488	3286	5	79183135	80411639
3243	5	79175814	84801081	3287	5	79183135	80446855
3244	5	79175814	84824103	3288	5	79183135	80492790
3245	5	79175814	84824203	3289	5	79183135	80670554
3246	5	79175814	84824816	3290	5	79183135	80674679
3247	5	79175814	84825422	3291	5	79183135	80720509
3248	5	79175814	84825763	3292	5	79183135	80800856
3249	5	79175814	84825942	3293	5	79183135	80804587
3250	5	79175814	84843411	3294	5	79183135	80807409
3251	5	79175814	84936441	3295	5	79183135	80835734
3252	5	79175814	84936493	3296	5	79183135	80971764
3253	5	79175814	84943705	3297	5	79183135	80972258
3254	5	79175814	169454950	3298	5	79183135	80974450
3255	5	79175814	181522829	3299	5	79183135	81047638
3256	5	79175814	204759879	3300	5	79183135	81082921
3257	5	79175814	209874191	3301	5	79183135	81157909
3258	5	79183135	79188028	3302	5	79183135	81265937
3259	5	79183135	79201760	3303	5	79183135	81265937
3260	5	79183135	79230005	3304	5	79183135	81267485
3261	5	79183135	79230318	3305	5	79183135	81267499
3262	5	79183135	79505592	3306	5	79183135	81274512
3263	5	79183135	79510072	3307	5	79183135	81763618
3264	5	79183135	79538012	3308	5	79183135	81797217
3265	5	79183135	79538048	3309	5	79183135	81800186
3266	5	79183135	79538367	3310	5	79183135	81806213

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
3311	5	79183135	81854583	3355	5	79183135	83861633
3312	5	79183135	81859374	3356	5	79183135	83865653
3313	5	79183135	81861368	3357	5	79183135	83865914
3314	5	79183135	81863686	3358	5	79183135	83865920
3315	5	79183135	81916850	3359	5	79183135	83868010
3316	5	79183135	81954891	3360	5	79183135	84019752
3317	5	79183135	81985250	3361	5	79183135	84065912
3318	5	79183135	82083752	3362	5	79183135	84086632
3319	5	79183135	82101253	3363	5	79183135	84089603
3320	5	79183135	82143124	3364	5	79183135	84104814
3321	5	79183135	82236318	3365	5	79183135	84105175
3322	5	79183135	82325587	3366	5	79183135	84251635
3323	5	79183135	82427210	3367	5	79183135	84252180
3324	5	79183135	82431853	3368	5	79183135	84253030
3325	5	79183135	82446714	3369	5	79183135	84254208
3326	5	79183135	82446794	3370	5	79183135	84314930
3327	5	79183135	82551111	3371	5	79183135	84340523
3328	5	79183135	82552090	3372	5	79183135	84516340
3329	5	79183135	82555641	3373	5	79183135	84706916
3330	5	79183135	82555670	3374	5	79183135	84799488
3331	5	79183135	82556511	3375	5	79183135	84801081
3332	5	79183135	82559047	3376	5	79183135	84824103
3333	5	79183135	82561535	3377	5	79183135	84824203
3334	5	79183135	82610100	3378	5	79183135	84824816
3335	5	79183135	82676822	3379	5	79183135	84825422
3336	5	79183135	82676901	3380	5	79183135	84825763
3337	5	79183135	82883691	3381	5	79183135	84825942
3338	5	79183135	82954942	3382	5	79183135	84843411
3339	5	79183135	82971688	3383	5	79183135	84936441
3340	5	79183135	83023965	3384	5	79183135	84936493
3341	5	79183135	83094205	3385	5	79183135	84943705
3342	5	79183135	83146355	3386	5	79183135	169454950
3343	5	79183135	83280630	3387	5	79183135	181522829
3344	5	79183135	83281412	3388	5	79183135	204759879
3345	5	79183135	83400242	3389	5	79183135	209874191
3346	5	79183135	83405797	3390	5	79200056	79201760
3347	5	79183135	83437132	3391	5	79200056	79230005
3348	5	79183135	83522252	3392	5	79200056	79230318
3349	5	79183135	83560095	3393	5	79200056	79505592
3350	5	79183135	83560204	3394	5	79200056	79510072
3351	5	79183135	83572400	3395	5	79200056	79538012
3352	5	79183135	83607661	3396	5	79200056	79538048
3353	5	79183135	83745342	3397	5	79200056	79538367
3354	5	79183135	83861275	3398	5	79200056	79669824

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
3399	5	79200056	79682242	3443	5	79200056	81859374
3400	5	79200056	79699261	3444	5	79200056	81861368
3401	5	79200056	79710673	3445	5	79200056	81863686
3402	5	79200056	79861902	3446	5	79200056	81916850
3403	5	79200056	79867710	3447	5	79200056	81954891
3404	5	79200056	79867868	3448	5	79200056	81985250
3405	5	79200056	79867873	3449	5	79200056	82083752
3406	5	79200056	79961961	3450	5	79200056	82101253
3407	5	79200056	80086268	3451	5	79200056	82143124
3408	5	79200056	80190673	3452	5	79200056	82236318
3409	5	79200056	80190777	3453	5	79200056	82325587
3410	5	79200056	80192546	3454	5	79200056	82427210
3411	5	79200056	80195395	3455	5	79200056	82431853
3412	5	79200056	80199923	3456	5	79200056	82446714
3413	5	79200056	80241911	3457	5	79200056	82446794
3414	5	79200056	80282785	3458	5	79200056	82551111
3415	5	79200056	80345337	3459	5	79200056	82552090
3416	5	79200056	80389787	3460	5	79200056	82555641
3417	5	79200056	80411639	3461	5	79200056	82555670
3418	5	79200056	80446855	3462	5	79200056	82556511
3419	5	79200056	80492790	3463	5	79200056	82559047
3420	5	79200056	80670554	3464	5	79200056	82561535
3421	5	79200056	80674679	3465	5	79200056	82610100
3422	5	79200056	80720509	3466	5	79200056	82676822
3423	5	79200056	80800856	3467	5	79200056	82676901
3424	5	79200056	80804587	3468	5	79200056	82883691
3425	5	79200056	80807409	3469	5	79200056	82954942
3426	5	79200056	80835734	3470	5	79200056	82971688
3427	5	79200056	80971764	3471	5	79200056	83023965
3428	5	79200056	80972258	3472	5	79200056	83094205
3429	5	79200056	80974450	3473	5	79200056	83146355
3430	5	79200056	81047638	3474	5	79200056	83280630
3431	5	79200056	81082921	3475	5	79200056	83281412
3432	5	79200056	81157909	3476	5	79200056	83400242
3433	5	79200056	81265937	3477	5	79200056	83405797
3434	5	79200056	81265937	3478	5	79200056	83437132
3435	5	79200056	81267485	3479	5	79200056	83522252
3436	5	79200056	81267499	3480	5	79200056	83560095
3437	5	79200056	81274512	3481	5	79200056	83560204
3438	5	79200056	81763618	3482	5	79200056	83572400
3439	5	79200056	81797217	3483	5	79200056	83607661
3440	5	79200056	81800186	3484	5	79200056	83745342
3441	5	79200056	81806213	3485	5	79200056	83861275
3442	5	79200056	81854583	3486	5	79200056	83861633

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
3487	5	79200056	83865653	3531	5	79229010	79710673
3488	5	79200056	83865914	3532	5	79229010	79861902
3489	5	79200056	83865920	3533	5	79229010	79867710
3490	5	79200056	83868010	3534	5	79229010	79867868
3491	5	79200056	84019752	3535	5	79229010	79867873
3492	5	79200056	84065912	3536	5	79229010	79961961
3493	5	79200056	84086632	3537	5	79229010	80086268
3494	5	79200056	84089603	3538	5	79229010	80190673
3495	5	79200056	84104814	3539	5	79229010	80190777
3496	5	79200056	84105175	3540	5	79229010	80192546
3497	5	79200056	84251635	3541	5	79229010	80195395
3498	5	79200056	84252180	3542	5	79229010	80199923
3499	5	79200056	84253030	3543	5	79229010	80241911
3500	5	79200056	84254208	3544	5	79229010	80282785
3501	5	79200056	84314930	3545	5	79229010	80345337
3502	5	79200056	84340523	3546	5	79229010	80389787
3503	5	79200056	84516340	3547	5	79229010	80411639
3504	5	79200056	84706916	3548	5	79229010	80446855
3505	5	79200056	84799488	3549	5	79229010	80492790
3506	5	79200056	84801081	3550	5	79229010	80670554
3507	5	79200056	84824103	3551	5	79229010	80674679
3508	5	79200056	84824203	3552	5	79229010	80720509
3509	5	79200056	84824816	3553	5	79229010	80800856
3510	5	79200056	84825422	3554	5	79229010	80804587
3511	5	79200056	84825763	3555	5	79229010	80807409
3512	5	79200056	84825942	3556	5	79229010	80835734
3513	5	79200056	84843411	3557	5	79229010	80971764
3514	5	79200056	84936441	3558	5	79229010	80972258
3515	5	79200056	84936493	3559	5	79229010	80974450
3516	5	79200056	84943705	3560	5	79229010	81047638
3517	5	79200056	169454950	3561	5	79229010	81082921
3518	5	79200056	181522829	3562	5	79229010	81157909
3519	5	79200056	204759879	3563	5	79229010	81265937
3520	5	79200056	209874191	3564	5	79229010	81265937
3521	5	79229010	79230005	3565	5	79229010	81267485
3522	5	79229010	79230318	3566	5	79229010	81267499
3523	5	79229010	79505592	3567	5	79229010	81274512
3524	5	79229010	79510072	3568	5	79229010	81763618
3525	5	79229010	79538012	3569	5	79229010	81797217
3526	5	79229010	79538048	3570	5	79229010	81800186
3527	5	79229010	79538367	3571	5	79229010	81806213
3528	5	79229010	79669824	3572	5	79229010	81854583
3529	5	79229010	79682242	3573	5	79229010	81859374
3530	5	79229010	79699261	3574	5	79229010	81861368

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
3575	5	79229010	81863686	3619	5	79229010	83865920
3576	5	79229010	81916850	3620	5	79229010	83868010
3577	5	79229010	81954891	3621	5	79229010	84019752
3578	5	79229010	81985250	3622	5	79229010	84065912
3579	5	79229010	82083752	3623	5	79229010	84086632
3580	5	79229010	82101253	3624	5	79229010	84089603
3581	5	79229010	82143124	3625	5	79229010	84104814
3582	5	79229010	82236318	3626	5	79229010	84105175
3583	5	79229010	82325587	3627	5	79229010	84251635
3584	5	79229010	82427210	3628	5	79229010	84252180
3585	5	79229010	82431853	3629	5	79229010	84253030
3586	5	79229010	82446714	3630	5	79229010	84254208
3587	5	79229010	82446794	3631	5	79229010	84314930
3588	5	79229010	82551111	3632	5	79229010	84340523
3589	5	79229010	82552090	3633	5	79229010	84516340
3590	5	79229010	82555641	3634	5	79229010	84706916
3591	5	79229010	82555670	3635	5	79229010	84799488
3592	5	79229010	82556511	3636	5	79229010	84801081
3593	5	79229010	82559047	3637	5	79229010	84824103
3594	5	79229010	82561535	3638	5	79229010	84824203
3595	5	79229010	82610100	3639	5	79229010	84824816
3596	5	79229010	82676822	3640	5	79229010	84825422
3597	5	79229010	82676901	3641	5	79229010	84825763
3598	5	79229010	82883691	3642	5	79229010	84825942
3599	5	79229010	82954942	3643	5	79229010	84843411
3600	5	79229010	82971688	3644	5	79229010	84936441
3601	5	79229010	83023965	3645	5	79229010	84936493
3602	5	79229010	83094205	3646	5	79229010	84943705
3603	5	79229010	83146355	3647	5	79229010	169454950
3604	5	79229010	83280630	3648	5	79229010	181522829
3605	5	79229010	83281412	3649	5	79229010	204759879
3606	5	79229010	83400242	3650	5	79229010	209874191
3607	5	79229010	83405797	3651	5	79229019	79230005
3608	5	79229010	83437132	3652	5	79229019	79230318
3609	5	79229010	83522252	3653	5	79229019	79505592
3610	5	79229010	83560095	3654	5	79229019	79510072
3611	5	79229010	83560204	3655	5	79229019	79538012
3612	5	79229010	83572400	3656	5	79229019	79538048
3613	5	79229010	83607661	3657	5	79229019	79538367
3614	5	79229010	83745342	3658	5	79229019	79669824
3615	5	79229010	83861275	3659	5	79229019	79682242
3616	5	79229010	83861633	3660	5	79229019	79699261
3617	5	79229010	83865653	3661	5	79229019	79710673
3618	5	79229010	83865914	3662	5	79229019	79861902

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
3663	5	79229019	79867710	3707	5	79229019	81954891
3664	5	79229019	79867868	3708	5	79229019	81985250
3665	5	79229019	79867873	3709	5	79229019	82083752
3666	5	79229019	79961961	3710	5	79229019	82101253
3667	5	79229019	80086268	3711	5	79229019	82143124
3668	5	79229019	80190673	3712	5	79229019	82236318
3669	5	79229019	80190777	3713	5	79229019	82325587
3670	5	79229019	80192546	3714	5	79229019	82427210
3671	5	79229019	80195395	3715	5	79229019	82431853
3672	5	79229019	80199923	3716	5	79229019	82446714
3673	5	79229019	80241911	3717	5	79229019	82446794
3674	5	79229019	80282785	3718	5	79229019	82551111
3675	5	79229019	80345337	3719	5	79229019	82552090
3676	5	79229019	80389787	3720	5	79229019	82555641
3677	5	79229019	80411639	3721	5	79229019	82555670
3678	5	79229019	80446855	3722	5	79229019	82556511
3679	5	79229019	80492790	3723	5	79229019	82559047
3680	5	79229019	80670554	3724	5	79229019	82561535
3681	5	79229019	80674679	3725	5	79229019	82610100
3682	5	79229019	80720509	3726	5	79229019	82676822
3683	5	79229019	80800856	3727	5	79229019	82676901
3684	5	79229019	80804587	3728	5	79229019	82883691
3685	5	79229019	80807409	3729	5	79229019	82954942
3686	5	79229019	80835734	3730	5	79229019	82971688
3687	5	79229019	80971764	3731	5	79229019	83023965
3688	5	79229019	80972258	3732	5	79229019	83094205
3689	5	79229019	80974450	3733	5	79229019	83146355
3690	5	79229019	81047638	3734	5	79229019	83280630
3691	5	79229019	81082921	3735	5	79229019	83281412
3692	5	79229019	81157909	3736	5	79229019	83400242
3693	5	79229019	81265937	3737	5	79229019	83405797
3694	5	79229019	81265937	3738	5	79229019	83437132
3695	5	79229019	81267485	3739	5	79229019	83522252
3696	5	79229019	81267499	3740	5	79229019	83560095
3697	5	79229019	81274512	3741	5	79229019	83560204
3698	5	79229019	81763618	3742	5	79229019	83572400
3699	5	79229019	81797217	3743	5	79229019	83607661
3700	5	79229019	81800186	3744	5	79229019	83745342
3701	5	79229019	81806213	3745	5	79229019	83861275
3702	5	79229019	81854583	3746	5	79229019	83861633
3703	5	79229019	81859374	3747	5	79229019	83865653
3704	5	79229019	81861368	3748	5	79229019	83865914
3705	5	79229019	81863686	3749	5	79229019	83865920
3706	5	79229019	81916850	3750	5	79229019	83868010

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
3751	5	79229019	84019752	3795	5	79503885	80086268
3752	5	79229019	84065912	3796	5	79503885	80190673
3753	5	79229019	84086632	3797	5	79503885	80190777
3754	5	79229019	84089603	3798	5	79503885	80192546
3755	5	79229019	84104814	3799	5	79503885	80195395
3756	5	79229019	84105175	3800	5	79503885	80199923
3757	5	79229019	84251635	3801	5	79503885	80241911
3758	5	79229019	84252180	3802	5	79503885	80282785
3759	5	79229019	84253030	3803	5	79503885	80345337
3760	5	79229019	84254208	3804	5	79503885	80389787
3761	5	79229019	84314930	3805	5	79503885	80411639
3762	5	79229019	84340523	3806	5	79503885	80446855
3763	5	79229019	84516340	3807	5	79503885	80492790
3764	5	79229019	84706916	3808	5	79503885	80670554
3765	5	79229019	84799488	3809	5	79503885	80674679
3766	5	79229019	84801081	3810	5	79503885	80720509
3767	5	79229019	84824103	3811	5	79503885	80800856
3768	5	79229019	84824203	3812	5	79503885	80804587
3769	5	79229019	84824816	3813	5	79503885	80807409
3770	5	79229019	84825422	3814	5	79503885	80835734
3771	5	79229019	84825763	3815	5	79503885	80971764
3772	5	79229019	84825942	3816	5	79503885	80972258
3773	5	79229019	84843411	3817	5	79503885	80974450
3774	5	79229019	84936441	3818	5	79503885	81047638
3775	5	79229019	84936493	3819	5	79503885	81082921
3776	5	79229019	84943705	3820	5	79503885	81157909
3777	5	79229019	169454950	3821	5	79503885	81265937
3778	5	79229019	181522829	3822	5	79503885	81265937
3779	5	79229019	204759879	3823	5	79503885	81267485
3780	5	79229019	209874191	3824	5	79503885	81267499
3781	5	79503885	79505592	3825	5	79503885	81274512
3782	5	79503885	79510072	3826	5	79503885	81763618
3783	5	79503885	79538012	3827	5	79503885	81797217
3784	5	79503885	79538048	3828	5	79503885	81800186
3785	5	79503885	79538367	3829	5	79503885	81806213
3786	5	79503885	79669824	3830	5	79503885	81854583
3787	5	79503885	79682242	3831	5	79503885	81859374
3788	5	79503885	79699261	3832	5	79503885	81861368
3789	5	79503885	79710673	3833	5	79503885	81863686
3790	5	79503885	79851902	3834	5	79503885	81916850
3791	5	79503885	79867710	3835	5	79503885	81954891
3792	5	79503885	79867868	3836	5	79503885	81985250
3793	5	79503885	79867873	3837	5	79503885	82083752
3794	5	79503885	79961961	3838	5	79503885	82101253

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
3839	5	79503885	82143124	3883	5	79503885	84104814
3840	5	79503885	82236318	3884	5	79503885	84105175
3841	5	79503885	82325587	3885	5	79503885	84251635
3842	5	79503885	82427210	3886	5	79503885	84252180
3843	5	79503885	82431853	3887	5	79503885	84253030
3844	5	79503885	82446714	3888	5	79503885	84254208
3845	5	79503885	82446794	3889	5	79503885	84314930
3846	5	79503885	82551111	3890	5	79503885	84340523
3847	5	79503885	82552090	3891	5	79503885	84516340
3848	5	79503885	82555641	3892	5	79503885	84706916
3849	5	79503885	82555670	3893	5	79503885	84799488
3850	5	79503885	82556511	3894	5	79503885	84801081
3851	5	79503885	82559047	3895	5	79503885	84824103
3852	5	79503885	82561535	3896	5	79503885	84824203
3853	5	79503885	82610100	3897	5	79503885	84824816
3854	5	79503885	82676822	3898	5	79503885	84825422
3855	5	79503885	82676901	3899	5	79503885	84825763
3856	5	79503885	82883691	3900	5	79503885	84825942
3857	5	79503885	82954942	3901	5	79503885	84843411
3858	5	79503885	82971688	3902	5	79503885	84936441
3859	5	79503885	83023965	3903	5	79503885	84936493
3860	5	79503885	83094205	3904	5	79503885	84943705
3861	5	79503885	83146355	3905	5	79503885	169454950
3862	5	79503885	83280630	3906	5	79503885	181522829
3863	5	79503885	83281412	3907	5	79503885	204759879
3864	5	79503885	83400242	3908	5	79503885	209874191
3865	5	79503885	83405797	3909	5	79505757	79505592
3866	5	79503885	83437132	3910	5	79505757	79510072
3867	5	79503885	83522252	3911	5	79505757	79538012
3868	5	79503885	83560095	3912	5	79505757	79538048
3869	5	79503885	83560204	3913	5	79505757	79538367
3870	5	79503885	83572400	3914	5	79505757	79669824
3871	5	79503885	83607661	3915	5	79505757	79682242
3872	5	79503885	83745342	3916	5	79505757	79699261
3873	5	79503885	83861275	3917	5	79505757	79710673
3874	5	79503885	83861633	3918	5	79505757	79861902
3875	5	79503885	83865653	3919	5	79505757	79867710
3876	5	79503885	83865914	3920	5	79505757	79867868
3877	5	79503885	83865920	3921	5	79505757	79867873
3878	5	79503885	83868010	3922	5	79505757	79961961
3879	5	79503885	84019752	3923	5	79505757	80086268
3880	5	79503885	84065912	3924	5	79505757	80190673
3881	5	79503885	84086632	3925	5	79505757	80190777
3882	5	79503885	84089603	3926	5	79505757	80192546

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
3927	5	79505757	80195395	3971	5	79505757	82431853
3928	5	79505757	80199923	3972	5	79505757	82446714
3929	5	79505757	80241911	3973	5	79505757	82446794
3930	5	79505757	80282785	3974	5	79505757	82551111
3931	5	79505757	80345337	3975	5	79505757	82552090
3932	5	79505757	80389787	3976	5	79505757	82555641
3933	5	79505757	80411639	3977	5	79505757	82555670
3934	5	79505757	80446855	3978	5	79505757	82555611
3935	5	79505757	80492790	3979	5	79505757	82559047
3936	5	79505757	80670554	3980	5	79505757	82561535
3937	5	79505757	80674679	3981	5	79505757	82610100
3938	5	79505757	80720509	3982	5	79505757	82676822
3939	5	79505757	80800856	3983	5	79505757	82676901
3940	5	79505757	80804587	3984	5	79505757	82883691
3941	5	79505757	80807409	3985	5	79505757	82954942
3942	5	79505757	80835734	3986	5	79505757	82971688
3943	5	79505757	80971764	3987	5	79505757	83023965
3944	5	79505757	80972258	3988	5	79505757	83094205
3945	5	79505757	80974450	3989	5	79505757	83146355
3946	5	79505757	81047638	3990	5	79505757	83280630
3947	5	79505757	81082921	3991	5	79505757	83281412
3948	5	79505757	81157909	3992	5	79505757	83400242
3949	5	79505757	81265937	3993	5	79505757	83405797
3950	5	79505757	81265937	3994	5	79505757	83437132
3951	5	79505757	81267485	3995	5	79505757	83522252
3952	5	79505757	81267499	3996	5	79505757	83560095
3953	5	79505757	81274512	3997	5	79505757	83560204
3954	5	79505757	81763618	3998	5	79505757	83572400
3955	5	79505757	81797217	3999	5	79505757	83607661
3956	5	79505757	81800186	4000	5	79505757	83745342
3957	5	79505757	81806213	4001	5	79505757	83861275
3958	5	79505757	81854583	4002	5	79505757	83861633
3959	5	79505757	81859374	4003	5	79505757	83865653
3960	5	79505757	81861368	4004	5	79505757	83865914
3961	5	79505757	81863686	4005	5	79505757	83865920
3962	5	79505757	81916850	4006	5	79505757	83868010
3963	5	79505757	81954891	4007	5	79505757	84019752
3964	5	79505757	81985250	4008	5	79505757	84065912
3965	5	79505757	82083752	4009	5	79505757	84086632
3966	5	79505757	82101253	4010	5	79505757	84089603
3967	5	79505757	82143124	4011	5	79505757	84104814
3968	5	79505757	82236318	4012	5	79505757	84105175
3969	5	79505757	82325587	4013	5	79505757	84251635
3970	5	79505757	82427210	4014	5	79505757	84252180

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
4015	5	79505757	84253030	4059	5	79531009	80411639
4016	5	79505757	84254208	4060	5	79531009	80446855
4017	5	79505757	84314930	4061	5	79531009	80492790
4018	5	79505757	84340523	4062	5	79531009	80670554
4019	5	79505757	84516340	4063	5	79531009	80674679
4020	5	79505757	84706916	4064	5	79531009	80720509
4021	5	79505757	84799488	4065	5	79531009	80800856
4022	5	79505757	84801081	4066	5	79531009	80804587
4023	5	79505757	84824103	4067	5	79531009	80807409
4024	5	79505757	84824203	4068	5	79531009	80835734
4025	5	79505757	84824816	4069	5	79531009	80971764
4026	5	79505757	84825422	4070	5	79531009	80972258
4027	5	79505757	84825763	4071	5	79531009	80974450
4028	5	79505757	84825942	4072	5	79531009	81047638
4029	5	79505757	84843411	4073	5	79531009	81082921
4030	5	79505757	84936441	4074	5	79531009	81157909
4031	5	79505757	84936493	4075	5	79531009	81265937
4032	5	79505757	84943705	4076	5	79531009	81265937
4033	5	79505757	169454950	4077	5	79531009	81267485
4034	5	79505757	181522829	4078	5	79531009	81267499
4035	5	79505757	204759879	4079	5	79531009	81274512
4036	5	79505757	209874191	4080	5	79531009	81763618
4037	5	79531009	79538012	4081	5	79531009	81797217
4038	5	79531009	79538048	4082	5	79531009	81800186
4039	5	79531009	79538367	4083	5	79531009	81806213
4040	5	79531009	79669824	4084	5	79531009	81854583
4041	5	79531009	79682242	4085	5	79531009	81859374
4042	5	79531009	79699261	4086	5	79531009	81861368
4043	5	79531009	79710673	4087	5	79531009	81863686
4044	5	79531009	79861902	4088	5	79531009	81916850
4045	5	79531009	79867710	4089	5	79531009	81954891
4046	5	79531009	79867868	4090	5	79531009	81985250
4047	5	79531009	79867873	4091	5	79531009	82083752
4048	5	79531009	79961961	4092	5	79531009	82101253
4049	5	79531009	80086268	4093	5	79531009	82143124
4050	5	79531009	80190673	4094	5	79531009	82236318
4051	5	79531009	80190777	4095	5	79531009	82325587
4052	5	79531009	80192546	4096	5	79531009	82427210
4053	5	79531009	80195395	4097	5	79531009	82431853
4054	5	79531009	80199923	4098	5	79531009	82446714
4055	5	79531009	80241911	4099	5	79531009	82446794
4056	5	79531009	80282785	4100	5	79531009	82551111
4057	5	79531009	80345337	4101	5	79531009	82552090
4058	5	79531009	80389787	4102	5	79531009	82555641

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
4103	5	79531009	82555670	4147	5	79531009	84799488
4104	5	79531009	82556511	4148	5	79531009	84801081
4105	5	79531009	82559047	4149	5	79531009	84824103
4106	5	79531009	82561535	4150	5	79531009	84824203
4107	5	79531009	82610100	4151	5	79531009	84824816
4108	5	79531009	82676822	4152	5	79531009	84825422
4109	5	79531009	82676901	4153	5	79531009	84825763
4110	5	79531009	82883691	4154	5	79531009	84825942
4111	5	79531009	82954942	4155	5	79531009	84843411
4112	5	79531009	82971688	4156	5	79531009	84936441
4113	5	79531009	83023965	4157	5	79531009	84936493
4114	5	79531009	83094205	4158	5	79531009	84943705
4115	5	79531009	83146355	4159	5	79531009	169454950
4116	5	79531009	83280630	4160	5	79531009	181522829
4117	5	79531009	83281412	4161	5	79531009	204759879
4118	5	79531009	83400242	4162	5	79531009	209874191
4119	5	79531009	83405797	4163	5	79531040	79538012
4120	5	79531009	83437132	4164	5	79531040	79538048
4121	5	79531009	83522252	4165	5	79531040	79538367
4122	5	79531009	83560095	4166	5	79531040	79669824
4123	5	79531009	83560204	4167	5	79531040	79682242
4124	5	79531009	83572400	4168	5	79531040	79699261
4125	5	79531009	83607661	4169	5	79531040	79710673
4126	5	79531009	83745342	4170	5	79531040	79861902
4127	5	79531009	83861275	4171	5	79531040	79867710
4128	5	79531009	83861633	4172	5	79531040	79867868
4129	5	79531009	83865653	4173	5	79531040	79867873
4130	5	79531009	83865914	4174	5	79531040	79961961
4131	5	79531009	83865920	4175	5	79531040	80086268
4132	5	79531009	83868010	4176	5	79531040	80190673
4133	5	79531009	84019752	4177	5	79531040	80190777
4134	5	79531009	84065912	4178	5	79531040	80192546
4135	5	79531009	84086632	4179	5	79531040	80195395
4136	5	79531009	84089603	4180	5	79531040	80199923
4137	5	79531009	84104814	4181	5	79531040	80241911
4138	5	79531009	84105175	4182	5	79531040	80282785
4139	5	79531009	84251635	4183	5	79531040	80345337
4140	5	79531009	84252180	4184	5	79531040	80389787
4141	5	79531009	84253030	4185	5	79531040	80411639
4142	5	79531009	84254208	4186	5	79531040	80446855
4143	5	79531009	84314930	4187	5	79531040	80492790
4144	5	79531009	84340523	4188	5	79531040	80670554
4145	5	79531009	84516340	4189	5	79531040	80674679
4146	5	79531009	84706916	4190	5	79531040	80720509

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
4191	5	79531040	80800856	4235	5	79531040	82676901
4192	5	79531040	80804587	4236	5	79531040	82883691
4193	5	79531040	80807409	4237	5	79531040	82954942
4194	5	79531040	80835734	4238	5	79531040	82971688
4195	5	79531040	80971764	4239	5	79531040	83023965
4196	5	79531040	80972258	4240	5	79531040	83094205
4197	5	79531040	80974450	4241	5	79531040	83146355
4198	5	79531040	81047638	4242	5	79531040	83280630
4199	5	79531040	81082921	4243	5	79531040	83281412
4200	5	79531040	81157909	4244	5	79531040	83400242
4201	5	79531040	81265937	4245	5	79531040	83405797
4202	5	79531040	81265937	4246	5	79531040	83437132
4203	5	79531040	81267485	4247	5	79531040	83522252
4204	5	79531040	81267499	4248	5	79531040	83560095
4205	5	79531040	81274512	4249	5	79531040	83560204
4206	5	79531040	81763618	4250	5	79531040	83572400
4207	5	79531040	81797217	4251	5	79531040	83607661
4208	5	79531040	81800186	4252	5	79531040	83745342
4209	5	79531040	81806213	4253	5	79531040	83861275
4210	5	79531040	81854583	4254	5	79531040	83861633
4211	5	79531040	81859374	4255	5	79531040	83865653
4212	5	79531040	81861368	4256	5	79531040	83865914
4213	5	79531040	81863686	4257	5	79531040	83865920
4214	5	79531040	81916850	4258	5	79531040	83868010
4215	5	79531040	81954891	4259	5	79531040	84019752
4216	5	79531040	81985250	4260	5	79531040	84065912
4217	5	79531040	82083752	4261	5	79531040	84086632
4218	5	79531040	82101253	4262	5	79531040	84089603
4219	5	79531040	82143124	4263	5	79531040	84104814
4220	5	79531040	82236318	4264	5	79531040	84105175
4221	5	79531040	82325587	4265	5	79531040	84251635
4222	5	79531040	82427210	4266	5	79531040	84252180
4223	5	79531040	82431853	4267	5	79531040	84253030
4224	5	79531040	82446714	4268	5	79531040	84254208
4225	5	79531040	82446794	4269	5	79531040	84314930
4226	5	79531040	82551111	4270	5	79531040	84340523
4227	5	79531040	82552090	4271	5	79531040	84516340
4228	5	79531040	82555641	4272	5	79531040	84706916
4229	5	79531040	82555670	4273	5	79531040	84799488
4230	5	79531040	82556511	4274	5	79531040	84801081
4231	5	79531040	82559047	4275	5	79531040	84824103
4232	5	79531040	82561535	4276	5	79531040	84824203
4233	5	79531040	82610100	4277	5	79531040	84824816
4234	5	79531040	82676822	4278	5	79531040	84825422

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
4279	5	79531040	84825763	4323	5	79537564	80974450
4280	5	79531040	84825942	4324	5	79537564	81047638
4281	5	79531040	84843411	4325	5	79537564	81082921
4282	5	79531040	84936441	4326	5	79537564	81157909
4283	5	79531040	84936493	4327	5	79537564	81265937
4284	5	79531040	84943705	4328	5	79537564	81265937
4285	5	79531040	169454950	4329	5	79537564	81267485
4286	5	79531040	181522829	4330	5	79537564	81267499
4287	5	79531040	204759879	4331	5	79537564	81274512
4288	5	79531040	209874191	4332	5	79537564	81763618
4289	5	79537564	79538012	4333	5	79537564	81797217
4290	5	79537564	79538048	4334	5	79537564	81800186
4291	5	79537564	79538367	4335	5	79537564	81806213
4292	5	79537564	79669824	4336	5	79537564	81854583
4293	5	79537564	79682242	4337	5	79537564	81859374
4294	5	79537564	79699261	4338	5	79537564	81861368
4295	5	79537564	79710673	4339	5	79537564	81863686
4296	5	79537564	79861902	4340	5	79537564	81916850
4297	5	79537564	79867710	4341	5	79537564	81954891
4298	5	79537564	79867868	4342	5	79537564	81985250
4299	5	79537564	79867873	4343	5	79537564	82083752
4300	5	79537564	79961961	4344	5	79537564	82101253
4301	5	79537564	80086268	4345	5	79537564	82143124
4302	5	79537564	80190673	4346	5	79537564	82236318
4303	5	79537564	80190777	4347	5	79537564	82325587
4304	5	79537564	80192546	4348	5	79537564	82427210
4305	5	79537564	80195395	4349	5	79537564	82431853
4306	5	79537564	80199923	4350	5	79537564	82446714
4307	5	79537564	80241911	4351	5	79537564	82446794
4308	5	79537564	80282785	4352	5	79537564	82551111
4309	5	79537564	80345337	4353	5	79537564	82552090
4310	5	79537564	80389787	4354	5	79537564	82555641
4311	5	79537564	80411639	4355	5	79537564	82555670
4312	5	79537564	80446855	4356	5	79537564	82556511
4313	5	79537564	80492790	4357	5	79537564	82559047
4314	5	79537564	80670554	4358	5	79537564	82561535
4315	5	79537564	80674679	4359	5	79537564	82610100
4316	5	79537564	80720509	4360	5	79537564	82676822
4317	5	79537564	80800856	4361	5	79537564	82676901
4318	5	79537564	80804587	4362	5	79537564	82883691
4319	5	79537564	80807409	4363	5	79537564	82954942
4320	5	79537564	80835734	4364	5	79537564	82971688
4321	5	79537564	80971764	4365	5	79537564	83023965
4322	5	79537564	80972258	4366	5	79537564	83094205

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
4367	5	79537564	83146355	4411	5	79537564	169454950
4368	5	79537564	83280630	4412	5	79537564	181522829
4369	5	79537564	83281412	4413	5	79537564	204759879
4370	5	79537564	83400242	4414	5	79537564	209874191
4371	5	79537564	83405797	4415	5	79538367	79669824
4372	5	79537564	83437132	4416	5	79538367	79682242
4373	5	79537564	83522252	4417	5	79538367	79699261
4374	5	79537564	83560095	4418	5	79538367	79710673
4375	5	79537564	83560204	4419	5	79538367	79861902
4376	5	79537564	83572400	4420	5	79538367	79867710
4377	5	79537564	83607661	4421	5	79538367	79867868
4378	5	79537564	83745342	4422	5	79538367	79867873
4379	5	79537564	83861275	4423	5	79538367	79961961
4380	5	79537564	83861633	4424	5	79538367	80086268
4381	5	79537564	83865653	4425	5	79538367	80190673
4382	5	79537564	83865914	4426	5	79538367	80190777
4383	5	79537564	83865920	4427	5	79538367	80192546
4384	5	79537564	83868010	4428	5	79538367	80195395
4385	5	79537564	84019752	4429	5	79538367	80199923
4386	5	79537564	84065912	4430	5	79538367	80241911
4387	5	79537564	84086632	4431	5	79538367	80282785
4388	5	79537564	84089603	4432	5	79538367	80345337
4389	5	79537564	84104814	4433	5	79538367	80389787
4390	5	79537564	84105175	4434	5	79538367	80411639
4391	5	79537564	84251635	4435	5	79538367	80446855
4392	5	79537564	84252180	4436	5	79538367	80492790
4393	5	79537564	84253030	4437	5	79538367	80670554
4394	5	79537564	84254208	4438	5	79538367	80674679
4395	5	79537564	84314930	4439	5	79538367	80720509
4396	5	79537564	84340523	4440	5	79538367	80800856
4397	5	79537564	84516340	4441	5	79538367	80804587
4398	5	79537564	84706916	4442	5	79538367	80807409
4399	5	79537564	84799488	4443	5	79538367	80835734
4400	5	79537564	84801081	4444	5	79538367	80971764
4401	5	79537564	84824103	4445	5	79538367	80972258
4402	5	79537564	84824203	4446	5	79538367	80974450
4403	5	79537564	84824816	4447	5	79538367	81047638
4404	5	79537564	84825422	4448	5	79538367	81082921
4405	5	79537564	84825763	4449	5	79538367	81157909
4406	5	79537564	84825942	4450	5	79538367	81265937
4407	5	79537564	84843411	4451	5	79538367	81265937
4408	5	79537564	84936441	4452	5	79538367	81267485
4409	5	79537564	84936493	4453	5	79538367	81267499
4410	5	79537564	84943705	4454	5	79538367	81274512

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
4455	5	79538367	81763618	4499	5	79538367	83572400
4456	5	79538367	81797217	4500	5	79538367	83607661
4457	5	79538367	81800186	4501	5	79538367	83745342
4458	5	79538367	81806213	4502	5	79538367	83861275
4459	5	79538367	81854583	4503	5	79538367	83861633
4460	5	79538367	81859374	4504	5	79538367	83865653
4461	5	79538367	81861358	4505	5	79538367	83865914
4462	5	79538367	81863686	4506	5	79538367	83865920
4463	5	79538367	81916850	4507	5	79538367	83868010
4464	5	79538367	81954891	4508	5	79538367	84019752
4465	5	79538367	81985250	4509	5	79538367	84065912
4466	5	79538367	82083752	4510	5	79538367	84086632
4467	5	79538367	82101253	4511	5	79538367	84089603
4468	5	79538367	82143124	4512	5	79538367	84104814
4469	5	79538367	82236318	4513	5	79538367	84105175
4470	5	79538367	82325587	4514	5	79538367	84251635
4471	5	79538367	82427210	4515	5	79538367	84252180
4472	5	79538367	82431853	4516	5	79538367	84253030
4473	5	79538367	82446714	4517	5	79538367	84254208
4474	5	79538367	82446794	4518	5	79538367	84314930
4475	5	79538367	82551111	4519	5	79538367	84340523
4476	5	79538367	82552090	4520	5	79538367	84516340
4477	5	79538367	82555641	4521	5	79538367	84706916
4478	5	79538367	82555670	4522	5	79538367	84799488
4479	5	79538367	82556511	4523	5	79538367	84801081
4480	5	79538367	82559047	4524	5	79538367	84824103
4481	5	79538367	82561535	4525	5	79538367	84824203
4482	5	79538367	82610100	4526	5	79538367	84824816
4483	5	79538367	82676822	4527	5	79538367	84825422
4484	5	79538367	82676901	4528	5	79538367	84825763
4485	5	79538367	82883691	4529	5	79538367	84825942
4486	5	79538367	82954942	4530	5	79538367	84843411
4487	5	79538367	82971688	4531	5	79538367	84936441
4488	5	79538367	83023965	4532	5	79538367	84936493
4489	5	79538367	83094205	4533	5	79538367	84943705
4490	5	79538367	83146355	4534	5	79538367	169454950
4491	5	79538367	83280630	4535	5	79538367	181522829
4492	5	79538367	83281412	4536	5	79538367	204759879
4493	5	79538367	83400242	4537	5	79538367	209874191
4494	5	79538367	83405797	4538	5	79666742	79538367
4495	5	79538367	83437132	4539	5	79666742	79666824
4496	5	79538367	83522252	4540	5	79666742	79682242
4497	5	79538367	83560095	4541	5	79666742	79699261
4498	5	79538367	83560204	4542	5	79666742	79710673

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
4543	5	79666742	79861902	4587	5	79666742	81916850
4544	5	79666742	79867710	4588	5	79666742	81954891
4545	5	79666742	79867868	4589	5	79666742	81985250
4546	5	79666742	79867873	4590	5	79666742	82083752
4547	5	79666742	79961961	4591	5	79666742	82101253
4548	5	79666742	80086268	4592	5	79666742	82143124
4549	5	79666742	80190673	4593	5	79666742	82236318
4550	5	79666742	80190777	4594	5	79666742	82325587
4551	5	79666742	80192546	4595	5	79666742	82427210
4552	5	79666742	80195395	4596	5	79666742	82431853
4553	5	79666742	80199923	4597	5	79666742	82446714
4554	5	79666742	80241911	4598	5	79666742	82446794
4555	5	79666742	80282785	4599	5	79666742	82551111
4556	5	79666742	80345337	4600	5	79666742	82552090
4557	5	79666742	80389787	4601	5	79666742	82555641
4558	5	79666742	80411639	4602	5	79666742	82555670
4559	5	79666742	80446855	4603	5	79666742	82556511
4560	5	79666742	80492790	4604	5	79666742	82559047
4561	5	79666742	80670554	4605	5	79666742	82561535
4562	5	79666742	80674679	4606	5	79666742	82610100
4563	5	79666742	80720509	4607	5	79666742	82676822
4564	5	79666742	80800856	4608	5	79666742	82676901
4565	5	79666742	80804587	4609	5	79666742	82883691
4566	5	79666742	80807409	4610	5	79666742	82954942
4567	5	79666742	80835734	4611	5	79666742	82971688
4568	5	79666742	80971764	4612	5	79666742	83023965
4569	5	79666742	80972258	4613	5	79666742	83094205
4570	5	79666742	80974450	4614	5	79666742	83146355
4571	5	79666742	81047638	4615	5	79666742	83280630
4572	5	79666742	81082921	4616	5	79666742	83281412
4573	5	79666742	81157909	4617	5	79666742	83400242
4574	5	79666742	81265937	4618	5	79666742	83405797
4575	5	79666742	81265937	4619	5	79666742	83437132
4576	5	79666742	81267485	4620	5	79666742	83522252
4577	5	79666742	81267499	4621	5	79666742	83560095
4578	5	79666742	81274512	4622	5	79666742	83560204
4579	5	79666742	81763618	4623	5	79666742	83572400
4580	5	79666742	81797217	4624	5	79666742	83607661
4581	5	79666742	81800186	4625	5	79666742	83745342
4582	5	79666742	81806213	4626	5	79666742	83861275
4583	5	79666742	81854583	4627	5	79666742	83861633
4584	5	79666742	81859374	4628	5	79666742	83865653
4585	5	79666742	81861368	4629	5	79666742	83865914
4586	5	79666742	81863686	4630	5	79666742	83865920

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
4631	5	79666742	83868010	4675	5	79679654	80199923
4632	5	79666742	84019752	4676	5	79679654	80241911
4633	5	79666742	84065912	4677	5	79679654	80282785
4634	5	79666742	84086532	4678	5	79679654	80345337
4635	5	79666742	84089603	4679	5	79679654	80389787
4636	5	79666742	84104814	4680	5	79679654	80411639
4637	5	79666742	84105175	4681	5	79679654	80446855
4638	5	79666742	84251635	4682	5	79679654	80492790
4639	5	79666742	84252180	4683	5	79679654	80670554
4640	5	79666742	84253030	4684	5	79679654	80674679
4641	5	79666742	84254208	4685	5	79679654	80720509
4642	5	79666742	84314930	4686	5	79679654	80800856
4643	5	79666742	84340523	4687	5	79679654	80804587
4644	5	79666742	84516340	4688	5	79679654	80807409
4645	5	79666742	84706916	4689	5	79679654	80835734
4646	5	79666742	84799488	4690	5	79679654	80971764
4647	5	79666742	84801081	4691	5	79679654	80972258
4648	5	79666742	84824103	4692	5	79679654	80974450
4649	5	79666742	84824203	4693	5	79679654	81047638
4650	5	79666742	84824816	4694	5	79679654	81082921
4651	5	79666742	84825422	4695	5	79679654	81157909
4652	5	79666742	84825763	4696	5	79679654	81265937
4653	5	79666742	84825942	4697	5	79679654	81265937
4654	5	79666742	84843411	4698	5	79679654	81267485
4655	5	79666742	84936441	4699	5	79679654	81267499
4656	5	79666742	84936493	4700	5	79679654	81274512
4657	5	79666742	84943705	4701	5	79679654	81763618
4658	5	79666742	169454950	4702	5	79679654	81797217
4659	5	79666742	181522829	4703	5	79679654	81800186
4660	5	79666742	204759879	4704	5	79679654	81806213
4661	5	79666742	209874191	4705	5	79679654	81854583
4662	5	79679654	79682242	4706	5	79679654	81859374
4663	5	79679654	79699261	4707	5	79679654	81861368
4664	5	79679654	79710573	4708	5	79679654	81863686
4665	5	79679654	79861902	4709	5	79679654	81916850
4666	5	79679654	79867710	4710	5	79679654	81954891
4667	5	79679654	79867868	4711	5	79679654	81985250
4668	5	79679654	79867873	4712	5	79679654	82083752
4669	5	79679654	79961961	4713	5	79679654	82101253
4670	5	79679654	80086268	4714	5	79679654	82143124
4671	5	79679654	80190673	4715	5	79679654	82236318
4672	5	79679654	80190777	4716	5	79679654	82325587
4673	5	79679654	80192546	4717	5	79679654	82427210
4674	5	79679654	80195395	4718	5	79679654	82431853

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
4719	5	79679654	82446714	4763	5	79679654	84254208
4720	5	79679654	82446794	4764	5	79679654	84314930
4721	5	79679654	82551111	4765	5	79679654	84340523
4722	5	79679654	82552090	4766	5	79679654	84516340
4723	5	79679654	82555641	4767	5	79679654	84706916
4724	5	79679654	82555670	4768	5	79679654	84799488
4725	5	79679654	82556511	4769	5	79679654	84801081
4726	5	79679654	82559047	4770	5	79679654	84824103
4727	5	79679654	82561535	4771	5	79679654	84824203
4728	5	79679654	82610100	4772	5	79679654	84824816
4729	5	79679654	82676822	4773	5	79679654	84825422
4730	5	79679654	82676901	4774	5	79679654	84825763
4731	5	79679654	82883691	4775	5	79679654	84825942
4732	5	79679654	82954942	4776	5	79679654	84843411
4733	5	79679654	82971688	4777	5	79679654	84936441
4734	5	79679654	83023965	4778	5	79679654	84936493
4735	5	79679654	83094205	4779	5	79679654	84943705
4736	5	79679654	83146355	4780	5	79679654	169454950
4737	5	79679654	83280630	4781	5	79679654	181522829
4738	5	79679654	83281412	4782	5	79679654	204759879
4739	5	79679654	83400242	4783	5	79679654	209874191
4740	5	79679654	83405797	4784	5	79697555	79699261
4741	5	79679654	83437132	4785	5	79697555	79710673
4742	5	79679654	83522252	4786	5	79697555	79861902
4743	5	79679654	83560095	4787	5	79697555	79867710
4744	5	79679654	83560204	4788	5	79697555	79867868
4745	5	79679654	83572400	4789	5	79697555	79867873
4746	5	79679654	83607661	4790	5	79697555	79961961
4747	5	79679654	83745342	4791	5	79697555	80086268
4748	5	79679654	83861275	4792	5	79697555	80190673
4749	5	79679654	83861633	4793	5	79697555	80190777
4750	5	79679654	83865653	4794	5	79697555	80192546
4751	5	79679654	83865914	4795	5	79697555	80195395
4752	5	79679654	83865920	4796	5	79697555	80199923
4753	5	79679654	83868010	4797	5	79697555	80241911
4754	5	79679654	84019752	4798	5	79697555	80282785
4755	5	79679654	84065912	4799	5	79697555	80345337
4756	5	79679654	84086632	4800	5	79697555	80389787
4757	5	79679654	84089603	4801	5	79697555	80411639
4758	5	79679654	84104814	4802	5	79697555	80446855
4759	5	79679654	84105175	4803	5	79697555	80492790
4760	5	79679654	84251635	4804	5	79697555	80670554
4761	5	79679654	84252180	4805	5	79697555	80674679
4762	5	79679654	84253030	4806	5	79697555	80720509

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
4807	5	79697555	80800856	4851	5	79697555	82676901
4808	5	79697555	80804587	4852	5	79697555	82883691
4809	5	79697555	80807409	4853	5	79697555	82954942
4810	5	79697555	80835734	4854	5	79697555	82971688
4811	5	79697555	80971764	4855	5	79697555	83023965
4812	5	79697555	80972258	4856	5	79697555	83094205
4813	5	79697555	80974450	4857	5	79697555	83146355
4814	5	79697555	81047638	4858	5	79697555	83280630
4815	5	79697555	81082921	4859	5	79697555	83281412
4816	5	79697555	81157909	4860	5	79697555	83400242
4817	5	79697555	81265937	4861	5	79697555	83405797
4818	5	79697555	81265937	4862	5	79697555	83437132
4819	5	79697555	81267485	4863	5	79697555	83522252
4820	5	79697555	81267499	4864	5	79697555	83560095
4821	5	79697555	81274512	4865	5	79697555	83560204
4822	5	79697555	81763618	4866	5	79697555	83572400
4823	5	79697555	81797217	4867	5	79697555	83607661
4824	5	79697555	81800186	4868	5	79697555	83745342
4825	5	79697555	81806213	4869	5	79697555	83861275
4826	5	79697555	81854583	4870	5	79697555	83861633
4827	5	79697555	81859374	4871	5	79697555	83865653
4828	5	79697555	81861368	4872	5	79697555	83865914
4829	5	79697555	81863686	4873	5	79697555	83865920
4830	5	79697555	81916850	4874	5	79697555	83868010
4831	5	79697555	81954891	4875	5	79697555	84019752
4832	5	79697555	81985250	4876	5	79697555	84065912
4833	5	79697555	82083752	4877	5	79697555	84086632
4834	5	79697555	82101253	4878	5	79697555	84089603
4835	5	79697555	82143124	4879	5	79697555	84104814
4836	5	79697555	82236318	4880	5	79697555	84105175
4837	5	79697555	82325587	4881	5	79697555	84251635
4838	5	79697555	82427210	4882	5	79697555	84252180
4839	5	79697555	82431853	4883	5	79697555	84253030
4840	5	79697555	82446714	4884	5	79697555	84254208
4841	5	79697555	82446794	4885	5	79697555	84314930
4842	5	79697555	82551111	4886	5	79697555	84340523
4843	5	79697555	82552090	4887	5	79697555	84516340
4844	5	79697555	82555641	4888	5	79697555	84706916
4845	5	79697555	82555670	4889	5	79697555	84799488
4846	5	79697555	82556511	4890	5	79697555	84801081
4847	5	79697555	82559047	4891	5	79697555	84824103
4848	5	79697555	82561535	4892	5	79697555	84824203
4849	5	79697555	82610100	4893	5	79697555	84824816
4850	5	79697555	82676822	4894	5	79697555	84825422

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
4895	5	79697555	84825763	4939	5	79857859	81267499
4896	5	79697555	84825942	4940	5	79857859	81274512
4897	5	79697555	84843411	4941	5	79857859	81763618
4898	5	79697555	84936441	4942	5	79857859	81797217
4899	5	79697555	84936493	4943	5	79857859	81800186
4900	5	79697555	84943705	4944	5	79857859	81806213
4901	5	79697555	169454950	4945	5	79857859	81854583
4902	5	79697555	181522829	4946	5	79857859	81859374
4903	5	79697555	204759879	4947	5	79857859	81861368
4904	5	79697555	209874191	4948	5	79857859	81863686
4905	5	79857859	79861902	4949	5	79857859	81916850
4906	5	79857859	79867710	4950	5	79857859	81954891
4907	5	79857859	79867868	4951	5	79857859	81985250
4908	5	79857859	79867873	4952	5	79857859	82083752
4909	5	79857859	79961961	4953	5	79857859	82101253
4910	5	79857859	80086268	4954	5	79857859	82143124
4911	5	79857859	80190673	4955	5	79857859	82236318
4912	5	79857859	80190777	4956	5	79857859	82325587
4913	5	79857859	80192546	4957	5	79857859	82427210
4914	5	79857859	80195395	4958	5	79857859	82431853
4915	5	79857859	80199923	4959	5	79857859	82446714
4916	5	79857859	80241911	4960	5	79857859	82446794
4917	5	79857859	80282785	4961	5	79857859	82551111
4918	5	79857859	80345337	4962	5	79857859	82552090
4919	5	79857859	80389787	4963	5	79857859	82555641
4920	5	79857859	80411639	4964	5	79857859	82555670
4921	5	79857859	80446855	4965	5	79857859	82556511
4922	5	79857859	80492790	4966	5	79857859	82559047
4923	5	79857859	80670554	4967	5	79857859	82561535
4924	5	79857859	80674679	4968	5	79857859	82610100
4925	5	79857859	80720509	4969	5	79857859	82676822
4926	5	79857859	80800856	4970	5	79857859	82676901
4927	5	79857859	80804587	4971	5	79857859	82883691
4928	5	79857859	80807409	4972	5	79857859	82954942
4929	5	79857859	80835734	4973	5	79857859	82971688
4930	5	79857859	80971764	4974	5	79857859	83023965
4931	5	79857859	80972258	4975	5	79857859	83094205
4932	5	79857859	80974450	4976	5	79857859	83146355
4933	5	79857859	81047638	4977	5	79857859	83280630
4934	5	79857859	81082921	4978	5	79857859	83281412
4935	5	79857859	81157909	4979	5	79857859	83400242
4936	5	79857859	81265937	4980	5	79857859	83405797
4937	5	79857859	81265937	4981	5	79857859	83437132
4938	5	79857859	81267485	4982	5	79857859	83522252

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
4983	5	79857859	83560095	5027	5	79862405	79961961
4984	5	79857859	83560204	5028	5	79862405	80086268
4985	5	79857859	83572400	5029	5	79862405	80190673
4986	5	79857859	83607661	5030	5	79862405	80190777
4987	5	79857859	83745342	5031	5	79862405	80192546
4988	5	79857859	83861275	5032	5	79862405	80195395
4989	5	79857859	83861633	5033	5	79862405	80199923
4990	5	79857859	83865653	5034	5	79862405	80241911
4991	5	79857859	83865914	5035	5	79862405	80282785
4992	5	79857859	83865920	5036	5	79862405	80345337
4993	5	79857859	83868010	5037	5	79862405	80389787
4994	5	79857859	84019752	5038	5	79862405	80411639
4995	5	79857859	84065912	5039	5	79862405	80446855
4996	5	79857859	84086632	5040	5	79862405	80492790
4997	5	79857859	84089603	5041	5	79862405	80670554
4998	5	79857859	84104814	5042	5	79862405	80674679
4999	5	79857859	84105175	5043	5	79862405	80720509
5000	5	79857859	84251635	5044	5	79862405	80800856
5001	5	79857859	84252180	5045	5	79862405	80804587
5002	5	79857859	84253030	5046	5	79862405	80807409
5003	5	79857859	84254208	5047	5	79862405	80835734
5004	5	79857859	84314930	5048	5	79862405	80971764
5005	5	79857859	84340523	5049	5	79862405	80972258
5006	5	79857859	84516340	5050	5	79862405	80974450
5007	5	79857859	84706916	5051	5	79862405	81047638
5008	5	79857859	84799488	5052	5	79862405	81082921
5009	5	79857859	84801081	5053	5	79862405	81157909
5010	5	79857859	84824103	5054	5	79862405	81265937
5011	5	79857859	84824203	5055	5	79862405	81265937
5012	5	79857859	84824816	5056	5	79862405	81267485
5013	5	79857859	84825422	5057	5	79862405	81267499
5014	5	79857859	84825763	5058	5	79862405	81274512
5015	5	79857859	84825942	5059	5	79862405	81763618
5016	5	79857859	84843411	5060	5	79862405	81797217
5017	5	79857859	84936441	5061	5	79862405	81800186
5018	5	79857859	84936493	5062	5	79862405	81806213
5019	5	79857859	84943705	5063	5	79862405	81854583
5020	5	79857859	169454950	5064	5	79862405	81859374
5021	5	79857859	181522829	5065	5	79862405	81861368
5022	5	79857859	204759879	5066	5	79862405	81863686
5023	5	79857859	209874191	5067	5	79862405	81916850
5024	5	79862405	79867710	5068	5	79862405	81954891
5025	5	79862405	79867868	5069	5	79862405	81985250
5026	5	79862405	79867873	5070	5	79862405	82083752

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
5071	5	79862405	82101253	5115	5	79862405	84089603
5072	5	79862405	82143124	5116	5	79862405	84104814
5073	5	79862405	82236318	5117	5	79862405	84105175
5074	5	79862405	82325587	5118	5	79862405	84251635
5075	5	79862405	82427210	5119	5	79862405	84252180
5076	5	79862405	82431853	5120	5	79862405	84253030
5077	5	79862405	82446714	5121	5	79862405	84254208
5078	5	79862405	82446794	5122	5	79862405	84314930
5079	5	79862405	82551111	5123	5	79862405	84340523
5080	5	79862405	82552090	5124	5	79862405	84516340
5081	5	79862405	82555641	5125	5	79862405	84706916
5082	5	79862405	82555670	5126	5	79862405	84799488
5083	5	79862405	82556511	5127	5	79862405	84801081
5084	5	79862405	82559047	5128	5	79862405	84824103
5085	5	79862405	82561535	5129	5	79862405	84824203
5086	5	79862405	82610100	5130	5	79862405	84824816
5087	5	79862405	82676822	5131	5	79862405	84825422
5088	5	79862405	82676901	5132	5	79862405	84825763
5089	5	79862405	82883691	5133	5	79862405	84825942
5090	5	79862405	82954942	5134	5	79862405	84843411
5091	5	79862405	82971688	5135	5	79862405	84936441
5092	5	79862405	83023965	5136	5	79862405	84936493
5093	5	79862405	83094205	5137	5	79862405	84943705
5094	5	79862405	83146355	5138	5	79862405	169454950
5095	5	79862405	83280630	5139	5	79862405	181522829
5096	5	79862405	83281412	5140	5	79862405	204759879
5097	5	79862405	83400242	5141	5	79862405	209874191
5098	5	79862405	83405797	5142	5	79960831	79961961
5099	5	79862405	83437132	5143	5	79960831	80086268
5100	5	79862405	83522252	5144	5	79960831	80190673
5101	5	79862405	83560095	5145	5	79960831	80190777
5102	5	79862405	83560204	5146	5	79960831	80192546
5103	5	79862405	83572400	5147	5	79960831	80195395
5104	5	79862405	83607661	5148	5	79960831	80199923
5105	5	79862405	83745342	5149	5	79960831	80241911
5106	5	79862405	83861275	5150	5	79960831	80282785
5107	5	79862405	83861633	5151	5	79960831	80345337
5108	5	79862405	83865653	5152	5	79960831	80389787
5109	5	79862405	83865914	5153	5	79960831	80411639
5110	5	79862405	83865920	5154	5	79960831	80446855
5111	5	79862405	83868010	5155	5	79960831	80492790
5112	5	79862405	84019752	5156	5	79960831	80670554
5113	5	79862405	84065912	5157	5	79960831	80674679
5114	5	79862405	84086632	5158	5	79960831	80720509

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
5159	5	79960831	80800856	5203	5	79960831	82676901
5160	5	79960831	80804587	5204	5	79960831	82883691
5161	5	79960831	80807409	5205	5	79960831	82954942
5162	5	79960831	80835734	5206	5	79960831	82971688
5163	5	79960831	80971764	5207	5	79960831	83023965
5164	5	79960831	80972258	5208	5	79960831	83094205
5165	5	79960831	80974450	5209	5	79960831	83146355
5166	5	79960831	81047638	5210	5	79960831	83280630
5167	5	79960831	81082921	5211	5	79960831	83281412
5168	5	79960831	81157909	5212	5	79960831	83400242
5169	5	79960831	81265937	5213	5	79960831	83405797
5170	5	79960831	81265937	5214	5	79960831	83437132
5171	5	79960831	81267485	5215	5	79960831	83522252
5172	5	79960831	81267499	5216	5	79960831	83560095
5173	5	79960831	81274512	5217	5	79960831	83560204
5174	5	79960831	81763618	5218	5	79960831	83572400
5175	5	79960831	81797217	5219	5	79960831	83607661
5176	5	79960831	81800186	5220	5	79960831	83745342
5177	5	79960831	81806213	5221	5	79960831	83861275
5178	5	79960831	81854583	5222	5	79960831	83861633
5179	5	79960831	81859374	5223	5	79960831	83865653
5180	5	79960831	81861368	5224	5	79960831	83865914
5181	5	79960831	81863686	5225	5	79960831	83865920
5182	5	79960831	81916850	5226	5	79960831	83868010
5183	5	79960831	81954891	5227	5	79960831	84019752
5184	5	79960831	81985250	5228	5	79960831	84065912
5185	5	79960831	82083752	5229	5	79960831	84086632
5186	5	79960831	82101253	5230	5	79960831	84089603
5187	5	79960831	82143124	5231	5	79960831	84104814
5188	5	79960831	82236318	5232	5	79960831	84105175
5189	5	79960831	82325587	5233	5	79960831	84251635
5190	5	79960831	82427210	5234	5	79960831	84252180
5191	5	79960831	82431853	5235	5	79960831	84253030
5192	5	79960831	82446714	5236	5	79960831	84254208
5193	5	79960831	82446794	5237	5	79960831	84314930
5194	5	79960831	82551111	5238	5	79960831	84340523
5195	5	79960831	82552090	5239	5	79960831	84516340
5196	5	79960831	82555641	5240	5	79960831	84706916
5197	5	79960831	82555670	5241	5	79960831	84799488
5198	5	79960831	82556511	5242	5	79960831	84801081
5199	5	79960831	82559047	5243	5	79960831	84824103
5200	5	79960831	82561535	5244	5	79960831	84824203
5201	5	79960831	82610100	5245	5	79960831	84824816
5202	5	79960831	82676822	5246	5	79960831	84825422

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
5247	5	79960831	84825763	5291	5	80084956	81806213
5248	5	79960831	84825942	5292	5	80084956	81854583
5249	5	79960831	84843411	5293	5	80084956	81859374
5250	5	79960831	84936441	5294	5	80084956	81861368
5251	5	79960831	84936493	5295	5	80084956	81863686
5252	5	79960831	84943705	5296	5	80084956	81916850
5253	5	79960831	169454950	5297	5	80084956	81954891
5254	5	79960831	181522829	5298	5	80084956	81985250
5255	5	79960831	204759879	5299	5	80084956	82083752
5256	5	79960831	209874191	5300	5	80084956	82101253
5257	5	80084956	80086268	5301	5	80084956	82143124
5258	5	80084956	80190673	5302	5	80084956	82236318
5259	5	80084956	80190777	5303	5	80084956	82325587
5260	5	80084956	80192546	5304	5	80084956	82427210
5261	5	80084956	80195395	5305	5	80084956	82431853
5262	5	80084956	80199923	5306	5	80084956	82446714
5263	5	80084956	80241911	5307	5	80084956	82446794
5264	5	80084956	80282785	5308	5	80084956	82551111
5265	5	80084956	80345337	5309	5	80084956	82552090
5266	5	80084956	80389787	5310	5	80084956	82555641
5267	5	80084956	80411639	5311	5	80084956	82555670
5268	5	80084956	80446855	5312	5	80084956	82556511
5269	5	80084956	80492790	5313	5	80084956	82559047
5270	5	80084956	80670554	5314	5	80084956	82561535
5271	5	80084956	80674679	5315	5	80084956	82610100
5272	5	80084956	80720509	5316	5	80084956	82676822
5273	5	80084956	80800856	5317	5	80084956	82676901
5274	5	80084956	80804587	5318	5	80084956	82883691
5275	5	80084956	80807409	5319	5	80084956	82954942
5276	5	80084956	80835734	5320	5	80084956	82971688
5277	5	80084956	80971764	5321	5	80084956	83023965
5278	5	80084956	80972258	5322	5	80084956	83094205
5279	5	80084956	80974450	5323	5	80084956	83146355
5280	5	80084956	81047638	5324	5	80084956	83280630
5281	5	80084956	81082921	5325	5	80084956	83281412
5282	5	80084956	81157909	5326	5	80084956	83400242
5283	5	80084956	81265937	5327	5	80084956	83405797
5284	5	80084956	81265937	5328	5	80084956	83437132
5285	5	80084956	81267485	5329	5	80084956	83522252
5286	5	80084956	81267499	5330	5	80084956	83560095
5287	5	80084956	81274512	5331	5	80084956	83560204
5288	5	80084956	81763618	5332	5	80084956	83572400
5289	5	80084956	81797217	5333	5	80084956	83607661
5290	5	80084956	81800186	5334	5	80084956	83745342

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
5335	5	80084956	83861275	5379	5	80187987	80389787
5336	5	80084956	83861633	5380	5	80187987	80411639
5337	5	80084956	83865653	5381	5	80187987	80446855
5338	5	80084956	83865914	5382	5	80187987	80492790
5339	5	80084956	83865920	5383	5	80187987	80670554
5340	5	80084956	83868010	5384	5	80187987	80674679
5341	5	80084956	84019752	5385	5	80187987	80720509
5342	5	80084956	84065912	5386	5	80187987	80800856
5343	5	80084956	84086632	5387	5	80187987	80804587
5344	5	80084956	84089603	5388	5	80187987	80807409
5345	5	80084956	84104814	5389	5	80187987	80835734
5346	5	80084956	84105175	5390	5	80187987	80971764
5347	5	80084956	84251635	5391	5	80187987	80972258
5348	5	80084956	84252180	5392	5	80187987	80974450
5349	5	80084956	84253030	5393	5	80187987	81047638
5350	5	80084956	84254208	5394	5	80187987	81082921
5351	5	80084956	84314930	5395	5	80187987	81157909
5352	5	80084956	84340523	5396	5	80187987	81265937
5353	5	80084956	84516340	5397	5	80187987	81265937
5354	5	80084956	84706916	5398	5	80187987	81267485
5355	5	80084956	84799488	5399	5	80187987	81267499
5356	5	80084956	84801081	5400	5	80187987	81274512
5357	5	80084956	84824103	5401	5	80187987	81763618
5358	5	80084956	84824203	5402	5	80187987	81797217
5359	5	80084956	84824816	5403	5	80187987	81800186
5360	5	80084956	84825422	5404	5	80187987	81806213
5361	5	80084956	84825763	5405	5	80187987	81854583
5362	5	80084956	84825942	5406	5	80187987	81859374
5363	5	80084956	84843411	5407	5	80187987	81861368
5364	5	80084956	84936441	5408	5	80187987	81863686
5365	5	80084956	84936493	5409	5	80187987	81916850
5366	5	80084956	84943705	5410	5	80187987	81954891
5367	5	80084956	169454950	5411	5	80187987	81985250
5368	5	80084956	181522829	5412	5	80187987	82083752
5369	5	80084956	204759879	5413	5	80187987	82101253
5370	5	80084956	209874191	5414	5	80187987	82143124
5371	5	80187987	80190673	5415	5	80187987	82236318
5372	5	80187987	80190777	5416	5	80187987	82235587
5373	5	80187987	80192546	5417	5	80187987	82427210
5374	5	80187987	80195395	5418	5	80187987	82431853
5375	5	80187987	80199923	5419	5	80187987	82446714
5376	5	80187987	80241911	5420	5	80187987	82446794
5377	5	80187987	80282785	5421	5	80187987	82551111
5378	5	80187987	80345337	5422	5	80187987	82552090

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
5423	5	80187987	82555641	5467	5	80187987	84706916
5424	5	80187987	82555670	5468	5	80187987	84799488
5425	5	80187987	82556511	5469	5	80187987	84801081
5426	5	80187987	82559047	5470	5	80187987	84824103
5427	5	80187987	82561535	5471	5	80187987	84824203
5428	5	80187987	82610100	5472	5	80187987	84824816
5429	5	80187987	82676822	5473	5	80187987	84825422
5430	5	80187987	82676901	5474	5	80187987	84825763
5431	5	80187987	82883691	5475	5	80187987	84825942
5432	5	80187987	82954942	5476	5	80187987	84843411
5433	5	80187987	82971688	5477	5	80187987	84936441
5434	5	80187987	83023965	5478	5	80187987	84936493
5435	5	80187987	83094205	5479	5	80187987	84943705
5436	5	80187987	83146355	5480	5	80187987	169454950
5437	5	80187987	83280630	5481	5	80187987	181522829
5438	5	80187987	83281412	5482	5	80187987	204759879
5439	5	80187987	83400242	5483	5	80187987	209874191
5440	5	80187987	83405797	5484	5	80188978	80190673
5441	5	80187987	83437132	5485	5	80188978	80190777
5442	5	80187987	83522252	5486	5	80188978	80192546
5443	5	80187987	83560095	5487	5	80188978	80195395
5444	5	80187987	83560204	5488	5	80188978	80199923
5445	5	80187987	83572400	5489	5	80188978	80241911
5446	5	80187987	83607661	5490	5	80188978	80282785
5447	5	80187987	83745342	5491	5	80188978	80345337
5448	5	80187987	83861275	5492	5	80188978	80389787
5449	5	80187987	83861633	5493	5	80188978	80411639
5450	5	80187987	83865653	5494	5	80188978	80446855
5451	5	80187987	83865914	5495	5	80188978	80492790
5452	5	80187987	83865920	5496	5	80188978	80670554
5453	5	80187987	83868010	5497	5	80188978	80674679
5454	5	80187987	84019752	5498	5	80188978	80720509
5455	5	80187987	84065912	5499	5	80188978	80800856
5456	5	80187987	84086632	5500	5	80188978	80804587
5457	5	80187987	84089603	5501	5	80188978	80807409
5458	5	80187987	84104814	5502	5	80188978	80835734
5459	5	80187987	84105175	5503	5	80188978	80971764
5460	5	80187987	84251635	5504	5	80188978	80972258
5461	5	80187987	84252180	5505	5	80188978	80974450
5462	5	80187987	84253030	5506	5	80188978	81047638
5463	5	80187987	84254208	5507	5	80188978	81082921
5464	5	80187987	84314930	5508	5	80188978	81157909
5465	5	80187987	84340523	5509	5	80188978	81265937
5466	5	80187987	84516340	5510	5	80188978	81265937

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
5511	5	80188978	81267485	5555	5	80188978	83522252
5512	5	80188978	81267499	5556	5	80188978	83560095
5513	5	80188978	81274512	5557	5	80188978	83560204
5514	5	80188978	81763618	5558	5	80188978	83572400
5515	5	80188978	81797217	5559	5	80188978	83607661
5516	5	80188978	81800186	5560	5	80188978	83745342
5517	5	80188978	81806213	5561	5	80188978	83861275
5518	5	80188978	81854583	5562	5	80188978	83861633
5519	5	80188978	81859374	5563	5	80188978	83865653
5520	5	80188978	81861358	5564	5	80188978	83865914
5521	5	80188978	81863686	5565	5	80188978	83865920
5522	5	80188978	81916850	5566	5	80188978	83868010
5523	5	80188978	81954891	5567	5	80188978	84019752
5524	5	80188978	81985250	5568	5	80188978	84065912
5525	5	80188978	82083752	5569	5	80188978	84086632
5526	5	80188978	82101253	5570	5	80188978	84089603
5527	5	80188978	82143124	5571	5	80188978	84104814
5528	5	80188978	82236318	5572	5	80188978	84105175
5529	5	80188978	82325587	5573	5	80188978	84251635
5530	5	80188978	82427210	5574	5	80188978	84252180
5531	5	80188978	82431853	5575	5	80188978	84253030
5532	5	80188978	82446714	5576	5	80188978	84254208
5533	5	80188978	82446794	5577	5	80188978	84314930
5534	5	80188978	82551111	5578	5	80188978	84340523
5535	5	80188978	82552090	5579	5	80188978	84516340
5536	5	80188978	82555641	5580	5	80188978	84706916
5537	5	80188978	82555670	5581	5	80188978	84799488
5538	5	80188978	82556511	5582	5	80188978	84801081
5539	5	80188978	82559047	5583	5	80188978	84824103
5540	5	80188978	82561535	5584	5	80188978	84824203
5541	5	80188978	82610100	5585	5	80188978	84824816
5542	5	80188978	82676822	5586	5	80188978	84825422
5543	5	80188978	82676901	5587	5	80188978	84825763
5544	5	80188978	82883691	5588	5	80188978	84825942
5545	5	80188978	82954942	5589	5	80188978	84843411
5546	5	80188978	82971688	5590	5	80188978	84936441
5547	5	80188978	83023965	5591	5	80188978	84936493
5548	5	80188978	83094205	5592	5	80188978	84943705
5549	5	80188978	83146355	5593	5	80188978	169454950
5550	5	80188978	83280630	5594	5	80188978	181522829
5551	5	80188978	83281412	5595	5	80188978	204759879
5552	5	80188978	83400242	5596	5	80188978	209874191
5553	5	80188978	83405797	5597	5	80191781	80192546
5554	5	80188978	83437132	5598	5	80191781	80195395

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
5599	5	80191781	80199923	5643	5	80191781	82446714
5600	5	80191781	80241911	5644	5	80191781	82446794
5601	5	80191781	80282785	5645	5	80191781	82551111
5602	5	80191781	80345337	5646	5	80191781	82552090
5603	5	80191781	80389787	5647	5	80191781	82555641
5604	5	80191781	80411639	5648	5	80191781	82555670
5605	5	80191781	80446855	5649	5	80191781	82556511
5606	5	80191781	80492790	5650	5	80191781	82559047
5607	5	80191781	80670554	5651	5	80191781	82561535
5608	5	80191781	80674679	5652	5	80191781	82610100
5609	5	80191781	80720509	5653	5	80191781	82676822
5610	5	80191781	80800856	5654	5	80191781	82676901
5611	5	80191781	80804587	5655	5	80191781	82883691
5612	5	80191781	80807409	5656	5	80191781	82954942
5613	5	80191781	80835734	5657	5	80191781	82971688
5614	5	80191781	80971764	5658	5	80191781	83023965
5615	5	80191781	80972258	5659	5	80191781	83094205
5616	5	80191781	80974450	5660	5	80191781	83146355
5617	5	80191781	81047638	5661	5	80191781	83280630
5618	5	80191781	81082921	5662	5	80191781	83281412
5619	5	80191781	81157909	5663	5	80191781	83400242
5620	5	80191781	81265937	5664	5	80191781	83405797
5621	5	80191781	81265937	5665	5	80191781	83437132
5622	5	80191781	81267485	5666	5	80191781	83522252
5623	5	80191781	81267499	5667	5	80191781	83560095
5624	5	80191781	81274512	5668	5	80191781	83560204
5625	5	80191781	81763618	5669	5	80191781	83572400
5626	5	80191781	81797217	5670	5	80191781	83607661
5627	5	80191781	81800186	5671	5	80191781	83745342
5628	5	80191781	81806213	5672	5	80191781	83861275
5629	5	80191781	81854583	5673	5	80191781	83861633
5630	5	80191781	81859374	5674	5	80191781	83865653
5631	5	80191781	81861368	5675	5	80191781	83865914
5632	5	80191781	81863686	5676	5	80191781	83865920
5633	5	80191781	81916850	5677	5	80191781	83868010
5634	5	80191781	81954891	5678	5	80191781	84019752
5635	5	80191781	81985250	5679	5	80191781	84065912
5636	5	80191781	82083752	5680	5	80191781	84086632
5637	5	80191781	82101253	5681	5	80191781	84089603
5638	5	80191781	82143124	5682	5	80191781	84104814
5639	5	80191781	82236318	5683	5	80191781	84105175
5640	5	80191781	82325587	5684	5	80191781	84251635
5641	5	80191781	82427210	5685	5	80191781	84252180
5642	5	80191781	82431853	5686	5	80191781	84253030

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
5687	5	80191781	84254208	5731	5	80195077	81265937
5688	5	80191781	84314930	5732	5	80195077	81267485
5689	5	80191781	84340523	5733	5	80195077	81267499
5690	5	80191781	84516340	5734	5	80195077	81274512
5691	5	80191781	84706916	5735	5	80195077	81763618
5692	5	80191781	84799488	5736	5	80195077	81797217
5693	5	80191781	84801081	5737	5	80195077	81800186
5694	5	80191781	84824103	5738	5	80195077	81806213
5695	5	80191781	84824203	5739	5	80195077	81854583
5696	5	80191781	84824816	5740	5	80195077	81859374
5697	5	80191781	84825422	5741	5	80195077	81861368
5698	5	80191781	84825763	5742	5	80195077	81863686
5699	5	80191781	84825942	5743	5	80195077	81916850
5700	5	80191781	84843411	5744	5	80195077	81954891
5701	5	80191781	84936441	5745	5	80195077	81985250
5702	5	80191781	84936493	5746	5	80195077	82083752
5703	5	80191781	84943705	5747	5	80195077	82101253
5704	5	80191781	169454950	5748	5	80195077	82143124
5705	5	80191781	181522829	5749	5	80195077	82236318
5706	5	80191781	204759879	5750	5	80195077	82325587
5707	5	80191781	209874191	5751	5	80195077	82427210
5708	5	80195077	80195395	5752	5	80195077	82431853
5709	5	80195077	80199923	5753	5	80195077	82446714
5710	5	80195077	80241911	5754	5	80195077	82446794
5711	5	80195077	80282785	5755	5	80195077	82551111
5712	5	80195077	80345337	5756	5	80195077	82552090
5713	5	80195077	80389787	5757	5	80195077	82555641
5714	5	80195077	80411639	5758	5	80195077	82555670
5715	5	80195077	80446855	5759	5	80195077	82556511
5716	5	80195077	80492790	5760	5	80195077	82559047
5717	5	80195077	80670554	5761	5	80195077	82561535
5718	5	80195077	80674679	5762	5	80195077	82610100
5719	5	80195077	80720509	5763	5	80195077	82676822
5720	5	80195077	80800856	5764	5	80195077	82676901
5721	5	80195077	80804587	5765	5	80195077	82883691
5722	5	80195077	80807409	5766	5	80195077	82954942
5723	5	80195077	80835734	5767	5	80195077	82971688
5724	5	80195077	80971764	5768	5	80195077	83023965
5725	5	80195077	80972258	5769	5	80195077	83094205
5726	5	80195077	80974450	5770	5	80195077	83146355
5727	5	80195077	81047638	5771	5	80195077	83280630
5728	5	80195077	81082921	5772	5	80195077	83281412
5729	5	80195077	81157909	5773	5	80195077	83400242
5730	5	80195077	81265937	5774	5	80195077	83405797

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
5775	5	80195077	83437132	5819	5	80195395	80241911
5776	5	80195077	83522252	5820	5	80195395	80282785
5777	5	80195077	83560095	5821	5	80195395	80345337
5778	5	80195077	83560204	5822	5	80195395	80389787
5779	5	80195077	83572400	5823	5	80195395	80411639
5780	5	80195077	83607661	5824	5	80195395	80446855
5781	5	80195077	83745342	5825	5	80195395	80492790
5782	5	80195077	83861275	5826	5	80195395	80670554
5783	5	80195077	83861633	5827	5	80195395	80674679
5784	5	80195077	83865653	5828	5	80195395	80720509
5785	5	80195077	83865914	5829	5	80195395	80800856
5786	5	80195077	83865920	5830	5	80195395	80804587
5787	5	80195077	83868010	5831	5	80195395	80807409
5788	5	80195077	84019752	5832	5	80195395	80835734
5789	5	80195077	84065912	5833	5	80195395	80971764
5790	5	80195077	84086632	5834	5	80195395	80972258
5791	5	80195077	84089603	5835	5	80195395	80974450
5792	5	80195077	84104814	5836	5	80195395	81047638
5793	5	80195077	84105175	5837	5	80195395	81082921
5794	5	80195077	84251635	5838	5	80195395	81157909
5795	5	80195077	84252180	5839	5	80195395	81265937
5796	5	80195077	84253030	5840	5	80195395	81265937
5797	5	80195077	84254208	5841	5	80195395	81267485
5798	5	80195077	84314930	5842	5	80195395	81267499
5799	5	80195077	84340523	5843	5	80195395	81274512
5800	5	80195077	84516340	5844	5	80195395	81763618
5801	5	80195077	84706916	5845	5	80195395	81797217
5802	5	80195077	84799488	5846	5	80195395	81800186
5803	5	80195077	84801081	5847	5	80195395	81806213
5804	5	80195077	84824103	5848	5	80195395	81854583
5805	5	80195077	84824203	5849	5	80195395	81859374
5806	5	80195077	84824816	5850	5	80195395	81861368
5807	5	80195077	84825422	5851	5	80195395	81863686
5808	5	80195077	84825763	5852	5	80195395	81916850
5809	5	80195077	84825942	5853	5	80195395	81954891
5810	5	80195077	84843411	5854	5	80195395	81985250
5811	5	80195077	84936441	5855	5	80195395	82083752
5812	5	80195077	84936493	5856	5	80195395	82101253
5813	5	80195077	84943705	5857	5	80195395	82143124
5814	5	80195077	169454950	5858	5	80195395	82236318
5815	5	80195077	181522829	5859	5	80195395	82325587
5816	5	80195077	204759879	5860	5	80195395	82427210
5817	5	80195077	209874191	5861	5	80195395	82431853
5818	5	80195395	80199923	5862	5	80195395	82446714

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
5863	5	80195395	82446794	5907	5	80195395	84314930
5864	5	80195395	82551111	5908	5	80195395	84340523
5865	5	80195395	82552090	5909	5	80195395	84516340
5866	5	80195395	82555641	5910	5	80195395	84706916
5867	5	80195395	82555670	5911	5	80195395	84799488
5868	5	80195395	82556511	5912	5	80195395	84801081
5869	5	80195395	82559047	5913	5	80195395	84824103
5870	5	80195395	82561535	5914	5	80195395	84824203
5871	5	80195395	82610100	5915	5	80195395	84824816
5872	5	80195395	82676822	5916	5	80195395	84825422
5873	5	80195395	82676901	5917	5	80195395	84825763
5874	5	80195395	82883691	5918	5	80195395	84825942
5875	5	80195395	82954942	5919	5	80195395	84843411
5876	5	80195395	82971688	5920	5	80195395	84936441
5877	5	80195395	83023965	5921	5	80195395	84936493
5878	5	80195395	83094205	5922	5	80195395	84943705
5879	5	80195395	83146355	5923	5	80195395	169454950
5880	5	80195395	83280630	5924	5	80195395	181522829
5881	5	80195395	83281412	5925	5	80195395	204759879
5882	5	80195395	83400242	5926	5	80195395	209874191
5883	5	80195395	83405797	5927	5	80195714	80199923
5884	5	80195395	83437132	5928	5	80195714	80241911
5885	5	80195395	83522252	5929	5	80195714	80282785
5886	5	80195395	83560095	5930	5	80195714	80345337
5887	5	80195395	83560204	5931	5	80195714	80389787
5888	5	80195395	83572400	5932	5	80195714	80411639
5889	5	80195395	83607661	5933	5	80195714	80446855
5890	5	80195395	83745342	5934	5	80195714	80492790
5891	5	80195395	83861275	5935	5	80195714	80670554
5892	5	80195395	83861633	5936	5	80195714	80674679
5893	5	80195395	83865653	5937	5	80195714	80720509
5894	5	80195395	83865914	5938	5	80195714	80800856
5895	5	80195395	83865920	5939	5	80195714	80804587
5896	5	80195395	83868010	5940	5	80195714	80807409
5897	5	80195395	84019752	5941	5	80195714	80835734
5898	5	80195395	84065912	5942	5	80195714	80971764
5899	5	80195395	84086632	5943	5	80195714	80972258
5900	5	80195395	84089603	5944	5	80195714	80974450
5901	5	80195395	84104814	5945	5	80195714	81047638
5902	5	80195395	84105175	5946	5	80195714	81082921
5903	5	80195395	84251635	5947	5	80195714	81157909
5904	5	80195395	84252180	5948	5	80195714	81265937
5905	5	80195395	84253030	5949	5	80195714	81265937
5906	5	80195395	84254208	5950	5	80195714	81267485

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
5951	5	80195714	81267499	5995	5	80195714	83560095
5952	5	80195714	81274512	5996	5	80195714	83560204
5953	5	80195714	81763618	5997	5	80195714	83572400
5954	5	80195714	81797217	5998	5	80195714	83607661
5955	5	80195714	81800186	5999	5	80195714	83745342
5956	5	80195714	81806213	6000	5	80195714	83861275
5957	5	80195714	81854583	6001	5	80195714	83861633
5958	5	80195714	81859374	6002	5	80195714	83865653
5959	5	80195714	81861368	6003	5	80195714	83865914
5960	5	80195714	81863686	6004	5	80195714	83865920
5961	5	80195714	81916850	6005	5	80195714	83868010
5962	5	80195714	81954891	6006	5	80195714	84019752
5963	5	80195714	81985250	6007	5	80195714	84065912
5964	5	80195714	82083752	6008	5	80195714	84086632
5965	5	80195714	82101253	6009	5	80195714	84089603
5966	5	80195714	82143124	6010	5	80195714	84104814
5967	5	80195714	82236318	6011	5	80195714	84105175
5968	5	80195714	82325587	6012	5	80195714	84251635
5969	5	80195714	82427210	6013	5	80195714	84252180
5970	5	80195714	82431853	6014	5	80195714	84253030
5971	5	80195714	82446714	6015	5	80195714	84254208
5972	5	80195714	82446794	6016	5	80195714	84314930
5973	5	80195714	82551111	6017	5	80195714	84340523
5974	5	80195714	82552090	6018	5	80195714	84516340
5975	5	80195714	82555641	6019	5	80195714	84706916
5976	5	80195714	82555670	6020	5	80195714	84799488
5977	5	80195714	82556511	6021	5	80195714	84801081
5978	5	80195714	82559047	6022	5	80195714	84824103
5979	5	80195714	82561535	6023	5	80195714	84824203
5980	5	80195714	82610100	6024	5	80195714	84824816
5981	5	80195714	82676822	6025	5	80195714	84825422
5982	5	80195714	82676901	6026	5	80195714	84825763
5983	5	80195714	82883691	6027	5	80195714	84825942
5984	5	80195714	82954942	6028	5	80195714	84843411
5985	5	80195714	82971688	6029	5	80195714	84936441
5986	5	80195714	83023965	6030	5	80195714	84936493
5987	5	80195714	83094205	6031	5	80195714	84943705
5988	5	80195714	83146355	6032	5	80195714	169454950
5989	5	80195714	83280630	6033	5	80195714	181522829
5990	5	80195714	83281412	6034	5	80195714	204759879
5991	5	80195714	83400242	6035	5	80195714	209874191
5992	5	80195714	83405797	6036	5	80236478	80241911
5993	5	80195714	83437132	6037	5	80236478	80282785
5994	5	80195714	83522252	6038	5	80236478	80345337

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
6039	5	80236478	80389787	6083	5	80236478	82555641
6040	5	80236478	80411639	6084	5	80236478	82555670
6041	5	80236478	80446855	6085	5	80236478	82555611
6042	5	80236478	80492790	6086	5	80236478	82559047
6043	5	80236478	80670554	6087	5	80236478	82561535
6044	5	80236478	80674679	6088	5	80236478	82610100
6045	5	80236478	80720509	6089	5	80236478	82676822
6046	5	80236478	80800856	6090	5	80236478	82676901
6047	5	80236478	80804587	6091	5	80236478	82883691
6048	5	80236478	80807409	6092	5	80236478	82954942
6049	5	80236478	80835734	6093	5	80236478	82971688
6050	5	80236478	80971764	6094	5	80236478	83023965
6051	5	80236478	80972258	6095	5	80236478	83094205
6052	5	80236478	80974450	6096	5	80236478	83146355
6053	5	80236478	81047638	6097	5	80236478	83280630
6054	5	80236478	81082921	6098	5	80236478	83281412
6055	5	80236478	81157909	6099	5	80236478	83400242
6056	5	80236478	81265937	6100	5	80236478	83405797
6057	5	80236478	81265937	6101	5	80236478	83437132
6058	5	80236478	81267485	6102	5	80236478	83522252
6059	5	80236478	81267499	6103	5	80236478	83560095
6060	5	80236478	81274512	6104	5	80236478	83560204
6061	5	80236478	81763618	6105	5	80236478	83572400
6062	5	80236478	81797217	6106	5	80236478	83607661
6063	5	80236478	81800186	6107	5	80236478	83745342
6064	5	80236478	81806213	6108	5	80236478	83861275
6065	5	80236478	81854583	6109	5	80236478	83861633
6066	5	80236478	81859374	6110	5	80236478	83865653
6067	5	80236478	81861368	6111	5	80236478	83865914
6068	5	80236478	81863686	6112	5	80236478	83865920
6069	5	80236478	81916850	6113	5	80236478	83868010
6070	5	80236478	81954891	6114	5	80236478	84019752
6071	5	80236478	81985250	6115	5	80236478	84065912
6072	5	80236478	82083752	6116	5	80236478	84086632
6073	5	80236478	82101253	6117	5	80236478	84089603
6074	5	80236478	82143124	6118	5	80236478	84104814
6075	5	80236478	82236318	6119	5	80236478	84105175
6076	5	80236478	82325587	6120	5	80236478	84251635
6077	5	80236478	82427210	6121	5	80236478	84252180
6078	5	80236478	82431853	6122	5	80236478	84253030
6079	5	80236478	82446714	6123	5	80236478	84254208
6080	5	80236478	82446794	6124	5	80236478	84314930
6081	5	80236478	82551111	6125	5	80236478	84340523
6082	5	80236478	82552090	6126	5	80236478	84516340

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
6127	5	80236478	84706916	6171	5	80238986	81800186
6128	5	80236478	84799488	6172	5	80238986	81806213
6129	5	80236478	84801081	6173	5	80238986	81854583
6130	5	80236478	84824103	6174	5	80238986	81859374
6131	5	80236478	84824203	6175	5	80238986	81861368
6132	5	80236478	84824816	6176	5	80238986	81863686
6133	5	80236478	84825422	6177	5	80238986	81916850
6134	5	80236478	84825763	6178	5	80238986	81954891
6135	5	80236478	84825942	6179	5	80238986	81985250
6136	5	80236478	84843411	6180	5	80238986	82083752
6137	5	80236478	84936441	6181	5	80238986	82101253
6138	5	80236478	84936493	6182	5	80238986	82143124
6139	5	80236478	84943705	6183	5	80238986	82236318
6140	5	80236478	169454950	6184	5	80238986	82325587
6141	5	80236478	181522829	6185	5	80238986	82427210
6142	5	80236478	204759879	6186	5	80238986	82431853
6143	5	80236478	209874191	6187	5	80238986	82446714
6144	5	80238986	80241911	6188	5	80238986	82446794
6145	5	80238986	80282785	6189	5	80238986	82551111
6146	5	80238986	80345337	6190	5	80238986	82552090
6147	5	80238986	80389787	6191	5	80238986	82555641
6148	5	80238986	80411639	6192	5	80238986	82555670
6149	5	80238986	80446855	6193	5	80238986	82556311
6150	5	80238986	80492790	6194	5	80238986	82559047
6151	5	80238986	80670554	6195	5	80238986	82561535
6152	5	80238986	80674679	6196	5	80238986	82610100
6153	5	80238986	80720509	6197	5	80238986	82676822
6154	5	80238986	80800856	6198	5	80238986	82676901
6155	5	80238986	80804587	6199	5	80238986	82883691
6156	5	80238986	80807409	6200	5	80238986	82954942
6157	5	80238986	80835734	6201	5	80238986	82971688
6158	5	80238986	80971764	6202	5	80238986	83023965
6159	5	80238986	80972258	6203	5	80238986	83094205
6160	5	80238986	80974450	6204	5	80238986	83146355
6161	5	80238986	81047638	6205	5	80238986	83280630
6162	5	80238986	81082921	6206	5	80238986	83281412
6163	5	80238986	81157909	6207	5	80238986	83400242
6164	5	80238986	81265937	6208	5	80238986	83405797
6165	5	80238986	81265937	6209	5	80238986	83437132
6166	5	80238986	81267485	6210	5	80238986	83522252
6167	5	80238986	81267499	6211	5	80238986	83560095
6168	5	80238986	81274512	6212	5	80238986	83560204
6169	5	80238986	81763618	6213	5	80238986	83572400
6170	5	80238986	81797217	6214	5	80238986	83607661

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
6215	5	80238986	83745342	6259	5	80239243	80670554
6216	5	80238986	83861275	6260	5	80239243	80674679
6217	5	80238986	83861633	6261	5	80239243	80720509
6218	5	80238986	83865653	6262	5	80239243	80800856
6219	5	80238986	83865914	6263	5	80239243	80804587
6220	5	80238986	83865920	6264	5	80239243	80807409
6221	5	80238986	83868010	6265	5	80239243	80835734
6222	5	80238986	84019752	6266	5	80239243	80971764
6223	5	80238986	84065912	6267	5	80239243	80972258
6224	5	80238986	84086632	6268	5	80239243	80974450
6225	5	80238986	84089603	6269	5	80239243	81047638
6226	5	80238986	84104814	6270	5	80239243	81082921
6227	5	80238986	84105173	6271	5	80239243	81157909
6228	5	80238986	84251635	6272	5	80239243	81265937
6229	5	80238986	84252180	6273	5	80239243	81265937
6230	5	80238986	84253030	6274	5	80239243	81267485
6231	5	80238986	84254208	6275	5	80239243	81267499
6232	5	80238986	84314930	6276	5	80239243	81274512
6233	5	80238986	84340523	6277	5	80239243	81763618
6234	5	80238986	84516340	6278	5	80239243	81797217
6235	5	80238986	84706916	6279	5	80239243	81800186
6236	5	80238986	84799488	6280	5	80239243	81806213
6237	5	80238986	84801081	6281	5	80239243	81854583
6238	5	80238986	84824103	6282	5	80239243	81859374
6239	5	80238986	84824203	6283	5	80239243	81861368
6240	5	80238986	84824816	6284	5	80239243	81863686
6241	5	80238986	84825422	6285	5	80239243	81916850
6242	5	80238986	84825763	6286	5	80239243	81954891
6243	5	80238986	84825942	6287	5	80239243	81985250
6244	5	80238986	84843411	6288	5	80239243	82083752
6245	5	80238986	84936441	6289	5	80239243	82101253
6246	5	80238986	84936493	6290	5	80239243	82143124
6247	5	80238986	84943705	6291	5	80239243	82236318
6248	5	80238986	169454950	6292	5	80239243	82325587
6249	5	80238986	181522829	6293	5	80239243	82427210
6250	5	80238986	204759879	6294	5	80239243	82431853
6251	5	80238986	209874191	6295	5	80239243	82446714
6252	5	80239243	80241911	6296	5	80239243	82446794
6253	5	80239243	80282785	6297	5	80239243	82551111
6254	5	80239243	80345337	6298	5	80239243	82552090
6255	5	80239243	80389787	6299	5	80239243	82555641
6256	5	80239243	80411639	6300	5	80239243	82555670
6257	5	80239243	80446855	6301	5	80239243	82556511
6258	5	80239243	80492790	6302	5	80239243	82559047

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
6303	5	80239243	82561535	6347	5	80239243	84824203
6304	5	80239243	82610100	6348	5	80239243	84824816
6305	5	80239243	82676822	6349	5	80239243	84825422
6306	5	80239243	82676901	6350	5	80239243	84825763
6307	5	80239243	82883691	6351	5	80239243	84825942
6308	5	80239243	82934942	6352	5	80239243	84843411
6309	5	80239243	82971688	6353	5	80239243	84936441
6310	5	80239243	83023965	6354	5	80239243	84936493
6311	5	80239243	83094205	6355	5	80239243	84943705
6312	5	80239243	83146355	6356	5	80239243	169454950
6313	5	80239243	83280630	6357	5	80239243	181522829
6314	5	80239243	83281412	6358	5	80239243	204759879
6315	5	80239243	83400242	6359	5	80239243	209874191
6316	5	80239243	83405797	6360	5	80273499	80282785
6317	5	80239243	83437132	6361	5	80273499	80345337
6318	5	80239243	83522252	6362	5	80273499	80389787
6319	5	80239243	83560095	6363	5	80273499	80411639
6320	5	80239243	83560204	6364	5	80273499	80446855
6321	5	80239243	83572400	6365	5	80273499	80492790
6322	5	80239243	83607661	6366	5	80273499	80670554
6323	5	80239243	83745342	6367	5	80273499	80674679
6324	5	80239243	83861275	6368	5	80273499	80720509
6325	5	80239243	83861633	6369	5	80273499	80800856
6326	5	80239243	83865653	6370	5	80273499	80804587
6327	5	80239243	83865914	6371	5	80273499	80807409
6328	5	80239243	83865920	6372	5	80273499	80835734
6329	5	80239243	83868010	6373	5	80273499	80971764
6330	5	80239243	84019752	6374	5	80273499	80972258
6331	5	80239243	84065912	6375	5	80273499	80974450
6332	5	80239243	84086632	6376	5	80273499	81047638
6333	5	80239243	84089603	6377	5	80273499	81082921
6334	5	80239243	84104814	6378	5	80273499	81157909
6335	5	80239243	84105175	6379	5	80273499	81265937
6336	5	80239243	84251635	6380	5	80273499	81265937
6337	5	80239243	84252180	6381	5	80273499	81267485
6338	5	80239243	84253030	6382	5	80273499	81267499
6339	5	80239243	84254208	6383	5	80273499	81274512
6340	5	80239243	84314930	6384	5	80273499	81763618
6341	5	80239243	84340523	6385	5	80273499	81797217
6342	5	80239243	84516340	6386	5	80273499	81800186
6343	5	80239243	84706916	6387	5	80273499	81806213
6344	5	80239243	84799488	6388	5	80273499	81854583
6345	5	80239243	84801081	6389	5	80273499	81859374
6346	5	80239243	84824103	6390	5	80273499	81861368

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
6391	5	80273499	81863686	6435	5	80273499	83865920
6392	5	80273499	81916850	6436	5	80273499	83868010
6393	5	80273499	81954891	6437	5	80273499	84019752
6394	5	80273499	81985250	6438	5	80273499	84065912
6395	5	80273499	82083752	6439	5	80273499	84086632
6396	5	80273499	82101253	6440	5	80273499	84089603
6397	5	80273499	82143124	6441	5	80273499	84104814
6398	5	80273499	82236318	6442	5	80273499	84105175
6399	5	80273499	82325587	6443	5	80273499	84251635
6400	5	80273499	82427210	6444	5	80273499	84252180
6401	5	80273499	82431853	6445	5	80273499	84253030
6402	5	80273499	82446714	6446	5	80273499	84254208
6403	5	80273499	82446794	6447	5	80273499	84314930
6404	5	80273499	82551111	6448	5	80273499	84340523
6405	5	80273499	82552090	6449	5	80273499	84516340
6406	5	80273499	82555641	6450	5	80273499	84706916
6407	5	80273499	82555670	6451	5	80273499	84799488
6408	5	80273499	82556511	6452	5	80273499	84801081
6409	5	80273499	82559047	6453	5	80273499	84824103
6410	5	80273499	82561535	6454	5	80273499	84824203
6411	5	80273499	82610100	6455	5	80273499	84824816
6412	5	80273499	82676822	6456	5	80273499	84825422
6413	5	80273499	82676901	6457	5	80273499	84825763
6414	5	80273499	82883691	6458	5	80273499	84825942
6415	5	80273499	82954942	6459	5	80273499	84843411
6416	5	80273499	82971688	6460	5	80273499	84936441
6417	5	80273499	83023965	6461	5	80273499	84936493
6418	5	80273499	83094205	6462	5	80273499	84943705
6419	5	80273499	83146355	6463	5	80273499	169454950
6420	5	80273499	83280630	6464	5	80273499	181522829
6421	5	80273499	83281412	6465	5	80273499	204759879
6422	5	80273499	83400242	6466	5	80273499	209874191
6423	5	80273499	83405797	6467	5	80344025	80345337
6424	5	80273499	83437132	6468	5	80344025	80389787
6425	5	80273499	83522252	6469	5	80344025	80411639
6426	5	80273499	83560095	6470	5	80344025	80446855
6427	5	80273499	83560204	6471	5	80344025	80492790
6428	5	80273499	83572400	6472	5	80344025	80670554
6429	5	80273499	83607661	6473	5	80344025	80674679
6430	5	80273499	83745342	6474	5	80344025	80720509
6431	5	80273499	83861275	6475	5	80344025	80800856
6432	5	80273499	83861633	6476	5	80344025	80804587
6433	5	80273499	83865653	6477	5	80344025	80807409
6434	5	80273499	83865914	6478	5	80344025	80835734

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
6479	5	80344025	80971764	6523	5	80344025	83023965
6480	5	80344025	80972258	6524	5	80344025	83094205
6481	5	80344025	80974450	6525	5	80344025	83146355
6482	5	80344025	81047638	6526	5	80344025	83280630
6483	5	80344025	81082921	6527	5	80344025	83281412
6484	5	80344025	81157909	6528	5	80344025	83400242
6485	5	80344025	81265937	6529	5	80344025	83405797
6486	5	80344025	81265937	6530	5	80344025	83437132
6487	5	80344025	81267485	6531	5	80344025	83522252
6488	5	80344025	81267499	6532	5	80344025	83560095
6489	5	80344025	81274512	6533	5	80344025	83560204
6490	5	80344025	81763618	6534	5	80344025	83572400
6491	5	80344025	81797217	6535	5	80344025	83607661
6492	5	80344025	81800186	6536	5	80344025	83745342
6493	5	80344025	81806213	6537	5	80344025	83861275
6494	5	80344025	81854583	6538	5	80344025	83861633
6495	5	80344025	81859374	6539	5	80344025	83865653
6496	5	80344025	81861368	6540	5	80344025	83865914
6497	5	80344025	81863686	6541	5	80344025	83865920
6498	5	80344025	81916850	6542	5	80344025	83868010
6499	5	80344025	81954891	6543	5	80344025	84019752
6500	5	80344025	81985250	6544	5	80344025	84065912
6501	5	80344025	82083752	6545	5	80344025	84086632
6502	5	80344025	82101253	6546	5	80344025	84089603
6503	5	80344025	82143124	6547	5	80344025	84104814
6504	5	80344025	82236318	6548	5	80344025	84105175
6505	5	80344025	82325587	6549	5	80344025	84251635
6506	5	80344025	82427210	6550	5	80344025	84252180
6507	5	80344025	82431853	6551	5	80344025	84253030
6508	5	80344025	82446714	6552	5	80344025	84254208
6509	5	80344025	82446794	6553	5	80344025	84314930
6510	5	80344025	82551111	6554	5	80344025	84340523
6511	5	80344025	82552090	6555	5	80344025	84516340
6512	5	80344025	82555641	6556	5	80344025	84706916
6513	5	80344025	82555670	6557	5	80344025	84799488
6514	5	80344025	82556511	6558	5	80344025	84801081
6515	5	80344025	82559047	6559	5	80344025	84824103
6516	5	80344025	82561535	6560	5	80344025	84824203
6517	5	80344025	82610100	6561	5	80344025	84824816
6518	5	80344025	82676822	6562	5	80344025	84825422
6519	5	80344025	82676901	6563	5	80344025	84825763
6520	5	80344025	82883691	6564	5	80344025	84825942
6521	5	80344025	82954942	6565	5	80344025	84843411
6522	5	80344025	82971688	6566	5	80344025	84936441

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
6567	5	80344025	84936493	6611	5	80387639	82427210
6568	5	80344025	84943705	6612	5	80387639	82431853
6569	5	80344025	169454950	6613	5	80387639	82446714
6570	5	80344025	181522829	6614	5	80387639	82446794
6571	5	80344025	204739879	6615	5	80387639	82551111
6572	5	80344025	209874191	6616	5	80387639	82552090
6573	5	80387639	80389787	6617	5	80387639	82555641
6574	5	80387639	80411639	6618	5	80387639	82555670
6575	5	80387639	80446855	6619	5	80387639	82556511
6576	5	80387639	80492790	6620	5	80387639	82559047
6577	5	80387639	80670554	6621	5	80387639	82561535
6578	5	80387639	80674679	6622	5	80387639	82610100
6579	5	80387639	80720509	6623	5	80387639	82676822
6580	5	80387639	80800856	6624	5	80387639	82676901
6581	5	80387639	80804587	6625	5	80387639	82883691
6582	5	80387639	80807409	6626	5	80387639	82954942
6583	5	80387639	80835734	6627	5	80387639	82971688
6584	5	80387639	80971764	6628	5	80387639	83023965
6585	5	80387639	80972258	6629	5	80387639	83094205
6586	5	80387639	80974450	6630	5	80387639	83146355
6587	5	80387639	81047638	6631	5	80387639	83280630
6588	5	80387639	81082921	6632	5	80387639	83281412
6589	5	80387639	81157909	6633	5	80387639	83400242
6590	5	80387639	81265937	6634	5	80387639	83405797
6591	5	80387639	81265937	6635	5	80387639	83437132
6592	5	80387639	81267485	6636	5	80387639	83522252
6593	5	80387639	81267499	6637	5	80387639	83560095
6594	5	80387639	81274512	6638	5	80387639	83560204
6595	5	80387639	81763618	6639	5	80387639	83572400
6596	5	80387639	81797217	6640	5	80387639	83607661
6597	5	80387639	81800186	6641	5	80387639	83745342
6598	5	80387639	81806213	6642	5	80387639	83861275
6599	5	80387639	81854583	6643	5	80387639	83861633
6600	5	80387639	81859374	6644	5	80387639	83865653
6601	5	80387639	81861368	6645	5	80387639	83865914
6602	5	80387639	81863686	6646	5	80387639	83865920
6603	5	80387639	81916850	6647	5	80387639	83868010
6604	5	80387639	81954891	6648	5	80387639	84019752
6605	5	80387639	81985250	6649	5	80387639	84065912
6606	5	80387639	82083752	6650	5	80387639	84086632
6607	5	80387639	82101253	6651	5	80387639	84089603
6608	5	80387639	82143124	6652	5	80387639	84104814
6609	5	80387639	82236318	6653	5	80387639	84105175
6610	5	80387639	82325587	6654	5	80387639	84251635

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
6655	5	80387639	84252180	6699	5	80388596	81274512
6656	5	80387639	84253030	6700	5	80388596	81763618
6657	5	80387639	84254208	6701	5	80388596	81797217
6658	5	80387639	84314930	6702	5	80388596	81800186
6659	5	80387639	84340523	6703	5	80388596	81806213
6660	5	80387639	84516340	6704	5	80388596	81854583
6661	5	80387639	84706916	6705	5	80388596	81859374
6662	5	80387639	84799488	6706	5	80388596	81861368
6663	5	80387639	84801081	6707	5	80388596	81863686
6664	5	80387639	84824103	6708	5	80388596	81916850
6665	5	80387639	84824203	6709	5	80388596	81954891
6666	5	80387639	84824816	6710	5	80388596	81985250
6667	5	80387639	84825422	6711	5	80388596	82083752
6668	5	80387639	84825763	6712	5	80388596	82101253
6669	5	80387639	84825942	6713	5	80388596	82143124
6670	5	80387639	84843411	6714	5	80388596	82236318
6671	5	80387639	84936441	6715	5	80388596	82325587
6672	5	80387639	84936493	6716	5	80388596	82427210
6673	5	80387639	84943705	6717	5	80388596	82431853
6674	5	80387639	169454950	6718	5	80388596	82446714
6675	5	80387639	181522829	6719	5	80388596	82446794
6676	5	80387639	204759879	6720	5	80388596	82551111
6677	5	80387639	209874191	6721	5	80388596	82552090
6678	5	80388596	80389787	6722	5	80388596	82555641
6679	5	80388596	80411639	6723	5	80388596	82555670
6680	5	80388596	80446855	6724	5	80388596	82556511
6681	5	80388596	80492790	6725	5	80388596	82559047
6682	5	80388596	80670554	6726	5	80388596	82561535
6683	5	80388596	80674679	6727	5	80388596	82610100
6684	5	80388596	80720509	6728	5	80388596	82676822
6685	5	80388596	80800856	6729	5	80388596	82676901
6686	5	80388596	80804587	6730	5	80388596	82883691
6687	5	80388596	80807409	6731	5	80388596	82954942
6688	5	80388596	80835734	6732	5	80388596	82971688
6689	5	80388596	80971764	6733	5	80388596	83023965
6690	5	80388596	80972258	6734	5	80388596	83094205
6691	5	80388596	80974450	6735	5	80388596	83146355
6692	5	80388596	81047638	6736	5	80388596	83280630
6693	5	80388596	81082921	6737	5	80388596	83281412
6694	5	80388596	81157909	6738	5	80388596	83400242
6695	5	80388596	81265937	6739	5	80388596	83405797
6696	5	80388596	81265937	6740	5	80388596	83437132
6697	5	80388596	81267485	6741	5	80388596	83522252
6698	5	80388596	81267499	6742	5	80388596	83560095

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
6743	5	80388596	83560204	6787	5	80411337	80674679
6744	5	80388596	83572400	6788	5	80411337	80720509
6745	5	80388596	83607661	6789	5	80411337	80800856
6746	5	80388596	83745342	6790	5	80411337	80804587
6747	5	80388596	83861275	6791	5	80411337	80807409
6748	5	80388596	83861633	6792	5	80411337	80835734
6749	5	80388596	83865653	6793	5	80411337	80971764
6750	5	80388596	83865914	6794	5	80411337	80972258
6751	5	80388596	83865920	6795	5	80411337	80974450
6752	5	80388596	83868010	6796	5	80411337	81047638
6753	5	80388596	84019752	6797	5	80411337	81082921
6754	5	80388596	84065912	6798	5	80411337	81157909
6755	5	80388596	84086632	6799	5	80411337	81265937
6756	5	80388596	84089603	6800	5	80411337	81265937
6757	5	80388596	84104814	6801	5	80411337	81267485
6758	5	80388596	84105175	6802	5	80411337	81267499
6759	5	80388596	84251635	6803	5	80411337	81274512
6760	5	80388596	84252180	6804	5	80411337	81763618
6761	5	80388596	84253030	6805	5	80411337	81797217
6762	5	80388596	84254208	6806	5	80411337	81800186
6763	5	80388596	84314930	6807	5	80411337	81806213
6764	5	80388596	84340523	6808	5	80411337	81854583
6765	5	80388596	84516340	6809	5	80411337	81859374
6766	5	80388596	84706916	6810	5	80411337	81861368
6767	5	80388596	84799488	6811	5	80411337	81863686
6768	5	80388596	84801081	6812	5	80411337	81916850
6769	5	80388596	84824103	6813	5	80411337	81954891
6770	5	80388596	84824203	6814	5	80411337	81985250
6771	5	80388596	84824816	6815	5	80411337	82083752
6772	5	80388596	84825422	6816	5	80411337	82101253
6773	5	80388596	84825763	6817	5	80411337	82143124
6774	5	80388596	84825942	6818	5	80411337	82236318
6775	5	80388596	84843411	6819	5	80411337	82325587
6776	5	80388596	84936441	6820	5	80411337	82427210
6777	5	80388596	84936493	6821	5	80411337	82431853
6778	5	80388596	84943705	6822	5	80411337	82446714
6779	5	80388596	169454950	6823	5	80411337	82446794
6780	5	80388596	181522829	6824	5	80411337	82551111
6781	5	80388596	204759879	6825	5	80411337	82552090
6782	5	80388596	209874191	6826	5	80411337	82555641
6783	5	80411337	80411639	6827	5	80411337	82555670
6784	5	80411337	80446855	6828	5	80411337	82556511
6785	5	80411337	80492790	6829	5	80411337	82559047
6786	5	80411337	80670554	6830	5	80411337	82561535

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
6831	5	80411337	82610100	6875	5	80411337	84824816
6832	5	80411337	82676822	6876	5	80411337	84825422
6833	5	80411337	82676901	6877	5	80411337	84825763
6834	5	80411337	82883691	6878	5	80411337	84825942
6835	5	80411337	82954942	6879	5	80411337	84843411
6836	5	80411337	82971688	6880	5	80411337	84936441
6837	5	80411337	83023965	6881	5	80411337	84936493
6838	5	80411337	83094205	6882	5	80411337	84943705
6839	5	80411337	83146355	6883	5	80411337	169454950
6840	5	80411337	83280630	6884	5	80411337	181522829
6841	5	80411337	83281412	6885	5	80411337	204759879
6842	5	80411337	83400242	6886	5	80411337	209874191
6843	5	80411337	83405797	6887	5	80446281	80446855
6844	5	80411337	83437132	6888	5	80446281	80492790
6845	5	80411337	83522252	6889	5	80446281	80670554
6846	5	80411337	83560095	6890	5	80446281	80674679
6847	5	80411337	83560204	6891	5	80446281	80720509
6848	5	80411337	83572400	6892	5	80446281	80800856
6849	5	80411337	83607661	6893	5	80446281	80804587
6850	5	80411337	83745342	6894	5	80446281	80807409
6851	5	80411337	83861275	6895	5	80446281	80835734
6852	5	80411337	83861633	6896	5	80446281	80971764
6853	5	80411337	83865653	6897	5	80446281	80972258
6854	5	80411337	83865914	6898	5	80446281	80974450
6855	5	80411337	83865920	6899	5	80446281	81047638
6856	5	80411337	83868010	6900	5	80446281	81082921
6857	5	80411337	84019752	6901	5	80446281	81157909
6858	5	80411337	84065912	6902	5	80446281	81265937
6859	5	80411337	84086632	6903	5	80446281	81265937
6860	5	80411337	84089603	6904	5	80446281	81267485
6861	5	80411337	84104814	6905	5	80446281	81267499
6862	5	80411337	84105175	6906	5	80446281	81274512
6863	5	80411337	84251635	6907	5	80446281	81763618
6864	5	80411337	84252180	6908	5	80446281	81797217
6865	5	80411337	84253030	6909	5	80446281	81800186
6866	5	80411337	84254208	6910	5	80446281	81806213
6867	5	80411337	84314930	6911	5	80446281	81854583
6868	5	80411337	84340523	6912	5	80446281	81859374
6869	5	80411337	84516340	6913	5	80446281	81861368
6870	5	80411337	84706916	6914	5	80446281	81863686
6871	5	80411337	84799488	6915	5	80446281	81916850
6872	5	80411337	84801081	6916	5	80446281	81954891
6873	5	80411337	84824103	6917	5	80446281	81985250
6874	5	80411337	84824203	6918	5	80446281	82083752

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
6919	5	80446281	82101253	6963	5	80446281	84089603
6920	5	80446281	82143124	6964	5	80446281	84104814
6921	5	80446281	82236318	6965	5	80446281	84105175
6922	5	80446281	82325587	6966	5	80446281	84251635
6923	5	80446281	82427210	6967	5	80446281	84252180
6924	5	80446281	82431853	6968	5	80446281	84253030
6925	5	80446281	82446714	6969	5	80446281	84254208
6926	5	80446281	82446794	6970	5	80446281	84314930
6927	5	80446281	82551111	6971	5	80446281	84340523
6928	5	80446281	82552090	6972	5	80446281	84516340
6929	5	80446281	82555641	6973	5	80446281	84706916
6930	5	80446281	82555670	6974	5	80446281	84799488
6931	5	80446281	82556511	6975	5	80446281	84801081
6932	5	80446281	82559047	6976	5	80446281	84824103
6933	5	80446281	82561535	6977	5	80446281	84824203
6934	5	80446281	82610100	6978	5	80446281	84824816
6935	5	80446281	82676822	6979	5	80446281	84825422
6936	5	80446281	82676901	6980	5	80446281	84825763
6937	5	80446281	82883691	6981	5	80446281	84825942
6938	5	80446281	82954942	6982	5	80446281	84843411
6939	5	80446281	82971688	6983	5	80446281	84936441
6940	5	80446281	83023965	6984	5	80446281	84936493
6941	5	80446281	83094205	6985	5	80446281	84943705
6942	5	80446281	83145355	6986	5	80446281	169454950
6943	5	80446281	83280630	6987	5	80446281	181522829
6944	5	80446281	83281412	6988	5	80446281	204759879
6945	5	80446281	83400242	6989	5	80446281	209874191
6946	5	80446281	83405797	6990	5	80491807	80492790
6947	5	80446281	83437132	6991	5	80491807	80670554
6948	5	80446281	83522252	6992	5	80491807	80674679
6949	5	80446281	83560095	6993	5	80491807	80720509
6950	5	80446281	83560204	6994	5	80491807	80800856
6951	5	80446281	83572400	6995	5	80491807	80804587
6952	5	80446281	83607661	6996	5	80491807	80807409
6953	5	80446281	83745342	6997	5	80491807	80835734
6954	5	80446281	83861275	6998	5	80491807	80971764
6955	5	80446281	83861633	6999	5	80491807	80972258
6956	5	80446281	83865653	7000	5	80491807	80974450
6957	5	80446281	83865914	7001	5	80491807	81047638
6958	5	80446281	83865920	7002	5	80491807	81082921
6959	5	80446281	83868010	7003	5	80491807	81157909
6960	5	80446281	84019752	7004	5	80491807	81265937
6961	5	80446281	84065912	7005	5	80491807	81265937
6962	5	80446281	84086632	7006	5	80491807	81267485

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
7007	5	80491807	81267499	7051	5	80491807	83560095
7008	5	80491807	81274512	7052	5	80491807	83560204
7009	5	80491807	81763618	7053	5	80491807	83572400
7010	5	80491807	81797217	7054	5	80491807	83607661
7011	5	80491807	81800186	7055	5	80491807	83745342
7012	5	80491807	81806213	7056	5	80491807	83861275
7013	5	80491807	81854583	7057	5	80491807	83861633
7014	5	80491807	81859374	7058	5	80491807	83865653
7015	5	80491807	81861368	7059	5	80491807	83865914
7016	5	80491807	81863686	7060	5	80491807	83865920
7017	5	80491807	81916850	7061	5	80491807	83868010
7018	5	80491807	81954891	7062	5	80491807	84019752
7019	5	80491807	81985250	7063	5	80491807	84065912
7020	5	80491807	82083752	7064	5	80491807	84086632
7021	5	80491807	82101253	7065	5	80491807	84089603
7022	5	80491807	82143124	7066	5	80491807	84104814
7023	5	80491807	82236318	7067	5	80491807	84105175
7024	5	80491807	82325587	7068	5	80491807	84251635
7025	5	80491807	82427210	7069	5	80491807	84252180
7026	5	80491807	82431853	7070	5	80491807	84253030
7027	5	80491807	82446714	7071	5	80491807	84254208
7028	5	80491807	82446794	7072	5	80491807	84314930
7029	5	80491807	82551111	7073	5	80491807	84340523
7030	5	80491807	82552090	7074	5	80491807	84516340
7031	5	80491807	82555641	7075	5	80491807	84706916
7032	5	80491807	82555670	7076	5	80491807	84799488
7033	5	80491807	82556511	7077	5	80491807	84801081
7034	5	80491807	82559047	7078	5	80491807	84824103
7035	5	80491807	82561535	7079	5	80491807	84824203
7036	5	80491807	82610100	7080	5	80491807	84824816
7037	5	80491807	82676822	7081	5	80491807	84825422
7038	5	80491807	82676901	7082	5	80491807	84825763
7039	5	80491807	82883691	7083	5	80491807	84825942
7040	5	80491807	82954942	7084	5	80491807	84843411
7041	5	80491807	82971688	7085	5	80491807	84936441
7042	5	80491807	83023965	7086	5	80491807	84936493
7043	5	80491807	83094205	7087	5	80491807	84943705
7044	5	80491807	83146355	7088	5	80491807	169454950
7045	5	80491807	83280630	7089	5	80491807	181522829
7046	5	80491807	83281412	7090	5	80491807	204759879
7047	5	80491807	83400242	7091	5	80491807	209874191
7048	5	80491807	83405797	7092	5	80669160	80670554
7049	5	80491807	83437132	7093	5	80669160	80674679
7050	5	80491807	83522252	7094	5	80669160	80720509

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
7095	5	80669160	80800856	7139	5	80669160	82676901
7096	5	80669160	80804587	7140	5	80669160	82883691
7097	5	80669160	80807409	7141	5	80669160	82954942
7098	5	80669160	80835734	7142	5	80669160	82971688
7099	5	80669160	80971764	7143	5	80669160	83023965
7100	5	80669160	80972258	7144	5	80669160	83094205
7101	5	80669160	80974450	7145	5	80669160	83146355
7102	5	80669160	81047638	7146	5	80669160	83280630
7103	5	80669160	81082921	7147	5	80669160	83281412
7104	5	80669160	81157909	7148	5	80669160	83400242
7105	5	80669160	81265937	7149	5	80669160	83405797
7106	5	80669160	81265937	7150	5	80669160	83437132
7107	5	80669160	81267485	7151	5	80669160	83522252
7108	5	80669160	81267499	7152	5	80669160	83560095
7109	5	80669160	81274512	7153	5	80669160	83560204
7110	5	80669160	81763618	7154	5	80669160	83572400
7111	5	80669160	81797217	7155	5	80669160	83607661
7112	5	80669160	81800186	7156	5	80669160	83745342
7113	5	80669160	81806213	7157	5	80669160	83861275
7114	5	80669160	81854583	7158	5	80669160	83861633
7115	5	80669160	81859374	7159	5	80669160	83865653
7116	5	80669160	81861368	7160	5	80669160	83865914
7117	5	80669160	81863686	7161	5	80669160	83865920
7118	5	80669160	81916850	7162	5	80669160	83868010
7119	5	80669160	81954891	7163	5	80669160	84019752
7120	5	80669160	81985250	7164	5	80669160	84065912
7121	5	80669160	82083752	7165	5	80669160	84086632
7122	5	80669160	82101253	7166	5	80669160	84089603
7123	5	80669160	82143124	7167	5	80669160	84104814
7124	5	80669160	82236518	7168	5	80669160	84105175
7125	5	80669160	82325587	7169	5	80669160	84251635
7126	5	80669160	82427210	7170	5	80669160	84252180
7127	5	80669160	82431853	7171	5	80669160	84253030
7128	5	80669160	82446714	7172	5	80669160	84254208
7129	5	80669160	82446794	7173	5	80669160	84314930
7130	5	80669160	82551111	7174	5	80669160	84340523
7131	5	80669160	82552090	7175	5	80669160	84516340
7132	5	80669160	82555641	7176	5	80669160	84706916
7133	5	80669160	82555670	7177	5	80669160	84799488
7134	5	80669160	82556511	7178	5	80669160	84801081
7135	5	80669160	82559047	7179	5	80669160	84824103
7136	5	80669160	82561535	7180	5	80669160	84824203
7137	5	80669160	82610100	7181	5	80669160	84824816
7138	5	80669160	82676822	7182	5	80669160	84825422

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
7183	5	80669160	84825763	7227	5	80715081	82446714
7184	5	80669160	84825942	7228	5	80715081	82446794
7185	5	80669160	84843411	7229	5	80715081	82551111
7186	5	80669160	84936441	7230	5	80715081	82552090
7187	5	80669160	84936493	7231	5	80715081	82555641
7188	5	80669160	84943705	7232	5	80715081	82555670
7189	5	80669160	169454950	7233	5	80715081	825556511
7190	5	80669160	181522829	7234	5	80715081	82559047
7191	5	80669160	204759879	7235	5	80715081	82561535
7192	5	80669160	209874191	7236	5	80715081	82610100
7193	5	80715081	80720509	7237	5	80715081	82676822
7194	5	80715081	80800856	7238	5	80715081	82676901
7195	5	80715081	80804587	7239	5	80715081	82883691
7196	5	80715081	80807409	7240	5	80715081	82954942
7197	5	80715081	80835734	7241	5	80715081	82971688
7198	5	80715081	80971764	7242	5	80715081	83023965
7199	5	80715081	80972258	7243	5	80715081	83094205
7200	5	80715081	80974450	7244	5	80715081	83146355
7201	5	80715081	81047638	7245	5	80715081	83280630
7202	5	80715081	81082921	7246	5	80715081	83281412
7203	5	80715081	81157909	7247	5	80715081	83400242
7204	5	80715081	81265937	7248	5	80715081	83405797
7205	5	80715081	81265937	7249	5	80715081	83437132
7206	5	80715081	81267485	7250	5	80715081	83522252
7207	5	80715081	81267499	7251	5	80715081	83560095
7208	5	80715081	81274512	7252	5	80715081	83560204
7209	5	80715081	81763618	7253	5	80715081	83572400
7210	5	80715081	81797217	7254	5	80715081	83607661
7211	5	80715081	81800186	7255	5	80715081	83745342
7212	5	80715081	81806213	7256	5	80715081	83861275
7213	5	80715081	81854583	7257	5	80715081	83861633
7214	5	80715081	81859374	7258	5	80715081	83865653
7215	5	80715081	81861368	7259	5	80715081	83865914
7216	5	80715081	81863686	7260	5	80715081	83865920
7217	5	80715081	81916850	7261	5	80715081	83868010
7218	5	80715081	81954891	7262	5	80715081	84019752
7219	5	80715081	81985250	7263	5	80715081	84065912
7220	5	80715081	82083752	7264	5	80715081	84086632
7221	5	80715081	82101253	7265	5	80715081	84089603
7222	5	80715081	82143124	7266	5	80715081	84104814
7223	5	80715081	82236318	7267	5	80715081	84105175
7224	5	80715081	82325587	7268	5	80715081	84251635
7225	5	80715081	82427210	7269	5	80715081	84252180
7226	5	80715081	82431853	7270	5	80715081	84253030

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
7271	5	80715081	84254208	7315	5	80795990	81916850
7272	5	80715081	84314930	7316	5	80795990	81954891
7273	5	80715081	84340523	7317	5	80795990	81985250
7274	5	80715081	84516340	7318	5	80795990	82083752
7275	5	80715081	84706916	7319	5	80795990	82101253
7276	5	80715081	84799488	7320	5	80795990	82143124
7277	5	80715081	84801081	7321	5	80795990	82236318
7278	5	80715081	84824103	7322	5	80795990	82325587
7279	5	80715081	84824203	7323	5	80795990	82427210
7280	5	80715081	84824816	7324	5	80795990	82431853
7281	5	80715081	84825422	7325	5	80795990	82446714
7282	5	80715081	84825763	7326	5	80795990	82446794
7283	5	80715081	84825942	7327	5	80795990	82551111
7284	5	80715081	84843411	7328	5	80795990	82552090
7285	5	80715081	84936441	7329	5	80795990	82555641
7286	5	80715081	84936493	7330	5	80795990	82555670
7287	5	80715081	84943705	7331	5	80795990	82556511
7288	5	80715081	169454950	7332	5	80795990	82559047
7289	5	80715081	181522829	7333	5	80795990	82561535
7290	5	80715081	204759879	7334	5	80795990	82610100
7291	5	80715081	209874191	7335	5	80795990	82676822
7292	5	80795990	80800856	7336	5	80795990	82676901
7293	5	80795990	80804587	7337	5	80795990	82883691
7294	5	80795990	80807409	7338	5	80795990	82954942
7295	5	80795990	80835734	7339	5	80795990	82971688
7296	5	80795990	80971764	7340	5	80795990	83023965
7297	5	80795990	80972258	7341	5	80795990	83094205
7298	5	80795990	80974450	7342	5	80795990	83146355
7299	5	80795990	81047638	7343	5	80795990	83280630
7300	5	80795990	81082921	7344	5	80795990	83281412
7301	5	80795990	81157909	7345	5	80795990	83400242
7302	5	80795990	81265937	7346	5	80795990	83405797
7303	5	80795990	81265937	7347	5	80795990	83437132
7304	5	80795990	81267485	7348	5	80795990	83522252
7305	5	80795990	81267499	7349	5	80795990	83560095
7306	5	80795990	81274512	7350	5	80795990	83560204
7307	5	80795990	81763618	7351	5	80795990	83572400
7308	5	80795990	81797217	7352	5	80795990	83607661
7309	5	80795990	81800186	7353	5	80795990	83745342
7310	5	80795990	81806213	7354	5	80795990	83861275
7311	5	80795990	81854583	7355	5	80795990	83861633
7312	5	80795990	81859374	7356	5	80795990	83865653
7313	5	80795990	81861368	7357	5	80795990	83865914
7314	5	80795990	81863686	7358	5	80795990	83865920

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
7359	5	80795990	83868010	7403	5	80803727	81274512
7360	5	80795990	84019752	7404	5	80803727	81763618
7361	5	80795990	84065912	7405	5	80803727	81797217
7362	5	80795990	84086632	7406	5	80803727	81800186
7363	5	80795990	84089603	7407	5	80803727	81806213
7364	5	80795990	84104814	7408	5	80803727	81854583
7365	5	80795990	84105175	7409	5	80803727	81859374
7366	5	80795990	84251635	7410	5	80803727	81861368
7367	5	80795990	84252180	7411	5	80803727	81863686
7368	5	80795990	84253030	7412	5	80803727	81916850
7369	5	80795990	84254208	7413	5	80803727	81954891
7370	5	80795990	84314930	7414	5	80803727	81985250
7371	5	80795990	84340523	7415	5	80803727	82083752
7372	5	80795990	84516340	7416	5	80803727	82101253
7373	5	80795990	84706916	7417	5	80803727	82143124
7374	5	80795990	84799488	7418	5	80803727	82236318
7375	5	80795990	84801081	7419	5	80803727	82325587
7376	5	80795990	84824103	7420	5	80803727	82427210
7377	5	80795990	84824203	7421	5	80803727	82431853
7378	5	80795990	84824816	7422	5	80803727	82446714
7379	5	80795990	84825422	7423	5	80803727	82446794
7380	5	80795990	84825763	7424	5	80803727	82551111
7381	5	80795990	84825942	7425	5	80803727	82552090
7382	5	80795990	84843411	7426	5	80803727	82555641
7383	5	80795990	84936441	7427	5	80803727	82555670
7384	5	80795990	84936493	7428	5	80803727	82556511
7385	5	80795990	84943705	7429	5	80803727	82559047
7386	5	80795990	169454950	7430	5	80803727	82561535
7387	5	80795990	181522829	7431	5	80803727	82610100
7388	5	80795990	204759879	7432	5	80803727	82676822
7389	5	80795990	209874191	7433	5	80803727	82676901
7390	5	80803727	80804587	7434	5	80803727	82883691
7391	5	80803727	80807409	7435	5	80803727	82954942
7392	5	80803727	80835734	7436	5	80803727	82971688
7393	5	80803727	80971764	7437	5	80803727	83023965
7394	5	80803727	80972258	7438	5	80803727	83094205
7395	5	80803727	80974450	7439	5	80803727	83146355
7396	5	80803727	81047638	7440	5	80803727	83280630
7397	5	80803727	81082921	7441	5	80803727	83281412
7398	5	80803727	81157909	7442	5	80803727	83400242
7399	5	80803727	81265937	7443	5	80803727	83405797
7400	5	80803727	81265937	7444	5	80803727	83437132
7401	5	80803727	81267485	7445	5	80803727	83522252
7402	5	80803727	81267499	7446	5	80803727	83560095

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
7447	5	80803727	83560204	7491	5	80804587	81047638
7448	5	80803727	83572400	7492	5	80804587	81082921
7449	5	80803727	83607661	7493	5	80804587	81157909
7450	5	80803727	83745342	7494	5	80804587	81265937
7451	5	80803727	83861275	7495	5	80804587	81265937
7452	5	80803727	83861633	7496	5	80804587	81267485
7453	5	80803727	83865653	7497	5	80804587	81267499
7454	5	80803727	83865914	7498	5	80804587	81274512
7455	5	80803727	83865920	7499	5	80804587	81763618
7456	5	80803727	83868010	7500	5	80804587	81797217
7457	5	80803727	84019752	7501	5	80804587	81800186
7458	5	80803727	84065912	7502	5	80804587	81806213
7459	5	80803727	84086632	7503	5	80804587	81854583
7460	5	80803727	84089603	7504	5	80804587	81859374
7461	5	80803727	84104814	7505	5	80804587	81861368
7462	5	80803727	84105175	7506	5	80804587	81863686
7463	5	80803727	84251635	7507	5	80804587	81916850
7464	5	80803727	84252180	7508	5	80804587	81954891
7465	5	80803727	84253030	7509	5	80804587	81985250
7466	5	80803727	84254208	7510	5	80804587	82083752
7467	5	80803727	84314930	7511	5	80804587	82101253
7468	5	80803727	84340523	7512	5	80804587	82143124
7469	5	80803727	84516340	7513	5	80804587	82236318
7470	5	80803727	84706916	7514	5	80804587	82325587
7471	5	80803727	84799488	7515	5	80804587	82427210
7472	5	80803727	84801081	7516	5	80804587	82431853
7473	5	80803727	84824103	7517	5	80804587	82446714
7474	5	80803727	84824203	7518	5	80804587	82446794
7475	5	80803727	84824816	7519	5	80804587	82551111
7476	5	80803727	84825422	7520	5	80804587	82552090
7477	5	80803727	84825763	7521	5	80804587	82555641
7478	5	80803727	84825942	7522	5	80804587	82555670
7479	5	80803727	84843411	7523	5	80804587	82556511
7480	5	80803727	84936441	7524	5	80804587	82559047
7481	5	80803727	84936493	7525	5	80804587	82561535
7482	5	80803727	84943705	7526	5	80804587	82610100
7483	5	80803727	169454950	7527	5	80804587	82676822
7484	5	80803727	181522829	7528	5	80804587	82676901
7485	5	80803727	204759879	7529	5	80804587	82883691
7486	5	80803727	209874191	7530	5	80804587	82954942
7487	5	80804587	80835734	7531	5	80804587	82971688
7488	5	80804587	80971764	7532	5	80804587	83023965
7489	5	80804587	80972258	7533	5	80804587	83094205
7490	5	80804587	80974450	7534	5	80804587	83146355

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
7535	5	80804587	83280630	7579	5	80804587	181522829
7536	5	80804587	83281412	7580	5	80804587	204759879
7537	5	80804587	83400242	7581	5	80804587	209874191
7538	5	80804587	83405797	7582	5	80828457	80835734
7539	5	80804587	83437132	7583	5	80828457	80971764
7540	5	80804587	83522252	7584	5	80828457	80972258
7541	5	80804587	83560095	7585	5	80828457	80974450
7542	5	80804587	83560204	7586	5	80828457	81047638
7543	5	80804587	83572400	7587	5	80828457	81082921
7544	5	80804587	83607661	7588	5	80828457	81157909
7545	5	80804587	83745342	7589	5	80828457	81265937
7546	5	80804587	83861275	7590	5	80828457	81265937
7547	5	80804587	83861633	7591	5	80828457	81267485
7548	5	80804587	83865653	7592	5	80828457	81267499
7549	5	80804587	83865914	7593	5	80828457	81274512
7550	5	80804587	83865920	7594	5	80828457	81763618
7551	5	80804587	83868010	7595	5	80828457	81797217
7552	5	80804587	84019752	7596	5	80828457	81800186
7553	5	80804587	84065912	7597	5	80828457	81806213
7554	5	80804587	84086632	7598	5	80828457	81854583
7555	5	80804587	84089603	7599	5	80828457	81859374
7556	5	80804587	84104814	7600	5	80828457	81861368
7557	5	80804587	84105175	7601	5	80828457	81863686
7558	5	80804587	84251635	7602	5	80828457	81916850
7559	5	80804587	84252180	7603	5	80828457	81954891
7560	5	80804587	84253030	7604	5	80828457	81985250
7561	5	80804587	84254208	7605	5	80828457	82083752
7562	5	80804587	84314930	7606	5	80828457	82101253
7563	5	80804587	84340523	7607	5	80828457	82143124
7564	5	80804587	84516340	7608	5	80828457	82236318
7565	5	80804587	84706916	7609	5	80828457	82325587
7566	5	80804587	84799488	7610	5	80828457	82427210
7567	5	80804587	84801081	7611	5	80828457	82431853
7568	5	80804587	84824103	7612	5	80828457	82446714
7569	5	80804587	84824203	7613	5	80828457	82446794
7570	5	80804587	84824816	7614	5	80828457	82551111
7571	5	80804587	84825422	7615	5	80828457	82552090
7572	5	80804587	84825763	7616	5	80828457	82555641
7573	5	80804587	84825942	7617	5	80828457	82555670
7574	5	80804587	84843411	7618	5	80828457	82556511
7575	5	80804587	84936441	7619	5	80828457	82559047
7576	5	80804587	84936493	7620	5	80828457	82561535
7577	5	80804587	84943705	7621	5	80828457	82610100
7578	5	80804587	169454950	7622	5	80828457	82676822

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
7623	5	80828457	82676901	7667	5	80828457	84825763
7624	5	80828457	82883591	7668	5	80828457	84825942
7625	5	80828457	82954942	7669	5	80828457	84843411
7626	5	80828457	82971688	7670	5	80828457	84936441
7627	5	80828457	83023965	7671	5	80828457	84936493
7628	5	80828457	83094205	7672	5	80828457	84943705
7629	5	80828457	83146355	7673	5	80828457	169454950
7630	5	80828457	83280630	7674	5	80828457	181522829
7631	5	80828457	83281412	7675	5	80828457	204759879
7632	5	80828457	83400242	7676	5	80828457	209874191
7633	5	80828457	83405797	7677	5	80828945	80835734
7634	5	80828457	83437132	7678	5	80828945	80971764
7635	5	80828457	83522252	7679	5	80828945	80972258
7636	5	80828457	83560095	7680	5	80828945	80974450
7637	5	80828457	83560204	7681	5	80828945	81047638
7638	5	80828457	83572400	7682	5	80828945	81082921
7639	5	80828457	83607661	7683	5	80828945	81157909
7640	5	80828457	83745342	7684	5	80828945	81265937
7641	5	80828457	83861275	7685	5	80828945	81265937
7642	5	80828457	83861633	7686	5	80828945	81267485
7643	5	80828457	83865653	7687	5	80828945	81267499
7644	5	80828457	83865914	7688	5	80828945	81274512
7645	5	80828457	83865920	7689	5	80828945	81763618
7646	5	80828457	83868010	7690	5	80828945	81797217
7647	5	80828457	84019752	7691	5	80828945	81800186
7648	5	80828457	84065912	7692	5	80828945	81806213
7649	5	80828457	84086632	7693	5	80828945	81854583
7650	5	80828457	84089603	7694	5	80828945	81859374
7651	5	80828457	84104814	7695	5	80828945	81861368
7652	5	80828457	84105175	7696	5	80828945	81863686
7653	5	80828457	84251635	7697	5	80828945	81916850
7654	5	80828457	84252180	7698	5	80828945	81954891
7655	5	80828457	84253030	7699	5	80828945	81985250
7656	5	80828457	84254208	7700	5	80828945	82083752
7657	5	80828457	84314930	7701	5	80828945	82101253
7658	5	80828457	84340523	7702	5	80828945	82143124
7659	5	80828457	84516340	7703	5	80828945	82236318
7660	5	80828457	84706916	7704	5	80828945	82325587
7661	5	80828457	84799488	7705	5	80828945	82427210
7662	5	80828457	84801081	7706	5	80828945	82431853
7663	5	80828457	84824103	7707	5	80828945	82446714
7664	5	80828457	84824203	7708	5	80828945	82446794
7665	5	80828457	84824816	7709	5	80828945	82551111
7666	5	80828457	84825422	7710	5	80828945	82552090

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
7711	5	80828945	82555641	7755	5	80828945	84706916
7712	5	80828945	82555670	7756	5	80828945	84799488
7713	5	80828945	82556511	7757	5	80828945	84801081
7714	5	80828945	82559047	7758	5	80828945	84824103
7715	5	80828945	82561535	7759	5	80828945	84824203
7716	5	80828945	82610100	7760	5	80828945	84824816
7717	5	80828945	82676822	7761	5	80828945	84825422
7718	5	80828945	82676901	7762	5	80828945	84825763
7719	5	80828945	82883691	7763	5	80828945	84825942
7720	5	80828945	82954942	7764	5	80828945	84843411
7721	5	80828945	82971688	7765	5	80828945	84936441
7722	5	80828945	83023965	7766	5	80828945	84936493
7723	5	80828945	83094205	7767	5	80828945	84943705
7724	5	80828945	83146355	7768	5	80828945	169454950
7725	5	80828945	83280630	7769	5	80828945	181522829
7726	5	80828945	83281412	7770	5	80828945	204759879
7727	5	80828945	83400242	7771	5	80828945	209874191
7728	5	80828945	83405797	7772	5	80969412	80971764
7729	5	80828945	83437132	7773	5	80969412	80972258
7730	5	80828945	83522252	7774	5	80969412	80974450
7731	5	80828945	83560095	7775	5	80969412	81047638
7732	5	80828945	83560204	7776	5	80969412	81082921
7733	5	80828945	83572400	7777	5	80969412	81137909
7734	5	80828945	83607661	7778	5	80969412	81265937
7735	5	80828945	83745342	7779	5	80969412	81265937
7736	5	80828945	83861275	7780	5	80969412	81267485
7737	5	80828945	83861633	7781	5	80969412	81267499
7738	5	80828945	83865653	7782	5	80969412	81274512
7739	5	80828945	83865914	7783	5	80969412	81763618
7740	5	80828945	83865920	7784	5	80969412	81797217
7741	5	80828945	83868010	7785	5	80969412	81800186
7742	5	80828945	84019752	7786	5	80969412	81806213
7743	5	80828945	84065912	7787	5	80969412	81854583
7744	5	80828945	84086632	7788	5	80969412	81859374
7745	5	80828945	84089603	7789	5	80969412	81861368
7746	5	80828945	84104814	7790	5	80969412	81863686
7747	5	80828945	84105175	7791	5	80969412	81916850
7748	5	80828945	84251635	7792	5	80969412	81954891
7749	5	80828945	84252180	7793	5	80969412	81985250
7750	5	80828945	84253030	7794	5	80969412	82083752
7751	5	80828945	84254208	7795	5	80969412	82101253
7752	5	80828945	84314930	7796	5	80969412	82143124
7753	5	80828945	84340523	7797	5	80969412	82236318
7754	5	80828945	84516340	7798	5	80969412	82325587

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
7799	5	80969412	82427210	7843	5	80969412	84252180
7800	5	80969412	82431853	7844	5	80969412	84253030
7801	5	80969412	82446714	7845	5	80969412	84254208
7802	5	80969412	82446794	7846	5	80969412	84314930
7803	5	80969412	82551111	7847	5	80969412	84340523
7804	5	80969412	82552090	7848	5	80969412	84516340
7805	5	80969412	82555641	7849	5	80969412	84706916
7806	5	80969412	82555670	7850	5	80969412	84799488
7807	5	80969412	82556511	7851	5	80969412	84801081
7808	5	80969412	82559047	7852	5	80969412	84824103
7809	5	80969412	82561535	7853	5	80969412	84824203
7810	5	80969412	82610100	7854	5	80969412	84824816
7811	5	80969412	82676822	7855	5	80969412	84825422
7812	5	80969412	82676901	7856	5	80969412	84825763
7813	5	80969412	82883691	7857	5	80969412	84825942
7814	5	80969412	82954942	7858	5	80969412	84843411
7815	5	80969412	82971688	7859	5	80969412	84936441
7816	5	80969412	83023965	7860	5	80969412	84936493
7817	5	80969412	83094205	7861	5	80969412	84943705
7818	5	80969412	83146355	7862	5	80969412	169454950
7819	5	80969412	83280630	7863	5	80969412	181522829
7820	5	80969412	83281412	7864	5	80969412	204759879
7821	5	80969412	83400242	7865	5	80969412	209874191
7822	5	80969412	83405797	7866	5	80970381	80974450
7823	5	80969412	83437132	7867	5	80970381	81047638
7824	5	80969412	83522252	7868	5	80970381	81082921
7825	5	80969412	83560095	7869	5	80970381	81157909
7826	5	80969412	83560204	7870	5	80970381	81265937
7827	5	80969412	83572400	7871	5	80970381	81265937
7828	5	80969412	83607661	7872	5	80970381	81267485
7829	5	80969412	83745342	7873	5	80970381	81267499
7830	5	80969412	83861275	7874	5	80970381	81274512
7831	5	80969412	83861633	7875	5	80970381	81763618
7832	5	80969412	83865653	7876	5	80970381	81797217
7833	5	80969412	83865914	7877	5	80970381	81800186
7834	5	80969412	83865920	7878	5	80970381	81806213
7835	5	80969412	83868010	7879	5	80970381	81854583
7836	5	80969412	84019752	7880	5	80970381	81859374
7837	5	80969412	84063912	7881	5	80970381	81861368
7838	5	80969412	84086632	7882	5	80970381	81863686
7839	5	80969412	84089603	7883	5	80970381	81916850
7840	5	80969412	84104814	7884	5	80970381	81954891
7841	5	80969412	84105175	7885	5	80970381	81985250
7842	5	80969412	84251635	7886	5	80970381	82083752

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
7887	5	80970381	82101253	7931	5	80970381	84089603
7888	5	80970381	82143124	7932	5	80970381	84104814
7889	5	80970381	82236318	7933	5	80970381	84105175
7890	5	80970381	82325587	7934	5	80970381	84251635
7891	5	80970381	82427210	7935	5	80970381	84252180
7892	5	80970381	82431853	7936	5	80970381	84253030
7893	5	80970381	82446714	7937	5	80970381	84254208
7894	5	80970381	82446794	7938	5	80970381	84314930
7895	5	80970381	82551111	7939	5	80970381	84340523
7896	5	80970381	82552090	7940	5	80970381	84516340
7897	5	80970381	82555641	7941	5	80970381	84706916
7898	5	80970381	82555670	7942	5	80970381	84799488
7899	5	80970381	82556511	7943	5	80970381	84801081
7900	5	80970381	82559047	7944	5	80970381	84824103
7901	5	80970381	82561535	7945	5	80970381	84824203
7902	5	80970381	82610100	7946	5	80970381	84824816
7903	5	80970381	82676822	7947	5	80970381	84825422
7904	5	80970381	82676901	7948	5	80970381	84825763
7905	5	80970381	82883691	7949	5	80970381	84825942
7906	5	80970381	82954942	7950	5	80970381	84843411
7907	5	80970381	82971688	7951	5	80970381	84936441
7908	5	80970381	83023965	7952	5	80970381	84936493
7909	5	80970381	83094205	7953	5	80970381	84943705
7910	5	80970381	83146355	7954	5	80970381	169454950
7911	5	80970381	83280630	7955	5	80970381	181522829
7912	5	80970381	83281412	7956	5	80970381	204759879
7913	5	80970381	83400242	7957	5	80970381	209874191
7914	5	80970381	83405797	7958	5	80971764	81047638
7915	5	80970381	83437132	7959	5	80971764	81082921
7916	5	80970381	83522252	7960	5	80971764	81157909
7917	5	80970381	83560095	7961	5	80971764	81265937
7918	5	80970381	83560204	7962	5	80971764	81265937
7919	5	80970381	83572400	7963	5	80971764	81267485
7920	5	80970381	83607661	7964	5	80971764	81267499
7921	5	80970381	83745342	7965	5	80971764	81274512
7922	5	80970381	83861275	7966	5	80971764	81763618
7923	5	80970381	83861533	7967	5	80971764	81797217
7924	5	80970381	83865653	7968	5	80971764	81800186
7925	5	80970381	83865914	7969	5	80971764	81806213
7926	5	80970381	83865920	7970	5	80971764	81854583
7927	5	80970381	83868010	7971	5	80971764	81859374
7928	5	80970381	84019752	7972	5	80971764	81861368
7929	5	80970381	84065912	7973	5	80971764	81863686
7930	5	80970381	84086632	7974	5	80971764	81916850

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
7975	5	80971764	81954891	8019	5	80971764	84019752
7976	5	80971764	81985250	8020	5	80971764	84065912
7977	5	80971764	82083752	8021	5	80971764	84086632
7978	5	80971764	82101253	8022	5	80971764	84089603
7979	5	80971764	82143124	8023	5	80971764	84104814
7980	5	80971764	82236318	8024	5	80971764	84105175
7981	5	80971764	82325587	8025	5	80971764	84251635
7982	5	80971764	82427210	8026	5	80971764	84252180
7983	5	80971764	82431853	8027	5	80971764	84253030
7984	5	80971764	82446714	8028	5	80971764	84254208
7985	5	80971764	82446794	8029	5	80971764	84314930
7986	5	80971764	82551111	8030	5	80971764	84340523
7987	5	80971764	82552090	8031	5	80971764	84516340
7988	5	80971764	82555641	8032	5	80971764	84706916
7989	5	80971764	82555670	8033	5	80971764	84799488
7990	5	80971764	82556511	8034	5	80971764	84801081
7991	5	80971764	82559047	8035	5	80971764	84824103
7992	5	80971764	82561535	8036	5	80971764	84824203
7993	5	80971764	82610100	8037	5	80971764	84824816
7994	5	80971764	82676822	8038	5	80971764	84825422
7995	5	80971764	82676901	8039	5	80971764	84825763
7996	5	80971764	82883691	8040	5	80971764	84825942
7997	5	80971764	82954942	8041	5	80971764	84843411
7998	5	80971764	82971688	8042	5	80971764	84936441
7999	5	80971764	83023965	8043	5	80971764	84936493
8000	5	80971764	83094205	8044	5	80971764	84943705
8001	5	80971764	83146355	8045	5	80971764	169454950
8002	5	80971764	83280630	8046	5	80971764	181522829
8003	5	80971764	83281412	8047	5	80971764	204759879
8004	5	80971764	83400242	8048	5	80971764	209874191
8005	5	80971764	83405797	8049	5	81031951	81047638
8006	5	80971764	83437132	8050	5	81031951	81082921
8007	5	80971764	83522252	8051	5	81031951	81157909
8008	5	80971764	83560095	8052	5	81031951	81265937
8009	5	80971764	83560204	8053	5	81031951	81265937
8010	5	80971764	83572400	8054	5	81031951	81267485
8011	5	80971764	83607661	8055	5	81031951	81267499
8012	5	80971764	83745342	8056	5	81031951	81274512
8013	5	80971764	83861275	8057	5	81031951	81763618
8014	5	80971764	83861633	8058	5	81031951	81797217
8015	5	80971764	83865653	8059	5	81031951	81800186
8016	5	80971764	83865914	8060	5	81031951	81806213
8017	5	80971764	83865920	8061	5	81031951	81854583
8018	5	80971764	83868010	8062	5	81031951	81859374

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
8063	5	81031951	81861368	8107	5	81031951	83865914
8064	5	81031951	81863686	8108	5	81031951	83865920
8065	5	81031951	81916850	8109	5	81031951	83868010
8066	5	81031951	81954891	8110	5	81031951	84019752
8067	5	81031951	81985250	8111	5	81031951	84065912
8068	5	81031951	82083752	8112	5	81031951	84086632
8069	5	81031951	82101253	8113	5	81031951	84089603
8070	5	81031951	82143124	8114	5	81031951	84104814
8071	5	81031951	82236318	8115	5	81031951	84105175
8072	5	81031951	82325587	8116	5	81031951	84251635
8073	5	81031951	82427210	8117	5	81031951	84252180
8074	5	81031951	82431853	8118	5	81031951	84253030
8075	5	81031951	82446714	8119	5	81031951	84254208
8076	5	81031951	82446794	8120	5	81031951	84314930
8077	5	81031951	82551111	8121	5	81031951	84340523
8078	5	81031951	82552090	8122	5	81031951	84516340
8079	5	81031951	82555641	8123	5	81031951	84706916
8080	5	81031951	82555670	8124	5	81031951	84799488
8081	5	81031951	82556511	8125	5	81031951	84801081
8082	5	81031951	82559047	8126	5	81031951	84824103
8083	5	81031951	82561535	8127	5	81031951	84824203
8084	5	81031951	82610100	8128	5	81031951	84824816
8085	5	81031951	82676822	8129	5	81031951	84825422
8086	5	81031951	82676901	8130	5	81031951	84825763
8087	5	81031951	82883691	8131	5	81031951	84825942
8088	5	81031951	82954942	8132	5	81031951	84843411
8089	5	81031951	82971688	8133	5	81031951	84936441
8090	5	81031951	83023965	8134	5	81031951	84936493
8091	5	81031951	83094205	8135	5	81031951	84943705
8092	5	81031951	83146355	8136	5	81031951	169454950
8093	5	81031951	83280630	8137	5	81031951	181522829
8094	5	81031951	83281412	8138	5	81031951	204759879
8095	5	81031951	83400242	8139	5	81031951	209874191
8096	5	81031951	83405797	8140	5	81076870	81082921
8097	5	81031951	83437132	8141	5	81076870	81157909
8098	5	81031951	83522252	8142	5	81076870	81265937
8099	5	81031951	83560095	8143	5	81076870	81265937
8100	5	81031951	83560204	8144	5	81076870	81267485
8101	5	81031951	83572400	8145	5	81076870	81267499
8102	5	81031951	83607661	8146	5	81076870	81274512
8103	5	81031951	83745342	8147	5	81076870	81763618
8104	5	81031951	83861275	8148	5	81076870	81797217
8105	5	81031951	83861633	8149	5	81076870	81800186
8106	5	81031951	83865653	8150	5	81076870	81806213

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
8151	5	81076870	81854583	8195	5	81076870	83861633
8152	5	81076870	81859374	8196	5	81076870	83865653
8153	5	81076870	81861368	8197	5	81076870	83865914
8154	5	81076870	81863686	8198	5	81076870	83865920
8155	5	81076870	81916850	8199	5	81076870	83868010
8156	5	81076870	81954891	8200	5	81076870	84019752
8157	5	81076870	81985250	8201	5	81076870	84065912
8158	5	81076870	82083752	8202	5	81076870	84086632
8159	5	81076870	82101253	8203	5	81076870	84089603
8160	5	81076870	82143124	8204	5	81076870	84104814
8161	5	81076870	82236318	8205	5	81076870	84105175
8162	5	81076870	82325587	8206	5	81076870	84251635
8163	5	81076870	82427210	8207	5	81076870	84252180
8164	5	81076870	82431853	8208	5	81076870	84253030
8165	5	81076870	82446714	8209	5	81076870	84254208
8166	5	81076870	82446794	8210	5	81076870	84314930
8167	5	81076870	82551111	8211	5	81076870	84340523
8168	5	81076870	82552090	8212	5	81076870	84516340
8169	5	81076870	82555641	8213	5	81076870	84706916
8170	5	81076870	82555670	8214	5	81076870	84799488
8171	5	81076870	82556511	8215	5	81076870	84801081
8172	5	81076870	82559047	8216	5	81076870	84824103
8173	5	81076870	82561535	8217	5	81076870	84824203
8174	5	81076870	82610100	8218	5	81076870	84824816
8175	5	81076870	82676822	8219	5	81076870	84825422
8176	5	81076870	82676901	8220	5	81076870	84825763
8177	5	81076870	82883691	8221	5	81076870	84825942
8178	5	81076870	82954942	8222	5	81076870	84843411
8179	5	81076870	82971688	8223	5	81076870	84936441
8180	5	81076870	83023965	8224	5	81076870	84936493
8181	5	81076870	83094205	8225	5	81076870	84943705
8182	5	81076870	83146355	8226	5	81076870	169454950
8183	5	81076870	83280630	8227	5	81076870	181522829
8184	5	81076870	83281412	8228	5	81076870	204759879
8185	5	81076870	83400242	8229	5	81076870	209874191
8186	5	81076870	83405797	8230	5	81155197	81157909
8187	5	81076870	83437132	8231	5	81155197	81265937
8188	5	81076870	83522252	8232	5	81155197	81265937
8189	5	81076870	83560095	8233	5	81155197	81267485
8190	5	81076870	83560204	8234	5	81155197	81267499
8191	5	81076870	83572400	8235	5	81155197	81274512
8192	5	81076870	83607661	8236	5	81155197	81763618
8193	5	81076870	83745342	8237	5	81155197	81797217
8194	5	81076870	83861275	8238	5	81155197	81800186

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
8239	5	81155197	81806213	8283	5	81155197	83861275
8240	5	81155197	81854583	8284	5	81155197	83861633
8241	5	81155197	81859374	8285	5	81155197	83865653
8242	5	81155197	81861368	8286	5	81155197	83865914
8243	5	81155197	81863686	8287	5	81155197	83865920
8244	5	81155197	81916850	8288	5	81155197	83868010
8245	5	81155197	81954891	8289	5	81155197	84019752
8246	5	81155197	81985250	8290	5	81155197	84065912
8247	5	81155197	82083752	8291	5	81155197	84086632
8248	5	81155197	82101253	8292	5	81155197	84089603
8249	5	81155197	82143124	8293	5	81155197	84104814
8250	5	81155197	82236318	8294	5	81155197	84105175
8251	5	81155197	82325587	8295	5	81155197	84251635
8252	5	81155197	82427210	8296	5	81155197	84252180
8253	5	81155197	82431853	8297	5	81155197	84253030
8254	5	81155197	82446714	8298	5	81155197	84254208
8255	5	81155197	82446794	8299	5	81155197	84314930
8256	5	81155197	82551111	8300	5	81155197	84340523
8257	5	81155197	82552090	8301	5	81155197	84516340
8258	5	81155197	82555641	8302	5	81155197	84706916
8259	5	81155197	82555670	8303	5	81155197	84799488
8260	5	81155197	82556511	8304	5	81155197	84801081
8261	5	81155197	82559047	8305	5	81155197	84824103
8262	5	81155197	82561535	8306	5	81155197	84824203
8263	5	81155197	82610100	8307	5	81155197	84824816
8264	5	81155197	82676822	8308	5	81155197	84825422
8265	5	81155197	82676901	8309	5	81155197	84825762
8266	5	81155197	82883691	8310	5	81155197	84825942
8267	5	81155197	82954942	8311	5	81155197	84843411
8268	5	81155197	82971688	8312	5	81155197	84936441
8269	5	81155197	83023965	8313	5	81155197	84936493
8270	5	81155197	83094205	8314	5	81155197	84943705
8271	5	81155197	83146355	8315	5	81155197	169454950
8272	5	81155197	83280630	8316	5	81155197	181522829
8273	5	81155197	83281412	8317	5	81155197	204759879
8274	5	81155197	83400242	8318	5	81155197	209874191
8275	5	81155197	83405797	8319	5	81155255	81157909
8276	5	81155197	83437132	8320	5	81155255	81265937
8277	5	81155197	83522252	8321	5	81155255	81265937
8278	5	81155197	83560095	8322	5	81155255	81267485
8279	5	81155197	83560204	8323	5	81155255	81267499
8280	5	81155197	83572400	8324	5	81155255	81274512
8281	5	81155197	83607661	8325	5	81155255	81763618
8282	5	81155197	83745342	8326	5	81155255	81797217

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
8327	5	81155255	81800186	8371	5	81155255	83745342
8328	5	81155255	81806213	8372	5	81155255	83861275
8329	5	81155255	81854583	8373	5	81155255	83861633
8330	5	81155255	81859374	8374	5	81155255	83865653
8331	5	81155255	81861368	8375	5	81155255	83865914
8332	5	81155255	81863686	8376	5	81155255	83865920
8333	5	81155255	81916850	8377	5	81155255	83868010
8334	5	81155255	81954891	8378	5	81155255	84019752
8335	5	81155255	81985250	8379	5	81155255	84065912
8336	5	81155255	82083752	8380	5	81155255	84086632
8337	5	81155255	82101253	8381	5	81155255	84089603
8338	5	81155255	82143124	8382	5	81155255	84104814
8339	5	81155255	82236318	8383	5	81155255	84105175
8340	5	81155255	82325587	8384	5	81155255	84251635
8341	5	81155255	82427210	8385	5	81155255	84252180
8342	5	81155255	82431853	8386	5	81155255	84253030
8343	5	81155255	82446714	8387	5	81155255	84254208
8344	5	81155255	82446794	8388	5	81155255	84314930
8345	5	81155255	82551111	8389	5	81155255	84340523
8346	5	81155255	82552090	8390	5	81155255	84516340
8347	5	81155255	82555641	8391	5	81155255	84706916
8348	5	81155255	82555670	8392	5	81155255	84799488
8349	5	81155255	82556511	8393	5	81155255	84801081
8350	5	81155255	82559047	8394	5	81155255	84824103
8351	5	81155255	82561535	8395	5	81155255	84824203
8352	5	81155255	82610100	8396	5	81155255	84824816
8353	5	81155255	82676822	8397	5	81155255	84825422
8354	5	81155255	82676901	8398	5	81155255	84825763
8355	5	81155255	82883691	8399	5	81155255	84825942
8356	5	81155255	82954942	8400	5	81155255	84843411
8357	5	81155255	82971688	8401	5	81155255	84936441
8358	5	81155255	83023965	8402	5	81155255	84936493
8359	5	81155255	83094205	8403	5	81155255	84943705
8360	5	81155255	83146355	8404	5	81155255	169454950
8361	5	81155255	83280630	8405	5	81155255	181522829
8362	5	81155255	83281412	8406	5	81155255	204759879
8363	5	81155255	83400242	8407	5	81155255	209874191
8364	5	81155255	83405797	8408	5	81155675	81157909
8365	5	81155255	83437132	8409	5	81155675	81265937
8366	5	81155255	83522252	8410	5	81155675	81265937
8367	5	81155255	83560095	8411	5	81155675	81267485
8368	5	81155255	83560204	8412	5	81155675	81267499
8369	5	81155255	83572400	8413	5	81155675	81274512
8370	5	81155255	83607661	8414	5	81155675	81763618

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
8415	5	81155675	81797217	8459	5	81155675	83607661
8416	5	81155675	81800186	8460	5	81155675	83745342
8417	5	81155675	81806213	8461	5	81155675	83861275
8418	5	81155675	81854583	8462	5	81155675	83861633
8419	5	81155675	81859374	8463	5	81155675	83865653
8420	5	81155675	81861368	8464	5	81155675	83865914
8421	5	81155675	81863686	8465	5	81155675	83865920
8422	5	81155675	81916850	8466	5	81155675	83868010
8423	5	81155675	81954891	8467	5	81155675	84019752
8424	5	81155675	81985250	8468	5	81155675	84065912
8425	5	81155675	82083752	8469	5	81155675	84086632
8426	5	81155675	82101253	8470	5	81155675	84089603
8427	5	81155675	82143124	8471	5	81155675	84104814
8428	5	81155675	82236318	8472	5	81155675	84105175
8429	5	81155675	82325587	8473	5	81155675	84251635
8430	5	81155675	82427210	8474	5	81155675	84252180
8431	5	81155675	82431853	8475	5	81155675	84253030
8432	5	81155675	82446714	8476	5	81155675	84254208
8433	5	81155675	82446794	8477	5	81155675	84314930
8434	5	81155675	82551111	8478	5	81155675	84340523
8435	5	81155675	82552090	8479	5	81155675	84516340
8436	5	81155675	82555641	8480	5	81155675	84706916
8437	5	81155675	82555670	8481	5	81155675	84799488
8438	5	81155675	82556511	8482	5	81155675	84801081
8439	5	81155675	82559047	8483	5	81155675	84824103
8440	5	81155675	82561535	8484	5	81155675	84824203
8441	5	81155675	82610100	8485	5	81155675	84824816
8442	5	81155675	82676822	8486	5	81155675	84825422
8443	5	81155675	82676901	8487	5	81155675	84825763
8444	5	81155675	82883691	8488	5	81155675	84825942
8445	5	81155675	82954942	8489	5	81155675	84843411
8446	5	81155675	82971688	8490	5	81155675	84936441
8447	5	81155675	83023965	8491	5	81155675	84936493
8448	5	81155675	83094205	8492	5	81155675	84943705
8449	5	81155675	83146355	8493	5	81155675	169454950
8450	5	81155675	83280630	8494	5	81155675	181522829
8451	5	81155675	83281412	8495	5	81155675	204759879
8452	5	81155675	83400242	8496	5	81155675	209874191
8453	5	81155675	83405797	8497	5	81156713	81157909
8454	5	81155675	83437132	8498	5	81156713	81265937
8455	5	81155675	83522252	8499	5	81156713	81265937
8456	5	81155675	83560095	8500	5	81156713	81267485
8457	5	81155675	83560204	8501	5	81156713	81267499
8458	5	81155675	83572400	8502	5	81156713	81274512

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
8503	5	81156713	81763618	8547	5	81156713	83572400
8504	5	81156713	81797217	8548	5	81156713	83607661
8505	5	81156713	81800186	8549	5	81156713	83745342
8506	5	81156713	81806213	8550	5	81156713	83861275
8507	5	81156713	81854583	8551	5	81156713	83861633
8508	5	81156713	81859374	8552	5	81156713	83865653
8509	5	81156713	81861368	8553	5	81156713	83865914
8510	5	81156713	81863686	8554	5	81156713	83865920
8511	5	81156713	81916850	8555	5	81156713	83868010
8512	5	81156713	81954891	8556	5	81156713	84019752
8513	5	81156713	81985250	8557	5	81156713	84065912
8514	5	81156713	82083752	8558	5	81156713	84086632
8515	5	81156713	82101253	8559	5	81156713	84089603
8516	5	81156713	82143124	8560	5	81156713	84104814
8517	5	81156713	82236318	8561	5	81156713	84105175
8518	5	81156713	82325587	8562	5	81156713	84251635
8519	5	81156713	82427210	8563	5	81156713	84252180
8520	5	81156713	82431853	8564	5	81156713	84253030
8521	5	81156713	82446714	8565	5	81156713	84254208
8522	5	81156713	82446794	8566	5	81156713	84314930
8523	5	81156713	82551111	8567	5	81156713	84340523
8524	5	81156713	82552090	8568	5	81156713	84516340
8525	5	81156713	82555641	8569	5	81156713	84706916
8526	5	81156713	82555670	8570	5	81156713	84799488
8527	5	81156713	82556511	8571	5	81156713	84801081
8528	5	81156713	82559047	8572	5	81156713	84824103
8529	5	81156713	82561535	8573	5	81156713	84824203
8530	5	81156713	82610100	8574	5	81156713	84824816
8531	5	81156713	82676822	8575	5	81156713	84825422
8532	5	81156713	82676901	8576	5	81156713	84825763
8533	5	81156713	82883691	8577	5	81156713	84825942
8534	5	81156713	82954942	8578	5	81156713	84843411
8535	5	81156713	82971688	8579	5	81156713	84936441
8536	5	81156713	83023965	8580	5	81156713	84936493
8537	5	81156713	83094205	8581	5	81156713	84943705
8538	5	81156713	83146355	8582	5	81156713	169454950
8539	5	81156713	83280630	8583	5	81156713	181522829
8540	5	81156713	83281412	8584	5	81156713	204759879
8541	5	81156713	83400242	8585	5	81156713	209874191
8542	5	81156713	83405797	8586	5	81265211	81265937
8543	5	81156713	83437132	8587	5	81265211	81265937
8544	5	81156713	83522252	8588	5	81265211	81267485
8545	5	81156713	83560095	8589	5	81265211	81267499
8546	5	81156713	83560204	8590	5	81265211	81274512

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
8591	5	81265211	81763618	8635	5	81265211	83572400
8592	5	81265211	81797217	8636	5	81265211	83607661
8593	5	81265211	81800186	8637	5	81265211	83745342
8594	5	81265211	81806213	8638	5	81265211	83861275
8595	5	81265211	81854583	8639	5	81265211	83861633
8596	5	81265211	81859374	8640	5	81265211	83865653
8597	5	81265211	81861368	8641	5	81265211	83865914
8598	5	81265211	81863686	8642	5	81265211	83865920
8599	5	81265211	81916850	8643	5	81265211	83868010
8600	5	81265211	81954891	8644	5	81265211	84019752
8601	5	81265211	81985250	8645	5	81265211	84065912
8602	5	81265211	82083752	8646	5	81265211	84086632
8603	5	81265211	82101253	8647	5	81265211	84089603
8604	5	81265211	82143124	8648	5	81265211	84104814
8605	5	81265211	82236318	8649	5	81265211	84105175
8606	5	81265211	82325587	8650	5	81265211	84251635
8607	5	81265211	82427210	8651	5	81265211	84252180
8608	5	81265211	82431853	8652	5	81265211	84253030
8609	5	81265211	82446714	8653	5	81265211	84254208
8610	5	81265211	82446794	8654	5	81265211	84314930
8611	5	81265211	82551111	8655	5	81265211	84340523
8612	5	81265211	82552090	8656	5	81265211	84516340
8613	5	81265211	82555641	8657	5	81265211	84706916
8614	5	81265211	82555670	8658	5	81265211	84799488
8615	5	81265211	82556511	8659	5	81265211	84801081
8616	5	81265211	82559047	8660	5	81265211	84824103
8617	5	81265211	82561535	8661	5	81265211	84824203
8618	5	81265211	82610100	8662	5	81265211	84824816
8619	5	81265211	82676822	8663	5	81265211	84825422
8620	5	81265211	82676901	8664	5	81265211	84825763
8621	5	81265211	82883691	8665	5	81265211	84825942
8622	5	81265211	82954942	8666	5	81265211	84843411
8623	5	81265211	82971688	8667	5	81265211	84936441
8624	5	81265211	83023965	8668	5	81265211	84936493
8625	5	81265211	83094205	8669	5	81265211	84943705
8626	5	81265211	83146355	8670	5	81265211	169454950
8627	5	81265211	83280630	8671	5	81265211	181522829
8628	5	81265211	83281412	8672	5	81265211	204759879
8629	5	81265211	83400242	8673	5	81265211	209874191
8630	5	81265211	83405797	8674	5	81265354	81265937
8631	5	81265211	83437132	8675	5	81265354	81265937
8632	5	81265211	83522252	8676	5	81265354	81267485
8633	5	81265211	83560095	8677	5	81265354	81274512
8634	5	81265211	83560204	8678	5	81265354	81763618

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
8679	5	81265354	81797217	8723	5	81265354	83607661
8680	5	81265354	81800186	8724	5	81265354	83745342
8681	5	81265354	81806213	8725	5	81265354	83861275
8682	5	81265354	81854583	8726	5	81265354	83861633
8683	5	81265354	81859374	8727	5	81265354	83865653
8684	5	81265354	81861368	8728	5	81265354	83865914
8685	5	81265354	81863686	8729	5	81265354	83865920
8686	5	81265354	81916850	8730	5	81265354	83868010
8687	5	81265354	81954891	8731	5	81265354	84019752
8688	5	81265354	81985250	8732	5	81265354	84065912
8689	5	81265354	82083752	8733	5	81265354	84086632
8690	5	81265354	82101253	8734	5	81265354	84089603
8691	5	81265354	82143124	8735	5	81265354	84104814
8692	5	81265354	82236318	8736	5	81265354	84105175
8693	5	81265354	82325587	8737	5	81265354	84251635
8694	5	81265354	82427210	8738	5	81265354	84252180
8695	5	81265354	82431853	8739	5	81265354	84253030
8696	5	81265354	82446714	8740	5	81265354	84254208
8697	5	81265354	82446794	8741	5	81265354	84314930
8698	5	81265354	82551111	8742	5	81265354	84340523
8699	5	81265354	82552090	8743	5	81265354	84516340
8700	5	81265354	82555641	8744	5	81265354	84706916
8701	5	81265354	82555670	8745	5	81265354	84799488
8702	5	81265354	82556511	8746	5	81265354	84801081
8703	5	81265354	82559047	8747	5	81265354	84824103
8704	5	81265354	82561535	8748	5	81265354	84824203
8705	5	81265354	82610100	8749	5	81265354	84824816
8706	5	81265354	82676822	8750	5	81265354	84825422
8707	5	81265354	82676901	8751	5	81265354	84825763
8708	5	81265354	82883691	8752	5	81265354	84825942
8709	5	81265354	82954942	8753	5	81265354	84843411
8710	5	81265354	82971688	8754	5	81265354	84936441
8711	5	81265354	83023965	8755	5	81265354	84936493
8712	5	81265354	83094205	8756	5	81265354	84943705
8713	5	81265354	83146355	8757	5	81265354	169454950
8714	5	81265354	83280630	8758	5	81265354	181522829
8715	5	81265354	83281412	8759	5	81265354	204759879
8716	5	81265354	83400242	8760	5	81265354	209874191
8717	5	81265354	83405797	8761	5	81265937	81274512
8718	5	81265354	83437132	8762	5	81265937	81763618
8719	5	81265354	83522252	8763	5	81265937	81797217
8720	5	81265354	83560095	8764	5	81265937	81800186
8721	5	81265354	83560204	8765	5	81265937	81806213
8722	5	81265354	83572400	8766	5	81265937	81854583

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
8767	5	81265937	81859374	8811	5	81265937	83865653
8768	5	81265937	81861368	8812	5	81265937	83865914
8769	5	81265937	81863686	8813	5	81265937	83865920
8770	5	81265937	81916850	8814	5	81265937	83868010
8771	5	81265937	81954891	8815	5	81265937	84019752
8772	5	81265937	81985250	8816	5	81265937	84065912
8773	5	81265937	82083752	8817	5	81265937	84086632
8774	5	81265937	82101253	8818	5	81265937	84089603
8775	5	81265937	82143124	8819	5	81265937	84104814
8776	5	81265937	82236318	8820	5	81265937	84105175
8777	5	81265937	82325587	8821	5	81265937	84251635
8778	5	81265937	82427210	8822	5	81265937	84252180
8779	5	81265937	82431853	8823	5	81265937	84253030
8780	5	81265937	82446714	8824	5	81265937	84254208
8781	5	81265937	82446794	8825	5	81265937	84314930
8782	5	81265937	82551111	8826	5	81265937	84340523
8783	5	81265937	82552090	8827	5	81265937	84516340
8784	5	81265937	82555641	8828	5	81265937	84706916
8785	5	81265937	82555670	8829	5	81265937	84799488
8786	5	81265937	82556511	8830	5	81265937	84801081
8787	5	81265937	82559047	8831	5	81265937	84824103
8788	5	81265937	82561535	8832	5	81265937	84824203
8789	5	81265937	82610100	8833	5	81265937	84824816
8790	5	81265937	82676822	8834	5	81265937	84825422
8791	5	81265937	82676901	8835	5	81265937	84825763
8792	5	81265937	82883691	8836	5	81265937	84825942
8793	5	81265937	82954942	8837	5	81265937	84843411
8794	5	81265937	82971688	8838	5	81265937	84936441
8795	5	81265937	83023965	8839	5	81265937	84936493
8796	5	81265937	83094205	8840	5	81265937	84943705
8797	5	81265937	83146355	8841	5	81265937	169454950
8798	5	81265937	83280630	8842	5	81265937	181522829
8799	5	81265937	83281412	8843	5	81265937	204759879
8800	5	81265937	83400242	8844	5	81265937	209874191
8801	5	81265937	83405797	8845	5	81273796	81265937
8802	5	81265937	83437132	8846	5	81273796	81274512
8803	5	81265937	83522252	8847	5	81273796	81763618
8804	5	81265937	83560095	8848	5	81273796	81797217
8805	5	81265937	83560204	8849	5	81273796	81800186
8806	5	81265937	83572400	8850	5	81273796	81806213
8807	5	81265937	83607661	8851	5	81273796	81854583
8808	5	81265937	83745342	8852	5	81273796	81859374
8809	5	81265937	83861275	8853	5	81273796	81861368
8810	5	81265937	83861633	8854	5	81273796	81863686

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
8855	5	81273796	81916850	8899	5	81273796	83868010
8856	5	81273796	81954891	8900	5	81273796	84019752
8857	5	81273796	81985250	8901	5	81273796	84065912
8858	5	81273796	82083752	8902	5	81273796	84086632
8859	5	81273796	82101253	8903	5	81273796	84089603
8860	5	81273796	82143124	8904	5	81273796	84104814
8861	5	81273796	82236318	8905	5	81273796	84105175
8862	5	81273796	82325587	8906	5	81273796	84251635
8863	5	81273796	82427210	8907	5	81273796	84252180
8864	5	81273796	82431853	8908	5	81273796	84253030
8865	5	81273796	82446714	8909	5	81273796	84254208
8866	5	81273796	82446794	8910	5	81273796	84314930
8867	5	81273796	82551111	8911	5	81273796	84340523
8868	5	81273796	82552090	8912	5	81273796	84516340
8869	5	81273796	82555641	8913	5	81273796	84706916
8870	5	81273796	82555670	8914	5	81273796	84799488
8871	5	81273796	82556511	8915	5	81273796	84801081
8872	5	81273796	82559047	8916	5	81273796	84824103
8873	5	81273796	82561535	8917	5	81273796	84824203
8874	5	81273796	82610100	8918	5	81273796	84824816
8875	5	81273796	82676822	8919	5	81273796	84825422
8876	5	81273796	82676901	8920	5	81273796	84825763
8877	5	81273796	82883691	8921	5	81273796	84825942
8878	5	81273796	82954942	8922	5	81273796	84843411
8879	5	81273796	82971688	8923	5	81273796	84936441
8880	5	81273796	83023965	8924	5	81273796	84936493
8881	5	81273796	83094205	8925	5	81273796	84943705
8882	5	81273796	83146355	8926	5	81273796	169454950
8883	5	81273796	83280630	8927	5	81273796	181522829
8884	5	81273796	83281412	8928	5	81273796	204759879
8885	5	81273796	83400242	8929	5	81273796	209874191
8886	5	81273796	83405797	8930	5	81761119	81265937
8887	5	81273796	83437132	8931	5	81761119	81265937
8888	5	81273796	83522252	8932	5	81761119	81267485
8889	5	81273796	83560095	8933	5	81761119	81267499
8890	5	81273796	83560204	8934	5	81761119	81274512
8891	5	81273796	83572400	8935	5	81761119	81763618
8892	5	81273796	83607661	8936	5	81761119	81797217
8893	5	81273796	83745342	8937	5	81761119	81800186
8894	5	81273796	83861275	8938	5	81761119	81806213
8895	5	81273796	83861633	8939	5	81761119	81854583
8896	5	81273796	83865653	8940	5	81761119	81859374
8897	5	81273796	83865914	8941	5	81761119	81861368
8898	5	81273796	83865920	8942	5	81761119	81863686

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
8943	5	81761119	81916850	8987	5	81761119	83868010
8944	5	81761119	81954891	8988	5	81761119	84019752
8945	5	81761119	81985250	8989	5	81761119	84065912
8946	5	81761119	82083752	8990	5	81761119	84086632
8947	5	81761119	82101253	8991	5	81761119	84089603
8948	5	81761119	82143124	8992	5	81761119	84104814
8949	5	81761119	82236318	8993	5	81761119	84105175
8950	5	81761119	82325587	8994	5	81761119	84251635
8951	5	81761119	82427210	8995	5	81761119	84252180
8952	5	81761119	82431853	8996	5	81761119	84253030
8953	5	81761119	82446714	8997	5	81761119	84254208
8954	5	81761119	82446794	8998	5	81761119	84314930
8955	5	81761119	82551111	8999	5	81761119	84340523
8956	5	81761119	82552090	9000	5	81761119	84516340
8957	5	81761119	82555641	9001	5	81761119	84706916
8958	5	81761119	82555670	9002	5	81761119	84799488
8959	5	81761119	82556511	9003	5	81761119	84801081
8960	5	81761119	82559047	9004	5	81761119	84824103
8961	5	81761119	82561535	9005	5	81761119	84824203
8962	5	81761119	82610100	9006	5	81761119	84824816
8963	5	81761119	82676822	9007	5	81761119	84825422
8964	5	81761119	82676901	9008	5	81761119	84825763
8965	5	81761119	82883691	9009	5	81761119	84825942
8966	5	81761119	82954942	9010	5	81761119	84843411
8967	5	81761119	82971688	9011	5	81761119	84936441
8968	5	81761119	83023965	9012	5	81761119	84936493
8969	5	81761119	83094205	9013	5	81761119	84943705
8970	5	81761119	83146355	9014	5	81761119	169454950
8971	5	81761119	83280630	9015	5	81761119	181522829
8972	5	81761119	83281412	9016	5	81761119	204759879
8973	5	81761119	83400242	9017	5	81761119	209874191
8974	5	81761119	83405797	9018	5	81793777	81265937
8975	5	81761119	83437132	9019	5	81793777	81797217
8976	5	81761119	83522252	9020	5	81793777	81800186
8977	5	81761119	83560095	9021	5	81793777	81806213
8978	5	81761119	83560204	9022	5	81793777	81854583
8979	5	81761119	83572400	9023	5	81793777	81859374
8980	5	81761119	83607661	9024	5	81793777	81861368
8981	5	81761119	83745342	9025	5	81793777	81863686
8982	5	81761119	83861275	9026	5	81793777	81916850
8983	5	81761119	83861633	9027	5	81793777	81954891
8984	5	81761119	83865653	9028	5	81793777	81985250
8985	5	81761119	83865914	9029	5	81793777	82083752
8986	5	81761119	83865920	9030	5	81793777	82101253

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
9031	5	81793777	82143124	9075	5	81793777	84104814
9032	5	81793777	82236318	9076	5	81793777	84105175
9033	5	81793777	82325587	9077	5	81793777	84251635
9034	5	81793777	82427210	9078	5	81793777	84252180
9035	5	81793777	82431853	9079	5	81793777	84253030
9036	5	81793777	82446714	9080	5	81793777	84254208
9037	5	81793777	82446794	9081	5	81793777	84314930
9038	5	81793777	82551111	9082	5	81793777	84340523
9039	5	81793777	82552090	9083	5	81793777	84516340
9040	5	81793777	82555641	9084	5	81793777	84706916
9041	5	81793777	82555670	9085	5	81793777	84799488
9042	5	81793777	82556511	9086	5	81793777	84801081
9043	5	81793777	82559047	9087	5	81793777	84824103
9044	5	81793777	82561533	9088	5	81793777	84824203
9045	5	81793777	82610100	9089	5	81793777	84824816
9046	5	81793777	82676822	9090	5	81793777	84825422
9047	5	81793777	82676901	9091	5	81793777	84825763
9048	5	81793777	82883691	9092	5	81793777	84825942
9049	5	81793777	82954942	9093	5	81793777	84843411
9050	5	81793777	82971688	9094	5	81793777	84936441
9051	5	81793777	83023965	9095	5	81793777	84936493
9052	5	81793777	83094205	9096	5	81793777	84943705
9053	5	81793777	83146355	9097	5	81793777	169454950
9054	5	81793777	83280630	9098	5	81793777	181522829
9055	5	81793777	83281412	9099	5	81793777	204759879
9056	5	81793777	83400242	9100	5	81793777	209874191
9057	5	81793777	83405797	9101	5	81798893	81265937
9058	5	81793777	83437132	9102	5	81798893	81800186
9059	5	81793777	83522252	9103	5	81798893	81806213
9060	5	81793777	83560095	9104	5	81798893	81854583
9061	5	81793777	83560204	9105	5	81798893	81859374
9062	5	81793777	83572400	9106	5	81798893	81861368
9063	5	81793777	83607661	9107	5	81798893	81863686
9064	5	81793777	83745342	9108	5	81798893	81916850
9065	5	81793777	83861275	9109	5	81798893	81954891
9066	5	81793777	83861633	9110	5	81798893	81985250
9067	5	81793777	83865653	9111	5	81798893	82083752
9068	5	81793777	83865914	9112	5	81798893	82101253
9069	5	81793777	83865920	9113	5	81798893	82143124
9070	5	81793777	83868010	9114	5	81798893	82236318
9071	5	81793777	84019752	9115	5	81798893	82325587
9072	5	81793777	84065912	9116	5	81798893	82427210
9073	5	81793777	84086632	9117	5	81798893	82431853
9074	5	81793777	84089603	9118	5	81798893	82446714

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
9119	5	81798893	82446794	9163	5	81798893	84314930
9120	5	81798893	82551111	9164	5	81798893	84340523
9121	5	81798893	82552090	9165	5	81798893	84516340
9122	5	81798893	82555641	9166	5	81798893	84706916
9123	5	81798893	82555670	9167	5	81798893	84799488
9124	5	81798893	82556511	9168	5	81798893	84801081
9125	5	81798893	82559047	9169	5	81798893	84824103
9126	5	81798893	82561535	9170	5	81798893	84824203
9127	5	81798893	82610100	9171	5	81798893	84824816
9128	5	81798893	82676822	9172	5	81798893	84825422
9129	5	81798893	82676901	9173	5	81798893	84825763
9130	5	81798893	82883691	9174	5	81798893	84825942
9131	5	81798893	82954942	9175	5	81798893	84843411
9132	5	81798893	82971688	9176	5	81798893	84936441
9133	5	81798893	83023965	9177	5	81798893	84936493
9134	5	81798893	83094205	9178	5	81798893	84943705
9135	5	81798893	83146355	9179	5	81798893	169454950
9136	5	81798893	83280630	9180	5	81798893	181522829
9137	5	81798893	83281412	9181	5	81798893	204759879
9138	5	81798893	83400242	9182	5	81798893	209874191
9139	5	81798893	83405797	9183	5	81801973	81265937
9140	5	81798893	83437132	9184	5	81801973	81806213
9141	5	81798893	83522252	9185	5	81801973	81854583
9142	5	81798893	83560095	9186	5	81801973	81859374
9143	5	81798893	83560204	9187	5	81801973	81861368
9144	5	81798893	83572400	9188	5	81801973	81863686
9145	5	81798893	83607661	9189	5	81801973	81916850
9146	5	81798893	83745342	9190	5	81801973	81954891
9147	5	81798893	83861275	9191	5	81801973	81985250
9148	5	81798893	83861633	9192	5	81801973	82083752
9149	5	81798893	83865653	9193	5	81801973	82101253
9150	5	81798893	83865914	9194	5	81801973	82143124
9151	5	81798893	83865920	9195	5	81801973	82236318
9152	5	81798893	83868010	9196	5	81801973	82325587
9153	5	81798893	84019752	9197	5	81801973	82427210
9154	5	81798893	84065912	9198	5	81801973	82431853
9155	5	81798893	84086632	9199	5	81801973	82446714
9156	5	81798893	84089603	9200	5	81801973	82446794
9157	5	81798893	84104814	9201	5	81801973	82551111
9158	5	81798893	84105175	9202	5	81801973	82552090
9159	5	81798893	84251635	9203	5	81801973	82555641
9160	5	81798893	84252180	9204	5	81801973	82555670
9161	5	81798893	84253030	9205	5	81801973	82556511
9162	5	81798893	84254208	9206	5	81801973	82559047

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
9207	5	81801973	82561535	9251	5	81801973	84824203
9208	5	81801973	82610100	9252	5	81801973	84824816
9209	5	81801973	82676822	9253	5	81801973	84825422
9210	5	81801973	82676901	9254	5	81801973	84825763
9211	5	81801973	82883691	9255	5	81801973	84825942
9212	5	81801973	82954942	9256	5	81801973	84843411
9213	5	81801973	82971688	9257	5	81801973	84936441
9214	5	81801973	83023965	9258	5	81801973	84936493
9215	5	81801973	83094205	9259	5	81801973	84943705
9216	5	81801973	83146355	9260	5	81801973	169454950
9217	5	81801973	83280630	9261	5	81801973	181522829
9218	5	81801973	83281412	9262	5	81801973	204759879
9219	5	81801973	83400242	9263	5	81801973	209874191
9220	5	81801973	83405797	9264	5	81854583	81859374
9221	5	81801973	83437132	9265	5	81854583	81861368
9222	5	81801973	83522252	9266	5	81854583	81863686
9223	5	81801973	83560095	9267	5	81854583	81916850
9224	5	81801973	83560204	9268	5	81854583	81954891
9225	5	81801973	83572400	9269	5	81854583	81985250
9226	5	81801973	83607661	9270	5	81854583	82083752
9227	5	81801973	83745342	9271	5	81854583	82101253
9228	5	81801973	83861275	9272	5	81854583	82143124
9229	5	81801973	83861633	9273	5	81854583	82236318
9230	5	81801973	83865653	9274	5	81854583	82325587
9231	5	81801973	83865914	9275	5	81854583	82427210
9232	5	81801973	83865920	9276	5	81854583	82431853
9233	5	81801973	83868010	9277	5	81854583	82446714
9234	5	81801973	84019752	9278	5	81854583	82446794
9235	5	81801973	84065912	9279	5	81854583	82551111
9236	5	81801973	84086632	9280	5	81854583	82552090
9237	5	81801973	84089603	9281	5	81854583	82555641
9238	5	81801973	84104814	9282	5	81854583	82555670
9239	5	81801973	84105175	9283	5	81854583	82556511
9240	5	81801973	84251635	9284	5	81854583	82559047
9241	5	81801973	84252180	9285	5	81854583	82561535
9242	5	81801973	84253030	9286	5	81854583	82610100
9243	5	81801973	84254208	9287	5	81854583	82676822
9244	5	81801973	84314930	9288	5	81854583	82676901
9245	5	81801973	84340523	9289	5	81854583	82883691
9246	5	81801973	84516340	9290	5	81854583	82954942
9247	5	81801973	84706916	9291	5	81854583	82971688
9248	5	81801973	84799488	9292	5	81854583	83023965
9249	5	81801973	84801081	9293	5	81854583	83094205
9250	5	81801973	84824103	9294	5	81854583	83146355

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
9295	5	81854583	83280630	9339	5	81854583	181522829
9296	5	81854583	83281412	9340	5	81854583	204759879
9297	5	81854583	83400242	9341	5	81854583	209874191
9298	5	81854583	83405797	9342	5	81858527	81859374
9299	5	81854583	83437132	9343	5	81858527	81861368
9300	5	81854583	83522252	9344	5	81858527	81863686
9301	5	81854583	83560095	9345	5	81858527	81916850
9302	5	81854583	83560204	9346	5	81858527	81954891
9303	5	81854583	83572400	9347	5	81858527	81985250
9304	5	81854583	83607661	9348	5	81858527	82083752
9305	5	81854583	83745342	9349	5	81858527	82101253
9306	5	81854583	83861275	9350	5	81858527	82143124
9307	5	81854583	83861633	9351	5	81858527	82236318
9308	5	81854583	83865653	9352	5	81858527	82325587
9309	5	81854583	83865914	9353	5	81858527	82427210
9310	5	81854583	83865920	9354	5	81858527	82431853
9311	5	81854583	83868010	9355	5	81858527	82446714
9312	5	81854583	84019752	9356	5	81858527	82446794
9313	5	81854583	84065912	9357	5	81858527	82551111
9314	5	81854583	84086632	9358	5	81858527	82552090
9315	5	81854583	84089603	9359	5	81858527	82555641
9316	5	81854583	84104814	9360	5	81858527	82555670
9317	5	81854583	84105175	9361	5	81858527	82556511
9318	5	81854583	84251635	9362	5	81858527	82559047
9319	5	81854583	84252180	9363	5	81858527	82561535
9320	5	81854583	84253030	9364	5	81858527	82610100
9321	5	81854583	84254208	9365	5	81858527	82676822
9322	5	81854583	84314930	9366	5	81858527	82676901
9323	5	81854583	84340523	9367	5	81858527	82883691
9324	5	81854583	84516340	9368	5	81858527	82954942
9325	5	81854583	84706916	9369	5	81858527	82971688
9326	5	81854583	84799488	9370	5	81858527	83023965
9327	5	81854583	84801081	9371	5	81858527	83094205
9328	5	81854583	84824103	9372	5	81858527	83146355
9329	5	81854583	84824203	9373	5	81858527	83280630
9330	5	81854583	84824816	9374	5	81858527	83281412
9331	5	81854583	84825422	9375	5	81858527	83400242
9332	5	81854583	84825763	9376	5	81858527	83405797
9333	5	81854583	84825942	9377	5	81858527	83437132
9334	5	81854583	84843411	9378	5	81858527	83522252
9335	5	81854583	84936441	9379	5	81858527	83560095
9336	5	81854583	84936493	9380	5	81858527	83560204
9337	5	81854583	84943705	9381	5	81858527	83572400
9338	5	81854583	169454950	9382	5	81858527	83607661

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
9383	5	81858527	83745342	9427	5	81859618	82101253
9384	5	81858527	83861275	9428	5	81859618	82143124
9385	5	81858527	83861633	9429	5	81859618	82236318
9386	5	81858527	83865653	9430	5	81859618	82325587
9387	5	81858527	83865914	9431	5	81859618	82427210
9388	5	81858527	83865920	9432	5	81859618	82431853
9389	5	81858527	83868010	9433	5	81859618	82446714
9390	5	81858527	84019752	9434	5	81859618	82446794
9391	5	81858527	84065912	9435	5	81859618	82551111
9392	5	81858527	84086632	9436	5	81859618	82552090
9393	5	81858527	84089603	9437	5	81859618	82555641
9394	5	81858527	84104814	9438	5	81859618	82555670
9395	5	81858527	84105175	9439	5	81859618	825556511
9396	5	81858527	84251635	9440	5	81859618	82559047
9397	5	81858527	84252180	9441	5	81859618	82561535
9398	5	81858527	84253030	9442	5	81859618	82610100
9399	5	81858527	84254208	9443	5	81859618	82676822
9400	5	81858527	84314930	9444	5	81859618	82676901
9401	5	81858527	84340523	9445	5	81859618	82883691
9402	5	81858527	84516340	9446	5	81859618	82954942
9403	5	81858527	84706916	9447	5	81859618	82971688
9404	5	81858527	84799488	9448	5	81859618	83023965
9405	5	81858527	84801081	9449	5	81859618	83094205
9406	5	81858527	84824103	9450	5	81859618	83146355
9407	5	81858527	84824203	9451	5	81859618	83280630
9408	5	81858527	84824816	9452	5	81859618	83281412
9409	5	81858527	84825422	9453	5	81859618	83400242
9410	5	81858527	84825763	9454	5	81859618	83405797
9411	5	81858527	84825942	9455	5	81859618	83437132
9412	5	81858527	84843411	9456	5	81859618	83522252
9413	5	81858527	84936441	9457	5	81859618	83560095
9414	5	81858527	84936493	9458	5	81859618	83560204
9415	5	81858527	84943705	9459	5	81859618	83572400
9416	5	81858527	169454950	9460	5	81859618	83607661
9417	5	81858527	181522829	9461	5	81859618	83745342
9418	5	81858527	204759879	9462	5	81859618	83861275
9419	5	81858527	209874191	9463	5	81859618	83861633
9420	5	81859618	81265937	9464	5	81859618	83865653
9421	5	81859618	81861368	9465	5	81859618	83865914
9422	5	81859618	81863686	9466	5	81859618	83865920
9423	5	81859618	81916850	9467	5	81859618	83868010
9424	5	81859618	81954891	9468	5	81859618	84019752
9425	5	81859618	81985250	9469	5	81859618	84065912
9426	5	81859618	82083752	9470	5	81859618	84086632

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
9471	5	81859618	84089603	9515	5	81863099	82555670
9472	5	81859618	84104814	9516	5	81863099	82555611
9473	5	81859618	84105175	9517	5	81863099	82559047
9474	5	81859618	84251635	9518	5	81863099	82561535
9475	5	81859618	84252180	9519	5	81863099	82610100
9476	5	81859618	84253030	9520	5	81863099	82676822
9477	5	81859618	84254208	9521	5	81863099	82676901
9478	5	81859618	84314930	9522	5	81863099	82883691
9479	5	81859618	84340523	9523	5	81863099	82954942
9480	5	81859618	84516340	9524	5	81863099	82971688
9481	5	81859618	84706916	9525	5	81863099	83023965
9482	5	81859618	84799488	9526	5	81863099	83094205
9483	5	81859618	84801081	9527	5	81863099	83146355
9484	5	81859618	84824103	9528	5	81863099	83280630
9485	5	81859618	84824203	9529	5	81863099	83281412
9486	5	81859618	84824816	9530	5	81863099	83400242
9487	5	81859618	84825422	9531	5	81863099	83405797
9488	5	81859618	84825763	9532	5	81863099	83437132
9489	5	81859618	84825942	9533	5	81863099	83522252
9490	5	81859618	84843411	9534	5	81863099	83560095
9491	5	81859618	84936441	9535	5	81863099	83560204
9492	5	81859618	84936493	9536	5	81863099	83572400
9493	5	81859618	84943705	9537	5	81863099	83607661
9494	5	81859618	169454950	9538	5	81863099	83745342
9495	5	81859618	181522829	9539	5	81863099	83861275
9496	5	81859618	204759879	9540	5	81863099	83861633
9497	5	81859618	209874191	9541	5	81863099	83865653
9498	5	81863099	81265937	9542	5	81863099	83865914
9499	5	81863099	81863686	9543	5	81863099	83865920
9500	5	81863099	81916850	9544	5	81863099	83868010
9501	5	81863099	81954891	9545	5	81863099	84019752
9502	5	81863099	81985250	9546	5	81863099	84065912
9503	5	81863099	82083752	9547	5	81863099	84086632
9504	5	81863099	82101253	9548	5	81863099	84089603
9505	5	81863099	82143124	9549	5	81863099	84104814
9506	5	81863099	82236318	9550	5	81863099	84105175
9507	5	81863099	82325587	9551	5	81863099	84251635
9508	5	81863099	82427210	9552	5	81863099	84252180
9509	5	81863099	82431853	9553	5	81863099	84253030
9510	5	81863099	82446714	9554	5	81863099	84254208
9511	5	81863099	82446794	9555	5	81863099	84314930
9512	5	81863099	82551111	9556	5	81863099	84340523
9513	5	81863099	82552090	9557	5	81863099	84516340
9514	5	81863099	82555641	9558	5	81863099	84706916

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
9559	5	81863099	84799488	9603	5	81914498	83146355
9560	5	81863099	84801081	9604	5	81914498	83280630
9561	5	81863099	84824103	9605	5	81914498	83281412
9562	5	81863099	84824203	9606	5	81914498	83400242
9563	5	81863099	84824816	9607	5	81914498	83405797
9564	5	81863099	84825422	9608	5	81914498	83437132
9565	5	81863099	84825763	9609	5	81914498	83522252
9566	5	81863099	84825942	9610	5	81914498	83560095
9567	5	81863099	84843411	9611	5	81914498	83560204
9568	5	81863099	84936441	9612	5	81914498	83572400
9569	5	81863099	84936493	9613	5	81914498	83607661
9570	5	81863099	84943705	9614	5	81914498	83745342
9571	5	81863099	169454950	9615	5	81914498	83861275
9572	5	81863099	181522829	9616	5	81914498	83861633
9573	5	81863099	204759879	9617	5	81914498	83865653
9574	5	81863099	209874191	9618	5	81914498	83865914
9575	5	81914498	81265937	9619	5	81914498	83865920
9576	5	81914498	81916850	9620	5	81914498	83868010
9577	5	81914498	81954891	9621	5	81914498	84019752
9578	5	81914498	81985250	9622	5	81914498	84065912
9579	5	81914498	82083752	9623	5	81914498	84086632
9580	5	81914498	82101253	9624	5	81914498	84089603
9581	5	81914498	82143124	9625	5	81914498	84104814
9582	5	81914498	82236318	9626	5	81914498	84105175
9583	5	81914498	82325587	9627	5	81914498	84251635
9584	5	81914498	82427210	9628	5	81914498	84252180
9585	5	81914498	82431853	9629	5	81914498	84253030
9586	5	81914498	82446714	9630	5	81914498	84254208
9587	5	81914498	82446794	9631	5	81914498	84314930
9588	5	81914498	82551111	9632	5	81914498	84340523
9589	5	81914498	82552090	9633	5	81914498	84516340
9590	5	81914498	82555641	9634	5	81914498	84706916
9591	5	81914498	82555670	9635	5	81914498	84799488
9592	5	81914498	82556511	9636	5	81914498	84801081
9593	5	81914498	82559047	9637	5	81914498	84824103
9594	5	81914498	82561535	9638	5	81914498	84824203
9595	5	81914498	82610100	9639	5	81914498	84824816
9596	5	81914498	82676822	9640	5	81914498	84825422
9597	5	81914498	82676901	9641	5	81914498	84825763
9598	5	81914498	82883691	9642	5	81914498	84825942
9599	5	81914498	82954942	9643	5	81914498	84843411
9600	5	81914498	82971688	9644	5	81914498	84936441
9601	5	81914498	83023965	9645	5	81914498	84936493
9602	5	81914498	83094205	9646	5	81914498	84943705

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
9647	5	81914498	169454950	9691	5	81950191	83861633
9648	5	81914498	181522829	9692	5	81950191	83865653
9649	5	81914498	204759879	9693	5	81950191	83865914
9650	5	81914498	209874191	9694	5	81950191	83865920
9651	5	81950191	81265937	9695	5	81950191	83868010
9652	5	81950191	81954891	9696	5	81950191	84019752
9653	5	81950191	81985250	9697	5	81950191	84065912
9654	5	81950191	82083752	9698	5	81950191	84086632
9655	5	81950191	82101253	9699	5	81950191	84089603
9656	5	81950191	82143124	9700	5	81950191	84104814
9657	5	81950191	82236318	9701	5	81950191	84105175
9658	5	81950191	82325587	9702	5	81950191	84251635
9659	5	81950191	82427210	9703	5	81950191	84252180
9660	5	81950191	82431853	9704	5	81950191	84253030
9661	5	81950191	82446714	9705	5	81950191	84254208
9662	5	81950191	82446794	9706	5	81950191	84314930
9663	5	81950191	82551111	9707	5	81950191	84340523
9664	5	81950191	82552090	9708	5	81950191	84516340
9665	5	81950191	82555641	9709	5	81950191	84706916
9666	5	81950191	82555670	9710	5	81950191	84799488
9667	5	81950191	82556511	9711	5	81950191	84801081
9668	5	81950191	82559047	9712	5	81950191	84824103
9669	5	81950191	82561535	9713	5	81950191	84824203
9670	5	81950191	82610100	9714	5	81950191	84824816
9671	5	81950191	82676822	9715	5	81950191	84825422
9672	5	81950191	82676901	9716	5	81950191	84825763
9673	5	81950191	82883691	9717	5	81950191	84825942
9674	5	81950191	82954942	9718	5	81950191	84843411
9675	5	81950191	82971688	9719	5	81950191	84936441
9676	5	81950191	83023965	9720	5	81950191	84936493
9677	5	81950191	83094205	9721	5	81950191	84943705
9678	5	81950191	83146355	9722	5	81950191	169454950
9679	5	81950191	83280630	9723	5	81950191	181522829
9680	5	81950191	83281412	9724	5	81950191	204759879
9681	5	81950191	83400242	9725	5	81950191	209874191
9682	5	81950191	83405797	9726	5	81951639	81265937
9683	5	81950191	83437132	9727	5	81951639	81954891
9684	5	81950191	83522252	9728	5	81951639	81985250
9685	5	81950191	83560095	9729	5	81951639	82083752
9686	5	81950191	83560204	9730	5	81951639	82101253
9687	5	81950191	83572400	9731	5	81951639	82143124
9688	5	81950191	83607661	9732	5	81951639	82236318
9689	5	81950191	83745342	9733	5	81951639	82325587
9690	5	81950191	83861275	9734	5	81951639	82427210

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
9735	5	81951639	82431853	9779	5	81951639	84253030
9736	5	81951639	82446714	9780	5	81951639	84254208
9737	5	81951639	82446794	9781	5	81951639	84314930
9738	5	81951639	82551111	9782	5	81951639	84340523
9739	5	81951639	82552090	9783	5	81951639	84516340
9740	5	81951639	82555641	9784	5	81951639	84706916
9741	5	81951639	82555670	9785	5	81951639	84799488
9742	5	81951639	82556511	9786	5	81951639	84801081
9743	5	81951639	82559047	9787	5	81951639	84824103
9744	5	81951639	82561535	9788	5	81951639	84824203
9745	5	81951639	82610100	9789	5	81951639	84824816
9746	5	81951639	82676822	9790	5	81951639	84825422
9747	5	81951639	82676901	9791	5	81951639	84825763
9748	5	81951639	82883691	9792	5	81951639	84825942
9749	5	81951639	82954942	9793	5	81951639	84843411
9750	5	81951639	82971688	9794	5	81951639	84936441
9751	5	81951639	83023965	9795	5	81951639	84936493
9752	5	81951639	83094205	9796	5	81951639	84943705
9753	5	81951639	83146355	9797	5	81951639	169454950
9754	5	81951639	83280630	9798	5	81951639	181522829
9755	5	81951639	83281412	9799	5	81951639	204759879
9756	5	81951639	83400242	9800	5	81951639	209874191
9757	5	81951639	83405797	9801	5	81984901	81265937
9758	5	81951639	83437132	9802	5	81984901	81985250
9759	5	81951639	83522252	9803	5	81984901	82083752
9760	5	81951639	83560095	9804	5	81984901	82101253
9761	5	81951639	83560204	9805	5	81984901	82143124
9762	5	81951639	83572400	9806	5	81984901	82236318
9763	5	81951639	83607661	9807	5	81984901	82325587
9764	5	81951639	83745342	9808	5	81984901	82427210
9765	5	81951639	83861275	9809	5	81984901	82431853
9766	5	81951639	83861633	9810	5	81984901	82446714
9767	5	81951639	83865653	9811	5	81984901	82446794
9768	5	81951639	83865914	9812	5	81984901	82551111
9769	5	81951639	83865920	9813	5	81984901	82552090
9770	5	81951639	83868010	9814	5	81984901	82555641
9771	5	81951639	84019752	9815	5	81984901	82555670
9772	5	81951639	84065912	9816	5	81984901	82556511
9773	5	81951639	84086632	9817	5	81984901	82559047
9774	5	81951639	84089603	9818	5	81984901	82561535
9775	5	81951639	84104814	9819	5	81984901	82610100
9776	5	81951639	84105175	9820	5	81984901	82676822
9777	5	81951639	84251635	9821	5	81984901	82676901
9778	5	81951639	84252180	9822	5	81984901	82883691

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
9823	5	81984901	82954942	9867	5	81984901	84843411
9824	5	81984901	82971688	9868	5	81984901	84936441
9825	5	81984901	83023965	9869	5	81984901	84936493
9826	5	81984901	83094205	9870	5	81984901	84943705
9827	5	81984901	83146355	9871	5	81984901	169454950
9828	5	81984901	83280630	9872	5	81984901	181522829
9829	5	81984901	83281412	9873	5	81984901	204759879
9830	5	81984901	83400242	9874	5	81984901	209874191
9831	5	81984901	83405797	9875	5	82083639	81265937
9832	5	81984901	83437132	9876	5	82083639	82083752
9833	5	81984901	83522252	9877	5	82083639	82101253
9834	5	81984901	83560095	9878	5	82083639	82143124
9835	5	81984901	83560204	9879	5	82083639	82236318
9836	5	81984901	83572400	9880	5	82083639	82325587
9837	5	81984901	83607661	9881	5	82083639	82427210
9838	5	81984901	83745342	9882	5	82083639	82431853
9839	5	81984901	83861275	9883	5	82083639	82446714
9840	5	81984901	83861633	9884	5	82083639	82446794
9841	5	81984901	83865653	9885	5	82083639	82551111
9842	5	81984901	83865914	9886	5	82083639	82552090
9843	5	81984901	83865920	9887	5	82083639	82555641
9844	5	81984901	83868010	9888	5	82083639	82555670
9845	5	81984901	84019752	9889	5	82083639	82556511
9846	5	81984901	84065912	9890	5	82083639	82559047
9847	5	81984901	84086632	9891	5	82083639	82561535
9848	5	81984901	84089603	9892	5	82083639	82610100
9849	5	81984901	84104814	9893	5	82083639	82676822
9850	5	81984901	84105175	9894	5	82083639	82676901
9851	5	81984901	84251635	9895	5	82083639	82883691
9852	5	81984901	84252180	9896	5	82083639	82954942
9853	5	81984901	84253030	9897	5	82083639	82971688
9854	5	81984901	84254208	9898	5	82083639	83023965
9855	5	81984901	84314930	9899	5	82083639	83094205
9856	5	81984901	84340523	9900	5	82083639	83146355
9857	5	81984901	84516340	9901	5	82083639	83280630
9858	5	81984901	84706916	9902	5	82083639	83281412
9859	5	81984901	84799488	9903	5	82083639	83400242
9860	5	81984901	84801081	9904	5	82083639	83405797
9861	5	81984901	84824103	9905	5	82083639	83437132
9862	5	81984901	84824203	9906	5	82083639	83522252
9863	5	81984901	84824816	9907	5	82083639	83560095
9864	5	81984901	84825422	9908	5	82083639	83560204
9865	5	81984901	84825763	9909	5	82083639	83572400
9866	5	81984901	84825942	9910	5	82083639	83607661

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
9911	5	82083639	83745342	9955	5	82083752	82446714
9912	5	82083639	83861275	9956	5	82083752	82446794
9913	5	82083639	83861633	9957	5	82083752	82551111
9914	5	82083639	83865653	9958	5	82083752	82552090
9915	5	82083639	83865914	9959	5	82083752	82555641
9916	5	82083639	83865920	9960	5	82083752	82555670
9917	5	82083639	83868010	9961	5	82083752	82556511
9918	5	82083639	84019752	9962	5	82083752	82559047
9919	5	82083639	84065912	9963	5	82083752	82561535
9920	5	82083639	84086632	9964	5	82083752	82610100
9921	5	82083639	84089603	9965	5	82083752	82676822
9922	5	82083639	84104814	9966	5	82083752	82676901
9923	5	82083639	84105175	9967	5	82083752	82883691
9924	5	82083639	84251635	9968	5	82083752	82954942
9925	5	82083639	84252180	9969	5	82083752	82971688
9926	5	82083639	84253030	9970	5	82083752	83023965
9927	5	82083639	84254208	9971	5	82083752	83094205
9928	5	82083639	84314930	9972	5	82083752	83146355
9929	5	82083639	84340523	9973	5	82083752	83280630
9930	5	82083639	84516340	9974	5	82083752	83281412
9931	5	82083639	84706916	9975	5	82083752	83400242
9932	5	82083639	84799488	9976	5	82083752	83405797
9933	5	82083639	84801081	9977	5	82083752	83437132
9934	5	82083639	84824103	9978	5	82083752	83522252
9935	5	82083639	84824203	9979	5	82083752	83560095
9936	5	82083639	84824816	9980	5	82083752	83560204
9937	5	82083639	84825422	9981	5	82083752	83572400
9938	5	82083639	84825763	9982	5	82083752	83607661
9939	5	82083639	84825942	9983	5	82083752	83745342
9940	5	82083639	84843411	9984	5	82083752	83861275
9941	5	82083639	84936441	9985	5	82083752	83861633
9942	5	82083639	84936493	9986	5	82083752	83865653
9943	5	82083639	84943705	9987	5	82083752	83865914
9944	5	82083639	169454950	9988	5	82083752	83865920
9945	5	82083639	181522829	9989	5	82083752	83868010
9946	5	82083639	204759879	9990	5	82083752	84019752
9947	5	82083639	209874191	9991	5	82083752	84065912
9948	5	82083752	81265937	9992	5	82083752	84086632
9949	5	82083752	82137780	9993	5	82083752	84089603
9950	5	82083752	82143124	9994	5	82083752	84104814
9951	5	82083752	82236318	9995	5	82083752	84105175
9952	5	82083752	82325587	9996	5	82083752	84251635
9953	5	82083752	82427210	9997	5	82083752	84252180
9954	5	82083752	82431853	9998	5	82083752	84253030

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
9999	5	82083752	84254208	10043	5	82137780	83146355
10000	5	82083752	84314930	10044	5	82137780	83280630
10001	5	82083752	84340523	10045	5	82137780	83281412
10002	5	82083752	84516340	10046	5	82137780	83400242
10003	5	82083752	84706916	10047	5	82137780	83405797
10004	5	82083752	84799488	10048	5	82137780	83437132
10005	5	82083752	84801081	10049	5	82137780	83522252
10006	5	82083752	84824103	10050	5	82137780	83560095
10007	5	82083752	84824203	10051	5	82137780	83560204
10008	5	82083752	84824816	10052	5	82137780	83572400
10009	5	82083752	84825422	10053	5	82137780	83607661
10010	5	82083752	84825763	10054	5	82137780	83745342
10011	5	82083752	84825942	10055	5	82137780	83861275
10012	5	82083752	84843411	10056	5	82137780	83861633
10013	5	82083752	84936441	10057	5	82137780	83865653
10014	5	82083752	84936493	10058	5	82137780	83865914
10015	5	82083752	84943705	10059	5	82137780	83865920
10016	5	82083752	169454950	10060	5	82137780	83868010
10017	5	82083752	181522829	10061	5	82137780	84019752
10018	5	82083752	204759879	10062	5	82137780	84065912
10019	5	82083752	209874191	10063	5	82137780	84086632
10020	5	82137780	81265937	10064	5	82137780	84089603
10021	5	82137780	82143124	10065	5	82137780	84104814
10022	5	82137780	82236318	10066	5	82137780	84105175
10023	5	82137780	82325587	10067	5	82137780	84251635
10024	5	82137780	82427210	10068	5	82137780	84252180
10025	5	82137780	82431853	10069	5	82137780	84253030
10026	5	82137780	82446714	10070	5	82137780	84254208
10027	5	82137780	82446794	10071	5	82137780	84314930
10028	5	82137780	82551111	10072	5	82137780	84340523
10029	5	82137780	82552090	10073	5	82137780	84516340
10030	5	82137780	82555641	10074	5	82137780	84706916
10031	5	82137780	82555670	10075	5	82137780	84799488
10032	5	82137780	82556511	10076	5	82137780	84801081
10033	5	82137780	82559047	10077	5	82137780	84824103
10034	5	82137780	82561535	10078	5	82137780	84824203
10035	5	82137780	82610100	10079	5	82137780	84824816
10036	5	82137780	82676822	10080	5	82137780	84825422
10037	5	82137780	82676901	10081	5	82137780	84825763
10038	5	82137780	82883691	10082	5	82137780	84825942
10039	5	82137780	82954942	10083	5	82137780	84843411
10040	5	82137780	82971688	10084	5	82137780	84936441
10041	5	82137780	83023965	10085	5	82137780	84936493
10042	5	82137780	83094205	10086	5	82137780	84943705

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
10087	5	82137780	169454950	10131	5	82139338	83868010
10088	5	82137780	181522829	10132	5	82139338	84019752
10089	5	82137780	204759879	10133	5	82139338	84065912
10090	5	82137780	209874191	10134	5	82139338	84086632
10091	5	82139338	81265937	10135	5	82139338	84089603
10092	5	82139338	82143124	10136	5	82139338	84104814
10093	5	82139338	82236318	10137	5	82139338	84105175
10094	5	82139338	82325587	10138	5	82139338	84251635
10095	5	82139338	82427210	10139	5	82139338	84252180
10096	5	82139338	82431853	10140	5	82139338	84253030
10097	5	82139338	82446714	10141	5	82139338	84254208
10098	5	82139338	82446794	10142	5	82139338	84314930
10099	5	82139338	82551111	10143	5	82139338	84340523
10100	5	82139338	82552090	10144	5	82139338	84516340
10101	5	82139338	82555641	10145	5	82139338	84706916
10102	5	82139338	82555670	10146	5	82139338	84799488
10103	5	82139338	82556511	10147	5	82139338	84801081
10104	5	82139338	82559047	10148	5	82139338	84824103
10105	5	82139338	82561535	10149	5	82139338	84824203
10106	5	82139338	82610100	10150	5	82139338	84824816
10107	5	82139338	82676822	10151	5	82139338	84825422
10108	5	82139338	82676901	10152	5	82139338	84825763
10109	5	82139338	82883691	10153	5	82139338	84825942
10110	5	82139338	82954942	10154	5	82139338	84843411
10111	5	82139338	82971688	10155	5	82139338	84936441
10112	5	82139338	83023965	10156	5	82139338	84936493
10113	5	82139338	83094205	10157	5	82139338	84943705
10114	5	82139338	83146355	10158	5	82139338	169454950
10115	5	82139338	83280630	10159	5	82139338	181522829
10116	5	82139338	83281412	10160	5	82139338	204759879
10117	5	82139338	83400242	10161	5	82139338	209874191
10118	5	82139338	83405797	10162	5	82234311	81265937
10119	5	82139338	83437132	10163	5	82234311	82236318
10120	5	82139338	83522252	10164	5	82234311	82325587
10121	5	82139338	83560095	10165	5	82234311	82427210
10122	5	82139338	83560204	10166	5	82234311	82431853
10123	5	82139338	83572400	10167	5	82234311	82446714
10124	5	82139338	83607661	10168	5	82234311	82446794
10125	5	82139338	83745342	10169	5	82234311	82551111
10126	5	82139338	83861275	10170	5	82234311	82552090
10127	5	82139338	83861633	10171	5	82234311	82555641
10128	5	82139338	83865653	10172	5	82234311	82555670
10129	5	82139338	83865914	10173	5	82234311	82556511
10130	5	82139338	83865920	10174	5	82234311	82559047

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
10175	5	82234311	82561535	10219	5	82234311	84824203
10176	5	82234311	82610100	10220	5	82234311	84824816
10177	5	82234311	82676822	10221	5	82234311	84825422
10178	5	82234311	82676901	10222	5	82234311	84825763
10179	5	82234311	82883691	10223	5	82234311	84825942
10180	5	82234311	82954942	10224	5	82234311	84843411
10181	5	82234311	82971688	10225	5	82234311	84936441
10182	5	82234311	83023965	10226	5	82234311	84936493
10183	5	82234311	83094205	10227	5	82234311	84943705
10184	5	82234311	83146355	10228	5	82234311	169454950
10185	5	82234311	83280630	10229	5	82234311	181522829
10186	5	82234311	83281412	10230	5	82234311	204759879
10187	5	82234311	83400242	10231	5	82234311	209874191
10188	5	82234311	83405797	10232	5	82236318	81265937
10189	5	82234311	83437132	10233	5	82325587	82423451
10190	5	82234311	83522252	10234	5	82325587	82427210
10191	5	82234311	83560095	10235	5	82325587	82431853
10192	5	82234311	83560204	10236	5	82325587	82446714
10193	5	82234311	83572400	10237	5	82325587	82446794
10194	5	82234311	83607661	10238	5	82325587	82551111
10195	5	82234311	83745342	10239	5	82325587	82552090
10196	5	82234311	83861275	10240	5	82325587	82555641
10197	5	82234311	83861633	10241	5	82325587	82555670
10198	5	82234311	83865653	10242	5	82325587	82556511
10199	5	82234311	83865914	10243	5	82325587	82559047
10200	5	82234311	83865920	10244	5	82325587	82561535
10201	5	82234311	83868010	10245	5	82325587	82610100
10202	5	82234311	84019752	10246	5	82325587	82676822
10203	5	82234311	84065912	10247	5	82325587	82676901
10204	5	82234311	84086632	10248	5	82325587	82883691
10205	5	82234311	84089603	10249	5	82325587	82954942
10206	5	82234311	84104814	10250	5	82325587	82971688
10207	5	82234311	84105175	10251	5	82325587	83023965
10208	5	82234311	84251635	10252	5	82325587	83094205
10209	5	82234311	84252180	10253	5	82325587	83146355
10210	5	82234311	84253030	10254	5	82325587	83280630
10211	5	82234311	84254208	10255	5	82325587	83281412
10212	5	82234311	84314930	10256	5	82325587	83400242
10213	5	82234311	84340523	10257	5	82325587	83405797
10214	5	82234311	84516340	10258	5	82325587	83437132
10215	5	82234311	84706916	10259	5	82325587	83522252
10216	5	82234311	84799488	10260	5	82325587	83560095
10217	5	82234311	84801081	10261	5	82325587	83560204
10218	5	82234311	84824103	10262	5	82325587	83572400

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
10263	5	82325587	83607661	10307	5	82423451	82555641
10264	5	82325587	83745342	10308	5	82423451	82555670
10265	5	82325587	83861275	10309	5	82423451	82556511
10266	5	82325587	83861633	10310	5	82423451	82559047
10267	5	82325587	83865653	10311	5	82423451	82561535
10268	5	82325587	83865914	10312	5	82423451	82610100
10269	5	82325587	83865920	10313	5	82423451	82676822
10270	5	82325587	83868010	10314	5	82423451	82676901
10271	5	82325587	84019752	10315	5	82423451	82883691
10272	5	82325587	84065912	10316	5	82423451	82954942
10273	5	82325587	84086632	10317	5	82423451	82971688
10274	5	82325587	84089603	10318	5	82423451	83023965
10275	5	82325587	84104814	10319	5	82423451	83094205
10276	5	82325587	84105175	10320	5	82423451	83146355
10277	5	82325587	84251635	10321	5	82423451	83280630
10278	5	82325587	84252180	10322	5	82423451	83281412
10279	5	82325587	84253030	10323	5	82423451	83400242
10280	5	82325587	84254208	10324	5	82423451	83405797
10281	5	82325587	84314930	10325	5	82423451	83437132
10282	5	82325587	84340523	10326	5	82423451	83522252
10283	5	82325587	84516340	10327	5	82423451	83560095
10284	5	82325587	84706916	10328	5	82423451	83560204
10285	5	82325587	84799488	10329	5	82423451	83572400
10286	5	82325587	84801081	10330	5	82423451	83607661
10287	5	82325587	84824103	10331	5	82423451	83745342
10288	5	82325587	84824203	10332	5	82423451	83861275
10289	5	82325587	84824816	10333	5	82423451	83861633
10290	5	82325587	84825422	10334	5	82423451	83865653
10291	5	82325587	84825763	10335	5	82423451	83865914
10292	5	82325587	84825942	10336	5	82423451	83865920
10293	5	82325587	84843411	10337	5	82423451	83868010
10294	5	82325587	84936441	10338	5	82423451	84019752
10295	5	82325587	84936493	10339	5	82423451	84065912
10296	5	82325587	84943705	10340	5	82423451	84086632
10297	5	82325587	169454950	10341	5	82423451	84089603
10298	5	82325587	181522829	10342	5	82423451	84104814
10299	5	82325587	204759879	10343	5	82423451	84105175
10300	5	82325587	209874191	10344	5	82423451	84251635
10301	5	82423451	82427210	10345	5	82423451	84252180
10302	5	82423451	82431853	10346	5	82423451	84253030
10303	5	82423451	82446714	10347	5	82423451	84254208
10304	5	82423451	82446794	10348	5	82423451	84314930
10305	5	82423451	82551111	10349	5	82423451	84340523
10306	5	82423451	82552090	10350	5	82423451	84516340

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
10351	5	82423451	84706916	10395	5	82427780	83572400
10352	5	82423451	84799488	10396	5	82427780	83607661
10353	5	82423451	84801081	10397	5	82427780	83745342
10354	5	82423451	84824103	10398	5	82427780	83861275
10355	5	82423451	84824203	10399	5	82427780	83861633
10356	5	82423451	84824816	10400	5	82427780	83865653
10357	5	82423451	84825422	10401	5	82427780	83865914
10358	5	82423451	84825763	10402	5	82427780	83865920
10359	5	82423451	84825942	10403	5	82427780	83868010
10360	5	82423451	84843411	10404	5	82427780	84019752
10361	5	82423451	84936441	10405	5	82427780	84065912
10362	5	82423451	84936493	10406	5	82427780	84086632
10363	5	82423451	84943705	10407	5	82427780	84089603
10364	5	82423451	169454950	10408	5	82427780	84104814
10365	5	82423451	181522829	10409	5	82427780	84105175
10366	5	82423451	204759879	10410	5	82427780	84251635
10367	5	82423451	209874191	10411	5	82427780	84252180
10368	5	82427780	82431853	10412	5	82427780	84253030
10369	5	82427780	82446714	10413	5	82427780	84254208
10370	5	82427780	82446794	10414	5	82427780	84314930
10371	5	82427780	82551111	10415	5	82427780	84340523
10372	5	82427780	82552090	10416	5	82427780	84516340
10373	5	82427780	82555641	10417	5	82427780	84706916
10374	5	82427780	82555670	10418	5	82427780	84799488
10375	5	82427780	82556511	10419	5	82427780	84801081
10376	5	82427780	82559047	10420	5	82427780	84824103
10377	5	82427780	82561535	10421	5	82427780	84824203
10378	5	82427780	82610100	10422	5	82427780	84824816
10379	5	82427780	82676822	10423	5	82427780	84825422
10380	5	82427780	82676901	10424	5	82427780	84825763
10381	5	82427780	82883691	10425	5	82427780	84825942
10382	5	82427780	82954942	10426	5	82427780	84843411
10383	5	82427780	82971688	10427	5	82427780	84936441
10384	5	82427780	83023965	10428	5	82427780	84936493
10385	5	82427780	83094205	10429	5	82427780	84943705
10386	5	82427780	83146355	10430	5	82427780	169454950
10387	5	82427780	83280630	10431	5	82427780	181522829
10388	5	82427780	83281412	10432	5	82427780	204759879
10389	5	82427780	83400242	10433	5	82427780	209874191
10390	5	82427780	83405797	10434	5	82443403	82446714
10391	5	82427780	83437132	10435	5	82443403	82446794
10392	5	82427780	83522252	10436	5	82443403	82551111
10393	5	82427780	83560095	10437	5	82443403	82552090
10394	5	82427780	83560204	10438	5	82443403	82555641

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
10439	5	82443403	82555670	10483	5	82443403	84799488
10440	5	82443403	82556511	10484	5	82443403	84801081
10441	5	82443403	82559047	10485	5	82443403	84824103
10442	5	82443403	82561535	10486	5	82443403	84824203
10443	5	82443403	82610100	10487	5	82443403	84824816
10444	5	82443403	82676822	10488	5	82443403	84825422
10445	5	82443403	82676901	10489	5	82443403	84825763
10446	5	82443403	82883691	10490	5	82443403	84825942
10447	5	82443403	82954942	10491	5	82443403	84843411
10448	5	82443403	82971688	10492	5	82443403	84936441
10449	5	82443403	83023965	10493	5	82443403	84936493
10450	5	82443403	83094205	10494	5	82443403	84943705
10451	5	82443403	83146355	10495	5	82443403	169454950
10452	5	82443403	83280630	10496	5	82443403	181522829
10453	5	82443403	83281412	10497	5	82443403	204759879
10454	5	82443403	83400242	10498	5	82443403	209874191
10455	5	82443403	83405797	10499	5	82443815	82446714
10456	5	82443403	83437132	10500	5	82443815	82446794
10457	5	82443403	83522252	10501	5	82443815	82551111
10458	5	82443403	83560095	10502	5	82443815	82552090
10459	5	82443403	83560204	10503	5	82443815	82555641
10460	5	82443403	83572400	10504	5	82443815	82555670
10461	5	82443403	83607661	10505	5	82443815	82556511
10462	5	82443403	83745342	10506	5	82443815	82559047
10463	5	82443403	83861275	10507	5	82443815	82561535
10464	5	82443403	83861633	10508	5	82443815	82610100
10465	5	82443403	83865653	10509	5	82443815	82676822
10466	5	82443403	83865914	10510	5	82443815	82676901
10467	5	82443403	83865920	10511	5	82443815	82883691
10468	5	82443403	83868010	10512	5	82443815	82954942
10469	5	82443403	84019752	10513	5	82443815	82971688
10470	5	82443403	84065912	10514	5	82443815	83023965
10471	5	82443403	84086632	10515	5	82443815	83094205
10472	5	82443403	84089603	10516	5	82443815	83146355
10473	5	82443403	84104814	10517	5	82443815	83280630
10474	5	82443403	84105175	10518	5	82443815	83281412
10475	5	82443403	84251635	10519	5	82443815	83400242
10476	5	82443403	84252180	10520	5	82443815	83405797
10477	5	82443403	84253030	10521	5	82443815	83437132
10478	5	82443403	84254208	10522	5	82443815	83522252
10479	5	82443403	84314930	10523	5	82443815	83560095
10480	5	82443403	84340523	10524	5	82443815	83560204
10481	5	82443403	84516340	10525	5	82443815	83572400
10482	5	82443403	84706916	10526	5	82443815	83607661

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
10527	5	82443815	83745342	10571	5	82443856	82559047
10528	5	82443815	83861275	10572	5	82443856	82561535
10529	5	82443815	83861633	10573	5	82443856	82610100
10530	5	82443815	83865653	10574	5	82443856	82676822
10531	5	82443815	83865914	10575	5	82443856	82676901
10532	5	82443815	83865920	10576	5	82443856	82883691
10533	5	82443815	83868010	10577	5	82443856	82954942
10534	5	82443815	84019752	10578	5	82443856	82971688
10535	5	82443815	84065912	10579	5	82443856	83023965
10536	5	82443815	84086632	10580	5	82443856	83094205
10537	5	82443815	84089603	10581	5	82443856	83146355
10538	5	82443815	84104814	10582	5	82443856	83280630
10539	5	82443815	84105175	10583	5	82443856	83281412
10540	5	82443815	84251635	10584	5	82443856	83400242
10541	5	82443815	84252180	10585	5	82443856	83405797
10542	5	82443815	84253030	10586	5	82443856	83437132
10543	5	82443815	84254208	10587	5	82443856	83522252
10544	5	82443815	84314930	10588	5	82443856	83560095
10545	5	82443815	84340523	10589	5	82443856	83560204
10546	5	82443815	84516340	10590	5	82443856	83572400
10547	5	82443815	84706916	10591	5	82443856	83607661
10548	5	82443815	84799488	10592	5	82443856	83745342
10549	5	82443815	84801081	10593	5	82443856	83861275
10550	5	82443815	84824103	10594	5	82443856	83861633
10551	5	82443815	84824203	10595	5	82443856	83865653
10552	5	82443815	84824816	10596	5	82443856	83865914
10553	5	82443815	84825422	10597	5	82443856	83865920
10554	5	82443815	84825763	10598	5	82443856	83868010
10555	5	82443815	84825942	10599	5	82443856	84019752
10556	5	82443815	84843411	10600	5	82443856	84065912
10557	5	82443815	84936441	10601	5	82443856	84086632
10558	5	82443815	84936493	10602	5	82443856	84089603
10559	5	82443815	84943705	10603	5	82443856	84104814
10560	5	82443815	169454950	10604	5	82443856	84105175
10561	5	82443815	181522829	10605	5	82443856	84251635
10562	5	82443815	204759879	10606	5	82443856	84252180
10563	5	82443815	209874191	10607	5	82443856	84253030
10564	5	82443856	82446714	10608	5	82443856	84254208
10565	5	82443856	82446794	10609	5	82443856	84314930
10566	5	82443856	82551111	10610	5	82443856	84340523
10567	5	82443856	82552090	10611	5	82443856	84516340
10568	5	82443856	82555641	10612	5	82443856	84706916
10569	5	82443856	82555670	10613	5	82443856	84799488
10570	5	82443856	82556511	10614	5	82443856	84801081

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
10615	5	82443856	84824103	10659	5	82549227	83865914
10616	5	82443856	84824203	10660	5	82549227	83865920
10617	5	82443856	84824816	10661	5	82549227	83868010
10618	5	82443856	84825422	10662	5	82549227	84019752
10619	5	82443856	84825763	10663	5	82549227	84065912
10620	5	82443856	84825942	10664	5	82549227	84086632
10621	5	82443856	84843411	10665	5	82549227	84089603
10622	5	82443856	84936441	10666	5	82549227	84104814
10623	5	82443856	84936493	10667	5	82549227	84105175
10624	5	82443856	84943705	10668	5	82549227	84251635
10625	5	82443856	169454950	10669	5	82549227	84252180
10626	5	82443856	181522829	10670	5	82549227	84253030
10627	5	82443856	204759879	10671	5	82549227	84254208
10628	5	82443856	209874191	10672	5	82549227	84314930
10629	5	82549227	82551111	10673	5	82549227	84340523
10630	5	82549227	82552090	10674	5	82549227	84516340
10631	5	82549227	82555641	10675	5	82549227	84706916
10632	5	82549227	82555670	10676	5	82549227	84799488
10633	5	82549227	82556511	10677	5	82549227	84801081
10634	5	82549227	82559047	10678	5	82549227	84824103
10635	5	82549227	82561535	10679	5	82549227	84824203
10636	5	82549227	82610100	10680	5	82549227	84824816
10637	5	82549227	82676822	10681	5	82549227	84825422
10638	5	82549227	82676901	10682	5	82549227	84825763
10639	5	82549227	82883691	10683	5	82549227	84825942
10640	5	82549227	82954942	10684	5	82549227	84843411
10641	5	82549227	82971688	10685	5	82549227	84936441
10642	5	82549227	83023965	10686	5	82549227	84936493
10643	5	82549227	83094205	10687	5	82549227	84943705
10644	5	82549227	83146355	10688	5	82549227	169454950
10645	5	82549227	83280630	10689	5	82549227	181522829
10646	5	82549227	83281412	10690	5	82549227	204759879
10647	5	82549227	83400242	10691	5	82549227	209874191
10648	5	82549227	83405797	10692	5	82549246	82551111
10649	5	82549227	83437132	10693	5	82549246	82552090
10650	5	82549227	83522252	10694	5	82549246	82555641
10651	5	82549227	83560095	10695	5	82549246	82555670
10652	5	82549227	83560204	10696	5	82549246	82556511
10653	5	82549227	83572400	10697	5	82549246	82559047
10654	5	82549227	83607661	10698	5	82549246	82561535
10655	5	82549227	83745342	10699	5	82549246	82610100
10656	5	82549227	83861275	10700	5	82549246	82676822
10657	5	82549227	83861633	10701	5	82549246	82676901
10658	5	82549227	83865653	10702	5	82549246	82883691

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
10703	5	82549246	82954942	10747	5	82549246	84843411
10704	5	82549246	82971688	10748	5	82549246	84936441
10705	5	82549246	83023965	10749	5	82549246	84936493
10706	5	82549246	83094205	10750	5	82549246	84943705
10707	5	82549246	83146355	10751	5	82549246	169454950
10708	5	82549246	83280630	10752	5	82549246	181522829
10709	5	82549246	83281412	10753	5	82549246	204759879
10710	5	82549246	83400242	10754	5	82549246	209874191
10711	5	82549246	83405797	10755	5	82549299	82551111
10712	5	82549246	83437132	10756	5	82549299	82552090
10713	5	82549246	83522252	10757	5	82549299	82555670
10714	5	82549246	83560095	10758	5	82549299	82556511
10715	5	82549246	83560204	10759	5	82549299	82559047
10716	5	82549246	83572400	10760	5	82549299	82561535
10717	5	82549246	83607661	10761	5	82549299	82610100
10718	5	82549246	83745342	10762	5	82549299	82676822
10719	5	82549246	83861275	10763	5	82549299	82676901
10720	5	82549246	83861633	10764	5	82549299	82883691
10721	5	82549246	83865653	10765	5	82549299	82954942
10722	5	82549246	83865914	10766	5	82549299	82971688
10723	5	82549246	83865920	10767	5	82549299	83023965
10724	5	82549246	83868010	10768	5	82549299	83094205
10725	5	82549246	84019752	10769	5	82549299	83146355
10726	5	82549246	84065912	10770	5	82549299	83280630
10727	5	82549246	84086632	10771	5	82549299	83281412
10728	5	82549246	84089603	10772	5	82549299	83400242
10729	5	82549246	84104814	10773	5	82549299	83405797
10730	5	82549246	84105175	10774	5	82549299	83437132
10731	5	82549246	84251635	10775	5	82549299	83522252
10732	5	82549246	84252180	10776	5	82549299	83560095
10733	5	82549246	84253030	10777	5	82549299	83560204
10734	5	82549246	84254208	10778	5	82549299	83572400
10735	5	82549246	84314930	10779	5	82549299	83607661
10736	5	82549246	84340523	10780	5	82549299	83745342
10737	5	82549246	84316340	10781	5	82549299	83861275
10738	5	82549246	84706916	10782	5	82549299	83861633
10739	5	82549246	84799488	10783	5	82549299	83865653
10740	5	82549246	84801081	10784	5	82549299	83865914
10741	5	82549246	84824103	10785	5	82549299	83865920
10742	5	82549246	84824203	10786	5	82549299	83868010
10743	5	82549246	84824816	10787	5	82549299	84019752
10744	5	82549246	84825422	10788	5	82549299	84065912
10745	5	82549246	84825763	10789	5	82549299	84086632
10746	5	82549246	84825942	10790	5	82549299	84089603

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
10791	5	82549299	84104814	10835	5	82554608	83522252
10792	5	82549299	84105175	10836	5	82554608	83560095
10793	5	82549299	84251635	10837	5	82554608	83560204
10794	5	82549299	84252180	10838	5	82554608	83572400
10795	5	82549299	84253030	10839	5	82554608	83607661
10796	5	82549299	84254208	10840	5	82554608	83745342
10797	5	82549299	84314930	10841	5	82554608	83861275
10798	5	82549299	84340523	10842	5	82554608	83861633
10799	5	82549299	84516340	10843	5	82554608	83863653
10800	5	82549299	84706916	10844	5	82554608	83865914
10801	5	82549299	84799488	10845	5	82554608	83865920
10802	5	82549299	84801081	10846	5	82554608	83868010
10803	5	82549299	84824103	10847	5	82554608	84019752
10804	5	82549299	84824203	10848	5	82554608	84065912
10805	5	82549299	84824816	10849	5	82554608	84086632
10806	5	82549299	84825422	10850	5	82554608	84089603
10807	5	82549299	84825763	10851	5	82554608	84104814
10808	5	82549299	84825942	10852	5	82554608	84105175
10809	5	82549299	84843411	10853	5	82554608	84251635
10810	5	82549299	84936441	10854	5	82554608	84252180
10811	5	82549299	84936493	10855	5	82554608	84253030
10812	5	82549299	84943705	10856	5	82554608	84254208
10813	5	82549299	169454950	10857	5	82554608	84314930
10814	5	82549299	181522829	10858	5	82554608	84340523
10815	5	82549299	204759879	10859	5	82554608	84516340
10816	5	82549299	209874191	10860	5	82554608	84706916
10817	5	82554608	82555670	10861	5	82554608	84799488
10818	5	82554608	82556511	10862	5	82554608	84801081
10819	5	82554608	82559047	10863	5	82554608	84824103
10820	5	82554608	82561535	10864	5	82554608	84824203
10821	5	82554608	82610100	10865	5	82554608	84824816
10822	5	82554608	82676822	10866	5	82554608	84825422
10823	5	82554608	82676901	10867	5	82554608	84825763
10824	5	82554608	82883691	10868	5	82554608	84825942
10825	5	82554608	82954942	10869	5	82554608	84843411
10826	5	82554608	82971688	10870	5	82554608	84936441
10827	5	82554608	83023965	10871	5	82554608	84936493
10828	5	82554608	83094205	10872	5	82554608	84943705
10829	5	82554608	83146355	10873	5	82554608	169454950
10830	5	82554608	83280630	10874	5	82554608	181522829
10831	5	82554608	83281412	10875	5	82554608	204759879
10832	5	82554608	83400242	10876	5	82554608	209874191
10833	5	82554608	83405797	10877	5	82554971	82555670
10834	5	82554608	83437132	10878	5	82554971	82556511

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
10879	5	82554971	82559047	10923	5	82554971	84824103
10880	5	82554971	82561535	10924	5	82554971	84824203
10881	5	82554971	82610100	10925	5	82554971	84824816
10882	5	82554971	82676822	10926	5	82554971	84825422
10883	5	82554971	82676901	10927	5	82554971	84825763
10884	5	82554971	82883691	10928	5	82554971	84825942
10885	5	82554971	82954942	10929	5	82554971	84843411
10886	5	82554971	82971688	10930	5	82554971	84936441
10887	5	82554971	83023965	10931	5	82554971	84936493
10888	5	82554971	83094205	10932	5	82554971	84943705
10889	5	82554971	83146355	10933	5	82554971	169454950
10890	5	82554971	83280630	10934	5	82554971	181522829
10891	5	82554971	83281412	10935	5	82554971	204759879
10892	5	82554971	83400242	10936	5	82554971	209874191
10893	5	82554971	83405797	10937	5	82556313	82556511
10894	5	82554971	83437132	10938	5	82556313	82559047
10895	5	82554971	83522252	10939	5	82556313	82561535
10896	5	82554971	83560095	10940	5	82556313	82610100
10897	5	82554971	83560204	10941	5	82556313	82676822
10898	5	82554971	83572400	10942	5	82556313	82676901
10899	5	82554971	83607661	10943	5	82556313	82883691
10900	5	82554971	83745342	10944	5	82556313	82954942
10901	5	82554971	83861275	10945	5	82556313	82971688
10902	5	82554971	83861633	10946	5	82556313	83023965
10903	5	82554971	83865653	10947	5	82556313	83094205
10904	5	82554971	83865914	10948	5	82556313	83146355
10905	5	82554971	83865920	10949	5	82556313	83280630
10906	5	82554971	83868010	10950	5	82556313	83281412
10907	5	82554971	84019752	10951	5	82556313	83400242
10908	5	82554971	84065912	10952	5	82556313	83405797
10909	5	82554971	84086632	10953	5	82556313	83437132
10910	5	82554971	84089603	10954	5	82556313	83522252
10911	5	82554971	84104814	10955	5	82556313	83560095
10912	5	82554971	84105175	10956	5	82556313	83560204
10913	5	82554971	84251635	10957	5	82556313	83572400
10914	5	82554971	84252180	10958	5	82556313	83607661
10915	5	82554971	84253030	10959	5	82556313	83745342
10916	5	82554971	84254208	10960	5	82556313	83861275
10917	5	82554971	84314930	10961	5	82556313	83861633
10918	5	82554971	84340523	10962	5	82556313	83865653
10919	5	82554971	84516340	10963	5	82556313	83865914
10920	5	82554971	84706916	10964	5	82556313	83865920
10921	5	82554971	84799488	10965	5	82556313	83868010
10922	5	82554971	84801081	10966	5	82556313	84019752

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
10967	5	82556313	84065912	11011	5	82556337	83405797
10968	5	82556313	84086632	11012	5	82556337	83437132
10969	5	82556313	84089603	11013	5	82556337	83522252
10970	5	82556313	84104814	11014	5	82556337	83560095
10971	5	82556313	84105175	11015	5	82556337	83560204
10972	5	82556313	84251635	11016	5	82556337	83572400
10973	5	82556313	84252180	11017	5	82556337	83607661
10974	5	82556313	84253030	11018	5	82556337	83745342
10975	5	82556313	84254208	11019	5	82556337	83861275
10976	5	82556313	84314930	11020	5	82556337	83861633
10977	5	82556313	84340523	11021	5	82556337	83865653
10978	5	82556313	84516340	11022	5	82556337	83865914
10979	5	82556313	84706916	11023	5	82556337	83865920
10980	5	82556313	84799488	11024	5	82556337	83868010
10981	5	82556313	84801081	11025	5	82556337	84019752
10982	5	82556313	84824103	11026	5	82556337	84065912
10983	5	82556313	84824203	11027	5	82556337	84086632
10984	5	82556313	84824816	11028	5	82556337	84089603
10985	5	82556313	84825422	11029	5	82556337	84104814
10986	5	82556313	84825763	11030	5	82556337	84105175
10987	5	82556313	84825942	11031	5	82556337	84251635
10988	5	82556313	84843411	11032	5	82556337	84252180
10989	5	82556313	84936441	11033	5	82556337	84253030
10990	5	82556313	84936493	11034	5	82556337	84254208
10991	5	82556313	84943705	11035	5	82556337	84314930
10992	5	82556313	169454950	11036	5	82556337	84340523
10993	5	82556313	181522829	11037	5	82556337	84516340
10994	5	82556313	204759879	11038	5	82556337	84706916
10995	5	82556313	209874191	11039	5	82556337	84799488
10996	5	82556337	82556511	11040	5	82556337	84801081
10997	5	82556337	82559047	11041	5	82556337	84824103
10998	5	82556337	82561535	11042	5	82556337	84824203
10999	5	82556337	82610100	11043	5	82556337	84824816
11000	5	82556337	82676822	11044	5	82556337	84825422
11001	5	82556337	82676901	11045	5	82556337	84825763
11002	5	82556337	82883691	11046	5	82556337	84825942
11003	5	82556337	82954942	11047	5	82556337	84843411
11004	5	82556337	82971688	11048	5	82556337	84936441
11005	5	82556337	83023965	11049	5	82556337	84936493
11006	5	82556337	83094205	11050	5	82556337	84943705
11007	5	82556337	83146355	11051	5	82556337	169454950
11008	5	82556337	83280630	11052	5	82556337	181522829
11009	5	82556337	83281412	11053	5	82556337	204759879
11010	5	82556337	83400242	11054	5	82556337	209874191

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
11055	5	82556511	82609175	11099	5	82556511	84824203
11056	5	82556511	82610100	11100	5	82556511	84824816
11057	5	82556511	82676822	11101	5	82556511	84825422
11058	5	82556511	82676901	11102	5	82556511	84825763
11059	5	82556511	82883691	11103	5	82556511	84825942
11060	5	82556511	82954942	11104	5	82556511	84843411
11061	5	82556511	82971688	11105	5	82556511	84936441
11062	5	82556511	83023965	11106	5	82556511	84936493
11063	5	82556511	83094205	11107	5	82556511	84943705
11064	5	82556511	83146355	11108	5	82556511	169454950
11065	5	82556511	83280630	11109	5	82556511	181522829
11066	5	82556511	83281412	11110	5	82556511	204759879
11067	5	82556511	83400242	11111	5	82556511	209874191
11068	5	82556511	83405797	11112	5	82609175	82610100
11069	5	82556511	83437132	11113	5	82609175	82676822
11070	5	82556511	83522252	11114	5	82609175	82676901
11071	5	82556511	83560095	11115	5	82609175	82883591
11072	5	82556511	83560204	11116	5	82609175	82954942
11073	5	82556511	83572400	11117	5	82609175	82971688
11074	5	82556511	83607661	11118	5	82609175	83023965
11075	5	82556511	83745342	11119	5	82609175	83094205
11076	5	82556511	83861275	11120	5	82609175	83146355
11077	5	82556511	83861633	11121	5	82609175	83280630
11078	5	82556511	83865653	11122	5	82609175	83281412
11079	5	82556511	83865914	11123	5	82609175	83400242
11080	5	82556511	83865920	11124	5	82609175	83405797
11081	5	82556511	83868010	11125	5	82609175	83437132
11082	5	82556511	84019752	11126	5	82609175	83522252
11083	5	82556511	84065912	11127	5	82609175	83560095
11084	5	82556511	84086632	11128	5	82609175	83560204
11085	5	82556511	84089603	11129	5	82609175	83572400
11086	5	82556511	84104814	11130	5	82609175	83607661
11087	5	82556511	84105175	11131	5	82609175	83745342
11088	5	82556511	84251635	11132	5	82609175	83861275
11089	5	82556511	84252180	11133	5	82609175	83861633
11090	5	82556511	84253030	11134	5	82609175	83865653
11091	5	82556511	84254208	11135	5	82609175	83865914
11092	5	82556511	84314930	11136	5	82609175	83865920
11093	5	82556511	84340523	11137	5	82609175	83868010
11094	5	82556511	84516340	11138	5	82609175	84019752
11095	5	82556511	84706916	11139	5	82609175	84065912
11096	5	82556511	84799488	11140	5	82609175	84086632
11097	5	82556511	84801081	11141	5	82609175	84089603
11098	5	82556511	84824103	11142	5	82609175	84104814

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
11143	5	82609175	84105175	11187	5	82675654	83861275
11144	5	82609175	84251635	11188	5	82675654	83861633
11145	5	82609175	84252180	11189	5	82675654	83865653
11146	5	82609175	84253030	11190	5	82675654	83865914
11147	5	82609175	84254208	11191	5	82675654	83865920
11148	5	82609175	84314930	11192	5	82675654	83868010
11149	5	82609175	84340523	11193	5	82675654	84019752
11150	5	82609175	84516340	11194	5	82675654	84065912
11151	5	82609175	84706916	11195	5	82675654	84086632
11152	5	82609175	84799488	11196	5	82675654	84089603
11153	5	82609175	84801081	11197	5	82675654	84104814
11154	5	82609175	84824103	11198	5	82675654	84105175
11155	5	82609175	84824203	11199	5	82675654	84251635
11156	5	82609175	84824816	11200	5	82675654	84252180
11157	5	82609175	84825422	11201	5	82675654	84253030
11158	5	82609175	84825763	11202	5	82675654	84254208
11159	5	82609175	84825942	11203	5	82675654	84314930
11160	5	82609175	84843411	11204	5	82675654	84340523
11161	5	82609175	84936441	11205	5	82675654	84516340
11162	5	82609175	84936493	11206	5	82675654	84706916
11163	5	82609175	84943705	11207	5	82675654	84799488
11164	5	82609175	169454950	11208	5	82675654	84801081
11165	5	82609175	181522829	11209	5	82675654	84824103
11166	5	82609175	204759879	11210	5	82675654	84824203
11167	5	82609175	209874191	11211	5	82675654	84824816
11168	5	82675654	82676822	11212	5	82675654	84825422
11169	5	82675654	82676901	11213	5	82675654	84825763
11170	5	82675654	82883691	11214	5	82675654	84825942
11171	5	82675654	82954942	11215	5	82675654	84843411
11172	5	82675654	82971688	11216	5	82675654	84936441
11173	5	82675654	83023965	11217	5	82675654	84936493
11174	5	82675654	83094205	11218	5	82675654	84943705
11175	5	82675654	83146355	11219	5	82675654	169454950
11176	5	82675654	83280630	11220	5	82675654	181522829
11177	5	82675654	83281412	11221	5	82675654	204759879
11178	5	82675654	83400242	11222	5	82675654	209874191
11179	5	82675654	83405797	11223	5	82675825	82676822
11180	5	82675654	83437132	11224	5	82675825	82676901
11181	5	82675654	83522252	11225	5	82675825	82883691
11182	5	82675654	83560095	11226	5	82675825	82954942
11183	5	82675654	83560204	11227	5	82675825	82971688
11184	5	82675654	83572400	11228	5	82675825	83023965
11185	5	82675654	83607661	11229	5	82675825	83094205
11186	5	82675654	83745342	11230	5	82675825	83146355

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
11231	5	82675825	83280630	11275	5	82675825	181522829
11232	5	82675825	83281412	11276	5	82675825	204759879
11233	5	82675825	83400242	11277	5	82675825	209874191
11234	5	82675825	83405797	11278	5	82882273	82883691
11235	5	82675825	83437132	11279	5	82882273	82954942
11236	5	82675825	83522252	11280	5	82882273	82971688
11237	5	82675825	83560095	11281	5	82882273	83023965
11238	5	82675825	83560204	11282	5	82882273	83094205
11239	5	82675825	83572400	11283	5	82882273	83146355
11240	5	82675825	83607661	11284	5	82882273	83280630
11241	5	82675825	83745342	11285	5	82882273	83281412
11242	5	82675825	83861275	11286	5	82882273	83400242
11243	5	82675825	83861633	11287	5	82882273	83405797
11244	5	82675825	83865653	11288	5	82882273	83437132
11245	5	82675825	83865914	11289	5	82882273	83522252
11246	5	82675825	83865920	11290	5	82882273	83560095
11247	5	82675825	83868010	11291	5	82882273	83560204
11248	5	82675825	84019752	11292	5	82882273	83572400
11249	5	82675825	84065912	11293	5	82882273	83607661
11250	5	82675825	84086632	11294	5	82882273	83745342
11251	5	82675825	84089603	11295	5	82882273	83861275
11252	5	82675825	84104814	11296	5	82882273	83861633
11253	5	82675825	84105175	11297	5	82882273	83865653
11254	5	82675825	84251635	11298	5	82882273	83865914
11255	5	82675825	84252180	11299	5	82882273	83865920
11256	5	82675825	84253030	11300	5	82882273	83868010
11257	5	82675825	84254208	11301	5	82882273	84019752
11258	5	82675825	84314930	11302	5	82882273	84065912
11259	5	82675825	84340523	11303	5	82882273	84086632
11260	5	82675825	84516340	11304	5	82882273	84089603
11261	5	82675825	84706916	11305	5	82882273	84104814
11262	5	82675825	84799488	11306	5	82882273	84105175
11263	5	82675825	84801081	11307	5	82882273	84251635
11264	5	82675825	84824103	11308	5	82882273	84252180
11265	5	82675825	84824203	11309	5	82882273	84253030
11266	5	82675825	84824816	11310	5	82882273	84254208
11267	5	82675825	84825422	11311	5	82882273	84314930
11268	5	82675825	84825763	11312	5	82882273	84340523
11269	5	82675825	84825942	11313	5	82882273	84516340
11270	5	82675825	84843411	11314	5	82882273	84706916
11271	5	82675825	84936441	11315	5	82882273	84799488
11272	5	82675825	84936493	11316	5	82882273	84801081
11273	5	82675825	84943705	11317	5	82882273	84824103
11274	5	82675825	169454950	11318	5	82882273	84824203

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
11319	5	82882273	84824816	11363	5	82953053	84314930
11320	5	82882273	84825422	11364	5	82953053	84340523
11321	5	82882273	84825763	11365	5	82953053	84516340
11322	5	82882273	84825942	11366	5	82953053	84706916
11323	5	82882273	84843411	11367	5	82953053	84799488
11324	5	82882273	84936441	11368	5	82953053	84801081
11325	5	82882273	84936493	11369	5	82953053	84824103
11326	5	82882273	84943705	11370	5	82953053	84824203
11327	5	82882273	169454950	11371	5	82953053	84824816
11328	5	82882273	181522829	11372	5	82953053	84825422
11329	5	82882273	204759879	11373	5	82953053	84825763
11330	5	82882273	209874191	11374	5	82953053	84825942
11331	5	82953053	82954942	11375	5	82953053	84843411
11332	5	82953053	82971688	11376	5	82953053	84936441
11333	5	82953053	83023965	11377	5	82953053	84936493
11334	5	82953053	83094205	11378	5	82953053	84943705
11335	5	82953053	83146355	11379	5	82953053	169454950
11336	5	82953053	83280630	11380	5	82953053	181522829
11337	5	82953053	83281412	11381	5	82953053	204759879
11338	5	82953053	83400242	11382	5	82953053	209874191
11339	5	82953053	83405797	11383	5	82971168	82971688
11340	5	82953053	83437132	11384	5	82971168	83023965
11341	5	82953053	83522252	11385	5	82971168	83094205
11342	5	82953053	83560095	11386	5	82971168	83146355
11343	5	82953053	83560204	11387	5	82971168	83280630
11344	5	82953053	83572400	11388	5	82971168	83281412
11345	5	82953053	83607661	11389	5	82971168	83400242
11346	5	82953053	83745342	11390	5	82971168	83405797
11347	5	82953053	83861275	11391	5	82971168	83437132
11348	5	82953053	83861633	11392	5	82971168	83522252
11349	5	82953053	83865653	11393	5	82971168	83560095
11350	5	82953053	83865914	11394	5	82971168	83560204
11351	5	82953053	83865920	11395	5	82971168	83572400
11352	5	82953053	83868010	11396	5	82971168	83607661
11353	5	82953053	84019752	11397	5	82971168	83745342
11354	5	82953053	84065912	11398	5	82971168	83861275
11355	5	82953053	84086632	11399	5	82971168	83861633
11356	5	82953053	84089603	11400	5	82971168	83865653
11357	5	82953053	84104814	11401	5	82971168	83865914
11358	5	82953053	84105175	11402	5	82971168	83865920
11359	5	82953053	84251635	11403	5	82971168	83868010
11360	5	82953053	84252180	11404	5	82971168	84019752
11361	5	82953053	84253030	11405	5	82971168	84065912
11362	5	82953053	84254208	11406	5	82971168	84086632

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
11407	5	82971168	84089603	11451	5	83023500	83865914
11408	5	82971168	84104814	11452	5	83023500	83865920
11409	5	82971168	84105175	11453	5	83023500	83868010
11410	5	82971168	84251635	11454	5	83023500	84019752
11411	5	82971168	84252180	11455	5	83023500	84065912
11412	5	82971168	84253030	11456	5	83023500	84086632
11413	5	82971168	84254208	11457	5	83023500	84089603
11414	5	82971168	84314930	11458	5	83023500	84104814
11415	5	82971168	84340523	11459	5	83023500	84105175
11416	5	82971168	84516340	11460	5	83023500	84251635
11417	5	82971168	84706916	11461	5	83023500	84252180
11418	5	82971168	84799488	11462	5	83023500	84253030
11419	5	82971168	84801081	11463	5	83023500	84254208
11420	5	82971168	84824103	11464	5	83023500	84314930
11421	5	82971168	84824203	11465	5	83023500	84340523
11422	5	82971168	84824816	11466	5	83023500	84516340
11423	5	82971168	84825422	11467	5	83023500	84706916
11424	5	82971168	84825763	11468	5	83023500	84799488
11425	5	82971168	84825942	11469	5	83023500	84801081
11426	5	82971168	84843411	11470	5	83023500	84824103
11427	5	82971168	84936441	11471	5	83023500	84824203
11428	5	82971168	84936493	11472	5	83023500	84824816
11429	5	82971168	84943705	11473	5	83023500	84825422
11430	5	82971168	169454950	11474	5	83023500	84825763
11431	5	82971168	181522829	11475	5	83023500	84825942
11432	5	82971168	204759879	11476	5	83023500	84843411
11433	5	82971168	209874191	11477	5	83023500	84936441
11434	5	83023500	83023965	11478	5	83023500	84936493
11435	5	83023500	83094205	11479	5	83023500	84943705
11436	5	83023500	83146355	11480	5	83023500	169454950
11437	5	83023500	83280630	11481	5	83023500	181522829
11438	5	83023500	83281412	11482	5	83023500	204759879
11439	5	83023500	83400242	11483	5	83023500	209874191
11440	5	83023500	83405797	11484	5	83093332	83094205
11441	5	83023500	83437132	11485	5	83093332	83146355
11442	5	83023500	83522252	11486	5	83093332	83280630
11443	5	83023500	83560095	11487	5	83093332	83281412
11444	5	83023500	83560204	11488	5	83093332	83400242
11445	5	83023500	83572400	11489	5	83093332	83405797
11446	5	83023500	83607661	11490	5	83093332	83437132
11447	5	83023500	83745342	11491	5	83093332	83522252
11448	5	83023500	83861275	11492	5	83093332	83560095
11449	5	83023500	83861633	11493	5	83093332	83560204
11450	5	83023500	83865653	11494	5	83093332	83572400

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
11495	5	83093332	83607661	11539	5	83145879	83522252
11496	5	83093332	83745342	11540	5	83145879	83560095
11497	5	83093332	83861275	11541	5	83145879	83560204
11498	5	83093332	83861633	11542	5	83145879	83572400
11499	5	83093332	83865653	11543	5	83145879	83607661
11500	5	83093332	83865914	11544	5	83145879	83745342
11501	5	83093332	83865920	11545	5	83145879	83861275
11502	5	83093332	83868010	11546	5	83145879	83861633
11503	5	83093332	84019752	11547	5	83145879	83865653
11504	5	83093332	84065912	11548	5	83145879	83865914
11505	5	83093332	84086632	11549	5	83145879	83865920
11506	5	83093332	84089603	11550	5	83145879	83868010
11507	5	83093332	84104814	11551	5	83145879	84019752
11508	5	83093332	84105175	11552	5	83145879	84065912
11509	5	83093332	84251635	11553	5	83145879	84086632
11510	5	83093332	84252180	11554	5	83145879	84089603
11511	5	83093332	84253030	11555	5	83145879	84104814
11512	5	83093332	84254208	11556	5	83145879	84105175
11513	5	83093332	84314930	11557	5	83145879	84251635
11514	5	83093332	84340523	11558	5	83145879	84252180
11515	5	83093332	84516340	11559	5	83145879	84253030
11516	5	83093332	84706916	11560	5	83145879	84254208
11517	5	83093332	84799488	11561	5	83145879	84314930
11518	5	83093332	84801081	11562	5	83145879	84340523
11519	5	83093332	84824103	11563	5	83145879	84516340
11520	5	83093332	84824203	11564	5	83145879	84706916
11521	5	83093332	84824816	11565	5	83145879	84799488
11522	5	83093332	84825422	11566	5	83145879	84801081
11523	5	83093332	84825763	11567	5	83145879	84824103
11524	5	83093332	84825942	11568	5	83145879	84824203
11525	5	83093332	84843411	11569	5	83145879	84824816
11526	5	83093332	84936441	11570	5	83145879	84825422
11527	5	83093332	84936493	11571	5	83145879	84825763
11528	5	83093332	84943705	11572	5	83145879	84825942
11529	5	83093332	169454950	11573	5	83145879	84843411
11530	5	83093332	181522829	11574	5	83145879	84936441
11531	5	83093332	204759879	11575	5	83145879	84936493
11532	5	83093332	209874191	11576	5	83145879	84943705
11533	5	83145879	83146355	11577	5	83145879	169454950
11534	5	83145879	83280630	11578	5	83145879	181522829
11535	5	83145879	83281412	11579	5	83145879	204759879
11536	5	83145879	83400242	11580	5	83145879	209874191
11537	5	83145879	83405797	11581	5	83277783	83280630
11538	5	83145879	83437132	11582	5	83277783	83281412

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
11583	5	83277783	83400242	11627	5	83277783	209874191
11584	5	83277783	83405797	11628	5	83277785	83280630
11585	5	83277783	83437132	11629	5	83277785	83281412
11586	5	83277783	83522252	11630	5	83277785	83400242
11587	5	83277783	83560095	11631	5	83277785	83405797
11588	5	83277783	83560204	11632	5	83277785	83437132
11589	5	83277783	83572400	11633	5	83277785	83522252
11590	5	83277783	83607661	11634	5	83277785	83560095
11591	5	83277783	83745342	11635	5	83277785	83560204
11592	5	83277783	83861275	11636	5	83277785	83572400
11593	5	83277783	83861633	11637	5	83277785	83607661
11594	5	83277783	83865653	11638	5	83277785	83745342
11595	5	83277783	83865914	11639	5	83277785	83861275
11596	5	83277783	83865920	11640	5	83277785	83861633
11597	5	83277783	83868010	11641	5	83277785	83865653
11598	5	83277783	84019752	11642	5	83277785	83865914
11599	5	83277783	84065912	11643	5	83277785	83865920
11600	5	83277783	84086632	11644	5	83277785	83868010
11601	5	83277783	84089603	11645	5	83277785	84019752
11602	5	83277783	84104814	11646	5	83277785	84065912
11603	5	83277783	84105175	11647	5	83277785	84086632
11604	5	83277783	84251635	11648	5	83277785	84089603
11605	5	83277783	84252180	11649	5	83277785	84104814
11606	5	83277783	84253030	11650	5	83277785	84105175
11607	5	83277783	84254208	11651	5	83277785	84251635
11608	5	83277783	84314930	11652	5	83277785	84252180
11609	5	83277783	84340523	11653	5	83277785	84253030
11610	5	83277783	84516340	11654	5	83277785	84254208
11611	5	83277783	84706916	11655	5	83277785	84314930
11612	5	83277783	84799488	11656	5	83277785	84340523
11613	5	83277783	84801081	11657	5	83277785	84516340
11614	5	83277783	84824103	11658	5	83277785	84706916
11615	5	83277783	84824203	11659	5	83277785	84799488
11616	5	83277783	84824816	11660	5	83277785	84801081
11617	5	83277783	84825422	11661	5	83277785	84824103
11618	5	83277783	84825763	11662	5	83277785	84824203
11619	5	83277783	84825942	11663	5	83277785	84824816
11620	5	83277783	84843411	11664	5	83277785	84825422
11621	5	83277783	84936441	11665	5	83277785	84825763
11622	5	83277783	84936493	11666	5	83277785	84825942
11623	5	83277783	84943705	11667	5	83277785	84843411
11624	5	83277783	169454950	11668	5	83277785	84936441
11625	5	83277783	181522829	11669	5	83277785	84936493
11626	5	83277783	204759879	11670	5	83277785	84943705

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
11671	5	83277785	169454950	11715	5	83279034	84936441
11672	5	83277785	181522829	11716	5	83279034	84936493
11673	5	83277785	204759879	11717	5	83279034	84943705
11674	5	83277785	209874191	11718	5	83279034	169454950
11675	5	83279034	83280630	11719	5	83279034	181522829
11676	5	83279034	83281412	11720	5	83279034	204759879
11677	5	83279034	83400242	11721	5	83279034	209874191
11678	5	83279034	83405797	11722	5	83397014	83400242
11679	5	83279034	83437132	11723	5	83397014	83405797
11680	5	83279034	83522252	11724	5	83397014	83437132
11681	5	83279034	83560095	11725	5	83397014	83522252
11682	5	83279034	83560204	11726	5	83397014	83560095
11683	5	83279034	83572400	11727	5	83397014	83560204
11684	5	83279034	83607661	11728	5	83397014	83572400
11685	5	83279034	83745342	11729	5	83397014	83607661
11686	5	83279034	83861275	11730	5	83397014	83745342
11687	5	83279034	83861633	11731	5	83397014	83861275
11688	5	83279034	83865653	11732	5	83397014	83861633
11689	5	83279034	83865914	11733	5	83397014	83865653
11690	5	83279034	83865920	11734	5	83397014	83865914
11691	5	83279034	83868010	11735	5	83397014	83865920
11692	5	83279034	84019752	11736	5	83397014	83868010
11693	5	83279034	84065912	11737	5	83397014	84019752
11694	5	83279034	84086632	11738	5	83397014	84065912
11695	5	83279034	84089603	11739	5	83397014	84086632
11696	5	83279034	84104814	11740	5	83397014	84089603
11697	5	83279034	84105175	11741	5	83397014	84104814
11698	5	83279034	84251635	11742	5	83397014	84105175
11699	5	83279034	84252180	11743	5	83397014	84251635
11700	5	83279034	84253030	11744	5	83397014	84252180
11701	5	83279034	84254208	11745	5	83397014	84253030
11702	5	83279034	84314930	11746	5	83397014	84254208
11703	5	83279034	84340523	11747	5	83397014	84314930
11704	5	83279034	84516340	11748	5	83397014	84340523
11705	5	83279034	84706916	11749	5	83397014	84516340
11706	5	83279034	84799488	11750	5	83397014	84706916
11707	5	83279034	84801081	11751	5	83397014	84799488
11708	5	83279034	84824103	11752	5	83397014	84801081
11709	5	83279034	84824203	11753	5	83397014	84824103
11710	5	83279034	84824816	11754	5	83397014	84824203
11711	5	83279034	84825422	11755	5	83397014	84824816
11712	5	83279034	84825763	11756	5	83397014	84825422
11713	5	83279034	84825942	11757	5	83397014	84825763
11714	5	83279034	84843411	11758	5	83397014	84825942

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
11759	5	83397014	84843411	11803	5	83402967	84843411
11760	5	83397014	84936441	11804	5	83402967	84936441
11761	5	83397014	84936493	11805	5	83402967	84936493
11762	5	83397014	84943705	11806	5	83402967	84943705
11763	5	83397014	169454950	11807	5	83402967	169454950
11764	5	83397014	181522829	11808	5	83402967	181522829
11765	5	83397014	204759879	11809	5	83402967	204759879
11766	5	83397014	209874191	11810	5	83402967	209874191
11767	5	83402967	83405797	11811	5	83435480	83437132
11768	5	83402967	83437132	11812	5	83435480	83522252
11769	5	83402967	83522252	11813	5	83435480	83560095
11770	5	83402967	83560095	11814	5	83435480	83560204
11771	5	83402967	83560204	11815	5	83435480	83572400
11772	5	83402967	83572400	11816	5	83435480	83607661
11773	5	83402967	83607661	11817	5	83435480	83745342
11774	5	83402967	83745342	11818	5	83435480	83861275
11775	5	83402967	83861275	11819	5	83435480	83861633
11776	5	83402967	83861633	11820	5	83435480	83865653
11777	5	83402967	83865653	11821	5	83435480	83865914
11778	5	83402967	83865914	11822	5	83435480	83865920
11779	5	83402967	83865920	11823	5	83435480	83868010
11780	5	83402967	83868010	11824	5	83435480	84019752
11781	5	83402967	84019752	11825	5	83435480	84065912
11782	5	83402967	84065912	11826	5	83435480	84086632
11783	5	83402967	84086632	11827	5	83435480	84089603
11784	5	83402967	84089603	11828	5	83435480	84104814
11785	5	83402967	84104814	11829	5	83435480	84105175
11786	5	83402967	84105175	11830	5	83435480	84251635
11787	5	83402967	84251635	11831	5	83435480	84252180
11788	5	83402967	84252180	11832	5	83435480	84253030
11789	5	83402967	84253030	11833	5	83435480	84254208
11790	5	83402967	84254208	11834	5	83435480	84314930
11791	5	83402967	84314930	11835	5	83435480	84340523
11792	5	83402967	84340523	11836	5	83435480	84516340
11793	5	83402967	84516340	11837	5	83435480	84706916
11794	5	83402967	84706916	11838	5	83435480	84799488
11795	5	83402967	84799488	11839	5	83435480	84801081
11796	5	83402967	84801081	11840	5	83435480	84824103
11797	5	83402967	84824103	11841	5	83435480	84824203
11798	5	83402967	84824203	11842	5	83435480	84824816
11799	5	83402967	84824816	11843	5	83435480	84825422
11800	5	83402967	84825422	11844	5	83435480	84825763
11801	5	83402967	84825763	11845	5	83435480	84825942
11802	5	83402967	84825942	11846	5	83435480	84843411

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
11847	5	83435480	84936441	11891	5	83521923	84943705
11848	5	83435480	84936493	11892	5	83521923	169454950
11849	5	83435480	84943705	11893	5	83521923	181522829
11850	5	83435480	169454950	11894	5	83521923	204759879
11851	5	83435480	181522829	11895	5	83521923	209874191
11852	5	83435480	204759879	11896	5	83557023	83560095
11853	5	83435480	209874191	11897	5	83557023	83560204
11854	5	83521923	83522252	11898	5	83557023	83572400
11855	5	83521923	83560095	11899	5	83557023	83607661
11856	5	83521923	83560204	11900	5	83557023	83745342
11857	5	83521923	83572400	11901	5	83557023	83861275
11858	5	83521923	83607661	11902	5	83557023	83861633
11859	5	83521923	83745342	11903	5	83557023	83865653
11860	5	83521923	83861275	11904	5	83557023	83865914
11861	5	83521923	83861633	11905	5	83557023	83865920
11862	5	83521923	83865653	11906	5	83557023	83868010
11863	5	83521923	83865914	11907	5	83557023	84019752
11864	5	83521923	83865920	11908	5	83557023	84065912
11865	5	83521923	83868010	11909	5	83557023	84086632
11866	5	83521923	84019752	11910	5	83557023	84089603
11867	5	83521923	84065912	11911	5	83557023	84104814
11868	5	83521923	84086632	11912	5	83557023	84105175
11869	5	83521923	84089603	11913	5	83557023	84251635
11870	5	83521923	84104814	11914	5	83557023	84252180
11871	5	83521923	84105175	11915	5	83557023	84253030
11872	5	83521923	84251635	11916	5	83557023	84254208
11873	5	83521923	84252180	11917	5	83557023	84314930
11874	5	83521923	84253030	11918	5	83557023	84340523
11875	5	83521923	84254208	11919	5	83557023	84516340
11876	5	83521923	84314930	11920	5	83557023	84706916
11877	5	83521923	84340523	11921	5	83557023	84799488
11878	5	83521923	84516340	11922	5	83557023	84801081
11879	5	83521923	84706916	11923	5	83557023	84824103
11880	5	83521923	84799488	11924	5	83557023	84824203
11881	5	83521923	84801081	11925	5	83557023	84824816
11882	5	83521923	84824103	11926	5	83557023	84825422
11883	5	83521923	84824203	11927	5	83557023	84825763
11884	5	83521923	84824816	11928	5	83557023	84825942
11885	5	83521923	84825422	11929	5	83557023	84843411
11886	5	83521923	84825763	11930	5	83557023	84936441
11887	5	83521923	84825942	11931	5	83557023	84936493
11888	5	83521923	84843411	11932	5	83557023	84943705
11889	5	83521923	84936441	11933	5	83557023	169454950
11890	5	83521923	84936493	11934	5	83557023	181522829

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
11935	5	83557023	204759879	11979	5	83567769	83745342
11936	5	83557023	209874191	11980	5	83567769	83861275
11937	5	83560204	83567769	11981	5	83567769	83861633
11938	5	83560204	83572400	11982	5	83567769	83865653
11939	5	83560204	83607661	11983	5	83567769	83865914
11940	5	83560204	83745342	11984	5	83567769	83865920
11941	5	83560204	83861275	11985	5	83567769	83868010
11942	5	83560204	83861633	11986	5	83567769	84019752
11943	5	83560204	83865653	11987	5	83567769	84065912
11944	5	83560204	83865914	11988	5	83567769	84086632
11945	5	83560204	83865920	11989	5	83567769	84089603
11946	5	83560204	83868010	11990	5	83567769	84104814
11947	5	83560204	84019752	11991	5	83567769	84105175
11948	5	83560204	84065912	11992	5	83567769	84251635
11949	5	83560204	84086632	11993	5	83567769	84252180
11950	5	83560204	84089603	11994	5	83567769	84253030
11951	5	83560204	84104814	11995	5	83567769	84254208
11952	5	83560204	84105175	11996	5	83567769	84314930
11953	5	83560204	84251635	11997	5	83567769	84340523
11954	5	83560204	84252180	11998	5	83567769	84516340
11955	5	83560204	84253030	11999	5	83567769	84706916
11956	5	83560204	84254208	12000	5	83567769	84799488
11957	5	83560204	84314930	12001	5	83567769	84801081
11958	5	83560204	84340523	12002	5	83567769	84824103
11959	5	83560204	84516340	12003	5	83567769	84824203
11960	5	83560204	84706916	12004	5	83567769	84824816
11961	5	83560204	84799488	12005	5	83567769	84825422
11962	5	83560204	84801081	12006	5	83567769	84825763
11963	5	83560204	84824103	12007	5	83567769	84825942
11964	5	83560204	84824203	12008	5	83567769	84843411
11965	5	83560204	84824816	12009	5	83567769	84936441
11966	5	83560204	84825422	12010	5	83567769	84936493
11967	5	83560204	84825763	12011	5	83567769	84943705
11968	5	83560204	84825942	12012	5	83567769	169454950
11969	5	83560204	84843411	12013	5	83567769	181522829
11970	5	83560204	84936441	12014	5	83567769	204759879
11971	5	83560204	84936493	12015	5	83567769	209874191
11972	5	83560204	84943705	12016	5	83606990	83607661
11973	5	83560204	169454950	12017	5	83606990	83745342
11974	5	83560204	181522829	12018	5	83606990	83861275
11975	5	83560204	204759879	12019	5	83606990	83861633
11976	5	83560204	209874191	12020	5	83606990	83865653
11977	5	83567769	83572400	12021	5	83606990	83865914
11978	5	83567769	83607661	12022	5	83606990	83865920

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
12023	5	83606990	83868010	12067	5	83743980	84251635
12024	5	83606990	84019752	12068	5	83743980	84252180
12025	5	83606990	84065912	12069	5	83743980	84253030
12026	5	83606990	84086632	12070	5	83743980	84254208
12027	5	83606990	84089603	12071	5	83743980	84314930
12028	5	83606990	84104814	12072	5	83743980	84340523
12029	5	83606990	84105175	12073	5	83743980	84516340
12030	5	83606990	84251635	12074	5	83743980	84706916
12031	5	83606990	84252180	12075	5	83743980	84799488
12032	5	83606990	84253030	12076	5	83743980	84801081
12033	5	83606990	84254208	12077	5	83743980	84824103
12034	5	83606990	84314930	12078	5	83743980	84824203
12035	5	83606990	84340523	12079	5	83743980	84824816
12036	5	83606990	84516340	12080	5	83743980	84825422
12037	5	83606990	84706916	12081	5	83743980	84825763
12038	5	83606990	84799488	12082	5	83743980	84825942
12039	5	83606990	84801081	12083	5	83743980	84843411
12040	5	83606990	84824103	12084	5	83743980	84936441
12041	5	83606990	84824203	12085	5	83743980	84936493
12042	5	83606990	84824816	12086	5	83743980	84943705
12043	5	83606990	84825422	12087	5	83743980	169454950
12044	5	83606990	84825763	12088	5	83743980	181522829
12045	5	83606990	84825942	12089	5	83743980	204759879
12046	5	83606990	84843411	12090	5	83743980	209874191
12047	5	83606990	84936441	12091	5	83859479	83861275
12048	5	83606990	84936493	12092	5	83859479	83861633
12049	5	83606990	84943705	12093	5	83859479	83865653
12050	5	83606990	169454950	12094	5	83859479	83865914
12051	5	83606990	181522829	12095	5	83859479	83865920
12052	5	83606990	204759879	12096	5	83859479	83868010
12053	5	83606990	209874191	12097	5	83859479	84019752
12054	5	83743980	83745342	12098	5	83859479	84065912
12055	5	83743980	83861275	12099	5	83859479	84086632
12056	5	83743980	83861633	12100	5	83859479	84089603
12057	5	83743980	83865653	12101	5	83859479	84104814
12058	5	83743980	83865914	12102	5	83859479	84105175
12059	5	83743980	83865920	12103	5	83859479	84251635
12060	5	83743980	83868010	12104	5	83859479	84252180
12061	5	83743980	84019752	12105	5	83859479	84253030
12062	5	83743980	84065912	12106	5	83859479	84254208
12063	5	83743980	84086632	12107	5	83859479	84314930
12064	5	83743980	84089603	12108	5	83859479	84340523
12065	5	83743980	84104814	12109	5	83859479	84516340
12066	5	83743980	84105175	12110	5	83859479	84706916

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
12111	5	83859479	84799488	12155	5	83860797	84936493
12112	5	83859479	84801081	12156	5	83860797	84943705
12113	5	83859479	84824103	12157	5	83860797	169454950
12114	5	83859479	84824203	12158	5	83860797	181522829
12115	5	83859479	84824816	12159	5	83860797	204759879
12116	5	83859479	84825422	12160	5	83860797	209874191
12117	5	83859479	84825763	12161	5	83861275	83861394
12118	5	83859479	84825942	12162	5	83861275	83865653
12119	5	83859479	84843411	12163	5	83861275	83865914
12120	5	83859479	84936441	12164	5	83861275	83865920
12121	5	83859479	84936493	12165	5	83861275	83868010
12122	5	83859479	84943705	12166	5	83861275	84019752
12123	5	83859479	169454950	12167	5	83861275	84065912
12124	5	83859479	181522829	12168	5	83861275	84086632
12125	5	83859479	204759879	12169	5	83861275	84089603
12126	5	83859479	209874191	12170	5	83861275	84104814
12127	5	83860797	83865653	12171	5	83861275	84105175
12128	5	83860797	83865914	12172	5	83861275	84251635
12129	5	83860797	83865920	12173	5	83861275	84252180
12130	5	83860797	83868010	12174	5	83861275	84253050
12131	5	83860797	84019752	12175	5	83861275	84254208
12132	5	83860797	84065912	12176	5	83861275	84314930
12133	5	83860797	84086632	12177	5	83861275	84340523
12134	5	83860797	84089603	12178	5	83861275	84516340
12135	5	83860797	84104814	12179	5	83861275	84706916
12136	5	83860797	84105175	12180	5	83861275	84799488
12137	5	83860797	84251635	12181	5	83861275	84801081
12138	5	83860797	84252180	12182	5	83861275	84824103
12139	5	83860797	84253030	12183	5	83861275	84824203
12140	5	83860797	84254208	12184	5	83861275	84824816
12141	5	83860797	84314930	12185	5	83861275	84825422
12142	5	83860797	84340523	12186	5	83861275	84825763
12143	5	83860797	84516340	12187	5	83861275	84825942
12144	5	83860797	84706916	12188	5	83861275	84843411
12145	5	83860797	84799488	12189	5	83861275	84936441
12146	5	83860797	84801081	12190	5	83861275	84936493
12147	5	83860797	84824103	12191	5	83861275	84943705
12148	5	83860797	84824203	12192	5	83861275	169454950
12149	5	83860797	84824816	12193	5	83861275	181522829
12150	5	83860797	84825422	12194	5	83861275	204759879
12151	5	83860797	84825763	12195	5	83861275	209874191
12152	5	83860797	84825942	12196	5	83861394	83865653
12153	5	83860797	84843411	12197	5	83861394	83865914
12154	5	83860797	84936441	12198	5	83861394	83865920

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
12199	5	83861394	83868010	12243	5	83864692	84254208
12200	5	83861394	84019752	12244	5	83864692	84314930
12201	5	83861394	84065912	12245	5	83864692	84340523
12202	5	83861394	84086632	12246	5	83864692	84516340
12203	5	83861394	84089603	12247	5	83864692	84706916
12204	5	83861394	84104814	12248	5	83864692	84799488
12205	5	83861394	84105175	12249	5	83864692	84801081
12206	5	83861394	84251635	12250	5	83864692	84824103
12207	5	83861394	84252180	12251	5	83864692	84824203
12208	5	83861394	84253030	12252	5	83864692	84824816
12209	5	83861394	84254208	12253	5	83864692	84825422
12210	5	83861394	84314930	12254	5	83864692	84825763
12211	5	83861394	84340523	12255	5	83864692	84825942
12212	5	83861394	84516340	12256	5	83864692	84843411
12213	5	83861394	84706916	12257	5	83864692	84936441
12214	5	83861394	84799488	12258	5	83864692	84936493
12215	5	83861394	84801081	12259	5	83864692	84943705
12216	5	83861394	84824103	12260	5	83864692	169454950
12217	5	83861394	84824203	12261	5	83864692	181522829
12218	5	83861394	84824816	12262	5	83864692	204759879
12219	5	83861394	84825422	12263	5	83864692	209874191
12220	5	83861394	84825763	12264	5	83867332	83868010
12221	5	83861394	84825942	12265	5	83867332	84019752
12222	5	83861394	84843411	12266	5	83867332	84065912
12223	5	83861394	84936441	12267	5	83867332	84086632
12224	5	83861394	84936493	12268	5	83867332	84089603
12225	5	83861394	84943705	12269	5	83867332	84104814
12226	5	83861394	169454950	12270	5	83867332	84105175
12227	5	83861394	181522829	12271	5	83867332	84251635
12228	5	83861394	204759879	12272	5	83867332	84252180
12229	5	83861394	209874191	12273	5	83867332	84253030
12230	5	83864692	83865653	12274	5	83867332	84254208
12231	5	83864692	83865914	12275	5	83867332	84314930
12232	5	83864692	83865920	12276	5	83867332	84340523
12233	5	83864692	83868010	12277	5	83867332	84516340
12234	5	83864692	84019752	12278	5	83867332	84706916
12235	5	83864692	84065912	12279	5	83867332	84799488
12236	5	83864692	84086632	12280	5	83867332	84801081
12237	5	83864692	84089603	12281	5	83867332	84824103
12238	5	83864692	84104814	12282	5	83867332	84824203
12239	5	83864692	84105175	12283	5	83867332	84824816
12240	5	83864692	84251635	12284	5	83867332	84825422
12241	5	83864692	84252180	12285	5	83867332	84825763
12242	5	83864692	84253030	12286	5	83867332	84825942

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
12287	5	83867332	84843411	12331	5	84061561	84252180
12288	5	83867332	84936441	12332	5	84061561	84253030
12289	5	83867332	84936493	12333	5	84061561	84254208
12290	5	83867332	84943705	12334	5	84061561	84314930
12291	5	83867332	169454950	12335	5	84061561	84340523
12292	5	83867332	181522829	12336	5	84061561	84516340
12293	5	83867332	204759879	12337	5	84061561	84706916
12294	5	83867332	209874191	12338	5	84061561	84799488
12295	5	84018779	84019752	12339	5	84061561	84801081
12296	5	84018779	84065912	12340	5	84061561	84824103
12297	5	84018779	84086632	12341	5	84061561	84824203
12298	5	84018779	84089603	12342	5	84061561	84824816
12299	5	84018779	84104814	12343	5	84061561	84825422
12300	5	84018779	84105175	12344	5	84061561	84825763
12301	5	84018779	84251635	12345	5	84061561	84825942
12302	5	84018779	84252180	12346	5	84061561	84843411
12303	5	84018779	84253030	12347	5	84061561	84936441
12304	5	84018779	84254208	12348	5	84061561	84936493
12305	5	84018779	84314930	12349	5	84061561	84943705
12306	5	84018779	84340523	12350	5	84061561	169454950
12307	5	84018779	84516340	12351	5	84061561	181522829
12308	5	84018779	84706916	12352	5	84061561	204759879
12309	5	84018779	84799488	12353	5	84061561	209874191
12310	5	84018779	84801081	12354	5	84083388	84086632
12311	5	84018779	84824103	12355	5	84083388	84089603
12312	5	84018779	84824203	12356	5	84083388	84104814
12313	5	84018779	84824816	12357	5	84083388	84105175
12314	5	84018779	84825422	12358	5	84083388	84251635
12315	5	84018779	84825763	12359	5	84083388	84252180
12316	5	84018779	84825942	12360	5	84083388	84253030
12317	5	84018779	84843411	12361	5	84083388	84254208
12318	5	84018779	84936441	12362	5	84083388	84314930
12319	5	84018779	84936493	12363	5	84083388	84340523
12320	5	84018779	84943705	12364	5	84083388	84516340
12321	5	84018779	169454950	12365	5	84083388	84706916
12322	5	84018779	181522829	12366	5	84083388	84799488
12323	5	84018779	204759879	12367	5	84083388	84801081
12324	5	84018779	209874191	12368	5	84083388	84824103
12325	5	84061561	84065912	12369	5	84083388	84824203
12326	5	84061561	84086632	12370	5	84083388	84824816
12327	5	84061561	84089603	12371	5	84083388	84825422
12328	5	84061561	84104814	12372	5	84083388	84825763
12329	5	84061561	84105175	12373	5	84083388	84825942
12330	5	84061561	84251635	12374	5	84083388	84843411

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
12375	5	84083388	84936441	12419	5	84101452	84799488
12376	5	84083388	84936493	12420	5	84101452	84801081
12377	5	84083388	84943705	12421	5	84101452	84824103
12378	5	84083388	169454950	12422	5	84101452	84824203
12379	5	84083388	181522829	12423	5	84101452	84824816
12380	5	84083388	204759879	12424	5	84101452	84825422
12381	5	84083388	209874191	12425	5	84101452	84825763
12382	5	84088707	84089603	12426	5	84101452	84825942
12383	5	84088707	84104814	12427	5	84101452	84843411
12384	5	84088707	84105175	12428	5	84101452	84936441
12385	5	84088707	84251635	12429	5	84101452	84936493
12386	5	84088707	84252180	12430	5	84101452	84943705
12387	5	84088707	84253030	12431	5	84101452	169454950
12388	5	84088707	84254208	12432	5	84101452	181522829
12389	5	84088707	84314930	12433	5	84101452	204759879
12390	5	84088707	84340523	12434	5	84101452	209874191
12391	5	84088707	84516340	12435	5	84103364	84104814
12392	5	84088707	84706916	12436	5	84103364	84105175
12393	5	84088707	84799488	12437	5	84103364	84251635
12394	5	84088707	84801081	12438	5	84103364	84252180
12395	5	84088707	84824103	12439	5	84103364	84253030
12396	5	84088707	84824203	12440	5	84103364	84254208
12397	5	84088707	84824816	12441	5	84103364	84314930
12398	5	84088707	84825422	12442	5	84103364	84340523
12399	5	84088707	84825763	12443	5	84103364	84516340
12400	5	84088707	84825942	12444	5	84103364	84706916
12401	5	84088707	84843411	12445	5	84103364	84799488
12402	5	84088707	84936441	12446	5	84103364	84801081
12403	5	84088707	84936493	12447	5	84103364	84824103
12404	5	84088707	84943705	12448	5	84103364	84824203
12405	5	84088707	169454950	12449	5	84103364	84824816
12406	5	84088707	181522829	12450	5	84103364	84825422
12407	5	84088707	204759879	12451	5	84103364	84825763
12408	5	84088707	209874191	12452	5	84103364	84825942
12409	5	84101452	84104814	12453	5	84103364	84843411
12410	5	84101452	84105175	12454	5	84103364	84936441
12411	5	84101452	84251635	12455	5	84103364	84936493
12412	5	84101452	84252180	12456	5	84103364	84943705
12413	5	84101452	84253030	12457	5	84103364	169454950
12414	5	84101452	84254208	12458	5	84103364	181522829
12415	5	84101452	84314930	12459	5	84103364	204759879
12416	5	84101452	84340523	12460	5	84103364	209874191
12417	5	84101452	84516340	12461	5	84248220	84251635
12418	5	84101452	84706916	12462	5	84248220	84252180

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
12463	5	84248220	84253030	12507	5	84248224	204759879
12464	5	84248220	84254208	12508	5	84248224	209874191
12465	5	84248220	84314930	12509	5	84252053	84252180
12466	5	84248220	84340523	12510	5	84252053	84253030
12467	5	84248220	84516340	12511	5	84252053	84254208
12468	5	84248220	84706916	12512	5	84252053	84314930
12469	5	84248220	84799488	12513	5	84252053	84340523
12470	5	84248220	84801081	12514	5	84252053	84516340
12471	5	84248220	84824103	12515	5	84252053	84706916
12472	5	84248220	84824203	12516	5	84252053	84799488
12473	5	84248220	84824816	12517	5	84252053	84801081
12474	5	84248220	84825422	12518	5	84252053	84824103
12475	5	84248220	84825763	12519	5	84252053	84824203
12476	5	84248220	84825942	12520	5	84252053	84824816
12477	5	84248220	84843411	12521	5	84252053	84825422
12478	5	84248220	84936441	12522	5	84252053	84825763
12479	5	84248220	84936493	12523	5	84252053	84825942
12480	5	84248220	84943705	12524	5	84252053	84843411
12481	5	84248220	169454950	12525	5	84252053	84936441
12482	5	84248220	181522829	12526	5	84252053	84936493
12483	5	84248220	204759879	12527	5	84252053	84943705
12484	5	84248220	209874191	12528	5	84252053	169454950
12485	5	84248224	84251635	12529	5	84252053	181522829
12486	5	84248224	84252180	12530	5	84252053	204759879
12487	5	84248224	84253030	12531	5	84252053	209874191
12488	5	84248224	84254208	12532	5	84253581	84254208
12489	5	84248224	84314930	12533	5	84253581	84314930
12490	5	84248224	84340523	12534	5	84253581	84340523
12491	5	84248224	84516340	12535	5	84253581	84516340
12492	5	84248224	84706916	12536	5	84253581	84706916
12493	5	84248224	84799488	12537	5	84253581	84799488
12494	5	84248224	84801081	12538	5	84253581	84801081
12495	5	84248224	84824103	12539	5	84253581	84824103
12496	5	84248224	84824203	12540	5	84253581	84824203
12497	5	84248224	84824816	12541	5	84253581	84824816
12498	5	84248224	84825422	12542	5	84253581	84825422
12499	5	84248224	84825763	12543	5	84253581	84825763
12500	5	84248224	84825942	12544	5	84253581	84825942
12501	5	84248224	84843411	12545	5	84253581	84843411
12502	5	84248224	84936441	12546	5	84253581	84936441
12503	5	84248224	84936493	12547	5	84253581	84936493
12504	5	84248224	84943705	12548	5	84253581	84943705
12505	5	84248224	169454950	12549	5	84253581	169454950
12506	5	84248224	181522829	12550	5	84253581	181522829

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
12551	5	84253581	204759879	12595	5	84516113	84801081
12552	5	84253581	209874191	12596	5	84516113	84824103
12553	5	84314151	84314930	12597	5	84516113	84824203
12554	5	84314151	84340523	12598	5	84516113	84824816
12555	5	84314151	84516340	12599	5	84516113	84825422
12556	5	84314151	84706916	12600	5	84516113	84825763
12557	5	84314151	84799488	12601	5	84516113	84825942
12558	5	84314151	84801081	12602	5	84516113	84843411
12559	5	84314151	84824103	12603	5	84516113	84936441
12560	5	84314151	84824203	12604	5	84516113	84936493
12561	5	84314151	84824816	12605	5	84516113	84943705
12562	5	84314151	84825422	12606	5	84516113	169454950
12563	5	84314151	84825763	12607	5	84516113	181522829
12564	5	84314151	84825942	12608	5	84516113	204759879
12565	5	84314151	84843411	12609	5	84516113	209874191
12566	5	84314151	84936441	12610	5	84706267	84706916
12567	5	84314151	84936493	12611	5	84706267	84799488
12568	5	84314151	84943705	12612	5	84706267	84801081
12569	5	84314151	169454950	12613	5	84706267	84824103
12570	5	84314151	181522829	12614	5	84706267	84824203
12571	5	84314151	204759879	12615	5	84706267	84824816
12572	5	84314151	209874191	12616	5	84706267	84825422
12573	5	84338664	84340523	12617	5	84706267	84825763
12574	5	84338664	84516340	12618	5	84706267	84825942
12575	5	84338664	84706916	12619	5	84706267	84843411
12576	5	84338664	84799488	12620	5	84706267	84936441
12577	5	84338664	84801081	12621	5	84706267	84936493
12578	5	84338664	84824103	12622	5	84706267	84943705
12579	5	84338664	84824203	12623	5	84706267	169454950
12580	5	84338664	84824816	12624	5	84706267	181522829
12581	5	84338664	84825422	12625	5	84706267	204759879
12582	5	84338664	84825763	12626	5	84706267	209874191
12583	5	84338664	84825942	12627	5	84796405	84799488
12584	5	84338664	84843411	12628	5	84796405	84801081
12585	5	84338664	84936441	12629	5	84796405	84824103
12586	5	84338664	84936493	12630	5	84796405	84824203
12587	5	84338664	84943705	12631	5	84796405	84824816
12588	5	84338664	169454950	12632	5	84796405	84825422
12589	5	84338664	181522829	12633	5	84796405	84825763
12590	5	84338664	204759879	12634	5	84796405	84825942
12591	5	84338664	209874191	12635	5	84796405	84843411
12592	5	84516113	84516340	12636	5	84796405	84936441
12593	5	84516113	84706916	12637	5	84796405	84936493
12594	5	84516113	84799488	12638	5	84796405	84943705

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
12639	5	84796405	169454950	12683	5	84822183	181522829
12640	5	84796405	181522829	12684	5	84822183	204759879
12641	5	84796405	204759879	12685	5	84822183	209874191
12642	5	84796405	209874191	12686	5	84822215	84824103
12643	5	84799805	84801081	12687	5	84822215	84824203
12644	5	84799805	84824103	12688	5	84822215	84824816
12645	5	84799805	84824203	12689	5	84822215	84825422
12646	5	84799805	84824816	12690	5	84822215	84825763
12647	5	84799805	84825422	12691	5	84822215	84825942
12648	5	84799805	84825763	12692	5	84822215	84843411
12649	5	84799805	84825942	12693	5	84822215	84936493
12650	5	84799805	84843411	12694	5	84822215	84943705
12651	5	84799805	84936441	12695	5	84822215	169454950
12652	5	84799805	84936493	12696	5	84822215	181522829
12653	5	84799805	84943705	12697	5	84822215	204759879
12654	5	84799805	169454950	12698	5	84822215	209874191
12655	5	84799805	181522829	12699	5	84824103	84824203
12656	5	84799805	204759879	12700	5	84824103	84824816
12657	5	84799805	209874191	12701	5	84824103	84840183
12658	5	84821810	84824103	12702	5	84824103	84843411
12659	5	84821810	84824203	12703	5	84824103	84936441
12660	5	84821810	84824816	12704	5	84824103	84936493
12661	5	84821810	84825422	12705	5	84824103	84943705
12662	5	84821810	84825763	12706	5	84824103	169454950
12663	5	84821810	84825942	12707	5	84824103	181522829
12664	5	84821810	84843411	12708	5	84824103	204759879
12665	5	84821810	84936441	12709	5	84824103	209874191
12666	5	84821810	84936493	12710	5	84824203	84934242
12667	5	84821810	84943705	12711	5	84824203	84936441
12668	5	84821810	169454950	12712	5	84824203	84936493
12669	5	84821810	181522829	12713	5	84824203	84943705
12670	5	84821810	204759879	12714	5	84824203	169454950
12671	5	84821810	209874191	12715	5	84824203	181522829
12672	5	84822183	84824103	12716	5	84824203	204759879
12673	5	84822183	84824203	12717	5	84824203	209874191
12674	5	84822183	84824816	12718	5	84840183	84843411
12675	5	84822183	84825422	12719	5	84840183	84936441
12676	5	84822183	84825763	12720	5	84840183	84936493
12677	5	84822183	84825942	12721	5	84840183	84943705
12678	5	84822183	84843411	12722	5	84840183	169454950
12679	5	84822183	84936441	12723	5	84840183	181522829
12680	5	84822183	84936493	12724	5	84840183	204759879
12681	5	84822183	84943705	12725	5	84840183	209874191
12682	5	84822183	169454950	12726	5	84934242	84936441

Table 1 (cont'd.)

Chromosomal Segment	Chr.	Boundary 1	Boundary 2	Chromosomal Segment	Chr.	Boundary 1	Boundary 2
12727	5	84934242	84936493	12748	6	165317744	167541488
12728	5	84934242	84943705	12749	6	165632140	167541488
12729	5	84934242	169454950	12750	7	17293606	33157904
12730	5	84934242	181522829	12751	7	17293606	52027945
12731	5	84934242	204759879	12752	7	17293606	134050244
12732	5	84934242	209874191	12753	7	33157904	52027945
12733	5	84938287	84943705	12754	7	33157904	134050244
12734	5	84938287	169454950	12755	7	52027945	134050244
12735	5	84938287	181522829	12756	8	120061025	173714727
12736	5	84938287	204759879	12757	9	23258800	128947590
12737	5	84938287	209874191	12758	9	23258800	145336391
12738	5	169454950	181522829	12759	9	23258800	147896266
12739	5	169454950	204759879	12760	9	128947590	145336391
12740	5	169454950	209874191	12761	9	128947590	147896266
12741	5	181522829	204759879	12762	9	145336391	147896266
12742	5	181522829	209874191	12763	10	5873450	140850928
12743	5	204759879	209874191	12764	10	5873450	142092409
12744	6	121671402	165317744	12765	10	5873450	145273700
12745	6	121671402	165632140	12766	10	140850928	142092409
12746	6	121671402	167541488	12767	10	140850928	145273700
12747	6	165317744	165632140	12768	10	142092409	145273700

Table 2. Examples of alleles associated with increased fertility in maize.

Chr.	Position	Desired Allele	Chr.	Position	Desired Allele	Chr.	Position	Desired Allele
5	77990414	A	5	79859447	A	5	80389419	C
5	77990442	C	5	79862605	G	5	80389432	A
5	77990478	T	5	79862609	A	5	80389533	C
5	77990499	A	5	79865888	T	5	80804587	G
5	77990523	G	5	79867527	A	5	80828757	C
5	77990545	A	5	80236641	G	5	80829669	T
5	77991998	G	5	80236734	T	5	81267278	G
5	77995135	C	5	80236789	T	5	81267320	T
5	77995150	A	5	80236810	T	5	81763802	G
5	77996710	T	5	80236933	T	5	81763824	C
5	78310107	A	5	80271911	A	5	81802220	A
5	78310132	T	5	80279798	C	5	81802574	C
5	78918620	G	5	80387964	C	5	81950558	T
5	79531947	A	5	80388968	T	5	81950582	T
5	79537908	G	5	80389273	A	5	82085147	C
5	79707038	C	5	80389290	C	5	82087667	A
5	79707074	A	5	80389380	C	5	82235558	A

Table 2 (cont'd)

Chr.	Position	Desired Allele	Chr.	Position	Desired Allele	Chr.	Position	Desired Allele
5	82236085	T	5	82549380	C	5	84824103	T
5	82236162	A	5	82549409	A	5	84824205	T
5	82325775	C	5	82549517	A	5	84824447	C
5	82325977	C	5	82549554	C	5	84824473	C
5	82326020	G	5	82549629	C	5	84824495	G
5	82326037	G	5	82549650	C	5	84824561	G
5	82326164	C	5	82549724	C	5	84824603	C
5	82326170	T	5	82549867	C	5	84824951	i
5	82326175	T	5	82549995	G	5	84825014	C
5	82423926	A	5	82550364	C	5	84825020	A
5	82424010	G	5	82550459	G	5	84825024	G
5	82424392	A	5	82550498	G	5	84825087	C
5	82424461	C	5	82550853	T	5	84825264	T
5	82424629	G	5	82550983	T	5	84825276	T
5	82424695	C	5	82551025	C	5	84825303	C
5	82424706	C	5	82552120	T	5	84825469	G
5	82424752	G	5	82552368	G	5	84825471	A
5	82424773	G	5	82553234	G	5	84825480	C
5	82424791	A	5	82555338	A	5	84825497	G
5	82425070	C	5	83560144	T	5	84825510	C
5	82425098	C	5	83560192	A	5	84825512	A
5	82425358	G	5	83860601	T	5	84825527	C
5	82443847	T	5	83860682	T	5	84825551	G
5	82443957	T	5	83861161	G	5	84825588	G
5	82443978	A/G	5	83861215	A	5	84825642	C
5	82444245	T	5	83861266	A	5	84841805	T
5	82444266	T	5	83861344	T	5	84842085	A
5	82444716	A	5	83861361	T	5	84843056	A
5	82445340	A	5	84086015	T	5	84938414	T
5	82445493	A	5	84796702	G	5	84938476	T
5	82446188	C	5	84822534	G	5	84938528	T
5	82446660	G	5	84822543	T			
5	82446684	T	5	84823992	A			
5	82446704	A	5	84823998	C			

Table 3. Examples of proteins of interest encoded by maize chromosome 5.

Protein Identifier	Chr.	Positions	Strand	SEQ ID NO:	SEQ ID NO:	SEQ ID NO:
GRMZM2G435796_P01	5	78022476 - 78023096	-	1	176	351
GRMZM5G832780_P01	5	78129898 - 78131652	-	2	177	352
GRMZM2G425559_P01	5	78129898 - 78131784	+	3	178	353
GRMZM2G006937_P01	5	78255163 - 78310499	+	4	179	354
GRMZM2G102912_P01	5	78380304 - 78381593	+	5	180	355

Table 3 (cont'd)

Protein Identifier	Chr.	Positions	Strand	SEQ ID NO:	SEQ ID NO:	SEQ ID NO:
GRMZM2G102845_P01	5	78381834 - 78389884	-	6	181	356
GRMZM5G865367_P01	5	78519893 - 78520683	+	7	182	357
GRMZM2G322493_P01	5	78758856 - 78765635	+	8	183	358
GRMZM2G167741_P01	5	78772058 - 78780292	+	9	184	359
GRMZM2G410357_P02	5	78804756 - 78813114	+	10	185	360
GRMZM2G410357_P01	5	78804756 - 78814710	+	11	186	361
GRMZM2G410357_P04	5	78805059 - 78815306	+	12	187	362
GRMZM2G410357_P03	5	78805059 - 78815306	+	13	188	363
GRMZM2G410357_P05	5	78805059 - 78815306	+	14	189	364
GRMZM2G410357_P06	5	78814424 - 78814976	+	15	190	365
GRMZM2G410393_P03	5	78819803 - 78826528	+	16	191	366
GRMZM2G410393_P04	5	78819803 - 78826528	+	17	192	367
GRMZM2G410393_P05	5	78819803 - 78826528	+	18	193	368
GRMZM2G410393_P02	5	78819803 - 78826538	+	19	194	369
GRMZM2G410393_P01	5	78819803 - 78826612	+	20	195	370
AC197118.3_FGP005	5	78820119 - 78821393	-	21	196	371
GRMZM2G133048_P01	5	78904639 - 78918850	+	22	197	372
GRMZM2G018686_P01	5	79055654 - 79056960	-	23	198	373
AC212103.3_FGP002	5	79162381 - 79163631	+	24	199	374
AC193606.2_FGP001	5	79175814 - 79176557	-	25	200	375
GRMZM2G332749_P01	5	79183135 - 79188028	+	26	201	376
GRMZM2G068176_P01	5	79200056 - 79201760	-	27	202	377
GRMZM2G369391_P01	5	79229010 - 79230318	+	28	203	378
GRMZM2G369396_P01	5	79229019 - 79230005	-	29	204	379
GRMZM2G314233_P01	5	79503885 - 79505592	+	30	205	380
GRMZM5G816609_P01	5	79505757 - 79510072	+	31	206	381
GRMZM2G063942_P06	5	79531009 - 79538012	+	32	207	382
GRMZM2G063942_P03	5	79531009 - 79538048	+	33	208	383
GRMZM2G063942_P02	5	79531009 - 79538048	+	34	209	384
GRMZM2G063942_P01	5	79531009 - 79538048	+	35	210	385
GRMZM2G063942_P08	5	79531040 - 79538012	+	36	211	386
GRMZM2G063942_P07	5	79531040 - 79538012	+	37	212	387
GRMZM2G063942_P04	5	79531040 - 79538048	+	38	213	388
GRMZM2G063942_P05	5	79537564 - 79538048	+	39	214	389
GRMZM5G853950_P01	5	79666742 - 79669824	+	40	215	390
GRMZM2G472708_P01	5	79679654 - 79682242	-	41	216	391
GRMZM2G033138_P04	5	79697555 - 79699261	+	42	217	392
GRMZM2G033138_P03	5	79697555 - 79710673	+	43	218	393
GRMZM2G033138_P01	5	79697555 - 79710673	+	44	219	394
GRMZM2G033138_P02	5	79697555 - 79710673	+	45	220	395
GRMZM2G062885_P01	5	79857859 - 79861902	+	46	221	396
GRMZM2G062914_P03	5	79862405 - 79867710	-	47	222	397
GRMZM2G062914_P02	5	79862405 - 79867868	-	48	223	398
GRMZM2G062914_P01	5	79862405 - 79867873	-	49	224	399

Table 3 (cont'd)

Protein Identifier	Chr.	Positions	Strand	SEQ ID NO:	SEQ ID NO:	SEQ ID NO:
GRMZM5G865405_P01	5	79960831 - 79961961	-	50	225	400
GRMZM2G353478_P01	5	80084956 - 80086268	-	51	226	401
GRMZM2G067313_P01	5	80187987 - 80190673	+	52	227	402
GRMZM2G067313_P02	5	80188978 - 80190777	+	53	228	403
GRMZM2G367431_P01	5	80191781 - 80192546	+	54	229	404
GRMZM2G067350_P01	5	80195077 - 80199923	-	55	230	405
GRMZM2G067350_P02	5	80195714 - 80199923	-	56	231	406
GRMZM2G031850_P01	5	80236478 - 80241911	-	57	232	407
GRMZM2G031850_P02	5	80238986 - 80241911	-	58	233	408
GRMZM2G031850_P03	5	80239243 - 80241911	-	59	234	409
GRMZM2G024612_P01	5	80273499 - 80282785	-	60	235	410
GRMZM5G852229_P01	5	80344025 - 80345337	+	61	236	411
GRMZM5G829894_P01	5	80387639 - 80389787	+	62	237	412
GRMZM5G829894_P02	5	80387639 - 80389787	+	63	238	413
GRMZM5G829894_P03	5	80388596 - 80389787	+	64	239	414
AC233959.1_FGP003	5	80411337 - 80411639	-	65	240	415
GRMZM2G701675_P01	5	80446281 - 80446855	+	66	241	416
AC233959.1_FGP006	5	80491807 - 80492790	-	67	242	417
GRMZM2G392320_P02	5	80669160 - 80670554	+	68	243	418
GRMZM2G392320_P01	5	80669160 - 80674679	+	69	244	419
GRMZM2G147800_P01	5	80715081 - 80720509	+	70	245	420
GRMZM2G093490_P01	5	80795990 - 80800856	-	71	246	421
GRMZM2G482256_P01	5	80803727 - 80807409	-	72	247	422
GRMZM2G425774_P01	5	80828457 - 80835734	-	73	248	423
GRMZM2G425774_P02	5	80828945 - 80835734	-	74	249	424
GRMZM2G165945_P02	5	80969412 - 80972258	+	75	250	425
GRMZM2G165945_P01	5	80969412 - 80974450	+	76	251	426
GRMZM2G165945_P03	5	80970381 - 80974450	+	77	252	427
GRMZM2G400197_P01	5	81031951 - 81047638	+	78	253	428
GRMZM2G104425_P01	5	81076870 - 81082921	-	79	254	429
GRMZM5G887054_P01	5	81155197 - 81157909	-	80	255	430
GRMZM5G887054_P02	5	81155255 - 81157909	-	81	256	431
GRMZM5G887054_P03	5	81155675 - 81157909	-	82	257	432
GRMZM5G887054_P04	5	81156713 - 81157909	-	83	258	433
GRMZM2G088880_P01	5	81265211 - 81267499	+	84	259	434
GRMZM2G088880_P02	5	81265211 - 81267499	+	85	260	435
GRMZM2G088880_P03	5	81265354 - 81267485	+	86	261	436
AC207104.3_FGP001	5	81273796 - 81274512	+	87	262	437
GRMZM2G322672_P01	5	81761119 - 81763618	+	88	263	438
GRMZM2G011888_P01	5	81793777 - 81797217	+	89	264	439
GRMZM2G085513_P01	5	81798893 - 81800186	-	90	265	440
GRMZM2G085469_P01	5	81801973 - 81806213	-	91	266	441
GRMZM5G817948_P01	5	81858527 - 81859374	+	92	267	442
GRMZM5G897067_P01	5	81859618 - 81861368	+	93	268	443

Table 3 (cont'd)

Protein Identifier	Chr.	Positions	Strand	SEQ ID NO:	SEQ ID NO:	SEQ ID NO:
AC199577.4_FGP004	5	81863099 - 81863686	-	94	269	444
GRMZM5G823733_P01	5	81914498 - 81916850	+	95	270	445
GRMZM5G812923_P02	5	81950191 - 81954891	-	96	271	446
GRMZM5G812923_P03	5	81950191 - 81954891	-	97	272	447
GRMZM5G812923_P01	5	81951639 - 81954891	-	98	273	448
GRMZM2G464846_P01	5	81984901 - 81985250	+	99	274	449
GRMZM2G024882_P01	5	82083639 - 82101253	-	100	275	450
GRMZM5G868120_P02	5	82137780 - 82143124	-	101	276	451
GRMZM5G868120_P01	5	82139338 - 82143124	-	102	277	452
GRMZM5G867030_P01	5	82234311 - 82236318	+	103	278	453
GRMZM2G409658_P01	5	82423451 - 82427210	-	104	279	454
GRMZM2G111201_P01	5	82427780 - 82431853	+	105	280	455
GRMZM2G409726_P01	5	82443403 - 82446794	-	106	281	456
GRMZM2G409726_P02	5	82443815 - 82446714	-	107	282	457
GRMZM2G409726_P03	5	82443856 - 82446714	-	108	283	458
GRMZM2G005562_P01	5	82549227 - 82555670	-	109	284	459
GRMZM2G005562_P04	5	82549246 - 82552090	-	110	285	460
GRMZM2G005562_P03	5	82549246 - 82555641	-	111	286	461
GRMZM2G005562_P02	5	82549246 - 82555641	-	112	287	462
GRMZM2G005562_P05	5	82549299 - 82551111	-	113	288	463
GRMZM2G005562_P06	5	82554608 - 82555670	-	114	289	464
GRMZM2G005562_P07	5	82554971 - 82555670	-	115	290	465
GRMZM2G006144_P01	5	82556313 - 82561535	-	116	291	466
GRMZM2G006144_P02	5	82556337 - 82559047	-	117	292	467
GRMZM2G443332_P01	5	82609175 - 82610100	-	118	293	468
GRMZM2G167578_P01	5	82675654 - 82676901	-	119	294	469
GRMZM5G844909_P01	5	82675825 - 82676822	+	120	295	470
GRMZM2G390350_P01	5	82882273 - 82883691	-	121	296	471
GRMZM2G158520_P01	5	82953053 - 82954942	+	122	297	472
GRMZM2G459142_P01	5	82971168 - 82971688	+	123	298	473
GRMZM5G844046_P01	5	83023500 - 83023965	-	124	299	474
GRMZM2G564932_P01	5	83093332 - 83094205	+	125	300	475
AC197265.3_FGP005	5	83145879 - 83146355	+	126	301	476
GRMZM2G087267_P01	5	83277783 - 83281412	+	127	302	477
GRMZM2G087267_P02	5	83277785 - 83281412	+	128	303	478
GRMZM2G087267_P03	5	83279034 - 83280630	+	129	304	479
GRMZM2G032280_P01	5	83397014 - 83400242	+	130	305	480
GRMZM2G087495_P01	5	83402967 - 83405797	-	131	306	481
GRMZM2G387127_P01	5	83435480 - 83437132	-	132	307	482
GRMZM5G889792_P01	5	83521923 - 83522252	-	133	308	483
AC234515.1_FGP003	5	83557023 - 83560095	+	134	309	484
AC234515.1_FGP002	5	83567769 - 83572400	+	135	310	485
GRMZM5G894416_P01	5	83606990 - 83607661	+	136	311	486
GRMZM2G050080_P01	5	83743980 - 83745342	-	137	312	487

Table 3 (cont'd)

Protein Identifier	Chr.	Positions	Strand	SEQ ID NO:	SEQ ID NO:	SEQ ID NO:
GRMZM2G088396_P01	5	83859479 - 83861633	+	138	313	488
GRMZM2G088235_P03	5	83860797 - 83865914	-	139	314	489
GRMZM2G088235_P02	5	83860797 - 83865920	-	140	315	490
GRMZM2G088235_P01	5	83860797 - 83865920	-	141	316	491
GRMZM2G088235_P04	5	83861394 - 83865914	-	142	317	492
GRMZM2G088235_P05	5	83864692 - 83865653	-	143	318	493
GRMZM2G387123_P01	5	83867332 - 83868010	-	144	319	494
GRMZM2G449843_P01	5	84018779 - 84019752	+	145	320	495
GRMZM2G322129_P01	5	84061561 - 84065912	+	146	321	496
GRMZM2G017741_P01	5	84083388 - 84086632	+	147	322	497
GRMZM2G017802_P01	5	84088707 - 84089603	-	148	323	498
GRMZM2G074634_P05	5	84101452 - 84104814	-	149	324	499
GRMZM2G074634_P01	5	84101452 - 84105175	-	150	325	500
GRMZM2G074634_P02	5	84101452 - 84105175	-	151	326	501
GRMZM2G074634_P04	5	84101452 - 84105175	-	152	327	502
GRMZM2G074634_P03	5	84101452 - 84105175	-	153	328	503
GRMZM2G074634_P06	5	84103364 - 84105175	-	154	329	504
GRMZM2G026117_P02	5	84248220 - 84251635	+	155	330	505
GRMZM2G026117_P01	5	84248220 - 84252180	+	156	331	506
GRMZM2G026117_P03	5	84248224 - 84252180	+	157	332	507
GRMZM2G005998_P02	5	84252053 - 84253030	-	158	333	508
GRMZM2G005998_P03	5	84252053 - 84254208	-	159	334	509
GRMZM2G005998_P01	5	84253581 - 84254208	-	160	335	510
GRMZM2G107026_P01	5	84314151 - 84314930	-	161	336	511
AC211514.2_FGP003	5	84338664 - 84340523	-	162	337	512
AC208217.3_FGP001	5	84516113 - 84516340	-	163	338	513
GRMZM2G127999_P01	5	84706267 - 84706916	+	164	339	514
GRMZM2G128012_P01	5	84796405 - 84799488	-	165	340	515
GRMZM2G427468_P01	5	84799805 - 84801081	-	166	341	516
GRMZM2G382914_P05	5	84821810 - 84824816	+	167	342	517
GRMZM2G382914_P04	5	84821810 - 84825422	+	168	343	518
GRMZM2G382914_P02	5	84822183 - 84825763	+	169	344	519
GRMZM2G382914_P03	5	84822215 - 84825763	+	170	345	520
GRMZM2G382914_P01	5	84822215 - 84825942	+	171	346	521
GRMZM2G007372_P01	5	84840183 - 84843411	+	172	347	522
GRMZM2G010321_P02	5	84934242 - 84936441	+	173	348	523
GRMZM2G010321_P01	5	84934242 - 84936493	+	174	349	524
GRMZM2G010754_P01	5	84938287 - 84943705	-	175	350	525

The above examples clearly illustrate the advantages of the invention. Although the present invention has been described with reference to specific details of certain

embodiments thereof, it is not intended that such details should be regarded as limitations upon the scope of the claimed invention except as and to the extent that they are included in the accompanying claims.

We claim:

1. A method of identifying a Vip3A-expressing maize plant or plant part thereof having increased male fertility compared to a Vip3A-expressing maize plant that has reduced male fertility or is male infertile, comprising:

detecting, in nucleic acid of said Vip3A-expressing maize plant or plant part, a quantitative trait locus (QTL) associated with increased male fertility in Vip3A-expressing maize plants, wherein said QTL is located on chromosome 5 and is flanked by and includes marker 7 (SEQ ID NO:561) and marker 8 (SEQ ID NO:566), and further comprises a haplotype that comprises i) an A polymorphism in marker 7 at position 181522829 on chromosome 5; and ii) a G polymorphism in marker 8 at position 77920728 on chromosome 5;

thereby identifying a Vip3A-expressing maize plant or plant part having increased male fertility compared to a Vip3A-expressing maize plant without said QTL.

2. The method of claim 1, wherein said QTL is detected in an amplification product from a nucleic acid sample from said Vip3A-expressing maize plant or plant part.

3. A breeding method, comprising:

detecting, in nucleic acid from a Vip3A-expressing maize plant or a part thereof, a QTL associated with increased male fertility, wherein said QTL is located on chromosome 5 and is flanked by and includes marker 7 (SEQ ID NO:561) and marker 8 (SEQ ID NO:566), and further comprises a haplotype that comprises i) an A polymorphism in marker 7 at position 181522829 on chromosome 5; and ii) a G polymorphism in marker 8 at position 77920728 on chromosome 5; and

selecting said Vip3A-expressing maize plant for breeding.

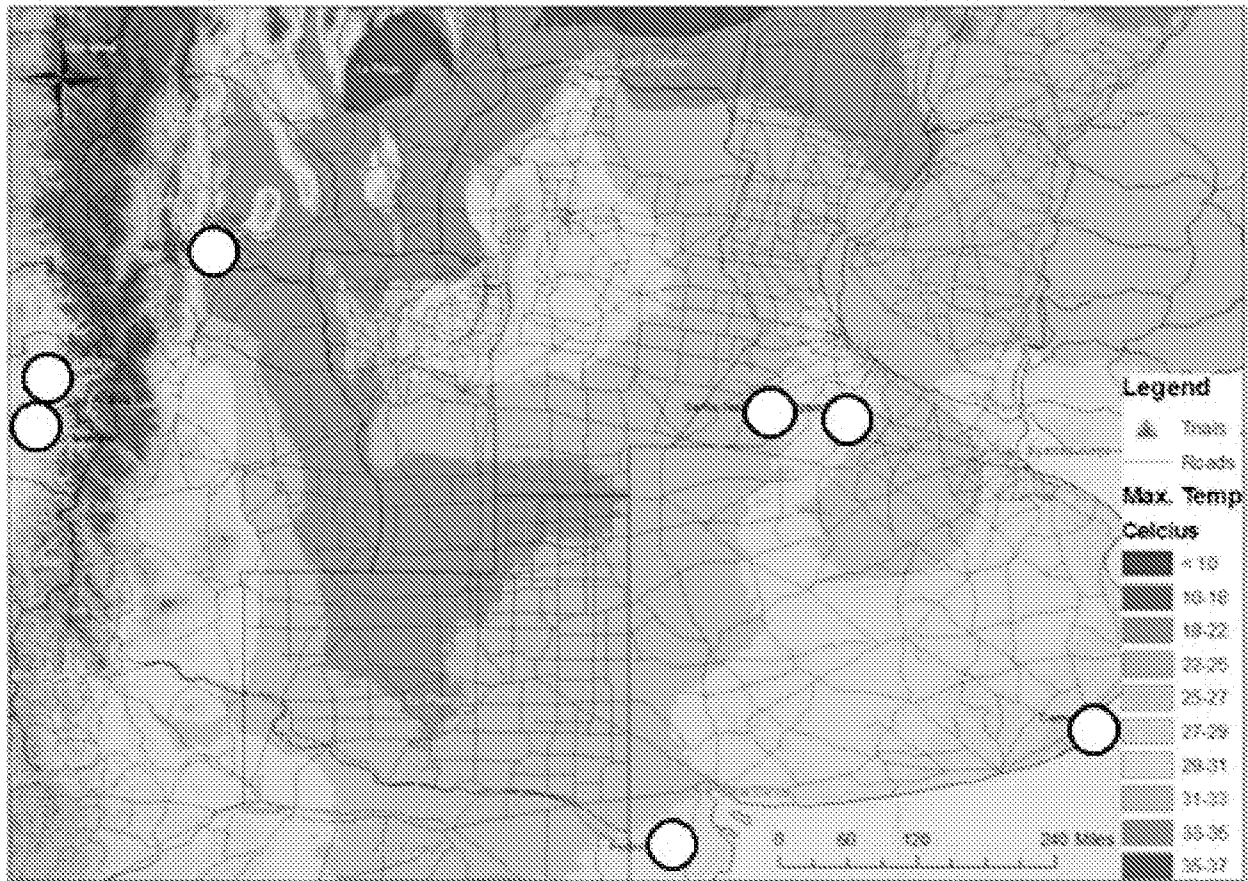
4. The method of claim 3, wherein said marker 7 and said marker 8 are detected in an amplification product from a nucleic acid sample from said Vip3A-expressing maize plant or plant part.

5. The method of any one of claims 1 to 4, wherein said Vip3A-expressing maize plant or plant part is hemizygous or homozygous for a *vip3a* coding sequence.
6. The method of claim 5, wherein said maize plant or plant part comprises maize event MIR162.
7. The method of claim 5, wherein said maize plant or plant part is an inbred maize plant or plant part.
8. The method of claim 5, wherein the genome of said maize plant or plant part is at least 95% identical to that of an elite maize line.
9. The method of claim 8, wherein said maize plant or plant part is an elite maize line.
10. The method of claim 9, wherein said elite maize line is NP2222, NP2660, NP2276, NP2391, NP2460 or ID3461.
11. The method of claim 10, wherein said maize plant or plant part is derived from NP2222, NP2660, NP2276, NP2391, NP2460 and/or ID3461.
12. The method of any one of claims 3 to 4, wherein the method further comprises crossing the maize plant with a second maize plant that lacks said marker 7 and said marker 8 to produce a progeny maize plant comprising the marker 7 and the marker 8.
13. The method of any one of claims 1 to 12, wherein said increased male fertility is associated with increased pollen production, enhanced tassel formation, enhanced anther formation, or any combination thereof.

Temperature (°F)	Relative Humidity (%)	Vip3 Homozygous	Vip3 Hemizygous	Vip Null
85	49	6.0	4.4	2.3
80	51	5.8	3.2	1.7
74	61	4.9	1.6	1.0

Final Anther Scale				
1 = exceptional anther extrusion				
2 = good anther extrusion, normal				
3 = reduced anther extrusion, below normal				
4 = sparse, scattered anthers				
5 = very sparse anthers, but more than 15 total				
6 = 15 or fewer total anthers extruded				

Fig. 1



Environmental Variables	Field Traits					
	Anther_N	Anther_Q	Central Spike Length	Final Weight	Initial Weight	Lateral Branch Number
Temp	-0.000975	0.00257	0.04046	0.01973	-0.03029	0.02788
Temp_Diff	0.01356	-0.00037	-0.08704	-0.0258	0.04125	-0.0562
Total Change in Trait	0.02331	0.00294	0.1275	0.04556	0.07154	0.08408
Unit	1-4 scale	1-4 scale	mms	grs	grs	count

Fig. 2

Temperature (°F)	Relative Humidity (%)	Vip3 Homozygous	Vip3 Hemizygous	Vip Null
85	49	6.0	4.4	2.3
80	51	5.8	3.2	1.7
74	61	4.9	1.6	1.0

Final Anther Scale

- 1 = exceptional anther extrusion
- 2 = good anther extrusion, normal
- 3 = reduced anther extrusion, below normal
- 4 = sparse, scattered anthers
- 5 = very sparse anthers, but more than 15 total
- 6 = 15 or fewer total anthers extruded