



- (51) **International Patent Classification:**
C12N 15/82 (2006.01) *A01H 5/10* (2006.01)
- (21) **International Application Number:**
PCT/US2014/063731
- (22) **International Filing Date:**
3 November 2014 (03.11.2014)
- (25) **Filing Language:** English
- (26) **Publication Language:** English
- (30) **Priority Data:**
61/899,598 4 November 2013 (04.11.2013) US
- (71) **Applicant:** DOW AGROSCIENCES LLC [US/US];
9330 Zionsville Road, Indianapolis, Indiana 46268 (US).
- (72) **Inventors:** SASTRY-DENT, Lakshmi; 2239 Stone Manor
Court, Avon, Indiana 46123 (US). CAO, Zehui; 13719
Stanford Drive, Westfield, Indiana 46074 (US). SRIRAM,
Shreedharan; 3619 Knickerbocker Place, Apt. 2A, Indi-
anapolis, Indiana 46240 (US). WEBB, Steven R.; 15416
Bloomfield Court, Westfield, Indiana 46074 (US).
CAMPER, Debra L.; 5340 North Delaware Street, Indi-
anapolis, Indiana 46220 (US).
- (74) **Agents:** ADDISON, Bradford, G. et al.; Barnes & Thorn-
burg LLP, 11 South Meridian Street, Indianapolis, IN
46204 (US).
- (81) **Designated States** (unless otherwise indicated, for every
kind of national protection available): AE, AG, AL, AM,
AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY,
BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM,
DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT,
HN, HR, HU, ID, IL, IN, IR, IS, JP, KE, KG, KN, KP, KR,
KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG,
MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM,
PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC,
SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN,
TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.
- (84) **Designated States** (unless otherwise indicated, for every
kind of regional protection available): ARIPO (BW, GH,
GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ,
TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU,
TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE,
DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU,
LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK,
SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ,
GW, KM, ML, MR, NE, SN, TD, TG).

[Continued on next page]

(54) Title: OPTIMAL MAIZE LOCI

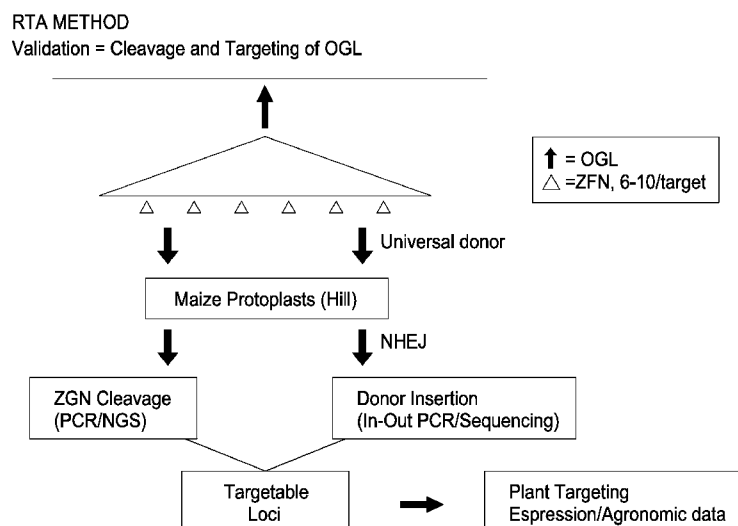


Fig. 13

(57) **Abstract:** As disclosed herein, optimal native genomic loci from maize plants have been identified that represent best sites for targeted insertion of exogenous sequences.

**Declarations under Rule 4.17:**

- *as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii))*
- *as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii))*

Published:

- *without international search report and to be republished upon receipt of that report (Rule 48.2(g))*
- *with sequence listing part of description (Rule 5.2(a))*

OPTIMAL MAIZE LOCI

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims the benefit, under 35 U.S.C. §119(e), to U.S. Provisional Patent
Application No. 61/899,598, filed on November 4, 2013, the contents of which are
incorporated by reference in their entirety into the present application.

REFERENCE TO SEQUENCE LISTING SUBMITTED ELECTRONICALLY

The official copy of the sequence listing is submitted electronically via EFS-Web as an
ASCII formatted sequence listing with a file named “7560232316_SeqList_ST25.txt”, created
on October 31, 2014, and having a size of 13 megabytes and is filed concurrently with the
specification. The sequence listing contained in this ASCII formatted document is part of the
specification and is herein incorporated by reference in its entirety.

REFERENCE TO TABLE LISTING SUBMITTED ELECTRONICALLY

The official copy of the table listing is submitted electronically via EFS-Web as a .PDF
formatted table listing with a file named “Table3”, created on November 04, 2013, and having
a size of 8 megabytes and is filed concurrently with the specification. The table listing
contained in this .PDF formatted document is part of the specification and is herein
incorporated by reference in its entirety.

BACKGROUND

The maize genome was successfully transformed with transgenes in the early 1990's.
Over the last twenty years, numerous methodologies have been developed for transforming the
maize genome, wherein a transgene is stably integrated into the maize genome. This evolution
of maize transformation methodologies has resulted in the capability to successfully introduce a
transgene comprising an agronomic trait within the maize genome. The introduction of insect
resistance and herbicide tolerant traits within maize plants in the late -1990's provided
producers with a new and convenient technological innovation for controlling insects and a
wide spectrum of weeds, which was unparalleled in cultivation farming methods. Currently,
transgenic maize is commercially available throughout the world, and new transgenic maize
products such as Enlist™ Corn offer improved solutions for ever-increasing weed challenges.
The utilization of transgenic maize in modern agronomic practices would not be possible, but
for the development and improvement of maize transformation methodologies.

However, current maize transformation methodologies rely upon the random insertion of transgenes within the maize genome. Reliance on random insertion of genes into a genome has several disadvantages. The transgenic events may randomly integrate within gene transcriptional sequences, thereby interrupting the expression of endogenous traits and altering the growth and development of the maize plant. In addition, the transgenic events may indiscriminately integrate into locations of the corn genome that are susceptible to gene silencing, culminating in the reduced or complete inhibition of transgene expression either in the first or subsequent generations of transgenic maize plants. Finally, the random integration of transgenes within the maize genome requires considerable effort and cost in identifying the location of the transgenic event and selecting transgenic events that perform as designed without agronomic impact to the plant. Novel assays must be continually developed to determine the precise location of the integrated transgene for each transgenic event, such as a maize event. The random nature of maize transformation methodologies results in a “position-effect” of the integrated transgene, which hinders the effectiveness and efficiency of maize transformation methodologies.

Targeted genome modification of plants has been a long-standing and elusive goal of both applied and basic research. Targeting genes and gene stacks to specific locations in the *Zea mays* genome will improve the quality of transgenic events, reduce costs associated with production of transgenic events and provide new methods for making transgenic plant products such as sequential gene stacking. Overall, targeting transgenes to specific genomic sites is likely to be commercially beneficial. Significant advances have been made in the last few years towards development of methods and compositions to target and cleave genomic DNA by site specific nucleases (e.g., Zinc Finger Nucleases (ZFNs), Meganucleases, Transcription Activator-Like Effector Nucleases (TALENs) and Clustered Regularly Interspaced Short Palindromic Repeats/CRISPR-associated nuclease (CRISPR/Cas) with an engineered crRNA/tracrRNA), to induce targeted mutagenesis, induce targeted deletions of cellular DNA sequences, and facilitate targeted recombination of an exogenous donor DNA polynucleotide within a predetermined genomic locus. See, for example, U.S. Patent Publication No. 20030232410; 20050208489; 20050026157; 20050064474; and 20060188987, and International Patent Publication No. WO 2007/014275, the disclosures of which are incorporated by reference in their entireties for all purposes. U.S. Patent Publication No. 20080182332 describes use of non-canonical zinc finger nucleases (ZFNs) for targeted modification of plant genomes and U.S. Patent Publication No. 20090205083 describes ZFN-

mediated targeted modification of a plant EPSPs genomic locus. Current methods for targeted insertion of exogenous DNA typically involve co-transformation of plant tissue with a donor DNA polynucleotide containing at least one transgene and a site specific nuclease (e.g., ZFN) which is designed to bind and cleave a specific genomic locus of an actively transcribed coding
5 sequence. This causes the donor DNA polynucleotide to stably insert within the cleaved genomic locus resulting in targeted gene addition at a specified genomic locus comprising an actively transcribed coding sequence.

An alternative approach is to target the transgene to preselected target nongenic loci within the corn genome. In recent years, several technologies have been developed and applied
10 to plant cells for the targeted delivery of a transgene within the corn genome. However, much less is known about the attributes of genomic sites that are suitable for targeting. Historically, non-essential genes and pathogen (viral) integration sites in genomes have been used as loci for targeting. The number of such sites in genomes is rather limiting and there is therefore a need for identification and characterization of targetable optimal genomic loci that can be used for
15 targeting of donor polynucleotide sequences. In addition to being amenable to targeting, optimal genomic loci are expected to be neutral sites that can support transgene expression and breeding applications. A need exists for compositions and methods that define criteria to identify optimal nongenic loci within the corn genome for targeted transgene integration.

20 SUMMARY

In accordance with one embodiment a recombinant sequence is provided comprising an optimal nongenic maize genomic sequence and an exogenous sequence, wherein the exogenous sequence is inserted into the optimal nongenic maize genomic sequence. In an embodiment, the subject disclosure relates to a recombinant sequence, comprising: a nucleic acid sequence of at
25 least 1 Kb and having at least 90%, 95%, or 99% sequence identity with a nongenic sequence selected from the group consisting of loci_137693_G1 (SEQ ID NO:387), loci_265551_G1 (SEQ ID NO:463), loci_128078_G1 (SEQ ID NO:560), loci_168286_G1 (SEQ ID NO:573), loci_3733_G1 (SEQ ID NO:1268), loci_203075_G1 (SEQ ID NO:2030), loci_232484_G1 (SEQ ID NO:2053), loci_136086_G1 (SEQ ID NO:4425), loci_203704_G1 (SEQ ID
30 NO:2033), loci_127268_G1 (SEQ ID NO:2709), loci_204637_G1 (SEQ ID NO:2731), loci_291068_G1 (SEQ ID NO:3230), loci_232222_G1 (SEQ ID NO:3357), loci_43577_G1 (SEQ ID NO:3428), loci_204726_G1 (SEQ ID NO:424), loci_232228_G1 (SEQ ID NO: 4529) with a DNA of interest inserted into the nongenic sequence. In one embodiment, the insertion

of the DNA of interest into the optimal nongenic maize genomic sequence modifies the original sequence of the nongenic loci by alterations of the nongenic loci sequence proximal to the insertion site. Such modifications include, for example, deletions, inversions, insertions, and duplications of the nongenic loci sequence. In a further aspect, an embodiment relates to a DNA of interest, wherein the DNA of interest is inserted into said nongenic sequence. In another aspect, an embodiment comprises the recombinant sequence, wherein a DNA of interest is inserted proximal to a zinc finger target site of Table 8. In another aspect, an embodiment comprises the recombinant sequence, wherein a DNA of interest is inserted at a zinc finger target site of Table 8. In another embodiment, the recombinant sequence comprises an inserted DNA of interest that further comprises an analytical domain. In another embodiment, the recombinant sequence comprises an inserted DNA of interest that does not encode a peptide. In a further embodiment, the recombinant sequence comprises a DNA of interest that encodes a peptide. In yet another embodiment, the recombinant sequence comprises an inserted DNA of interest that further comprises a gene expression cassette. In an embodiment, the gene expressions cassette contains a gene comprising an insecticidal resistance gene, herbicide tolerance gene, nitrogen use efficiency gene, water use efficiency gene, nutritional quality gene, DNA binding gene, and selectable marker gene. In a further embodiment, the recombinant sequence comprises two or more gene expression cassettes. In another embodiment, the recombinant sequence comprises two or more of said nongenic sequences each comprise an inserted DNA of interest to produce two or more recombinant sequences wherein the two or more recombinant sequences that are located on a same chromosome. In an additional embodiment, the recombinant sequence comprises the DNA of interest and/or the nongenic sequence are modified during insertion of said DNA of interest into the nongenic sequence. In another embodiment, the subject disclosure relates to a maize plant, maize plant part, or maize plant cell comprising a recombinant sequence comprising a nucleic acid sequence of at least 1 Kb and having at least 90%, 95%, or 99% sequence identity with a nongenic sequence selected from the group consisting of loci_137693_G1 (SEQ ID NO:387), loci_265551_G1 (SEQ ID NO:463), loci_128078_G1 (SEQ ID NO:560), loci_168286_G1 (SEQ ID NO:573), loci_3733_G1 (SEQ ID NO:1268), loci_203075_G1 (SEQ ID NO:2030), loci_232484_G1 (SEQ ID NO:2053), loci_136086_G1 (SEQ ID NO:4425), loci_203704_G1 (SEQ ID NO:2033), loci_127268_G1 (SEQ ID NO:2709), loci_204637_G1 (SEQ ID NO:2731), loci_291068_G1 (SEQ ID NO:3230), loci_232222_G1 (SEQ ID NO:3357), loci_43577_G1

(SEQ ID NO:3428), loci_204726_G1 (SEQ ID NO:424), loci_232228_G1 (SEQ ID NO: 4529) with a DNA of interest inserted into the nongenic sequence.

In a further embodiment, the disclosure relates to a method of making a transgenic plant cell comprising a DNA of interest. In another aspect of the disclosure, the method comprises
 5 selecting a target nongenic maize genomic locus having at least 90%, 95%, or 99% sequence identity with a target nongenic maize genomic locus selected from the group consisting of loci_137693_G1 (SEQ ID NO:387), loci_265551_G1 (SEQ ID NO:463), loci_128078_G1 (SEQ ID NO:560), loci_168286_G1 (SEQ ID NO:573), loci_3733_G1 (SEQ ID NO:1268), loci_203075_G1 (SEQ ID NO:2030), loci_232484_G1 (SEQ ID NO:2053), loci_136086_G1
 10 (SEQ ID NO:4425), loci_203704_G1 (SEQ ID NO:2033), loci_127268_G1 (SEQ ID NO:2709), loci_204637_G1 (SEQ ID NO:2731), loci_291068_G1 (SEQ ID NO:3230), loci_232222_G1 (SEQ ID NO:3357), loci_43577_G1 (SEQ ID NO:3428), loci_204726_G1 (SEQ ID NO:424), and loci_232228_G1 (SEQ ID NO: 4529); selecting a site specific nuclease that specifically binds and cleaves said target nongenic maize genomic locus; introducing said
 15 site specific nuclease into a maize plant cell; introducing the DNA of interest into the plant cell; inserting the DNA of interest into said target nongenic maize genomic loci; and, selecting transgenic plant cells comprising the DNA of interest targeted to said nongenic locus. In a further aspect, an embodiment relates to a method of making a transgenic plant cell. In another embodiment, the DNA of interest comprises an analytical domain. In an embodiment, the
 20 DNA of interest does not encode a peptide. In yet another embodiment, the DNA of interest encodes a peptide. In a further embodiment, the DNA of interest comprises a gene expression cassette comprising a transgene. In another embodiment, the DNA of interest comprises two or more gene expression cassettes. In a subsequent embodiment, the site specific nuclease is selected from the group consisting of a zinc finger nuclease, a CRISPR nuclease, a TALEN, a
 25 homing endonuclease or a meganuclease. In an embodiment, the DNA of interest is integrated within said nongenic locus via a homology directed repair integration method. In another embodiment, the DNA of interest is integrated within said nongenic locus via a non-homologous end joining integration method. In a further embodiment, the method of making a transgenic plant cell provides for two or more of said DNA of interest that are inserted into two
 30 or more of said target nongenic maize genomic loci. In another embodiment, the method of making a transgenic plant cell comprises two or more of said target nongenic maize genomic loci that are located on a same chromosome. In an additional embodiment, the method of

making a transgenic plant cell comprises the DNA of interest and/or the nongenic sequence that are modified during insertion of said DNA of interest into the nongenic sequence.

In accordance with one embodiment, a purified maize polynucleotide loci is disclosed herein, wherein the purified sequence comprises a nongenic sequence of at least 1 Kb. In one embodiment the nongenic sequence is hypomethylated, exemplifies evidence of recombination and is located in proximal location to an expressing genic region in the maize genome. In one embodiment, the nongenic sequence has a length ranging from about 1 Kb to about 8.4 Kb. In one embodiment, the DNA of interest comprises exogenous DNA sequences, including for example regulatory sequences, restriction cleavage sites, RNA encoding regions or protein encoding regions. In one embodiment, the DNA of interest comprises a gene expression cassette comprising one or more transgenes. In another embodiment, the purified sequence comprises a nongenic sequence having at least 90%, 95%, or 99% sequence identity with a nongenic sequence selected from the group consisting of loci_137693_G1 (SEQ ID NO:387), loci_265551_G1 (SEQ ID NO:463), loci_128078_G1 (SEQ ID NO:560), loci_168286_G1 (SEQ ID NO:573), loci_3733_G1 (SEQ ID NO:1268), loci_203075_G1 (SEQ ID NO:2030), loci_232484_G1 (SEQ ID NO:2053), loci_136086_G1 (SEQ ID NO:4425), loci_203704_G1 (SEQ ID NO:2033), loci_127268_G1 (SEQ ID NO:2709), loci_204637_G1 (SEQ ID NO:2731), loci_291068_G1 (SEQ ID NO:3230), loci_232222_G1 (SEQ ID NO:3357), loci_43577_G1 (SEQ ID NO:3428), loci_204726_G1 (SEQ ID NO:424), and loci_232228_G1 (SEQ ID NO: 4529). In a further embodiment, the purified nongenic maize genomic loci comprise a DNA of interest, wherein said DNA of interest is inserted into said nongenic sequence. In another aspect, an embodiment comprises the purified nongenic maize genomic loci, wherein said DNA of interest is inserted proximal to a zinc finger target site of Table 8. In a different aspect, an embodiment comprises the purified nongenic maize genomic loci, wherein said DNA of interest is inserted between a pair of zinc finger target sites selected from Table 8. In yet another aspect, an embodiment comprises the purified nongenic maize genomic loci and a DNA of interest inserted into the nongenic maize genomic loci, wherein said DNA of interest comprises an analytical domain. In another aspect, an embodiment comprises the purified recombinant nongenic maize genomic loci, wherein said DNA of interest does not encode a peptide. In a subsequent aspect, an embodiment comprises the purified recombinant nongenic maize genomic loci, wherein said DNA of interest encodes a peptide. In an embodiment, the purified recombinant nongenic maize genomic loci comprises a gene expression cassette, wherein the gene cassette comprises a gene including, for example, an insecticidal resistance

gene, herbicide tolerance gene, nitrogen use efficiency gene, water use efficiency gene, nutritional quality gene, DNA binding gene, and selectable marker gene. In one embodiment a DNA of interest is inserted into the nongenic maize genomic loci using a site specific nuclease wherein the site specific nuclease is selected from the group consisting of a zinc finger nuclease, a CRISPR nuclease, a TALEN, a homing endonuclease or a meganuclease. In an embodiment, the said DNA of interest is integrated within said nongenic sequence via a homology directed repair integration method. In another embodiment, the said DNA of interest is integrated within said nongenic sequence via a non-homologous end joining integration method. In a further embodiment, the DNA of interest comprises two or more gene expression cassettes. In a further embodiment, two or more of DNA of interest are inserted into two or more of said target nongenic maize genomic loci. In one embodiment, two or more of said target nongenic maize genomic loci are provided wherein each comprise an inserted DNA of interest to produce two or more recombinant sequences wherein the said target nongenic maize genomic loci are located on a same chromosome. In an additional embodiment, the purified nongenic maize genomic comprises the DNA of interest and/or the nongenic sequence that are modified during insertion of said DNA of interest into the nongenic sequence. In another embodiment, the DNA of interest is inserted via a homology directed repair or a non-homologous end joining repair mechanism.

In another embodiment, the subject disclosure provides for a plant comprising a recombinant sequence, said recombinant sequence comprising: a DNA of interest and a nucleic acid sequence having at least 90%, 95%, or 99% sequence identity with a nongenic sequence, wherein the DNA of interest is inserted into said nongenic sequence. In another embodiment, the nongenic sequence is selected from the group consisting of loci_137693_G1 (SEQ ID NO:387), loci_265551_G1 (SEQ ID NO:463), loci_128078_G1 (SEQ ID NO:560), loci_168286_G1 (SEQ ID NO:573), loci_3733_G1 (SEQ ID NO:1268), loci_203075_G1 (SEQ ID NO:2030), loci_232484_G1 (SEQ ID NO:2053), loci_136086_G1 (SEQ ID NO:4425), loci_203704_G1 (SEQ ID NO:2033), loci_127268_G1 (SEQ ID NO:2709), loci_204637_G1 (SEQ ID NO:2731), loci_291068_G1 (SEQ ID NO:3230), loci_232222_G1 (SEQ ID NO:3357), loci_43577_G1 (SEQ ID NO:3428), loci_204726_G1 (SEQ ID NO:424), and loci_232228_G1 (SEQ ID NO: 4529). In an additional embodiment, the plant comprises two or more of said recombinant sequences. In a further embodiment the plant comprises two recombinant sequences that are located on the same chromosome. In another embodiment the plant comprises a DNA of interest inserted proximal to a zinc finger target site of Table 8. In

one embodiment the plant comprises a DNA of interest inserted between a pair of zinc finger target sites selected from Table 8. In an embodiment, said DNA of interest comprises an analytical domain. In a further embodiment, said DNA of interest does not encode a peptide. In yet another embodiment, said DNA of interest encodes a peptide. In a subsequent
5 embodiment, said DNA of interest comprises a gene expression cassette encoding a gene product, including for example, an insecticidal resistance gene, herbicide tolerance gene, nitrogen use efficiency gene, water use efficiency gene, nutritional quality gene, DNA binding gene, and selectable marker gene. In another embodiment the plant comprises a DNA of interest and/or a nongenic sequence that are modified during insertion of said DNA of interest into said
10 nongenic sequence.

In an embodiment, the subject disclosure relates to a recombinant sequence, comprising: a nucleic acid sequence of at least 1 Kb and having at least 90%, 95%, or 99% sequence identity with a nongenic sequence selected from the group consisting of loci_137693_G1 (SEQ ID NO:387), loci_203075_G1 (SEQ ID NO:2030), and loci_204637_G1 (SEQ ID NO:2731),
15 with a DNA of interest inserted into the nongenic sequence.

In an embodiment, the subject disclosure relates to a recombinant sequence, comprising: a nucleic acid sequence of at least 1 Kb and having at least 90%, 95%, or 99% sequence identity with a nongenic sequence selected from the group consisting of loci_265551_G1 (SEQ ID NO:463), loci_128078_G1 (SEQ ID NO:560), loci_168286_G1 (SEQ ID NO:573),
20 loci_3733_G1 (SEQ ID NO:1268), and loci_232484_G1 (SEQ ID NO:2053), with a DNA of interest inserted into the nongenic sequence.

In an embodiment, the subject disclosure relates to a recombinant sequence, comprising: a nucleic acid sequence of at least 1 Kb and having at least 90%, 95%, or 99% sequence identity with a nongenic sequence selected from the group consisting of loci_127268_G1 (SEQ ID NO:2709), loci_232222_G1 (SEQ ID NO:3357), and loci_204726_G1 (SEQ ID NO:424),
25 with a DNA of interest inserted into the nongenic sequence.

In an embodiment, the subject disclosure relates to a recombinant sequence, comprising: a nucleic acid sequence of at least 1 Kb and having at least 90%, 95%, or 99% sequence identity with a nongenic sequence selected from the group consisting of loci_136086_G1 (SEQ ID NO:4425), loci_203704_G1 (SEQ ID NO:2033), loci_291068_G1 (SEQ ID NO:3230),
30 loci_43577_G1 (SEQ ID NO:3428), and loci_232228_G1 (SEQ ID NO: 4529) with a DNA of interest inserted into the nongenic sequence.

In an embodiment, the subject disclosure relates to a recombinant sequence, comprising: a nucleic acid sequence of at least 1 Kb and having at least 90%, 95%, or 99% sequence identity with a nongenic sequence selected from the group consisting of loci_137693_G1 (SEQ ID NO:387), loci_265551_G1 (SEQ ID NO:463), loci_128078_G1 (SEQ ID NO:560), loci_168286_G1 (SEQ ID NO:573), loci_3733_G1 (SEQ ID NO:1268), loci_203075_G1 (SEQ ID NO:2030), loci_232484_G1 (SEQ ID NO:2053), and loci_204637_G1 (SEQ ID NO:2731), with a DNA of interest inserted into the nongenic sequence.

In an embodiment, the subject disclosure relates to a recombinant sequence, comprising: a nucleic acid sequence of at least 1 Kb and having at least 90%, 95%, or 99% sequence identity with a nongenic sequence selected from the group consisting of loci_137693_G1 (SEQ ID NO:387), loci_265551_G1 (SEQ ID NO:463), loci_128078_G1 (SEQ ID NO:560), loci_168286_G1 (SEQ ID NO:573), loci_3733_G1 (SEQ ID NO:1268), loci_203075_G1 (SEQ ID NO:2030), loci_232484_G1 (SEQ ID NO:2053), loci_127268_G1 (SEQ ID NO:2709), loci_204637_G1 (SEQ ID NO:2731), loci_232222_G1 (SEQ ID NO:3357), and loci_204726_G1 (SEQ ID NO:424), with a DNA of interest inserted into the nongenic sequence.

In an embodiment, the subject disclosure relates to a recombinant sequence, comprising: a nucleic acid sequence of at least 1 Kb and having at least 90%, 95%, or 99% sequence identity with a nongenic sequence selected from the group consisting of loci_136086_G1 (SEQ ID NO:4425), loci_203704_G1 (SEQ ID NO:2033), loci_127268_G1 (SEQ ID NO:2709), loci_291068_G1 (SEQ ID NO:3230), loci_232222_G1 (SEQ ID NO:3357), loci_43577_G1 (SEQ ID NO:3428), loci_204726_G1 (SEQ ID NO:424), and loci_232228_G1 (SEQ ID NO:4529) with a DNA of interest inserted into the nongenic sequence.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1. Illustrates a screen-shot sample of a wiggle plot for the DNA methylation profile of root and shoot tissues obtained from *Zea mays* c.v. B73 chromosome number 1.

Fig. 2. Illustrates a distribution of the polynucleotide sequence lengths of the resulting hypomethylated genomic locations of the *Zea mays* c.v. B73 genome.

Fig. 3. Represents a three dimensional graph of the 5,286 optimal maize loci. The Principal Component Analysis (PCA) statistical approach was used to cluster the set of 5,286 identified optimal genomic loci into 32 distinct clusters based on their feature values (see Example 1). During the PCA process, five principal components (PC) were generated, with the

top three PCs containing about 90% of the total variation in the dataset. These top three PCAs were used to graphically represent the 32 clusters in a three dimensional plot as shown in Fig. 3.

Fig. 4. Provides a schematic drawing indicating the chromosomal distribution of the 81 optimal genomic loci, and their relative positions on the maize chromosomes.

5 Fig. 5. Provides a graph showing the coverage of the 72 optimal genomic loci within *Zea mays* c.v. B104 and c.v.Hi-II genomic databases that were selected for targeting validation.

Fig. 6. Provides a schematic drawing indicating the *Zea mays* chromosomal location of 72 optimal genomic loci selected for targeting validation.

10 Fig. 7. Provides a plasmid map of pDAB111845 (SEQ ID NO:5418). The numbered elements (i.e., 5, 7, 8, 9, 10, 11, 12, 15, 16, 25, and 26) correspond with zinc finger nuclease binding sequences of about 20 to 35 base pairs in length that are recognized and cleaved by corresponding zinc finger nuclease proteins. These zinc finger binding sequences and the annotated "UZI Sequence" (which is a 100-150 bp template region containing restriction sites and DNA sequences for primer design or coding sequences) comprise the universal donor
15 cassette.

Fig. 8. Representation of the universal donor polynucleotide sequence for integration via non-homologous end joining (NHEJ). Two proposed vectors are provide wherein a DNA of interest (DNA X) comprises one or more (i.e., "1-N") zinc finger binding sites (ZFN BS) at either end of the DNA of interest. Vertical arrows show unique restriction sites and horizontal
20 arrows represent potential PCR primer sites.

Fig. 9. Representation of the universal donor polynucleotide sequence for integration via homologous-directed repair (HDR). A DNA of interest (DNA X) comprising two regions of homologous sequences (HA) flanking the DNA of interest with zinc finger nuclease binding sites (ZFN) bracketing the DNAX and HA sequences. Vertical arrows show unique restriction
25 sites and horizontal arrows represent potential PCR primer sites.

Fig. 10A-10C. Illustrates the constructs used for targeting and validation of the universal donor polynucleotide system integration within the *Zea mays* optimal genomic loci targeting and validation. Fig. 10A) ZFN design space with location of the ZFN pairs as previously shown in pDAB111845 of Figure 5. The ZFN pairs are labelled numerically and
30 correspond with specific ZFN binding sequences that are specifically recognized by ZFN proteins for binding and cleavage. Fig. 10B) Configuration of the ZFN expression construct. The ZFN expression construct contains a constitutive plant promoter (Zm Ubi1) which is used to drive expression of the ZFN protein. The ZFN protein contains the nuclear localization

sequence (NLS), the zinc finger proteins (ZFP-L and ZFP-R, where L indicates left hand binding ZFN protein and R indicates right hand binding protein), Fok-1 endonuclease (Fok1) and the self-hydrolyzing 2A (2A). Fig. 10C) universal donor polynucleotide for NHEJ mediated targeting of *Zea mays* optimal genomic loci. Z1-Z6 represent ZFN binding sites specific for a *Zea mays* optimal genomic loci target. The number of ZFN sites can vary from 3-6. Vertical arrows show unique restriction sites and horizontal arrows represent potential PCR primer sites. The universal donor polynucleotide system is a short (110 bp) sequence that is common to donors used for integration within *Zea mays* optimal genomic loci.

Fig. 11. Plasmid map of pDAB8393.

Fig. 12. ZFN cleavage activity at *Zea mays* selected genomic loci targets. Cleavage activity is represented as number of sequences with indels (insertions and deletions) at the ZFN cleavage site per 1 million high quality reads.

Fig. 13. Validation of *Zea mays* selected genomic loci targets using NHEJ based Rapid Targeting Analysis (RTA) method.

Fig. 14 & 14B. Plasmid constructs transformed into *Zea mays* via random integration that comprise the events used for flanking sequence analysis and transgene expression studies. Fig. 14 represents the insertion of pDAB105817, a 1871 bp fragment; Fig. 14B represents the insertion of a 6128 pb fragment of pEPS105817.

Fig. 15. Plasmid map of pDAB111846 (SEQ ID NO:5419). The numbered elements (i.e., 1, 2, 5, 6, 11, 12, 15, 16, 21, 22, 29 and 30) correspond with zinc finger nuclease binding sequences of about 20 to 35 base pairs in length that are recognized and cleaved by corresponding zinc finger nuclease proteins. These zinc finger binding sequences and the annotated "UZI Sequence" (which is a 100-150 bp template region containing restriction sites and DNA sequences for primer design or coding sequences) comprise the universal donor cassette.

Fig. 16. Plasmid map of pDAB117415 (SEQ ID NO:5420). The numbered elements (i.e., ZFN51 and ZFN52) correspond with zinc finger nuclease binding sequences of about 20 to 35 base pairs in length that are recognized and cleaved by corresponding zinc finger nuclease proteins. These zinc finger binding sequences and the annotated "UZI Sequence" (which is a 100-150 bp template region containing restriction sites and DNA sequences for primer design or coding sequences) comprise the universal donor cassette. Further included in this plasmid design is the "104113 Overlap" which are sequences that share homology to the plasmid vector

for high throughput assembly of the universal donor cassettes within a plasmid vector (i.e., via Gibson assembly).

Fig. 17. Plasmid map of pDAB117416 (SEQ ID NO:5421). The numbered elements (i.e., ZFN54 and ZFN53) correspond with zinc finger nuclease binding sequences of about 20 to 35 base pairs in length that are recognized and cleaved by corresponding zinc finger nuclease proteins. These zinc finger binding sequences and the annotated “UZI Sequence” (which is a 100-150 bp template region containing restriction sites and DNA sequences for primer design or coding sequences) comprise the universal donor cassette. Further included in this plasmid design is the “104113 Overlap” which are sequences that share homology to the plasmid vector for high throughput assembly of the universal donor cassettes within a plasmid vector (i.e., via Gibson assembly).

Fig. 18. Plasmid map of pDAB117417 (SEQ ID NO:5422). The numbered element (i.e., ZFN55) correspond with zinc finger nuclease binding sequences of about 20 to 35 base pairs in length that are recognized and cleaved by corresponding zinc finger nuclease proteins. These zinc finger binding sequences and the annotated “UZI Sequence” (which is a 100-150 bp template region containing restriction sites and DNA sequences for primer design or coding sequences) comprise the universal donor cassette. Further included in this plasmid design is the “104113 Overlap” which are sequences that share homology to the plasmid vector for high throughput assembly of the universal donor cassettes within a plasmid vector (i.e., via Gibson assembly).

Fig. 19. Plasmid map of pDAB117419 (SEQ ID NO:5423). The numbered elements (i.e., ZFN59 and ZFN60) correspond with zinc finger nuclease binding sequences of about 20 to 35 base pairs in length that are recognized and cleaved by corresponding zinc finger nuclease proteins. These zinc finger binding sequences and the annotated “UZI Sequence” (which is a 100-150 bp template region containing restriction sites and DNA sequences for primer design or coding sequences) comprise the universal donor cassette. Further included in this plasmid design is the “104113 Overlap” which are sequences that share homology to the plasmid vector for high throughput assembly of the universal donor cassettes within a plasmid vector (i.e., via Gibson assembly).

Fig. 20. Plasmid map of pDAB117434 (SEQ ID NO:5424). The numbered elements (i.e., ZFN66, ZFN67, ZFN68 and ZFN69) correspond with zinc finger nuclease binding sequences of about 20 to 35 base pairs in length that are recognized and cleaved by corresponding zinc finger nuclease proteins. These zinc finger binding sequences and the

annotated “UZI Sequence” (which is a 100-150 bp template region containing restriction sites and DNA sequences for primer design or coding sequences) comprise the universal donor cassette. Further included in this plasmid design is the “104113 Overlap” which are sequences that share homology to the plasmid vector for high throughput assembly of the universal donor cassettes within a plasmid vector (i.e., via Gibson assembly).

Fig. 21. Plasmid map of pDAB117418 (SEQ ID NO:5425). The numbered elements (i.e., ZFN56, ZFN57, and ZFN58) correspond with zinc finger nuclease binding sequences of about 20 to 35 base pairs in length that are recognized and cleaved by corresponding zinc finger nuclease proteins. These zinc finger binding sequences and the annotated “UZI Sequence” (which is a 100-150 bp template region containing restriction sites and DNA sequences for primer design or coding sequences) comprise the universal donor cassette. Further included in this plasmid design is the “104113 Overlap” which are sequences that share homology to the plasmid vector for high throughput assembly of the universal donor cassettes within a plasmid vector (i.e., via Gibson assembly).

Fig. 22. Plasmid map of pDAB117420 (SEQ ID NO:5426). The numbered elements (i.e., ZFN61 and ZFN62) correspond with zinc finger nuclease binding sequences of about 20 to 35 base pairs in length that are recognized and cleaved by corresponding zinc finger nuclease proteins. These zinc finger binding sequences and the annotated “UZI Sequence” (which is a 100-150 bp template region containing restriction sites and DNA sequences for primer design or coding sequences) comprise the universal donor cassette. Further included in this plasmid design is the “104113 Overlap” which are sequences that share homology to the plasmid vector for high throughput assembly of the universal donor cassettes within a plasmid vector (i.e., via Gibson assembly).

Fig. 23. Plasmid map of pDAB117421 (SEQ ID NO:5427). The numbered elements (i.e., PPL17 Pair 3, PPL17 Pair 1, and PPL17 Pair2) correspond with zinc finger nuclease binding sequences of about 20 to 35 base pairs in length that are recognized and cleaved by corresponding zinc finger nuclease proteins. These zinc finger binding sequences and the annotated “UZI Sequence” (which is a 100-150 bp template region containing restriction sites and DNA sequences for primer design or coding sequences) comprise the universal donor cassette. Further included in this plasmid design is the “104113 Overlap” which are sequences that share homology to the plasmid vector for high throughput assembly of the universal donor cassettes within a plasmid vector (i.e., via Gibson assembly).

Figs. 24A-24C. Histogram of characteristics (length, expression of coding region within 40 Kb of loci, and recombination frequency) for the identified optimal nongenic maize loci. Fig. 24A illustrates a distribution of the polynucleotide sequence lengths of the optimal genomic loci (OGL). Fig. 24B illustrates the distribution of expressed nucleic acid sequences relative to their proximity (log scale) to the optimal genomic loci (OGL). Fig. 24C illustrates the distribution of the optimal nongenic maize loci relative to their recombination frequency.

Fig. 25A & 25B. Histogram of characteristics (distance to actively transcribed endogenous gene and distance from centromere) for the identified optimal nongenic maize loci. Fig. 25A illustrates the distribution of the optimal genomic loci sequences relative to their distance to actively transcribed endogenous genes. Fig. 25B illustrates the distribution of the optimal genomic loci sequences relative to their distance to the chromosomal centromere.

DETAILED DESCRIPTION

DEFINITIONS

In describing and claiming the invention, the following terminology will be used in accordance with the definitions set forth below.

The term "about" as used herein means greater or lesser than the value or range of values stated by 10 percent, but is not intended to designate any value or range of values to only this broader definition. Each value or range of values preceded by the term "about" is also intended to encompass the embodiment of the stated absolute value or range of values.

As used herein, the term "plant" includes a whole plant and any descendant, cell, tissue, or part of a plant. The term "plant parts" include any part(s) of a plant, including, for example and without limitation: seed (including mature seed and immature seed); a plant cutting; a plant cell; a plant cell culture; a plant organ (*e.g.*, pollen, embryos, flowers, fruits, shoots, leaves, roots, stems, and explants). A plant tissue or plant organ may be a seed, callus, or any other group of plant cells that is organized into a structural or functional unit. A plant cell or tissue culture may be capable of regenerating a plant having the physiological and morphological characteristics of the plant from which the cell or tissue was obtained, and of regenerating a plant having substantially the same genotype as the plant. In contrast, some plant cells are not capable of being regenerated to produce plants. Regenerable cells in a plant cell or tissue culture may be embryos, protoplasts, meristematic cells, callus, pollen, leaves, anthers, roots, root tips, silk, flowers, kernels, ears, cobs, husks, or stalks.

Plant parts include harvestable parts and parts useful for propagation of progeny plants. Plant parts useful for propagation include, for example and without limitation: seed; fruit; a cutting; a seedling; a tuber; and a rootstock. A harvestable part of a plant may be any useful part of a plant, including, for example and without limitation: flower; pollen; seedling; tuber; leaf; stem; fruit; seed; and root.

A plant cell is the structural and physiological unit of the plant. Plant cells, as used herein, includes protoplasts and protoplasts with a cell wall. A plant cell may be in the form of an isolated single cell, or an aggregate of cells (*e.g.*, a friable callus and a cultured cell), and may be part of a higher organized unit (*e.g.*, a plant tissue, plant organ, and plant). Thus, a plant cell may be a protoplast, a gamete producing cell, or a cell or collection of cells that can regenerate into a whole plant. As such, a seed, which comprises multiple plant cells and is capable of regenerating into a whole plant, is considered a "plant part" in embodiments herein.

The term "protoplast", as used herein, refers to a plant cell that had its cell wall completely or partially removed, with the lipid bilayer membrane thereof naked. Typically, a protoplast is an isolated plant cell without cell walls which has the potency for regeneration into cell culture or a whole plant.

As used herein the terms "native" or "natural" define a condition found in nature. A "native DNA sequence" is a DNA sequence present in nature that was produced by natural means or traditional breeding techniques but not generated by genetic engineering (*e.g.*, using molecular biology/transformation techniques).

As used herein, "endogenous sequence" defines the native form of a polynucleotide, gene or polypeptide in its natural location in the organism or in the genome of an organism.

The term "isolated" as used herein means having been removed from its natural environment.

The term "purified", as used herein relates to the isolation of a molecule or compound in a form that is substantially free of contaminants normally associated with the molecule or compound in a native or natural environment and means having been increased in purity as a result of being separated from other components of the original composition. The term "purified nucleic acid" is used herein to describe a nucleic acid sequence which has been separated from other compounds including, but not limited to polypeptides, lipids and carbohydrates.

The terms "polypeptide", "peptide" and "protein" are used interchangeably to refer to a polymer of amino acid residues. The term also applies to amino acid polymers in which one or

more amino acids are chemical analogues or modified derivatives of a corresponding naturally-occurring amino acids.

As used herein the terms "optimal maize genomic loci", "optimal nongenic maize loci", "optimal nongenic loci", or "optimal genomic loci (OGL)" are used interchangeably to designate a native DNA sequence found in the nuclear genome of a maize plant that has the following properties: nongenic, hypomethylated, targetable, and in proximal location to a genic region, wherein the genomic region around the optimal maize genomic loci exemplifies evidence of recombination.

As used herein, the terms "nongenic maize sequence" or "nongenic maize genomic sequence" are used interchangeably to designate a native DNA sequence found in the nuclear genome of a maize plant, having a length of at least 1 Kb, and devoid of any open reading frames, gene sequences, or gene regulatory sequences. Furthermore, the nongenic maize sequence does not comprise any intron sequence (i.e., introns are excluded from the definition of nongenic). The nongenic sequence cannot be transcribed or translated into protein. Many plant genomes contain nongenic regions. As much as 95% of the genome can be nongenic, and these regions may be comprised of mainly repetitive DNA.

As used herein, a "genic region" is defined as a polynucleotide sequence that comprises an open reading frame encoding an RNA and/or polypeptide. The genic region may also encompass any identifiable adjacent 5' and 3' non-coding nucleotide sequences involved in the regulation of expression of the open reading frame up to about 2 Kb upstream of the coding region and 1 Kb downstream of the coding region, but possibly further upstream or downstream. A genic region further includes any introns that may be present in the genic region. Further, the genic region may comprise a single gene sequence, or multiple gene sequences interspersed with short spans (less than 1 Kb) of nongenic sequences.

As used herein a "nucleic acid of interest", "DNA of interest", or "donor" is defined as a nucleic acid/DNA sequence that has been selected for site directed, targeted insertion into the maize genome. A nucleic acid of interest can be of any length, for example between 2 and 50,000 nucleotides in length (or any integer value therebetween or thereabove), preferably between about 1,000 and 5,000 nucleotides in length (or any integer value therebetween). A nucleic acid of interest may comprise one or more gene expression cassettes that further comprise actively transcribed and/or translated gene sequences. Conversely, the nucleic acid of interest may comprise a polynucleotide sequence which does not comprise a functional gene expression cassette or an entire gene (e.g., may simply comprise regulatory sequences such as a

promoter), or may not contain any identifiable gene expression elements or any actively transcribed gene sequence. The nucleic acid of interest may optionally contain an analytical domain. Upon insertion of the nucleic acid of interest into the maize genome, the inserted sequences are referred to as the "inserted DNA of interest". Further, the nucleic acid of interest
5 can be DNA or RNA, can be linear or circular, and can be single-stranded or double-stranded. It can be delivered to the cell as naked nucleic acid, as a complex with one or more delivery agents (e.g., liposomes, poloxamers, T-strand encapsulated with proteins, etc.) or contained in a bacterial or viral delivery vehicle, such as, for example, *Agrobacterium tumefaciens* or an adenovirus or an adeno-associated Virus (AAV), respectively.

10 As used herein the term "analytical domain" defines a nucleic acid sequence that contains functional elements that assist in the targeted insertion of nucleic acid sequences. For example, an analytical domain may contain specifically designed restriction enzyme sites, zinc finger binding sites, engineered landing pads or engineered transgene integration platforms and may or may not comprise gene regulatory elements or an open reading frame. See, for
15 example, U.S. Patent Publication No 20110191899, incorporated herein by reference in its entirety.

As used herein the term "selected maize sequence" defines a native genomic DNA sequence of maize that has been chosen for analysis to determine if the sequence qualifies as an optimal nongenic maize genomic loci.

20 As used herein, the term "hypomethylation" or "hypomethylated", in reference to a DNA sequence, defines a reduced state of methylated DNA nucleotide residues in a given sequence of DNA. Typically, the decreased methylation relates to the number of methylated adenine or cytosine residues, relative to the average level of methylation found in nongenic sequences present in the maize genome.

25 As used herein a "targetable sequence" is a polynucleotide sequence that is sufficiently unique in a nuclear genome to allow site specific, targeted insertion of a nucleic acid of interest into one specific sequence.

As used herein the term "non-repeating" sequence is defined as a sequence of at least 1Kb in length that shares less than 40% identity to any other sequence within the *Zea mays*
30 genome. Calculations of sequence identity can be determined using any standard technique known to those skilled in the art including, for example, scanning a selected maize sequence against the *Zea mays* c.v. B73 genome using a BLAST™ based homology search using the NCBI BLAST™ software (version 2.2.23) run using the default parameter settings (Stephen F.

Altschul et al (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402). For example, as the selected maize sequences (from the *Zea mays* c.v. B73 genome) were analyzed, the first BLAST™ hit identified from such a search represents the *Zea mays* c.v. B73 sequence itself. The second
5 BLAST™ hit for each selected maize sequence was identified and the alignment coverage (represented as the percent of the selected maize sequence covered by the BLAST™ hit) of the hit was used as a measure of uniqueness of the selected maize sequence within the *Zea mays* genome. These alignment coverage values for the second BLAST™ hit ranged from a minimum of 0% to a maximum of 39.98% sequence identity. Any sequences that aligned at
10 higher levels of sequence identity were not considered.

The term "in proximal location to a genic region" when used in reference to a nongenic sequence defines the relative location of the nongenic sequence to a genic region. Specifically, the number of genic regions within a 40 Kb neighborhood (i.e., within 40 Kb on either end of the selected optimal maize genomic loci sequence) is analyzed. This analysis was completed by
15 assaying gene annotation information and the locations of known genes in the *Zea mays* genome were extracted from Maize Genome Database. For each of the 5,286 optimal nongenic maize genomic loci, a 40 Kb window around the optimal genomic loci sequence was defined and the number of annotated genes with locations overlapping this window was counted. The number of genic regions ranged from a minimum of 1 gene to a maximum of 9 genes within the
20 40 Kb neighborhood.

The term "known maize coding sequence" as used herein relates to any polynucleotide sequence identified from the Maize Genomic Database (available at www.maizegdb.org and Monaco, M., et al., Maize Metabolic Network Construction and Transcriptome Analysis. doi:10.3835/plantgenome2012.09.0025; Posted online 23 Jan. 2013) that comprise an open
25 reading frame, either before or after processing of intron sequences, and are transcribed into mRNA and optionally translated into a protein sequence when placed under the control of the appropriate genetic regulatory elements. The known maize coding sequence can be a cDNA sequence or a genomic sequence. In some instances, the known maize coding sequence can be annotated as a functional protein. In other instances, the known maize coding sequence may
30 not be annotated.

The term "predicted maize coding sequence" as used herein relates to any Expressed Sequence Tag (EST) polynucleotide sequences described in the Maize Genomic Database. ESTs are identified from cDNA libraries constructed using oligo(dT) primers to direct first-

strand synthesis by reverse transcriptase. The resulting ESTs are single-pass sequencing reads of less than 500 bp obtained from either the 5' or 3' end of the cDNA insert. Multiple ESTs may be aligned into a single contig. The identified EST sequences are uploaded into the Maize Genomic Database, and can be searched via bioinformatics methods to predict corresponding
5 genomic polynucleotide sequences that comprise a coding sequence that is transcribed into mRNA and optionally translated into a protein sequence when placed under the control of the appropriate genetic regulatory elements.

The term "evidence of recombination" as used herein relates to the meiotic recombination frequencies between any pair of *Zea mays* genomic markers across a
10 chromosome region comprising the selected maize sequence. The recombination frequencies were calculated based on the ratio of the genetic distance between markers (in centimorgan (cM)) to the physical distance between the markers (in megabases (Mb)). For a selected maize sequence to have evidence of recombination, the selected maize sequence must contain at least one recombination event between two markers flanking the selected maize sequence as detected
15 using a high resolution marker dataset generated from multiple mapping populations. (See for example, Jafar Mammadov, Wei Chen, Anastasia Chueva, Karthik Muthuraman, Ruihua Ren, David Meyer, and Siva Kumpatla. 2011. Distribution of Recombinant Frequencies across the Maize Genome. 52nd Annual Maize Genetics Conference).

As used herein the term "relative location value" is a calculated value defining the
20 distance of a genomic locus from its corresponding chromosomal centromere. For each selected maize sequence, the genomic distance from the native location of the selected maize sequence to the centromere of the chromosome that it is located on, is measured (in Bp). The relative location of selected maize sequence within the chromosome is represented as the ratio of its genomic distance to the centromere relative to the length of the specific chromosomal arm
25 (measured in Bp) that it lies on. These relative location values for the optimal nongenic maize genomic loci dataset ranged from a minimum of 0.00373 to a maximum of 0.99908 ratio of genomic distance.

The term "exogenous DNA sequence" as used herein is any nucleic acid sequence that has been removed from its native location and inserted into a new location altering the
30 sequences that flank the nucleic acid sequence that has been moved. For example, an exogenous DNA sequence may comprise a sequence from another species.

"Binding" refers to a sequence-specific, interaction between macromolecules (e.g., between a protein and a nucleic acid). Not all components of a binding interaction need be

sequence-specific (e.g., contacts with phosphate residues in a DNA backbone), as long as the interaction as a whole is sequence-specific. Such interactions are generally characterized by a dissociation constant (K_d). "Affinity" refers to the strength of binding: increased binding affinity being correlated with a lower binding constant (K_d).

5 A "binding protein" is a protein that is able to bind to another molecule. A binding protein can bind to, for example, a DNA molecule (a DNA-binding protein), an RNA molecule (an RNA-binding protein) and/or a protein molecule (a protein-binding protein). In the case of a protein-binding protein, it can bind to itself (to form homodimers, homotrimers, etc.) and/or it can bind to one or more molecules of a different protein or proteins. A binding protein can have
10 more than one type of binding activity. For example, zinc finger proteins have DNA-binding, RNA-binding and protein-binding activity.

As used herein the term "zinc fingers," defines regions of amino acid sequence within a DNA binding protein binding domain whose structure is stabilized through coordination of a zinc ion.

15 A "zinc finger DNA binding protein" (or binding domain) is a protein, or a domain within a larger protein, that binds DNA in a sequence-specific manner through one or more zinc fingers, which are regions of amino acid sequence within the binding domain whose structure is stabilized through coordination of a zinc ion. The term zinc finger DNA binding protein is often abbreviated as zinc finger protein or ZFP. Zinc finger binding domains can be "engineered" to
20 bind to a predetermined nucleotide sequence. Non-limiting examples of methods for engineering zinc finger proteins are design and selection. A designed zinc finger protein is a protein not occurring in nature whose design/composition results principally from rational criteria. Rational criteria for design include application of substitution rules and computerized algorithms for processing information in a database storing information of existing ZFP designs
25 and binding data. See, for example, U.S. Pat. Nos. 6,140,081; 6,453,242; 6,534,261 and 6,794,136; see also WO 98/53058; WO 98/53059; WO 98/53060; WO 02/016536 and WO 03/016496.

A "TALE DNA binding domain" or "TALE" is a polypeptide comprising one or more TALE repeat domains/units. The repeat domains are involved in binding of the TALE to its
30 cognate target DNA sequence. A single "repeat unit" (also referred to as a "repeat") is typically 33-35 amino acids in length and exhibits at least some sequence homology with other TALE repeat sequences within a naturally occurring TALE protein. *See, e.g.*, U.S. Patent Publication No. 20110301073, incorporated by reference herein in its entirety.

The CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats)/Cas (CRISPR Associated) nuclease system. Briefly, a "CRISPR DNA binding domain" is a short stranded RNA molecule that acting in concert with the CAS enzyme can selectively recognize, bind, and cleave genomic DNA. The CRISPR/Cas system can be engineered to create a double-stranded break (DSB) at a desired target in a genome, and repair of the DSB can be influenced by the use of repair inhibitors to cause an increase in error prone repair. *See, e.g.,* Jinek et al (2012) Science 337, p. 816-821, Jinek et al, (2013), eLife 2:e00471, and David Segal, (2013) eLife 2:e00563).

Zinc finger, CRISPR and TALE binding domains can be "engineered" to bind to a predetermined nucleotide sequence, for example via engineering (altering one or more amino acids) of the recognition helix region of a naturally occurring zinc finger. Similarly, TALEs can be "engineered" to bind to a predetermined nucleotide sequence, for example by engineering of the amino acids involved in DNA binding (the repeat variable diresidue or RVD region). Therefore, engineered DNA binding proteins (zinc fingers or TALEs) are proteins that are non-naturally occurring. Non-limiting examples of methods for engineering DNA-binding proteins are design and selection. A designed DNA binding protein is a protein not occurring in nature whose design/composition results principally from rational criteria. Rational criteria for design include application of substitution rules and computerized algorithms for processing information in a database storing information of existing ZFP and/or TALE designs and binding data. *See, for example,* U.S. Patents 6,140,081; 6,453,242; and 6,534,261; *see also* WO 98/53058; WO 98/53059; WO 98/53060; WO 02/016536 and WO 03/016496 and U.S. Publication Nos. 20110301073, 20110239315 and 20119145940.

A "selected" zinc finger protein, CRISPR or TALE is a protein not found in nature whose production results primarily from an empirical process such as phage display, interaction trap or hybrid selection. *See e.g.,* U.S. Patent Nos. 5,789,538; US 5,925,523; US 6,007,988; US 6,013,453; US 6,200,759; WO 95/19431; WO 96/06166; WO 98/53057; WO 98/54311; WO 00/27878; WO 01/60970 WO 01/88197 and WO 02/099084 and U.S. Publication Nos. 20110301073, 20110239315 and 20119145940.

"Recombination" refers to a process of exchange of genetic information between two polynucleotides, including but not limited to, donor capture by non-homologous end joining (NHEJ) and homologous recombination. For the purposes of this disclosure, "homologous recombination (HR)" refers to the specialized form of such exchange that takes place, for example, during repair of double-strand breaks in cells via homology-directed repair

mechanisms. This process requires nucleotide sequence homology, uses a "donor" molecule to template repair of a "target" molecule (*i.e.*, the nucleotide sequence that experienced the double-strand break), and is variously known as "non-crossover gene conversion" or "short tract gene conversion," because it leads to the transfer of genetic information from the donor to the target. Without wishing to be bound by any particular theory, such transfer can involve mismatch correction of heteroduplex DNA that forms between the broken target and the donor, and/or "synthesis-dependent strand annealing," in which the donor is used to resynthesize genetic information that will become part of the target, and/or related processes. Such specialized HR often results in an alteration of the sequence of the target molecule such that part or all of the sequence of the donor polynucleotide is incorporated into the target polynucleotide. For HR-directed integration, the donor molecule contains at least 2 regions of homology to the genome ("homology arms") of least 50-100 base pairs in length. *See, e.g.*, U.S. Patent Publication No. 20110281361.

In the methods of the disclosure, one or more targeted nucleases as described herein create a double-stranded break in the target sequence (*e.g.*, cellular chromatin) at a predetermined site, and a "donor" polynucleotide, having homology to the nucleotide sequence in the region of the break for HR mediated integration or having no homology to the nucleotide sequence in the region of the break for NHEJ mediated integration, can be introduced into the cell. The presence of the double-stranded break has been shown to facilitate integration of the donor sequence. The donor sequence may be physically integrated or, alternatively, the donor polynucleotide is used as a template for repair of the break via homologous recombination, resulting in the introduction of all or part of the nucleotide sequence as in the donor into the cellular chromatin. Thus, a first sequence in cellular chromatin can be altered and, in certain embodiments, can be converted into a sequence present in a donor polynucleotide. Thus, the use of the terms "replace" or "replacement" can be understood to represent replacement of one nucleotide sequence by another, (*i.e.*, replacement of a sequence in the informational sense), and does not necessarily require physical or chemical replacement of one polynucleotide by another. In any of the methods described herein, additional pairs of zinc-finger proteins, CRISPRs or TALEN can be used for additional double-stranded cleavage of additional target sites within the cell.

Any of the methods described herein can be used for insertion of a donor of any size and/or partial or complete inactivation of one or more target sequences in a cell by targeted

integration of donor sequence that disrupts expression of the gene(s) of interest. Cell lines with partially or completely inactivated genes are also provided.

Furthermore, the methods of targeted integration as described herein can also be used to integrate one or more exogenous sequences. The exogenous nucleic acid sequence can comprise, for example, one or more genes or cDNA molecules, or any type of coding or noncoding sequence, as well as one or more control elements (*e.g.*, promoters). In addition, the exogenous nucleic acid sequence (transgene) may produce one or more RNA molecules (*e.g.*, small hairpin RNAs (shRNAs), inhibitory RNAs (RNAis), microRNAs (miRNAs), *etc.*), or protein.

"Cleavage" as used herein defines the breakage of the phosphate-sugar backbone of a DNA molecule. Cleavage can be initiated by a variety of methods including, but not limited to, enzymatic or chemical hydrolysis of a phosphodiester bond. Both single-stranded cleavage and double-stranded cleavage are possible, and double-stranded cleavage can occur as a result of two distinct single-stranded cleavage events. DNA cleavage can result in the production of either blunt ends or staggered ends. In certain embodiments, fusion polypeptides are used for targeted double-stranded DNA cleavage. A "cleavage domain" comprises one or more polypeptide sequences which possesses catalytic activity for DNA cleavage. A cleavage domain can be contained in a single polypeptide chain or cleavage activity can result from the association of two (or more) polypeptides.

A "cleavage half-domain" is a polypeptide sequence which, in conjunction with a second polypeptide (either identical or different) forms a complex having cleavage activity (preferably double-strand cleavage activity). The terms "first and second cleavage half-domains;" "+ and – cleavage half-domains" and "right and left cleavage half-domains" are used interchangeably to refer to pairs of cleavage half-domains that dimerize.

An "engineered cleavage half-domain" is a cleavage half-domain that has been modified so as to form obligate heterodimers with another cleavage half-domain (*e.g.*, another engineered cleavage half-domain). See, also, U.S. Patent Publication Nos. 2005/0064474, 20070218528, 2008/0131962 and 2011/0201055, incorporated herein by reference in their entireties.

A "target site" or "target sequence" refers to a portion of a nucleic acid to which a binding molecule will bind, provided sufficient conditions for binding exist.

Nucleic acids include DNA and RNA, can be single- or double-stranded; can be linear, branched or circular; and can be of any length. Nucleic acids include those capable of forming duplexes, as well as triplex-forming nucleic acids. See, for example, U.S. Pat. Nos. 5,176,996

and 5,422,251. Proteins include, but are not limited to, DNA-binding proteins, transcription factors, chromatin remodeling factors, methylated DNA binding proteins, polymerases, methylases, demethylases, acetylases, deacetylases, kinases, phosphatases, integrases, recombinases, ligases, topoisomerases, gyrases and helicases.

5 A "product of an exogenous nucleic acid" includes both polynucleotide and polypeptide products, for example, transcription products (polynucleotides such as RNA) and translation products (polypeptides).

A "fusion" molecule is a molecule in which two or more subunit molecules are linked, for example, covalently. The subunit molecules can be the same chemical type of molecule, or
10 can be different chemical types of molecules. Examples of the first type of fusion molecule include, but are not limited to, fusion proteins (for example, a fusion between a ZFP DNA-binding domain and a cleavage domain) and fusion nucleic acids (for example, a nucleic acid encoding the fusion protein described supra). Examples of the second type of fusion molecule include, but are not limited to, a fusion between a triplex-forming nucleic acid and a
15 polypeptide, and a fusion between a minor groove binder and a nucleic acid. Expression of a fusion protein in a cell can result from delivery of the fusion protein to the cell or by delivery of a polynucleotide encoding the fusion protein to a cell, wherein the polynucleotide is transcribed, and the transcript is translated, to generate the fusion protein. Trans-splicing, polypeptide cleavage and polypeptide ligation can also be involved in expression of a protein in a cell.
20 Methods for polynucleotide and polypeptide delivery to cells are presented elsewhere in this disclosure.

For the purposes of the present disclosure, a "gene", includes a DNA region encoding a gene product (*see infra*), as well as all DNA regions which regulate the production of the gene product, whether or not such regulatory sequences are adjacent or operably linked to coding
25 and/or transcribed sequences. Accordingly, a gene includes, but is not necessarily limited to, promoter sequences, terminators, translational regulatory sequences such as ribosome binding sites and internal ribosome entry sites, enhancers, silencers, insulators, boundary elements, replication origins, matrix attachment sites and locus control regions.

"Gene expression" refers to the conversion of the information, contained in a gene, into
30 a gene product. A gene product can be the direct transcriptional product of a gene (e.g., mRNA, tRNA, rRNA, antisense RNA, interfering RNA, ribozyme, structural RNA or any other type of RNA) or a protein produced by translation of a mRNA. Gene products also include RNAs which are modified, by processes such as capping, polyadenylation, methylation, and editing,

and proteins modified by, for example, methylation, acetylation, phosphorylation, ubiquitination, ADP-ribosylation, myristilation, and glycosylation.

Sequence identity: The term “sequence identity” or “identity,” as used herein in the context of two nucleic acid or polypeptide sequences, refers to the residues in the two sequences that are the same when aligned for maximum correspondence over a specified comparison window.

As used herein, the term “percentage of sequence identity” refers to the value determined by comparing two optimally aligned sequences (e.g., nucleic acid sequences, and amino acid sequences) over a comparison window, wherein the portion of the sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleotide or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the comparison window, and multiplying the result by 100 to yield the percentage of sequence identity.

Methods for aligning sequences for comparison are well-known in the art. Various programs and alignment algorithms are described in, for example: Smith and Waterman (1981) *Adv. Appl. Math.* 2:482; Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443; Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. U.S.A.* 85:2444; Higgins and Sharp (1988) *Gene* 73:237-44; Higgins and Sharp (1989) *CABIOS* 5:151-3; Corpet et al. (1988) *Nucleic Acids Res.* 16:10881-90; Huang et al. (1992) *Comp. Appl. Biosci.* 8:155-65; Pearson et al. (1994) *Methods Mol. Biol.* 24:307-31; Tatiana et al. (1999) *FEMS Microbiol. Lett.* 174:247-50. A detailed consideration of sequence alignment methods and homology calculations can be found in, e.g., Altschul et al. (1990) *J. Mol. Biol.* 215:403-10. The National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST™; Altschul et al. (1990)) is available from several sources, including the National Center for Biotechnology Information (Bethesda, MD), and on the internet, for use in connection with several sequence analysis programs. A description of how to determine sequence identity using this program is available on the internet under the “help” section for BLAST™. For comparisons of nucleic acid sequences, the “Blast 2 sequences” function of the BLAST™ (Blastn) program may be employed using the default parameters. Nucleic acid sequences with even greater similarity to the reference sequences will show increasing percentage identity when assessed by this method.

Specifically hybridizable/Specifically complementary: As used herein, the terms “specifically hybridizable” and “specifically complementary” are terms that indicate a sufficient degree of complementarity, such that stable and specific binding occurs between the nucleic acid molecule and a target nucleic acid molecule. Hybridization between two nucleic acid molecules involves the formation of an anti-parallel alignment between the nucleic acid sequences of the two nucleic acid molecules. The two molecules are then able to form hydrogen bonds with corresponding bases on the opposite strand to form a duplex molecule that, if it is sufficiently stable, is detectable using methods well known in the art. A nucleic acid molecule need not be 100% complementary to its target sequence to be specifically hybridizable. However, the amount of sequence complementarity that must exist for hybridization to be specific is a function of the hybridization conditions used.

Hybridization conditions resulting in particular degrees of stringency will vary depending upon the nature of the hybridization method of choice and the composition and length of the hybridizing nucleic acid sequences. Generally, the temperature of hybridization and the ionic strength (especially the Na⁺ and/or Mg⁺⁺ concentration) of the hybridization buffer will determine the stringency of hybridization, though wash times also influence stringency. Calculations regarding hybridization conditions required for attaining particular degrees of stringency are known to those of ordinary skill in the art, and are discussed, for example, in Sambrook et al. (ed.) *Molecular Cloning: A Laboratory Manual*, 2nd ed., vol. 1-3, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989, chapters 9 and 11; and Hames and Higgins (eds.) *Nucleic Acid Hybridization*, IRL Press, Oxford, 1985. Further detailed instruction and guidance with regard to the hybridization of nucleic acids may be found, for example, in Tijssen, “Overview of principles of hybridization and the strategy of nucleic acid probe assays,” in *Laboratory Techniques in Biochemistry and Molecular Biology-Hybridization with Nucleic Acid Probes*, Part I, Chapter 2, Elsevier, NY, 1993; and Ausubel et al., Eds., *Current Protocols in Molecular Biology*, Chapter 2, Greene Publishing and Wiley-Interscience, NY, 1995.

As used herein, “stringent conditions” encompass conditions under which hybridization will only occur if there is less than 20% mismatch between the hybridization molecule and a sequence within the target nucleic acid molecule. “Stringent conditions” include further particular levels of stringency. Thus, as used herein, “moderate stringency” conditions are those under which molecules with more than 20% sequence mismatch will not hybridize; conditions of “high stringency” are those under which sequences with more than 10% mismatch

will not hybridize; and conditions of "very high stringency" are those under which sequences with more than 5% mismatch will not hybridize. The following are representative, non-limiting hybridization conditions.

High Stringency condition (detects sequences that share at least 90% sequence identity):

- 5 Hybridization in 5x SSC buffer (wherein the SSC buffer contains a detergent such as SDS, and additional reagents like salmon sperm DNA, EDTA, etc.) at 65 °C for 16 hours; wash twice in 2x SSC buffer (wherein the SSC buffer contains a detergent such as SDS, and additional reagents like salmon sperm DNA, EDTA, etc.) at room temperature for 15 minutes each; and wash twice in 0.5x SSC buffer (wherein the SSC buffer contains a detergent such as SDS, and additional reagents like salmon sperm DNA, EDTA, etc.) at 65 °C for 20 minutes each.

- Moderate Stringency condition (detects sequences that share at least 80% sequence identity): Hybridization in 5x-6x SSC buffer (wherein the SSC buffer contains a detergent such as SDS, and additional reagents like salmon sperm DNA, EDTA, etc.) at 65-70 °C for 16-20 hours; wash twice in 2x SSC buffer (wherein the SSC buffer contains a detergent such as SDS, and additional reagents like salmon sperm DNA, EDTA, etc.) at room temperature for 5-20 minutes each; and wash twice in 1x SSC buffer (wherein the SSC buffer contains a detergent such as SDS, and additional reagents like salmon sperm DNA, EDTA, etc.) at 55-70 °C for 30 minutes each.

- Non-stringent control condition (sequences that share at least 50% sequence identity will hybridize): Hybridization in 6x SSC buffer (wherein the SSC buffer contains a detergent such as SDS, and additional reagents like salmon sperm DNA, EDTA, etc.) at room temperature to 55 °C for 16-20 hours; wash at least twice in 2x-3x SSC buffer (wherein the SSC buffer contains a detergent such as SDS, and additional reagents like salmon sperm DNA, EDTA, etc.) at room temperature to 55 °C for 20-30 minutes each.

- 25 As used herein, the term "substantially homologous" or "substantial homology," with regard to a contiguous nucleic acid sequence, refers to contiguous nucleotide sequences that hybridize under stringent conditions to the reference nucleic acid sequence. For example, nucleic acid sequences that are substantially homologous to a reference nucleic acid sequence are those nucleic acid sequences that hybridize under stringent conditions (e.g., the Moderate Stringency conditions set forth, supra) to the reference nucleic acid sequence. Substantially homologous sequences may have at least 80% sequence identity. For example, substantially homologous sequences may have from about 80% to 100% sequence identity, such as about 81%; about 82%; about 83%; about 84%; about 85%; about 86%; about 87%; about 88%; about

89%; about 90%; about 91%; about 92%; about 93%; about 94% about 95%; about 96%; about 97%; about 98%; about 98.5%; about 99%; about 99.5%; and about 100%. The property of substantial homology is closely related to specific hybridization. For example, a nucleic acid molecule is specifically hybridizable when there is a sufficient degree of complementarity to avoid non-specific binding of the nucleic acid to non-target sequences under conditions where specific binding is desired, for example, under stringent hybridization conditions.

In some instances "homologous" may be used to refer to the relationship of a first gene to a second gene by descent from a common ancestral DNA sequence. In such instances, the term, homolog, indicates a relationship between genes separated by the event of speciation (see ortholog) or to the relationship between genes separated by the event of genetic duplication (see paralog). In other instances "homologous" may be used to refer to the level of sequence identity between one or more polynucleotide sequences, in such instances the one or more polynucleotide sequences do not necessarily descend from a common ancestral DNA sequence. Those with skill in the art are aware of the interchangeability of the term "homologous" and appreciate the proper application of the term.

As used herein, the term "ortholog" (or "orthologous") refers to a gene in two or more species that has evolved from a common ancestral nucleotide sequence, and may retain the same function in the two or more species.

As used herein, the term "paralogous" refers to genes related by duplication within a genome. Orthologs retain the same function in the course of evolution, whereas paralogs evolve new functions, even if these new functions are unrelated to the original gene function.

As used herein, two nucleic acid sequence molecules are said to exhibit "complete complementarity" when every nucleotide of a sequence read in the 5' to 3' direction is complementary to every nucleotide of the other sequence when read in the 3' to 5' direction. A nucleotide sequence that is complementary to a reference nucleotide sequence will exhibit a sequence identical to the reverse complement sequence of the reference nucleotide sequence. These terms and descriptions are well defined in the art and are easily understood by those of ordinary skill in the art.

When determining the percentage of sequence identity between amino acid sequences, it is well-known by those of skill in the art that the identity of the amino acid in a given position provided by an alignment may differ without affecting desired properties of the polypeptides comprising the aligned sequences. In these instances, the percent sequence identity may be adjusted to account for similarity between conservatively substituted amino acids. These

adjustments are well-known and commonly used by those of skill in the art. See, e.g., Myers and Miller (1988) *Computer Applications in Biosciences* 4:11-7. Statistical methods are known in the art and can be used in analysis of the identified 5,286 optimal genomic loci.

As an embodiment, the identified optimal genomic loci comprising 5,286 individual
5 optimal genomic loci sequences can be analyzed via an F-distribution test. In probability theory and statistics, the F-distribution is a continuous probability distribution. The F-distribution test is a statistical significance test that has an F-distribution, and is used when comparing statistical models that have been fit to a data set, to identify the best-fitting model. An F-distribution is a continuous probability distribution, and is also known as Snedecor's F-distribution or the
10 Fisher-Snedecor distribution. The F-distribution arises frequently as the null distribution of a test statistic, most notably in the analysis of variance. The F-distribution is a right-skewed distribution. The F-distribution is an asymmetric distribution that has a minimum value of 0, but no maximum value. The curve reaches a peak not far to the right of 0, and then gradually approaches the horizontal axis the larger the F value is. The F-distribution approaches, but
15 never quite touches the horizontal axis. It will be appreciated that in other embodiments, variations on this equation, or indeed different equations, may be derived and used by the skilled person and are applicable to the analysis of 5,286 individual optimal genomic loci sequences.

Operably linked: A first nucleotide sequence is "operably linked" with a second
20 nucleotide sequence when the first nucleotide sequence is in a functional relationship with the second nucleotide sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. When recombinantly produced, operably linked nucleotide sequences are generally contiguous and, where necessary to join two protein-coding regions, in the same reading frame. However,
25 nucleotide sequences need not be contiguous to be operably linked.

The term, "operably linked," when used in reference to a regulatory sequence and a coding sequence, means that the regulatory sequence affects the expression of the linked coding sequence. "Regulatory sequences," "regulatory elements", or "control elements," refer to nucleotide sequences that influence the timing and level/amount of transcription, RNA
30 processing or stability, or translation of the associated coding sequence. Regulatory sequences may include promoters; translation leader sequences; introns; enhancers; stem-loop structures; repressor binding sequences; termination sequences; polyadenylation recognition sequences; etc. Particular regulatory sequences may be located upstream and/or downstream of a coding

sequence operably linked thereto. Also, particular regulatory sequences operably linked to a coding sequence may be located on the associated complementary strand of a double-stranded nucleic acid molecule.

When used in reference to two or more amino acid sequences, the term “operably linked” means that the first amino acid sequence is in a functional relationship with at least one of the additional amino acid sequences.

The disclosed methods and compositions include fusion proteins comprising a cleavage domain operably linked to a DNA-binding domain (e.g., a ZFP) in which the DNA-binding domain by binding to a sequence in the *Zea mays* optimal genomic locus directs the activity of the cleavage domain to the vicinity of the sequence and, hence, induces a double stranded break in the optimal genomic locus. As set forth elsewhere in this disclosure, a zinc finger domain can be engineered to bind to virtually any desired sequence. Accordingly, one or more DNA-binding domains can be engineered to bind to one or more sequences in the optimal genomic locus. Expression of a fusion protein comprising a DNA-binding domain and a cleavage domain in a cell, effects cleavage at or near the target site.

EMBODIMENTS

Targeting transgenes and transgene stacks to specific locations in the *Zea mays* genome will improve the quality of transgenic events, reduce costs associated with production of transgenic events and provide new methods for making transgenic plant products such as sequential gene stacking. Overall, targeting transgenes to specific genomic sites is likely to be commercially beneficial. Significant advances have been made in the last few years towards development of site-specific nucleases such as ZFNs, CRISPRs, and TALENs that can facilitate addition of donor polynucleotides to pre-selected sites in plant and other genomes. However, much less is known about the attributes of genomic sites that are suitable for targeting. Historically, non-essential genes and pathogen (viral) integration sites in genomes have been used as loci for targeting. The number of such sites in genomes is rather limiting and there is therefore a need for identification and characterization of optimal genomic loci that can be used for targeting of donor polynucleotide sequences. In addition to being amenable to targeting, optimal genomic loci are expected to be neutral sites that can support transgene expression and breeding applications.

Applicants have recognized that additional criteria are desirable for insertion sites and have combined these criteria to identify and select optimal sites in the maize genome for the

insertion of exogenous sequences. For targeting purposes, the site of selected insertion needs to be unique and in a non-repetitive region of the *Zea mays* genome. Likewise, the optimal genomic site for insertion should possess minimal undesirable phenotypic effects and be susceptible to recombination events to facilitate introgression into agronomically elite lines using traditional breeding techniques. In order to identify the genomic loci that meet the listed criteria, the *Zea mays* genome was scanned using a customized bioinformatics approach and genome scale datasets to identify novel genomic loci possessing characteristics that are beneficial for the integration of polynucleotide donor sequence and the subsequent expression of a inserted coding sequence.

I. Identification of Nongenic Maize Genomic Loci

In accordance with one embodiment a method is provided for identifying optimal nongenic maize genomic sequence for insertion of exogenous sequences. The method comprises the steps of first identifying maize genomic sequences of at least 1 Kb in length that are hypomethylated. In one embodiment the hypomethylated genomic sequence is 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, 10, 11, 12, 13, 14, 15, 16 or 17 Kb in length. In one embodiment the hypomethylated genomic sequence is about 1 to about 4Kb in length and in a further embodiment is about 2 Kb in length. A sequence is considered hypomethylated if it has less than 1% DNA methylation within the sequence. In one embodiment the methylation status is measured based on the presence of 5-methylcytosine at one or more CpG dinucleotides, CHG or CHH trinucleotides within a selected maize sequence, relative to the amount of total cytosines found at corresponding CpG dinucleotides, CHG or CHH trinucleotides within a normal control DNA sample. CHH methylation indicates a 5-methylcytosine followed by two nucleotides that many not be guanine and CHG methylation refers to a 5-methylcytosine preceding an adenine, thymine or cytosine based followed by guanine. More particularly, in one embodiment the selected maize sequence has less than 1, 2 or 3 methylated nucleotides per 500 nucleotides of the selected maize sequence. In one embodiment the selected maize sequence has less than one, two, or three 5-methylcytosines at CpG dinucleotides per 500 nucleotides of the selected maize sequence. In one embodiment the selected maize sequence is 1 to 4Kb in length and comprises a 1Kb sequence devoid of 5-methylcytosines. In one embodiment the selected maize sequence is 1, 1.5, 2, 2.5, 3, 3.5, 4, 4.5, 5, 5.5, 6, 6.5, 7, 7.5, 8, or 8.5 Kb in length and contains 1 or 0 methylated nucleotides in its entire length. In one embodiment the selected maize sequence is 1, 1.5, 2, 2.5, 3, 3.5, 4, 4.5, 5,

5.5, 6, 6.5, 7, 7.5, 8, or 8.5 Kb in length and contains no 5-methylcytosines at CpG dinucleotides within its entire length. In accordance with one embodiment the methylation of a selected maize sequence may vary based on source tissue. In such embodiments the methylation levels used to determine if a sequence is hypomethylated represents the average amount of methylation in the sequences isolated from two or more tissues (e.g., from root and shoot).

In addition to the requirement that an optimal genomic site be hypomethylated, the selected maize sequence must also be nongenic. Accordingly, all hypomethylated genomic sequences are further screened to eliminate hypomethylated sequences that contain a genic region. This includes any open reading frames regardless of whether the transcript encodes a protein. Hypomethylated genomic sequences that include genic regions, including any identifiable adjacent 5' and 3' non-coding nucleotide sequences involved in the regulation of expression of an open reading frame and any introns that may be present in the genic region, are excluded from the optimal nongenic maize genomic locus of the present disclosure.

Optimal nongenic maize genomic loci must also be sequences that have demonstrated evidence of recombination. In one embodiment the selected maize sequence must be one where at least one recombination event has been detected between two markers flanking the selected maize sequence as detected using a high resolution marker dataset generated from multiple mapping populations. In one embodiment the pair of markers flanking a 0.5, 1, 1.5 Mb maize genomic sequence comprising the selected maize sequence are used to calculate the recombinant frequency for the selected maize sequence. Recombination frequencies between each pairs of markers (measured in centimorgan (cM)) to the genomic physical distance between the markers (in Mb)) must be greater than 0 cM/Mb. In one embodiment the recombination frequency for a 1 Mb maize genomic sequence comprising the selected maize sequence ranges from about 0.00041 to about 4.0. In one embodiment the recombination frequency for a 1 Mb maize genomic sequence comprising the selected maize sequence ranges from about 0.5 to about 5.0. In one embodiment an optimal genomic loci is one where recombination events have been detected within the selected maize sequence.

An optimal nongenic maize genomic loci will also be a targetable sequence, i.e., a sequence that is relatively unique in the maize genome such that a gene targeted to the selected maize sequence will only insert in one location of the maize genome. In one embodiment the entire length of the optimal genomic sequence shares less than 30%, 35%, or 40%, sequence identity with another sequence of similar length contained in the maize genome. Accordingly

in one embodiment the selected maize sequence cannot comprise a 1 Kb sequence that shares more than 25%, 30%, 35%, or 40% sequence identity with another 1 Kb sequence contained in the maize genome. In a further embodiment the selected maize sequence cannot comprise a 500bp sequence that shares more than 30%, 35%, or 40% sequence identity with another 500bp sequence contained in the maize genome. In one embodiment the selected maize sequence cannot comprise a 1KB sequence that shares more than 40% sequence identity with another 1Kb sequence contained in the maize genome.

An optimal nongenic maize genomic loci will also be proximal to a genic region. More particularly, a selected maize sequence must be located in the vicinity of a genic region (e.g., a genic region must be located within 40Kb of genomic sequence flanking and contiguous with either end of the selected maize as found in the native genome). In one embodiment a genic region is located within 10, 20, 30 or 40 Kb of contiguous genomic sequence located at either end of the selected maize sequence as found in the native maize genome. In one embodiment two or more genic regions are located within 10, 20, 30 or 40 Kb of contiguous genomic sequence flanking the two ends of the selected maize sequence. In one embodiment 1-9 genic regions are located within 10, 20, 30 or 40 Kb of contiguous genomic sequence flanking the two ends of the selected maize sequence. In one embodiment two or more genic regions are located within a 20, 30 or 40 Kb genomic sequence comprising the selected maize sequence. In one embodiment 1-9 genic regions are located within a 40Kb genomic sequence comprising the selected maize sequence. In one embodiment the genic region located within a 10, 20, 30 or 40 Kb of contiguous genomic sequence flanking the selected maize sequence comprises a known gene in the *Zea mays* genome.

In accordance with one embodiment a modified nongenic maize genomic loci is provided wherein the loci is at least 1KB in length, is nongenic, comprises no methylated cytosine residues, has a recombination frequency of greater than 0.00041 cM/Mb over a 1Mb genomic region encompassing the maize genomic loci and a 1Kb sequence of the maize genomic loci shares less than 40% sequence identity with any other 1Kb sequence contained in the maize genome, wherein the nongenic maize genomic loci is modified by the insertion of a DNA of interest into the nongenic maize genomic loci.

In accordance with one embodiment a method for identifying optimal nongenic maize genomic loci is provided. In some embodiments, the method first comprises screening the maize genome to create a first pool of selected maize sequences that have a minimal length of 1Kb and are hypomethylated, optionally wherein the genomic sequence has less than 1%

methylation or wherein the genomic sequence is devoid of any methylated cytosine residues. This first pool of selected maize sequences can be further screened to eliminate loci that do not meet the requirements for optimal nongenic maize genomic loci. Maize genomic sequences that encode maize transcripts, share greater than 40% or higher sequence identity with another sequence of similar length, do not exhibit evidence of recombination, and do not have a known open reading frame within 40Kb of the selected maize sequence, are eliminated from the first pool of sequences, leaving a second pool of sequences that qualify as optimal nongenic maize loci. In one embodiment any selected maize sequences that do not have a known maize gene, or a sequence comprising a 2Kb upstream and/or 1Kb downstream region of a known maize gene, within 40Kb of one end of said nongenic sequence are eliminated from the first pool of sequences. In one embodiment any selected maize sequences that do not contain a known gene that expresses a protein within 40Kb of the selected maize sequence are eliminated. In one embodiment any selected maize sequences that do not have a recombination frequency of greater than 0.00041 cM/Mb are eliminated.

Using these selection criteria applicants have identified select optimal genomic loci of *Zea mays* that serve as optimal nongenic maize genomic loci, the sequences of which are disclosed as SEQ ID NO: 1-SEQ ID NO: 5,286. The present disclosure also encompasses natural variants or modified derivatives of the identified optimal nongenic maize genomic loci wherein the variant or derivative loci comprise a sequence that differs from any sequence of SEQ ID NO: 1-SEQ ID NO: 5,286 by 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 nucleotides. In one embodiment optimal nongenic maize genomic loci for use in accordance with the present disclosure comprise sequences selected from SEQ ID NO: 1-SEQ ID NO: 5,286 or sequences that share 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity with a sequence selected from SEQ ID NO: 1-SEQ ID NO: 5,286.

In another embodiment, optimal nongenic maize genomic loci for use in accordance with the present disclosure comprise sequences selected from any variety of maize or corn plants. In a further embodiment optimal nongenic maize genomic loci for use in accordance with the present disclosure comprise sequences selected from yellow corn inbreds. Accordingly, a yellow corn inbred includes dent or flint yellow corn inbred plants, including agronomically elite varieties thereof. In a subsequent embodiment, optimal nongenic maize genomic loci for use in accordance with the present disclosure comprise sequences selected from transformable corn lines. In an embodiment, representative transformable corn lines include; Hi-II, B73, B104, Mo 17, W22, A188, H99, and derivatives thereof. One of skill in the

art will appreciate that as a result of phylogenetic divergence, various types of corn lines do not contain identical genomic DNA sequences, and that polymorphisms or allelic variation may be present within genomic sequences. In an embodiment, the present disclosure encompasses such polymorphism or allelic variations of the identified optimal nongenic maize genomic loci wherein the polymorphisms or allelic variation comprise a sequence that differs from any sequence of SEQ ID NO: 1-SEQ ID NO: 5,286 by 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 nucleotides. In a further embodiment, the present disclosure encompasses such polymorphisms or allelic variations of the identified optimal nongenic maize genomic loci wherein the polymorphisms or allelic variations comprise a sequence that shares 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity with any sequence of SEQ ID NO: 1-SEQ ID NO: 5,286.

The identified optimal genomic loci comprising 5,286 individual sequences can be categorized into various subgroupings by further analysis using a multivariate analysis method. Application of any multivariate analysis statistical programs is used to uncover the latent structure (dimensions) of a set of variables. A number of different types of multivariate algorithms can be used, for example the data set can be analyzed using multiple regression analysis, logistic regression analysis, discriminate analysis, multivariate analysis of variance (MANOVA), factor analysis (including both common factor analysis, and principal component analysis), cluster analysis, multidimensional scaling, correspondence analysis, conjoint analysis, canonical analysis, canonical correlation, and structural equation modeling.

In accordance with one embodiment the optimal nongenic maize genomic loci are further analyzed using multivariate data analysis such as Principal Component Analysis (PCA). Only a brief description will be given here, more information can be found in H. Martens, T. Naes, Multivariate Calibration, Wiley, N.Y., 1989. PCA evaluates the underlying dimensionality (latent variables) of the data, and gives an overview of the dominant patterns and major trends in the data. In one embodiment, the optimal nongenic maize genomic loci can be sorted into clusters via a principal component analysis (PCA) statistical method. The PCA is a mathematical procedure that uses an orthogonal transformation to convert a set of observations of possibly correlated variables into a set of values of linearly uncorrelated variables called principal components. The number of principal components is less than or equal to the number of original variables. This transformation is defined in such a way that the first principal component has the largest possible variance (that is, accounts for as much of the variability in the data as possible), and each succeeding component in turn has the highest variance possible under the constraint that it be orthogonal to (i.e., uncorrelated with) the

preceding components. Principal components are guaranteed to be independent if the data set is jointly normally distributed. PCA is sensitive to the relative scaling of the original variables. Examples of the use of PCA to cluster a set of entities based on features of the entities include; Ciampitti, I. et al., (2012) *Crop Science*, 52(6); 2728-2742, *Chemometrics: A Practical Guide*, Kenneth R. Beebe, Randy J. Pell, and Mary Beth Seasholtz, Wiley-Interscience, 1 edition, 1998, U.S. Patent No. 8,385,662, and European Patent No. 2,340,975.

In accordance with one embodiment a principal component analysis (PCA) was conducted on the 5,286 optimal maize genomic loci using the following 10 features for each identified optimal maize genomic loci:

1. Length of the hypo-methylated region around the optimal genomic loci (OGL)
 - a. Genome wide methylation profiles for root and shoot tissues were established using Illumina/Solexa 1G parallel sequencing data after digesting genomic DNA with a methylation-sensitive restriction enzyme (Wang *et al.*, (2009) *Genome-Wide and Organ-Specific Landscapes of Epigenetic Modifications and Their Relationships to mRNA and Small RNA Transcriptomes in Maize. Plant Cell* 21(4): 1053–1069). Sequences mapping to the genome indicated the presence of DNA methylation at the mapped locations and chromosomal stretches without mapped sequences indicated an absence of methylation (hypo-methylation). The length of the hypo-methylated region around each of the OGLs was calculated using the described methylation profiles.
2. Rate of Recombination in a 1MB region around the OGL
 - a. For each OGL, a pair of markers on either side of the OGL, within a 1Mb window, was identified. Recombination frequencies between each pairs of markers across the chromosome were calculated based on the ratio of the genetic distance between markers (in centimorgan (cM)) to the genomic physical distance between the markers (in Mb).
3. Level of OGL sequence uniqueness
 - a. For each OGL, the nucleotide sequence of the OGL was scanned against the *Zea mays* c.v. B73 genome using a BLAST based homology search. As these OGL sequences are identified from the *Zea mays* c.v. B73 genome, the first BLAST hit identified through this search represents the OGL sequence itself. The second BLAST hit for each OGL was identified and the alignment coverage of the hit was used as a measure of uniqueness of the OGL sequence within the *Zea mays* genome.
4. Distance from the OGL to the closest gene in its neighborhood
 - a. Gene annotation information and the location of known genes in the *Zea mays* c.v. B73 genome were extracted from Maize Genome DB (www.maizegdb.org). For each OGL, the closest annotated gene in its upstream or downstream neighborhood was identified and the distance between the OGL sequence and the gene was measured (in bp).

5. GC % in the OGLneighborhood
 - a. For each OGL, the nucleotide sequence was analyzed to estimate the number of Guanine and Cytosine bases present. This count was represented as a percentage of the sequence length of each OGL and provides a measure for GC %.
6. Number of genes in a 40 Kb neighborhood around the OGL
 - a. Gene annotation information and the location of known genes in the *Zea mays* c.v. B73 genome were extracted from Maize Genome DB (www.maizegdb.org). For each OGL, a 40 Kb window around the OGL was defined and the number of annotated genes with locations overlapping this window was counted.
7. Average gene expression in a 40 Kb neighborhood around the OGL.
 - a. Transcript level expression of Maize genes was measured by analyzing transcriptome profiling data generated from *Zea mays* c.v. B73 root and shoot tissues using RNAseq technology. For each OGL, annotated genes within the *Zea mays* c.v. B73 genome that were present in a 40 Kb neighborhood around the OGL were identified. Expression levels for each of the genes in the window were extracted from the transcriptome profiles and an average gene expression level was calculated.
8. Level of Nucleosome occupancy around the OGL
 - a. Discerning the level of nucleosome occupancy for a particular nucleotide sequence provides information about chromosomal functions and the genomic context of the sequence. The NuPoP™ statistical package provides a user-friendly software tool for predicting the nucleosome occupancy and the most probable nucleosome positioning map for genomic sequences of any size (Xi, L., Fondufe-Mittendor, Y., Xia, L., Flatow, J., Widom, J. and Wang, J.-P., Predicting nucleosome positioning using a duration Hidden Markov Model, BMC Bioinformatics, 2010, doi:10.1186/1471-2105-11-346). For each OGL, the nucleotide sequence was submitted to the NuPoP™ software and a nucleosome occupancy score was calculated.
9. Relative location within the chromosome (proximity to centromere)
 - a. Information on position of the centromere in each of the Maize chromosomes and the lengths of the chromosome arms was extracted from Maize genome DB (www.maizegdb.org). For each OGL, the genomic distance from the OGLsequence to the centromere of the chromosome that it is located on, is measured (in bp). The relative location of a OGL within the chromosome is represented as the ratio of its genomic distance to the centromere relative to the length of the specific chromosomal arm that it lies on.
10. Number of OGLs in a 1Mb region around the OGL
 - a. For each OGL, a 1Mb genomic window around the OGL location is defined and the number of OGLs, in the Maize 1Kb OGL dataset, whose genomic locations overlap with this window is tallied.

The results or values for the score of the features and attributes of each optimal nongenicmaize genomic loci are further described in Table 3 of Example 2. The resulting

dataset was used in the PCA statistical method to cluster the 5,286 identified optimal nongenic maize genomic loci into clusters. During the clustering process, after estimating the “p” principle components of the optimal genomic loci, the assignment of the optimal genomic loci to one of the 32 clusters proceeded in the “p” dimensional Euclidean space. Each of the “p” axes was divided into “k” intervals. Optimal genomic loci assigned to the same interval were grouped together to form clusters. Using this analysis, each PCA axis was divided into two intervals, which was chosen based on *a priori* information regarding the number of clusters required for experimental validation. All analysis and the visualization of the resulting clusters were carried out with the Molecular Operating Environment™ (MOE) software from Chemical Computing Group Inc. (Montreal, Quebec, Canada). The PCA approach was used to cluster the set of 5,286 optimal maize genomic loci into 32 distinct clusters based on their feature values, described above.

During the PCA process, five principal components (PC) were generated, with the top three PCs containing about 90% of the total variation in the dataset (Table 4). These three PCs were used to graphically represent the 32 clusters in a three dimensional plot (see Fig. 3). After the clustering process, was completed, one representative optimal genomic loci was chosen from each cluster. This was performed by choosing a select optimal genomic locus, within each cluster, that was closest to the centroid of that cluster by computational methods (Table 4). The chromosomal locations of the 32 representative optimal genomic loci are uniformly distributed among the maize chromosomes as shown in Fig. 4.

In accordance with one embodiment a purified optimal nongenic sequence is provided wherein the purified sequence is at least 1Kb in length and has at least 90, 95%, or 99% sequence identity with a nongenic sequence selected from any sequence described in Table 15 of Example 8. In one embodiment the optimal nongenic maize genomic loci to be modified is a genomic sequence selected from loci_137693_G1 (SEQ ID NO:387), loci_265551_G1 (SEQ ID NO:463), loci_128078_G1 (SEQ ID NO:560), loci_168286_G1 (SEQ ID NO:573), loci_3733_G1 (SEQ ID NO:1268), loci_203075_G1 (SEQ ID NO:2030), loci_232484_G1 (SEQ ID NO:2053), loci_136086_G1 (SEQ ID NO:4425), loci_203704_G1 (SEQ ID NO:2033), loci_127268_G1 (SEQ ID NO:2709), loci_204637_G1 (SEQ ID NO:2731), loci_291068_G1 (SEQ ID NO:3230), loci_232222_G1 (SEQ ID NO:3357), loci_43577_G1 (SEQ ID NO:3428), loci_204726_G1 (SEQ ID NO:424), and loci_232228_G1 (SEQ ID NO:4529). In one embodiment the purified sequence is at least 1Kb in length and has at least 90%, 95%, or 99% sequence identity with a sequence present in a nongenic sequence selected from

the group consisting of loci_137693_G1 (SEQ ID NO:387), loci_265551_G1 (SEQ ID NO:463), loci_128078_G1 (SEQ ID NO:560), loci_168286_G1 (SEQ ID NO:573), loci_3733_G1 (SEQ ID NO:1268), loci_203075_G1 (SEQ ID NO:2030), loci_232484_G1 (SEQ ID NO:2053), loci_136086_G1 (SEQ ID NO:4425), loci_203704_G1 (SEQ ID NO:2033), loci_127268_G1 (SEQ ID NO:2709), loci_204637_G1 (SEQ ID NO:2731), loci_291068_G1 (SEQ ID NO:3230), loci_232222_G1 (SEQ ID NO:3357), loci_43577_G1 (SEQ ID NO:3428), loci_204726_G1 (SEQ ID NO:424), and loci_232228_G1 (SEQ ID NO:4529). In one embodiment a purified sequence is provided that is at least 1Kb in length and has at least 90%, 95%, or 99% sequence identity with a sequence present in a nongenic sequence selected from the group consisting of optimal loci_204637 (SEQ ID NO:2731), optimal_loci_136086 (SEQ ID NO:4425), optimal_loci_232484 (SEQ ID NO:2053), optimal_loci_203075 (SEQ ID NO:2030), optimal_loci_3733 (SEQ ID NO:1268), optimal_loci_168286 (SEQ ID NO:573), optimal_loci_128078 (SEQ ID NO:560), optimal_loci_265551 (SEQ ID NO:463), optimal_loci_127268 (SEQ ID NO:2709), optimal_loci_204726 (SEQ ID NO:424), and optimal_loci_232222 (SEQ ID NO:3357). In one embodiment a purified sequence is provided that is at least 1Kb in length and has at least 90%, 95%, or 99% sequence identity with a sequence present in a nongenic sequence selected from the group consisting of optimal loci_204637 (SEQ ID NO:2731), optimal_loci_136086 (SEQ ID NO:4425), optimal_loci_232484 (SEQ ID NO:2053), optimal_loci_203075 (SEQ ID NO:2030), optimal_loci_3733 (SEQ ID NO:1268), optimal_loci_168286 (SEQ ID NO:573), optimal_loci_128078 (SEQ ID NO:560) and optimal_loci_265551 (SEQ ID NO:463). In one embodiment a purified sequence is provided that is at least 1Kb in length and has at least 90%, 95%, or 99% sequence identity with a sequence present in a nongenic sequence selected from the group consisting of optimal loci_204637 (SEQ ID NO:2731), optimal_loci_203075 (SEQ ID NO:2030) and optimal_loci_128078 (SEQ ID NO:560).

In one embodiment a purified sequence is provided comprising a 1Kb sequence identical to a sequence present in a nongenic sequence selected from the group consisting of optimal loci_204637 (SEQ ID NO:2731), optimal_loci_136086 (SEQ ID NO:4425), optimal_loci_232484 (SEQ ID NO:2053), optimal_loci_203075 (SEQ ID NO:2030), optimal_loci_3733 (SEQ ID NO:1268), optimal_loci_168286 (SEQ ID NO:573), optimal_loci_128078 (SEQ ID NO:560) and optimal_loci_265551 (SEQ ID NO:463). In one embodiment a purified sequence is provided comprising a 1Kb sequence identical to a sequence present in a nongenic sequence selected from the group consisting of optimal loci_204637

(SEQ ID NO:2731), optimal_loci_203075 (SEQ ID NO:2030) and optimal_loci_128078 (SEQ ID NO:560).

In an embodiment, the subject disclosure relates to a recombinant sequence, comprising: a nucleic acid sequence of at least 1 Kb and having at least 90%, 95%, or 99% sequence identity with a nongenic sequence selected from the group consisting of loci_137693_G1 (SEQ ID NO:387), loci_265551_G1 (SEQ ID NO:463), loci_128078_G1 (SEQ ID NO:560), loci_168286_G1 (SEQ ID NO:573), loci_3733_G1 (SEQ ID NO:1268), loci_203075_G1 (SEQ ID NO:2030), loci_232484_G1 (SEQ ID NO:2053), and loci_204637_G1 (SEQ ID NO:2731), with a DNA of interest inserted into the nongenic sequence.

In accordance with one embodiment a modified optimal nongenic maize genomic loci is provided wherein the optimal nongenic maize genomic loci has been modified to comprise one or more nucleotide substitutions, deletions or insertions. In one embodiment the optimal nongenic maize genomic loci is modified by the insertion of a DNA of interest optionally accompanied with further nucleotide duplications, deletions or inversions of genomic loci sequence.

In an embodiment the optimal nongenic maize genomic loci to be modified is a genomic sequence selected from any sequence described in Table 15 of Example 8. In one embodiment the optimal nongenic maize genomic loci to be modified is a genomic sequence selected from loci_137693_G1 (SEQ ID NO:387), loci_265551_G1 (SEQ ID NO:463), loci_128078_G1 (SEQ ID NO:560), loci_168286_G1 (SEQ ID NO:573), loci_3733_G1 (SEQ ID NO:1268), loci_203075_G1 (SEQ ID NO:2030), loci_232484_G1 (SEQ ID NO:2053), loci_136086_G1 (SEQ ID NO:4425), loci_203704_G1 (SEQ ID NO:2033), loci_127268_G1 (SEQ ID NO:2709), loci_204637_G1 (SEQ ID NO:2731), loci_291068_G1 (SEQ ID NO:3230), loci_232222_G1 (SEQ ID NO:3357), loci_43577_G1 (SEQ ID NO:3428), loci_204726_G1 (SEQ ID NO:424), and loci_232228_G1 (SEQ ID NO: 4529). In one embodiment the optimal nongenic maize genomic loci to be modified is a genomic sequence from loci_137693_G1 (SEQ ID NO:387). In one embodiment the optimal nongenic maize genomic loci to be modified is a genomic sequence from loci_265551_G1 (SEQ ID NO:463). In one embodiment the optimal nongenic maize genomic loci to be modified is a genomic sequence from loci_128078_G1 (SEQ ID NO:560). In one embodiment the optimal nongenic maize genomic loci to be modified is a genomic sequence from loci_168286_G1 (SEQ ID NO:573). In one embodiment the optimal nongenic maize genomic loci to be modified is a genomic sequence from loci_3733_G1 (SEQ ID NO:1268). In one embodiment the optimal nongenic maize

genomic loci to be modified is a genomic sequence from loci_203075_G1 (SEQ ID NO:2030). In one embodiment the optimal nongenic maize genomic loci to be modified is a genomic sequence from loci_232484_G1 (SEQ ID NO:2053). In one embodiment the optimal nongenic maize genomic loci to be modified is a genomic sequence from loci_136086_G1 (SEQ ID NO:4425). In one embodiment the optimal nongenic maize genomic loci to be modified is a genomic sequence from loci_203704_G1 (SEQ ID NO:2033). In one embodiment the optimal nongenic maize genomic loci to be modified is a genomic sequence from loci_127268_G1 (SEQ ID NO:2709). In one embodiment the optimal nongenic maize genomic loci to be modified is a genomic sequence s from loci_204637_G1 (SEQ ID NO:2731). In one embodiment the optimal nongenic maize genomic loci to be modified is a genomic sequence from loci_291068_G1 (SEQ ID NO:3230). In one embodiment the optimal nongenic maize genomic loci to be modified is a genomic sequence from loci_232222_G1 (SEQ ID NO:3357). In one embodiment the optimal nongenic maize genomic loci to be modified is a genomic sequence from loci_43577_G1 (SEQ ID NO:3428). In one embodiment the optimal nongenic maize genomic loci to be modified is a genomic sequence from loci_204726_G1 (SEQ ID NO:424). In one embodiment the optimal nongenic maize genomic loci to be modified is a genomic sequence from loci_232228_G1 (SEQ ID NO: 4529).

In a further embodiment the optimal nongenic maize genomic loci to be modified is a genomic sequence selected from loci_137693_G1 (SEQ ID NO:387), loci_265551_G1 (SEQ ID NO:463), loci_128078_G1 (SEQ ID NO:560), loci_168286_G1 (SEQ ID NO:573), loci_3733_G1 (SEQ ID NO:1268), loci_203075_G1 (SEQ ID NO:2030), loci_232484_G1 (SEQ ID NO:2053), loci_136086_G1 (SEQ ID NO:4425), and loci_203704_G1 (SEQ ID NO:2033). In a further embodiment the optimal nongenic maize genomic loci to be modified is a genomic sequence selected from loci_137693_G1 (SEQ ID NO:387), loci_265551_G1 (SEQ ID NO:463), loci_128078_G1 (SEQ ID NO:560), loci_168286_G1 (SEQ ID NO:573), loci_3733_G1 (SEQ ID NO:1268), loci_203075_G1 (SEQ ID NO:2030), loci_232484_G1 (SEQ ID NO:2053), and loci_136086_G1 (SEQ ID NO:4425). In a further embodiment the optimal nongenic maize genomic loci to be modified is a genomic sequence selected from loci_137693_G1 (SEQ ID NO:387), loci_265551_G1 (SEQ ID NO:463), loci_128078_G1 (SEQ ID NO:560), loci_168286_G1 (SEQ ID NO:573), loci_3733_G1 (SEQ ID NO:1268), loci_203075_G1 (SEQ ID NO:2030), and loci_232484_G1 (SEQ ID NO:2053). In a further embodiment the optimal nongenic maize genomic loci to be modified is a genomic sequence selected from loci_137693_G1 (SEQ ID NO:387), loci_265551_G1 (SEQ ID NO:463),

loci_128078_G1 (SEQ ID NO:560), loci_168286_G1 (SEQ ID NO:573), loci_3733_G1 (SEQ ID NO:1268), and loci_203075_G1 (SEQ ID NO:2030). In a further embodiment the optimal nongenic maize genomic loci to be modified is a genomic sequence selected from loci_137693_G1 (SEQ ID NO:387), loci_265551_G1 (SEQ ID NO:463), loci_128078_G1 (SEQ ID NO:560), loci_168286_G1 (SEQ ID NO:573), and loci_3733_G1 (SEQ ID NO:1268). In a further embodiment the optimal nongenic maize genomic loci to be modified is a genomic sequence selected from loci_137693_G1 (SEQ ID NO:387), loci_265551_G1 (SEQ ID NO:463), loci_128078_G1 (SEQ ID NO:560), and loci_168286_G1 (SEQ ID NO:573). In a further embodiment the optimal nongenic maize genomic loci to be modified is a genomic sequence selected from loci_137693_G1 (SEQ ID NO:387), loci_265551_G1 (SEQ ID NO:463), and loci_128078_G1 (SEQ ID NO:560). In a further embodiment the optimal nongenic maize genomic loci to be modified is a genomic sequence selected from loci_137693_G1 (SEQ ID NO:387), and loci_265551_G1 (SEQ ID NO:463).

In a further embodiment the optimal nongenic maize genomic loci to be modified is a genomic sequence selected from loci_127268_G1 (SEQ ID NO:2709), loci_204637_G1 (SEQ ID NO:2731), loci_291068_G1 (SEQ ID NO:3230), loci_232222_G1 (SEQ ID NO:3357), loci_43577_G1 (SEQ ID NO:3428), loci_204726_G1 (SEQ ID NO:424), and loci_232228_G1 (SEQ ID NO: 4529). In a further embodiment the optimal nongenic maize genomic loci to be modified is a genomic sequence selected from loci_127268_G1 (SEQ ID NO:2709), loci_204637_G1 (SEQ ID NO:2731), loci_291068_G1 (SEQ ID NO:3230), loci_232222_G1 (SEQ ID NO:3357), loci_43577_G1 (SEQ ID NO:3428), and loci_204726_G1 (SEQ ID NO:424). In a further embodiment the optimal nongenic maize genomic loci to be modified is a genomic sequence selected from loci_127268_G1 (SEQ ID NO:2709), loci_204637_G1 (SEQ ID NO:2731), loci_291068_G1 (SEQ ID NO:3230), loci_232222_G1 (SEQ ID NO:3357), and loci_43577_G1 (SEQ ID NO:3428). In a further embodiment the optimal nongenic maize genomic loci to be modified is a genomic sequence selected from loci_127268_G1 (SEQ ID NO:2709), loci_204637_G1 (SEQ ID NO:2731), loci_291068_G1 (SEQ ID NO:3230), and loci_232222_G1 (SEQ ID NO:3357). In a further embodiment the optimal nongenic maize genomic loci to be modified is a genomic sequence selected from loci_127268_G1 (SEQ ID NO:2709), loci_204637_G1 (SEQ ID NO:2731), and loci_291068_G1 (SEQ ID NO:3230). In a further embodiment the optimal nongenic maize genomic loci to be modified is a genomic sequence selected from loci_127268_G1 (SEQ ID NO:2709), and loci_204637_G1 (SEQ ID NO:2731).

In one embodiment the optimal nongenic maize genomic loci is selected from the genomic sequences of loci_59517_G1 (SEQ ID NO: 1), loci_159525_G1 (SEQ ID NO: 199), loci_9811_G1 (SEQ ID NO: 365), loci_7507_G1 (SEQ ID NO: 543), loci_178978_G1 (SEQ ID NO: 687), loci_285621_G1 (SEQ ID NO: 875), loci_221721_G1 (SEQ ID NO: 1089),
 5 loci_83937_G1 (SEQ ID NO: 1233), loci_37146_G1 (SEQ ID NO: 1369), loci_156393_G1 (SEQ ID NO: 1571), loci_343678_G1 (SEQ ID NO: 1795), loci_60209_G1 (SEQ ID NO: 1980), loci_282323_G1 (SEQ ID NO: 2171), loci_64542_G1 (SEQ ID NO: 2349), loci_162531_G1 (SEQ ID NO: 2557), loci_337001_G1 (SEQ ID NO: 2693), loci_66202_G1 (SEQ ID NO: 2855), loci_185454_G1 (SEQ ID NO: 3004), loci_239863_G1 (SEQ ID NO: 3151),
 10 loci_257541_G1 (SEQ ID NO: 3289), loci_217939_G1 (SEQ ID NO: 3455), loci_326869_G1 (SEQ ID NO: 3586), loci_31710_G1 (SEQ ID NO: 3731), loci_81941_G1 (SEQ ID NO: 3849), loci_198387_G1 (SEQ ID NO: 3981), loci_197372_G1 (SEQ ID NO: 4192), loci_106202_G1 (SEQ ID NO: 4401), loci_232228_G1 (SEQ ID NO: 4529),
 15 loci_244324_G1 (SEQ ID NO: 4646), loci_157315_G1 (SEQ ID NO: 4836), loci_137489_G1 (SEQ ID NO: 5046), and loci_31764_G1 (SEQ ID NO: 5162).

In one embodiment the optimal nongenic maize genomic loci is selected from the genomic sequences of loci_59517_G1 (SEQ ID NO: 1), loci_25001_G1 (SEQ ID NO: 100), loci_112632_G1 (SEQ ID NO: 203), loci_28905_G1 (SEQ ID NO: 295), loci_129164_G1 (SEQ ID NO: 384), loci_204726_G1 (SEQ ID NO: 424), loci_2425_G1 (SEQ ID NO: 451),
 20 loci_122036_G1 (SEQ ID NO: 547), loci_5735_G1 (SEQ ID NO: 671), loci_178978_G1 (SEQ ID NO: 687), loci_288388_G1 (SEQ ID NO: 781), loci_60310_G1 (SEQ ID NO: 843), loci_285621_G1 (SEQ ID NO: 875), loci_243330_G1 (SEQ ID NO: 967), loci_127038_G1 (SEQ ID NO: 1107), loci_262784_G1 (SEQ ID NO: 1147), loci_344662_G1 (SEQ ID NO: 1190),
 25 loci_153894_G1 (SEQ ID NO: 1252), loci_28771_G1 (SEQ ID NO: 1300), loci_1098_G1 (SEQ ID NO: 1371), loci_97772_G1 (SEQ ID NO: 1569), loci_156393_G1 (SEQ ID NO: 1571), loci_236662_G1 (SEQ ID NO: 1663), loci_139485_G1 (SEQ ID NO: 1822), loci_301175_G1 (SEQ ID NO: 1906), loci_152337_G1 (SEQ ID NO: 2003), loci_202616_G1 (SEQ ID NO: 2027), loci_203704_G1 (SEQ ID NO: 2033), loci_282323_G1 (SEQ ID NO: 2171),
 30 loci_262782_G1 (SEQ ID NO: 2256), loci_64542_G1 (SEQ ID NO: 2349), loci_236455_G1 (SEQ ID NO: 2428), loci_162531_G1 (SEQ ID NO: 2557), loci_301774_G1 (SEQ ID NO: 2632), loci_344663_G1 (SEQ ID NO: 2649), loci_337001_G1

(SEQ ID NO: 2693), loci_204637_G1 (SEQ ID NO: 2731), loci_238100_G1 (SEQ ID NO: 2753), loci_66202_G1 (SEQ ID NO: 2855), loci_264359_G1 (SEQ ID NO: 2934), loci_282653_G1 (SEQ ID NO: 3086), loci_80282_G1 (SEQ ID NO: 3139), loci_291068_G1 (SEQ ID NO: 3230), loci_56395_G1 (SEQ ID NO: 3270), loci_200497_G1 (SEQ ID NO: 3334), loci_232222_G1 (SEQ ID NO: 3357), loci_43577_G1 (SEQ ID NO: 3428), loci_5607_G1 (SEQ ID NO: 3435), loci_114664_G1 (SEQ ID NO: 3457), loci_228254_G1 (SEQ ID NO: 3497), loci_120993_G1 (SEQ ID NO: 3593), loci_53137_G1 (SEQ ID NO: 3702), loci_31710_G1 (SEQ ID NO: 3731), loci_344664_G1 (SEQ ID NO: 3815), loci_81941_G1 (SEQ ID NO: 3849), loci_321514_G1 (SEQ ID NO: 3939), loci_198387_G1 (SEQ ID NO: 3981), loci_301180_G1 (SEQ ID NO: 4113), loci_197372_G1 (SEQ ID NO: 4192), loci_348776_G1 (SEQ ID NO: 4350), loci_244439_G1 (SEQ ID NO: 4458), loci_348258_G1 (SEQ ID NO: 4487), loci_232228_G1 (SEQ ID NO: 4529), loci_322501_G1 (SEQ ID NO: 4610), loci_244324_G1 (SEQ ID NO: 4646), loci_97232_G1 (SEQ ID NO: 4832), loci_157315_G1 (SEQ ID NO: 4836), loci_282499_G1 (SEQ ID NO: 4953), loci_155031_G1 (SEQ ID NO: 5060), loci_301773_G1 (SEQ ID NO: 5110), loci_283161_G1 (SEQ ID NO: 5213), loci_55524_G1 (SEQ ID NO: 5264), loci_127268_G1 (SEQ ID NO: 21492709), loci_136086_G1 (SEQ ID NO: 34844425), loci_232484_G1 (SEQ ID NO: 34172053), loci_3733_G1 (SEQ ID NO: 36261923), loci_168286_G1 (SEQ ID NO: 3473571), loci_128078_G1 (SEQ ID NO: 3047560), loci_265551_G1 (SEQ ID NO: 3547463), and loci_137693_G1 (SEQ ID NO: 387).

In one embodiment the optimal nongenic maize genomic loci is targeted with a DNA of interest, wherein the DNA of interest integrates within or proximal to the zinc finger nuclease target sites. In accordance with an embodiment, exemplary zinc finger target sites of optimal maize select genomic loci are provided in Table 8. In accordance with an embodiment, integration of a DNA of interest occurs within or proximal to the exemplary target sites of: 111879ZFN5 and 111879ZFN7; 111885ZFN1 and 111885ZFN2; SIG115737_31v1 and SIG115737_32v1; SIG120523_11v1 and SIG120523_12v1; SIG115246_5 and SIG115246_6; SIG115636_1v1 and SIG115636_2v1; SIG120417_11v1 and SIG120417_12v1; SIG120621_15v1 and SIG120621_16v1; SIG12078_11v1 and SIG12078_12v1; and, SIG157315_1v1 and SIG157315_2v1, ZFN_binding_1 and ZFN_binding_2, ZFN_binding_3 and ZFN_binding_4, ZFN_binding_5 and ZFN_binding_6, ZFN_binding_7 and ZFN_binding_8, ZFN_binding_9 and ZFN_binding_10, ZFN_binding_11 and

	ZFN_binding_12,	ZFN_binding_13	and	ZFN_binding_14,	ZFN_binding_15	and
	ZFN_binding_16,	ZFN_binding_17	and	ZFN_binding_18,	ZFN_binding_19	and
	ZFN_binding_20,	ZFN_binding_21	and	ZFN_binding_22,	ZFN_binding_23	and
	ZFN_binding_24,	ZFN_binding_25	and	ZFN_binding_26,	ZFN_binding_27	and
5	ZFN_binding_28,	ZFN_binding_29	and	ZFN_binding_30,	ZFN_binding_31	and
	ZFN_binding_32,	ZFN_binding_33	and	ZFN_binding_34,	ZFN_binding_35	and
	ZFN_binding_36,	ZFN_binding_37	and	ZFN_binding_38,	ZFN_binding_39	and
	ZFN_binding_40,	ZFN_binding_41	and	ZFN_binding_42,	ZFN_binding_43	and
	ZFN_binding_44,	ZFN_binding_45	and	ZFN_binding_46,	ZFN_binding_47	and
10	ZFN_binding_48,	ZFN_binding_49	and	ZFN_binding_50,	ZFN_binding_51	and
	ZFN_binding_52,	ZFN_binding_53	and	ZFN_binding_54,	ZFN_binding_55	and
	ZFN_binding_56,	ZFN_binding_57	and	ZFN_binding_58,	ZFN_binding_59	and
	ZFN_binding_60,	ZFN_binding_61	and	ZFN_binding_62,	ZFN_binding_63	and
	ZFN_binding_64,	ZFN_binding_65	and	ZFN_binding_66,	ZFN_binding_67	and
15	ZFN_binding_68,	ZFN_binding_69	and	ZFN_binding_70,	ZFN_binding_71	and
	ZFN_binding_72,	ZFN_binding_73	and	ZFN_binding_74,	ZFN_binding_75	and
	ZFN_binding_76,	ZFN_binding_77	and	ZFN_binding_78,	ZFN_binding_79	and
	ZFN_binding_80,	ZFN_binding_81	and	ZFN_binding_82,	ZFN_binding_83	and
	ZFN_binding_84,	ZFN_binding_85	and	ZFN_binding_86,	ZFN_binding_87	and
20	ZFN_binding_88,	ZFN_binding_89	and	ZFN_binding_90,	ZFN_binding_91	and
	ZFN_binding_92,	ZFN_binding_93	and	ZFN_binding_94,	ZFN_binding_95	and
	ZFN_binding_96,	ZFN_binding_97	and	ZFN_binding_98,	ZFN_binding_99	and
	ZFN_binding_100,	ZFN_binding_101	and	ZFN_binding_102,	ZFN_binding_103	and
	ZFN_binding_104,	ZFN_binding_105	and	ZFN_binding_106,	ZFN_binding_107	and
25	ZFN_binding_108,	ZFN_binding_109	and	ZFN_binding_110,	ZFN_binding_111	and
	ZFN_binding_112,	ZFN_binding_113	and	ZFN_binding_114,	ZFN_binding_115	and
	ZFN_binding_116,	ZFN_binding_117	and	ZFN_binding_118,	ZFN_binding_119	and
	ZFN_binding_120,	ZFN_binding_121	and	ZFN_binding_122,	ZFN_binding_123	and
	ZFN_binding_124,	ZFN_binding_125	and	ZFN_binding_126,	ZFN_binding_127	and
30	ZFN_binding_128,	ZFN_binding_129	and	ZFN_binding_130,	ZFN_binding_131	and
	ZFN_binding_132.					

In accordance with an embodiment, the zinc finger nuclease binds to the zinc finger target site and cleaves the unique maize genomic polynucleotide target sites, whereupon the

DNA of interest integrates within or proximal to the maize genomic polynucleotide target sites. In an embodiment, integration of the DNA of interest occurs within the zinc finger target site may result with rearrangements. In accordance with one embodiment, the rearrangements may comprise deletions, insertions, inversions, and repeats. In an embodiment, integration of the DNA of interest occurs proximal to the zinc finger target site. According to an aspect of the embodiment, the integration of the DNA is proximal to the zinc finger target site, and may integrate within 1.5 Kb, 1.25 Kb, 1.0 Kb, 0.75 Kb, 0.5 Kb, or 0.25 Kb to the zinc finger target site. Insertion within a genomic region proximal to the zinc finger target site is known in the art, see US Patent Pub No. 2010/0257638 A1 (herein incorporated by reference in its entirety).

In accordance with one embodiment the selected nongenic sequence comprises the following characteristics:

- a) the nongenic sequence does not contain greater than 1% DNA methylation within the sequence;
- b) the nongenic sequence has a relative location value from 0.0984 to 0.973 ratio of genomic distance from a maize chromosomal centromere;
- c) the nongenic sequence has a guanine/cytosine percent content range of 34.38 to 61.2%; and,
- d) the nongenic sequence is from about 1Kb to about 4.9Kb in length.

II. Recombinant Derivatives of Identified Optimal Nongenic Maize Genomic Loci

In accordance with one embodiment, after having identified a genomic loci of *Zea mays* as a highly desirable location for inserting polynucleotide donor sequences, one or more nucleic acids of interest can be inserted into the identified genomic locus. In one embodiment the nucleic acid of interest comprises exogenous gene sequences or other desirable polynucleotide donor sequences. In another embodiment, after having identified a genomic loci of *Zea mays* as a highly desirable location for inserting polynucleotide donor sequences, one or more nucleic acids of interest of the optimal nongenic maize genomic loci can optionally be deleted, excised or removed with the subsequent integration of the DNA of interest into the identified genomic locus. In one embodiment the insertion of a nucleic acid of interest into the optimal nongenic maize genomic loci comprises removal, deletion, or excision of the exogenous gene sequences or other desirable polynucleotide donor sequences.

The present disclosure further relates to methods and compositions for targeted integration into the select *Zea mays* genomic locus using ZFNs and a polynucleotide donor

construct. The methods for inserting a nucleic acid sequence of interest into the optimal nongenic maize genomic loci, unless otherwise indicated, use conventional techniques in molecular biology, biochemistry, chromatin structure and analysis, cell culture, recombinant DNA and related fields as are within the skill of the art. These techniques are fully explained in the literature. See, for example, Sambrook et al. MOLECULAR CLONING: A LABORATORY MANUAL, Second edition, Cold Spring Harbor Laboratory Press, 1989 and Third edition, 2001; Ausubel et al., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, 1987 and periodic updates; the series METHODS IN ENZYMOLOGY, Academic Press, San Diego; Wolfe, CHROMATIN STRUCTURE AND FUNCTION, Third edition, Academic Press, San Diego, 1998; METHODS IN ENZYMOLOGY, Vol. 304, "Chromatin" (P. M. Wassarman and A. P. Wolffe, eds.), Academic Press, San Diego, 1999; and METHODS IN MOLECULAR BIOLOGY, Vol. 119, "Chromatin Protocols" (P. B. Becker, ed.) Humana Press, Totowa, 1999.

Methods for Nucleic Acid Insertion into the Maize Genome

Any of the well known procedures for introducing polynucleotide donor sequences and nuclease sequences as a DNA construct into host cells may be used in accordance with the present disclosure. These include the use of calcium phosphate transfection, polybrene, protoplast fusion, PEG, electroporation, ultrasonic methods (e.g., sonoporation), liposomes, microinjection, naked DNA, plasmid vectors, viral vectors, both episomal and integrative, and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (see, e.g., Sambrook et al., supra). It is only necessary that the particular nucleic acid insertion procedure used be capable, of successfully introducing at least one gene into the host cell capable of expressing the protein of choice.

As noted above, DNA constructs may be introduced into the genome of a desired plant species by a variety of conventional techniques. For reviews of such techniques see, for example, Weissbach & Weissbach Methods for Plant Molecular Biology (1988, Academic Press, N.Y.) Section VIII, pp. 421-463; and Grierson & Corey, Plant Molecular Biology (1988, 2d Ed.), Blackie, London, Ch. 7-9. A DNA construct may be introduced directly into the genomic DNA of the plant cell using techniques such as electroporation and microinjection of plant cell protoplasts, by agitation with silicon carbide fibers (See, e.g., U.S. Patents 5,302,523 and 5,464,765), or the DNA constructs can be introduced directly to plant tissue using biolistic

methods, such as DNA particle bombardment (see, e.g., Klein et al. (1987) Nature 327:70-73). Alternatively, the DNA construct can be introduced into the plant cell via nanoparticle transformation (see, e.g., US Patent Publication No. 20090104700, which is incorporated herein by reference in its entirety). Alternatively, the DNA constructs may be combined with suitable T-DNA border/flanking regions and introduced into a conventional *Agrobacterium tumefaciens* host vector. *Agrobacterium tumefaciens*-mediated transformation techniques, including disarming and use of binary vectors, are well described in the scientific literature. See, for example Horsch et al. (1984) Science 233:496-498, and Fraley et al. (1983) Proc. Nat'l. Acad. Sci. USA 80:4803.

In addition, gene transfer may be achieved using non-*Agrobacterium* bacteria or viruses such as *Rhizobium* sp. NGR234, *Sinorhizobium meliloti*, *Mesorhizobium loti*, potato virus X, cauliflower mosaic virus and cassava vein mosaic virus and/or tobacco mosaic virus, See, e.g., Chung et al. (2006) Trends Plant Sci. 11(1):1-4. The virulence functions of the *Agrobacterium tumefaciens* host will direct the insertion of a T-strand containing the construct and adjacent marker into the plant cell DNA when the cell is infected by the bacteria using binary T DNA vector (Bevan (1984) Nuc. Acid Res. 12:8711-8721) or the co-cultivation procedure (Horsch et al. (1985) Science 227:1229-1231). Generally, the *Agrobacterium* transformation system is used to engineer dicotyledonous plants (Bevan et al. (1982) Ann. Rev. Genet. 16:357-384; Rogers et al. (1986) Methods Enzymol. 118:627-641). The *Agrobacterium* transformation system may also be used to transform, as well as transfer, DNA to monocotyledonous plants and plant cells. See U.S. Pat. No. 5,591,616; Hernalsteen et al. (1984) EMBO J. 3:3039-3041; Hooykass-Van Slogteren et al. (1984) Nature 311:763-764; Grimsley et al. (1987) Nature 325:1677-179; Boulton et al. (1989) Plant Mol. Biol. 12:31-40; and Gould et al. (1991) Plant Physiol. 95:426-434.

Alternative gene transfer and transformation methods include, but are not limited to, protoplast transformation through calcium-, polyethylene glycol (PEG)- or electroporation-mediated uptake of naked DNA (see Paszkowski et al. (1984) EMBO J. 3:2717-2722, Potrykus et al. (1985) Molec. Gen. Genet. 199:169-177; Fromm et al. (1985) Proc. Nat. Acad. Sci. USA 82:5824-5828; and Shimamoto (1989) Nature 338:274-276) and electroporation of plant tissues (D'Halluin et al. (1992) Plant Cell 4:1495-1505). Additional methods for plant cell transformation include microinjection, silicon carbide mediated DNA uptake (Kaeppeler et al. (1990) Plant Cell Reporter 9:415-418), and microprojectile bombardment (see Klein et al.

(1988) Proc. Nat. Acad. Sci. USA 85:4305-4309; and Gordon-Kamm et al. (1990) Plant Cell 2:603-618).

In one embodiment a nucleic acid of interest introduced into a host cell for targeted insertion into the genome comprises homologous flanking sequences on one or both ends of the targeted nucleic acid of interest. In such an embodiment, the homologous flanking sequences contain sufficient levels of sequence identity to a maize genomic sequence to support homologous recombination between it and the genomic sequence to which it bears homology. Approximately 25, 50, 100, 200, 500, 750, 1000, 1500, or 2000 nucleotides, or more of sequence identity, ranging from 70% to 100%, between a donor and a genomic sequence (or any integral value between 10 and 200 nucleotides, or more) will support homologous recombination therebetween.

In another embodiment the targeted nucleic acid of interest lacks homologous flanking sequences, and the targeted nucleic acid of interest shares low to very low levels of sequence identity with a genomic sequence.

In other embodiments of targeted recombination and/or replacement and/or alteration of a sequence in a region of interest in cellular chromatin, a chromosomal sequence is altered by homologous recombination with an exogenous "donor" nucleotide sequence. Such homologous recombination is stimulated by the presence of a double-stranded break in cellular chromatin, if sequences homologous to the region of the break are present. Double-strand breaks in cellular chromatin can also stimulate cellular mechanisms of non-homologous end joining. In any of the methods described herein, the first nucleotide sequence (the "donor sequence") can contain sequences that are homologous, but not identical, to genomic sequences in the region of interest, thereby stimulating homologous recombination to insert a non-identical sequence in the region of interest. Thus, in certain embodiments, portions of the donor sequence that are homologous to sequences in the region of interest exhibit between about 80, 85, 90, 95, 97.5, to 99% (or any integer therebetween) sequence identity to the genomic sequence that is replaced. In other embodiments, the homology between the donor and genomic sequence is higher than 99%, for example if only 1 nucleotide differs as between donor and genomic sequences of over 100 contiguous base pairs.

In certain cases, a non-homologous portion of the donor sequence can contain sequences not present in the region of interest, such that new sequences are introduced into the region of interest. In these instances, the non-homologous sequence is generally flanked by sequences of 50 to 2,000 base pairs (or any integral value therebetween) or any number of base pairs greater

than 2,000, that are homologous or identical to sequences in the region of interest. In other embodiments, the donor sequence is non-homologous to the region of interest, and is inserted into the genome by non-homologous recombination mechanisms.

In accordance with one embodiment a zinc finger nuclease (ZFN) is used to introduce a double strand break in a targeted genomic locus to facilitate the insertion of a nucleic acid of interest. Selection of a target site within the selected genomic locus for binding by a zinc finger domain can be accomplished, for example, according to the methods disclosed in U.S. Patent 6,453,242, the disclosure of which is incorporated herein, that also discloses methods for designing zinc finger proteins (ZFPs) to bind to a selected sequence. It will be clear to those skilled in the art that simple visual inspection of a nucleotide sequence can also be used for selection of a target site. Accordingly, any means for target site selection can be used in the methods described herein.

For ZFP DNA-binding domains, target sites are generally composed of a plurality of adjacent target subsites. A target subsite refers to the sequence, usually either a nucleotide triplet or a nucleotide quadruplet which may overlap by one nucleotide with an adjacent quadruplet that is bound by an individual zinc finger. See, for example, WO 02/077227, the disclosure of which is incorporated herein. A target site generally has a length of at least 9 nucleotides and, accordingly, is bound by a zinc finger binding domain comprising at least three zinc fingers. However binding of, for example, a 4-finger binding domain to a 12-nucleotide target site, a 5-finger binding domain to a 15-nucleotide target site or a 6-finger binding domain to an 18-nucleotide target site, is also possible. As will be apparent, binding of larger binding domains (e.g., 7-, 8-, 9-finger and more) to longer target sites is also consistent with the subject disclosure.

In accordance with one embodiment, it is not necessary for a target site to be a multiple of three nucleotides. In cases in which cross-strand interactions occur (see, e.g., U.S. Patent 6,453,242 and WO 02/077227), one or more of the individual zinc fingers of a multi-finger binding domain can bind to overlapping quadruplet subsites. As a result, a three-finger protein can bind a 10-nucleotide sequence, wherein the tenth nucleotide is part of a quadruplet bound by a terminal finger, a four-finger protein can bind a 13-nucleotide sequence, wherein the thirteenth nucleotide is part of a quadruplet bound by a terminal finger, etc.

The length and nature of amino acid linker sequences between individual zinc fingers in a multi-finger binding domain also affects binding to a target sequence. For example, the presence of a so-called "non-canonical linker," "long linker" or "structured linker" between

adjacent zinc fingers in a multi-finger binding domain can allow those fingers to bind subsites which are not immediately adjacent. Non-limiting examples of such linkers are described, for example, in U.S. Pat. No. 6,479,626 and WO 01/53480. Accordingly, one or more subsites, in a target site for a zinc finger binding domain, can be separated from each other by 1, 2, 3, 4, 5 or more nucleotides. One nonlimiting example would be a four-finger binding domain that binds to a 13-nucleotide target site comprising, in sequence, two contiguous 3-nucleotide subsites, an intervening nucleotide, and two contiguous triplet subsites.

While DNA-binding polypeptides identified from proteins that exist in nature typically bind to a discrete nucleotide sequence or motif (*e.g.*, a consensus recognition sequence), methods exist and are known in the art for modifying many such DNA-binding polypeptides to recognize a different nucleotide sequence or motif. DNA-binding polypeptides include, for example and without limitation: zinc finger DNA-binding domains; leucine zippers; UPA DNA-binding domains; GAL4; TAL; LexA; a Tet repressor; LacR; and a steroid hormone receptor.

In some examples, a DNA-binding polypeptide is a zinc finger. Individual zinc finger motifs can be designed to target and bind specifically to any of a large range of DNA sites. Canonical Cys₂His₂ (as well as non-canonical Cys₃His) zinc finger polypeptides bind DNA by inserting an α -helix into the major groove of the target DNA double helix. Recognition of DNA by a zinc finger is modular; each finger contacts primarily three consecutive base pairs in the target, and a few key residues in the polypeptide mediate recognition. By including multiple zinc finger DNA-binding domains in a targeting endonuclease, the DNA-binding specificity of the targeting endonuclease may be further increased (and hence the specificity of any gene regulatory effects conferred thereby may also be increased). *See, e.g.*, Urnov *et al.* (2005) *Nature* 435:646-51. Thus, one or more zinc finger DNA-binding polypeptides may be engineered and utilized such that a targeting endonuclease introduced into a host cell interacts with a DNA sequence that is unique within the genome of the host cell. Preferably, the zinc finger protein is non-naturally occurring in that it is engineered to bind to a target site of choice. *See, for example*, Beerli *et al.* (2002) *Nature Biotechnol.* 20:135-141; Pabo *et al.* (2001) *Ann. Rev. Biochem.* 70:313-340; Isalan *et al.* (2001) *Nature Biotechnol.* 19:656-660; Segal *et al.* (2001) *Curr. Opin. Biotechnol.* 12:632-637; Choo *et al.* (2000) *Curr. Opin. Struct. Biol.* 10:411-416; U.S. Patent Nos. 6,453,242; 6,534,261; 6,599,692; 6,503,717; 6,689,558; 7,030,215; 6,794,136; 7,067,317; 7,262,054; 7,070,934; 7,361,635; 7,253,273; and U.S. Patent Publication Nos. 2005/0064474; 2007/0218528; 2005/0267061, all incorporated herein by reference in their entireties.

An engineered zinc finger binding domain can have a novel binding specificity, compared to a naturally-occurring zinc finger protein. Engineering methods include, but are not limited to, rational design and various types of selection. Rational design includes, for example, using databases comprising triplet (or quadruplet) nucleotide sequences and individual
5 zinc finger amino acid sequences, in which each triplet or quadruplet nucleotide sequence is associated with one or more amino acid sequences of zinc fingers which bind the particular triplet or quadruplet sequence. See, for example, co-owned U.S. Patents 6,453,242 and 6,534,261, incorporated by reference herein in their entireties.

Alternatively, the DNA-binding domain may be derived from a nuclease. For example,
10 the recognition sequences of homing endonucleases and meganucleases such as I-SceI, I-CeuI, PI-PspI, PI-Sce, I-SceIV, I-CsmI, I-PanI, I-SceII, I-PpoI, I-SceIII, I-CreI, I-TevI, I-TevII and I-TevIII are known. See also U.S. Patent No. 5,420,032; U.S. Patent No. 6,833,252; Belfort et al. (1997) *Nucleic Acids Res.* 25:3379–3388; Dujon et al. (1989) *Gene* 82:115–118; Perler et al. (1994) *Nucleic Acids Res.* 22, 1125–1127; Jasin (1996) *Trends Genet.* 12:224–228; Gimble
15 et al. (1996) *J. Mol. Biol.* 263:163–180; Argast et al. (1998) *J. Mol. Biol.* 280:345–353 and the New England Biolabs catalogue. In addition, the DNA-binding specificity of homing endonucleases and meganucleases can be engineered to bind non-natural target sites. See, for example, Chevalier et al. (2002) *Molec. Cell* 10:895-905; Epinat et al. (2003) *Nucleic Acids Res.* 31:2952-2962; Ashworth et al. (2006) *Nature* 441:656-659; Paques et al. (2007) *Current*
20 *Gene Therapy* 7:49-66; U.S. Patent Publication No. 20070117128.

As another alternative, the DNA-binding domain may be derived from a leucine zipper protein. Leucine zippers are a class of proteins that are involved in protein-protein interactions in many eukaryotic regulatory proteins that are important transcription factors associated with gene expression. The leucine zipper refers to a common structural motif shared in these
25 transcriptional factors across several kingdoms including animals, plants, yeasts, etc. The leucine zipper is formed by two polypeptides (homodimer or heterodimer) that bind to specific DNA sequences in a manner where the leucine residues are evenly spaced through an α -helix, such that the leucine residues of the two polypeptides end up on the same face of the helix. The DNA binding specificity of leucine zippers can be utilized in the DNA-binding domains
30 disclosed herein.

In some embodiments, the DNA-binding domain is an engineered domain from a TAL effector derived from the plant pathogen *Xanthomonas* (see, Miller et al. (2011) *Nature Biotechnology* 29(2):143-8; Boch et al, (2009) *Science* 29 Oct 2009 (10.1126/science.117881)

and Moscou and Bogdanove, (2009) Science 29 Oct 2009 (10.1126/science.1178817; and U.S. Patent Publication Nos. 20110239315, 20110145940 and 20110301073).

The CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats)/Cas (CRISPR Associated) nuclease system is a recently engineered nuclease system based on a bacterial system that can be used for genome engineering. It is based on part of the adaptive immune response of many bacteria and Archea. When a virus or plasmid invades a bacterium, segments of the invader's DNA are converted into CRISPR RNAs (crRNA) by the 'immune' response. This crRNA then associates, through a region of partial complementarity, with another type of RNA called tracrRNA to guide the Cas9 nuclease to a region homologous to the crRNA in the target DNA called a "protospacer". Cas9 cleaves the DNA to generate blunt ends at the DSB at sites specified by a 20-nucleotide guide sequence contained within the crRNA transcript. Cas9 requires both the crRNA and the tracrRNA for site specific DNA recognition and cleavage. This system has now been engineered such that the crRNA and tracrRNA can be combined into one molecule (the "single guide RNA"), and the crRNA equivalent portion of the single guide RNA can be engineered to guide the Cas9 nuclease to target any desired sequence (see Jinek et al (2012) Science 337, p. 816-821, Jinek et al, (2013), eLife 2:e00471, and David Segal, (2013) eLife 2:e00563). Thus, the CRISPR/Cas system can be engineered to create a double-stranded break (DSB) at a desired target in a genome, and repair of the DSB can be influenced by the use of repair inhibitors to cause an increase in error prone repair.

In certain embodiments, Cas protein may be a "functional derivative" of a naturally occurring Cas protein. A "functional derivative" of a native sequence polypeptide is a compound having a qualitative biological property in common with a native sequence polypeptide. "Functional derivatives" include, but are not limited to, fragments of a native sequence and derivatives of a native sequence polypeptide and its fragments, provided that they have a biological activity in common with a corresponding native sequence polypeptide. A biological activity contemplated herein is the ability of the functional derivative to hydrolyze a DNA substrate into fragments. The term "derivative" encompasses both amino acid sequence variants of polypeptide, covalent modifications, and fusions thereof. Suitable derivatives of a Cas polypeptide or a fragment thereof include but are not limited to mutants, fusions, covalent modifications of Cas protein or a fragment thereof. Cas protein, which includes Cas protein or a fragment thereof, as well as derivatives of Cas protein or a fragment thereof, may be obtainable from a cell or synthesized chemically or by a combination of these two procedures. The cell may be a cell that naturally produces Cas protein, or a cell that naturally produces Cas protein

and is genetically engineered to produce the endogenous Cas protein at a higher expression level or to produce a Cas protein from an exogenously introduced nucleic acid, which nucleic acid encodes a Cas that is same or different from the endogenous Cas. In some case, the cell does not naturally produce Cas protein and is genetically engineered to produce a Cas protein.

5 The Cas protein is deployed in mammalian cells (and putatively within plant cells) by co-expressing the Cas nuclease with guide RNA. Two forms of guide RNAs can be used to facilitate Cas-mediated genome cleavage as disclosed in Le Cong, F., *et al.*, (2013) *Science* 339(6121):819-823.

In other embodiments, the DNA-binding domain may be associated with a cleavage
10 (nuclease) domain. For example, homing endonucleases may be modified in their DNA-binding specificity while retaining nuclease function. In addition, zinc finger proteins may also be fused to a cleavage domain to form a zinc finger nuclease (ZFN). The cleavage domain portion of the fusion proteins disclosed herein can be obtained from any endonuclease or exonuclease. Exemplary endonucleases from which a cleavage domain can be derived include,
15 but are not limited to, restriction endonucleases and homing endonucleases. See, for example, 2002-2003 Catalogue, New England Biolabs, Beverly, MA; and Belfort et al. (1997) *Nucleic Acids Res.* 25:3379-3388. Additional enzymes which cleave DNA are known (e.g., S1 Nuclease; mung bean nuclease; pancreatic DNase I; micrococcal nuclease; yeast HO endonuclease; see also Linn et al. (eds.) *Nucleases*, Cold Spring Harbor Laboratory
20 Press, 1993). Non limiting examples of homing endonucleases and meganucleases include I-SceI, I-CeuI, PI-PspI, PI-Sce, I-SceIV, I-CsmI, I-PanI, I-SceII, I-PpoI, I-SceIII, I-CreI, I-TevI, I-TevII and I-TevIII are known. See also U.S. Patent No. 5,420,032; U.S. Patent No. 6,833,252; Belfort et al. (1997) *Nucleic Acids Res.* 25:3379-3388; Dujon et al. (1989) *Gene* 82:115-118; Perler et al. (1994) *Nucleic Acids Res.* 22, 1125-1127; Jasin (1996) *Trends*
25 *Genet.* 12:224-228; Gimble et al. (1996) *J. Mol. Biol.* 263:163-180; Argast et al. (1998) *J. Mol. Biol.* 280:345-353 and the New England Biolabs catalogue. One or more of these enzymes (or functional fragments thereof) can be used as a source of cleavage domains and cleavage half-domains.

Restriction endonucleases (restriction enzymes) are present in many species and are
30 capable of sequence-specific binding to DNA (at a recognition site), and cleaving DNA at or near the site of binding. Certain restriction enzymes (e.g., Type IIS) cleave DNA at sites removed from the recognition site and have separable binding and cleavage domains. For example, the Type IIS enzyme FokI catalyzes double-stranded cleavage of DNA, at 9

nucleotides from its recognition site on one strand and 13 nucleotides from its recognition site on the other. See, for example, US Patents 5,356,802; 5,436,150 and 5,487,994; as well as Li et al. (1992) Proc. Natl. Acad. Sci. USA 89:4275-4279; Li et al. (1993) Proc. Natl. Acad. Sci. USA 90:2764-2768; Kim et al. (1994a) Proc. Natl. Acad. Sci. USA 91:883-887; Kim et al. (1994b) J. Biol. Chem. 269:31,978-31,982. Thus, in one embodiment, fusion proteins comprise the cleavage domain (or cleavage half-domain) from at least one Type IIS restriction enzyme and one or more zinc finger binding domains, which may or may not be engineered.

An exemplary Type IIS restriction enzyme, whose cleavage domain is separable from the binding domain, is FokI. This particular enzyme is active as a dimer. Bitinaite et al. (1998) Proc. Natl. Acad. Sci. USA 95: 10,570-10,575. Accordingly, for the purposes of the present disclosure, the portion of the FokI enzyme used in the disclosed fusion proteins is considered a cleavage half-domain. Thus, for targeted double-stranded cleavage and/or targeted replacement of cellular sequences using zinc finger-FokI fusions, two fusion proteins, each comprising a FokI cleavage half-domain, can be used to reconstitute a catalytically active cleavage domain. Alternatively, a single polypeptide molecule containing a zinc finger binding domain and two FokI cleavage half-domains can also be used. Parameters for targeted cleavage and targeted sequence alteration using zinc finger-FokI fusions are provided elsewhere in this disclosure.

A cleavage domain or cleavage half-domain can be any portion of a protein that retains cleavage activity, or that retains the ability to multimerize (e.g., dimerize) to form a functional cleavage domain. Exemplary Type IIS restriction enzymes are described in International Publication WO 2007/014275, incorporated by reference herein in its entirety.

To enhance cleavage specificity, cleavage domains may also be modified. In certain embodiments, variants of the cleavage half-domain are employed these variants minimize or prevent homodimerization of the cleavage half-domains. Non-limiting examples of such modified cleavage half-domains are described in detail in WO 2007/014275, incorporated by reference in its entirety herein. In certain embodiments, the cleavage domain comprises an engineered cleavage half-domain (also referred to as dimerization domain mutants) that minimize or prevent homodimerization. Such embodiments are known to those of skill the art and described for example in U.S. Patent Publication Nos. 20050064474; 20060188987; 20070305346 and 20080131962, the disclosures of all of which are incorporated by reference in their entirety herein. Amino acid residues at positions 446, 447, 479, 483, 484, 486, 487, 490, 491, 496, 498, 499, 500, 531, 534, 537, and 538 of FokI are all targets for influencing dimerization of the FokI cleavage half-domains.

Additional engineered cleavage half-domains of FokI that form obligate heterodimers can also be used in the ZFNs described herein. Exemplary engineered cleavage half-domains of Fok I that form obligate heterodimers include a pair in which a first cleavage half-domain includes mutations at amino acid residues at positions 490 and 538 of Fok I and a second
5 cleavage half-domain includes mutations at amino acid residues 486 and 499. In one embodiment, a mutation at 490 replaces Glu (E) with Lys (K); the mutation at 538 replaces Iso (I) with Lys (K); the mutation at 486 replaced Gln (Q) with Glu (E); and the mutation at position 499 replaces Iso (I) with Lys (K). Specifically, the engineered cleavage half-domains described herein were prepared by mutating positions 490 (E→K) and 538 (I→K) in one
10 cleavage half-domain to produce an engineered cleavage half-domain designated “E490K:I538K” and by mutating positions 486 (Q→E) and 499 (I→L) in another cleavage half-domain to produce an engineered cleavage half-domain designated “Q486E:I499L”. The engineered cleavage half-domains described herein are obligate heterodimer mutants in which aberrant cleavage is minimized or abolished. See, e.g., U.S. Patent Publication No.
15 2008/0131962, the disclosure of which is incorporated by reference in its entirety for all purposes. In certain embodiments, the engineered cleavage half-domain comprises mutations at positions 486, 499 and 496 (numbered relative to wild-type FokI), for instance mutations that replace the wild type Gln (Q) residue at position 486 with a Glu (E) residue, the wild type Iso (I) residue at position 499 with a Leu (L) residue and the wild-type Asn (N) residue at position
20 496 with an Asp (D) or Glu (E) residue (also referred to as a “ELD” and “ELE” domains, respectively). In other embodiments, the engineered cleavage half-domain comprises mutations at positions 490, 538 and 537 (numbered relative to wild-type FokI), for instance mutations that replace the wild type Glu (E) residue at position 490 with a Lys (K) residue, the wild type Iso (I) residue at position 538 with a Lys (K) residue, and the wild-type His (H) residue at position
25 537 with a Lys (K) residue or a Arg (R) residue (also referred to as “KKK” and “KKR” domains, respectively). In other embodiments, the engineered cleavage half-domain comprises mutations at positions 490 and 537 (numbered relative to wild-type FokI), for instance mutations that replace the wild type Glu (E) residue at position 490 with a Lys (K) residue and the wild-type His (H) residue at position 537 with a Lys (K) residue or a Arg (R) residue (also
30 referred to as “KIK” and “KIR” domains, respectively). (See US Patent Publication No. 20110201055). In other embodiments, the engineered cleavage half domain comprises the “Sharkey” and/or “Sharkey’ ” mutations (see Guo et al, (2010) J. Mol. Biol. 400(1):96-107).

Engineered cleavage half-domains described herein can be prepared using any suitable method, for example, by site-directed mutagenesis of wild-type cleavage half-domains (Fok I) as described in U.S. Patent Publication Nos. 20050064474; 20080131962; and 20110201055. Alternatively, nucleases may be assembled *in vivo* at the nucleic acid target site using so-called “split-enzyme” technology (see e.g. U.S. Patent Publication No. 20090068164). Components of such split enzymes may be expressed either on separate expression constructs, or can be linked in one open reading frame where the individual components are separated, for example, by a self-cleaving 2A peptide or IRES sequence. Components may be individual zinc finger binding domains or domains of a meganuclease nucleic acid binding domain.

Nucleases can be screened for activity prior to use, for example in a yeast-based chromosomal system as described in WO 2009/042163 and 20090068164. Nuclease expression constructs can be readily designed using methods known in the art. See, e.g., United States Patent Publications 20030232410; 20050208489; 20050026157; 20050064474; 20060188987; 20060063231; and International Publication WO 07/014275. Expression of the nuclease may be under the control of a constitutive promoter or an inducible promoter, for example the galactokinase promoter which is activated (de-repressed) in the presence of raffinose and/or galactose and repressed in presence of glucose.

Distance between target sites refers to the number of nucleotides or nucleotide pairs intervening between two target sites as measured from the edges of the sequences nearest each other. In certain embodiments in which cleavage depends on the binding of two zinc finger domain/cleavage half-domain fusion molecules to separate target sites, the two target sites can be on opposite DNA strands. In other embodiments, both target sites are on the same DNA strand. For targeted integration into the optimal genomic locus, one or more ZFPs are engineered to bind a target site at or near the predetermined cleavage site, and a fusion protein comprising the engineered DNA-binding domain and a cleavage domain is expressed in the cell. Upon binding of the zinc finger portion of the fusion protein to the target site, the DNA is cleaved, preferably via a double-stranded break, near the target site by the cleavage domain.

The presence of a double-stranded break in the optimal genomic locus facilitates integration of exogenous sequences via homologous recombination. Thus, in one embodiment the polynucleotide comprising the nucleic acid sequence of interest to be inserted into the targeted genomic locus will include one or more regions of homology with the targeted genomic locus to facilitate homologous recombination.

In addition to the fusion molecules described herein, targeted replacement of a selected genomic sequence also involves the introduction of a donor sequence. The polynucleotide donor sequence can be introduced into the cell prior to, concurrently with, or subsequent to, expression of the fusion protein(s). In one embodiment the donor polynucleotide contains sufficient homology to the optimal genomic locus to support homologous recombination between it and the optimal genomic locus genomic sequence to which it bears homology. Approximately 25, 50, 100, 200, 500, 750, 1,000, 1,500, 2,000 nucleotides or more of sequence homology between a donor and a genomic sequence, or any integral value between 10 and 2,000 nucleotides or more, will support homologous recombination. In certain embodiments, the homology arms are less than 1,000 basepairs in length. In other embodiments, the homology arms are less than 750 base pairs in length. In one embodiment, donor polynucleotide sequences can comprise a vector molecule containing sequences that are not homologous to the region of interest in cellular chromatin. A donor polynucleotide molecule can contain several, discontinuous regions of homology to cellular chromatin. For example, for targeted insertion of sequences not normally present in a region of interest, said sequences can be present in a donor nucleic acid molecule and flanked by regions of homology to sequence in the region of interest. The donor polynucleotide can be DNA or RNA, single-stranded or double-stranded and can be introduced into a cell in linear or circular form. *See, e.g.*, U.S. Patent Publication Nos. 20100047805, 20110281361, 20110207221 and U.S. Application No. 13/889,162. If introduced in linear form, the ends of the donor sequence can be protected (*e.g.*, from exonucleolytic degradation) by methods known to those of skill in the art. For example, one or more dideoxynucleotide residues are added to the 3' terminus of a linear molecule and/or self-complementary oligonucleotides are ligated to one or both ends. *See, for example*, Chang *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84:4959-4963; Nehls *et al.* (1996) *Science* 272:886-889. Additional methods for protecting exogenous polynucleotides from degradation include, but are not limited to, addition of terminal amino group(s) and the use of modified internucleotide linkages such as, for example, phosphorothioates, phosphoramidates, and O-methyl ribose or deoxyribose residues.

In accordance with one embodiment a method of preparing a transgenic maize plant is provided wherein a DNA of interest has been inserted into an optimal nongenic maize genomic locus. The method comprises the steps of:

- a. selecting an optimal nongenic maize locus as a target for insertion of the nucleic acid of interest;

- b. introducing a site specific nuclease into a maize plant cell, wherein the site specific nuclease cleaves the nongenic sequence;
- c. introducing the DNA of interest into the plant cell; and
- d. selecting transgenic plant cells comprising the DNA of interest targeted to said
5 nongenic sequence.

In accordance with one embodiment a method of preparing a transgenic maize protoplast cell is provided wherein a DNA of interest has been inserted into an optimal nongenic maize genomic locus. The method comprises the steps of:

- a. selecting an optimal nongenic maize locus as a target for insertion of the nucleic
10 acid of interest;
- b. introducing a site specific nuclease into a maize protoplast cell, wherein the site specific nuclease cleaves the nongenic sequence;
- c. introducing the DNA of interest into the maize protoplast cell; and
- d. selecting the transgenic maize protoplast cell comprising the DNA of interest
15 targeted to said nongenic sequence.

In one embodiment the site specific nuclease is selected from the group consisting of a Zinc Finger nuclease, a CRISPR nuclease, a TALEN nuclease, or a meganuclease, and more particularly in one embodiment the site specific nuclease is a Zinc Finger nuclease. In accordance with one embodiment the DNA of interest is integrated within said nongenic
20 sequence via a homology directed repair integration method. Alternatively, in some embodiments the DNA of interest is integrated within said nongenic sequence via a non-homologous end joining integration method. In additional embodiments, the DNA of interest is integrated within said nongenic sequence via a previously undescribed integration method. In one embodiment the method comprises selecting a optimal nongenic maize genomic locus for
25 targeted insertion of a DNA of interest that has 2, 3, 4, 5, 6, 7, or 8 of the following characteristics:

- a. the nongenic sequence is at least 1 Kb in length and does not contain greater than 1% DNA methylation within the sequence;
- b. the nongenic sequence exhibits a 0.00041 to 62.42 cM/Mb rate of recombination
30 within the maize genome;
- c. the nongenic sequence exhibits a 0 to 0.962 level of nucleosome occupancy of the maize genome;

d. the nongenic sequence shares less than 40% sequence identity with any other sequence contained in the maize genome;

e. the nongenic sequence has a relative location value from 0.00373 to 0.99908 ratio of genomic distance from a maize chromosomal centromere;

5 f. the nongenic sequence has a guanine/cytosine percent content range of 25.17 to 68.3%;

g. the nongenic sequence is located proximally to a genic sequence; and,

h. a 1 Mb region of maize genomic sequence comprising said nongenic sequence comprises one or more additional nongenic sequences. In one embodiment the optimal
10 nongenic maize locus is selected from a loci of cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 2, 3, 4, 5, 6, 7, 8, 9, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32.

Delivery

The donor molecules disclosed herein are integrated into a genome of a cell via targeted,
15 homology-independent and/or homology-dependent methods. For such targeted integration, the genome is cleaved at a desired location (or locations) using a nuclease, for example, a fusion between a DNA-binding domain (*e.g.*, zinc finger binding domain, CRISPR or TAL effector domain is engineered to bind a target site at or near the predetermined cleavage site) and nuclease domain (*e.g.*, cleavage domain or cleavage half-domain). In certain embodiments, two
20 fusion proteins, each comprising a DNA-binding domain and a cleavage half-domain, are expressed in a cell, and bind to target sites which are juxtaposed in such a way that a functional cleavage domain is reconstituted and DNA is cleaved in the vicinity of the target sites. In one embodiment, cleavage occurs between the target sites of the two DNA-binding domains. One or both of the DNA-binding domains can be engineered. *See, also*, U.S. Patent No. 7,888,121;
25 U.S. Patent Publication 20050064474 and International Patent Publications WO05/084190, WO05/014791 and WO 03/080809.

The nucleases as described herein can be introduced as polypeptides and/or polynucleotides. For example, two polynucleotides, each comprising sequences encoding one of the aforementioned polypeptides, can be introduced into a cell, and when the polypeptides
30 are expressed and each binds to its target sequence, cleavage occurs at or near the target sequence. Alternatively, a single polynucleotide comprising sequences encoding both fusion polypeptides is introduced into a cell. Polynucleotides can be DNA, RNA or any modified forms or analogues or DNA and/or RNA.

Following the introduction of a double-stranded break in the region of interest, the transgene is integrated into the region of interest in a targeted manner via non-homology dependent methods (*e.g.*, non-homologous end joining (NHEJ)) following linearization of a double-stranded donor molecule as described herein. The double-stranded donor is preferably linearized *in vivo* with a nuclease, for example one or more of the same or different nucleases that are used to introduce the double-stranded break in the genome. Synchronized cleavage of the chromosome and the donor in the cell may limit donor DNA degradation (as compared to linearization of the donor molecule prior to introduction into the cell). The nuclease target sites used for linearization of the donor preferably do not disrupt the transgene(s) sequence(s).

The transgene may be integrated into the genome in the direction expected by simple ligation of the nuclease overhangs (designated “forward” or “AB” orientation) or in the alternate direction (designated “reverse” or “BA” orientation). In certain embodiments, the transgene is integrated following accurate ligation of the donor and chromosome overhangs. In other embodiments, integration of the transgene in either the BA or AB orientation results in deletion of several nucleotides.

Through the application of techniques such as these, the cells of virtually any species may be stably transformed. In some embodiments, transforming DNA is integrated into the genome of the host cell. In the case of multicellular species, transgenic cells may be regenerated into a transgenic organism. Any of these techniques may be used to produce a transgenic plant, for example, comprising one or more donor polynucleotide acid sequences in the genome of the transgenic plant.

The delivery of nucleic acids may be introduced into a plant cell in embodiments of the invention by any method known to those of skill in the art, including, for example and without limitation: by transformation of protoplasts (*See, e.g.*, U.S. Patent 5,508,184); by desiccation/inhibition-mediated DNA uptake (*See, e.g.*, Potrykus *et al.* (1985) *Mol. Gen. Genet.* 199:183-8); by electroporation (*See, e.g.*, U.S. Patent 5,384,253); by agitation with silicon carbide fibers (*See, e.g.*, U.S. Patents 5,302,523 and 5,464,765); by *Agrobacterium*-mediated transformation (*See, e.g.*, U.S. Patents 5,563,055, 5,591,616, 5,693,512, 5,824,877, 5,981,840, and 6,384,301);, by acceleration of DNA-coated particles (*See, e.g.*, U.S. Patents 5,015,580, 5,550,318, 5,538,880, 6,160,208, 6,399,861, and 6,403,865) and by Nanoparticles, nanocarriers and cell penetrating peptides (WO201126644A2; WO2009046384A1; WO2008148223A1) in the methods to deliver DNA, RNA, Peptides and/or proteins or combinations of nucleic acids and peptides into plant cells.

The most widely-utilized method for introducing an expression vector into plants is based on the natural transformation system of *Agrobacterium*. *A. tumefaciens* and *A. rhizogenes* are plant pathogenic soil bacteria that genetically transform plant cells. The T_i and R_i plasmids of *A. tumefaciens* and *A. rhizogenes*, respectively, carry genes responsible for genetic transformation of the plant. The T_i (tumor-inducing)-plasmids contain a large segment, known as T-DNA, which is transferred to transformed plants. Another segment of the T_i plasmid, the vir region, is responsible for T-DNA transfer. The T-DNA region is bordered by left-hand and right-hand borders that are each composed of terminal repeated nucleotide sequences. In some modified binary vectors, the tumor-inducing genes have been deleted, and the functions of the vir region are utilized to transfer foreign DNA bordered by the T-DNA border sequences. The T-region may also contain, for example, a selectable marker for efficient recovery of transgenic plants and cells, and a multiple cloning site for inserting sequences for transfer such as a nucleic acid encoding a fusion protein of the invention.

Thus, in some embodiments, a plant transformation vector is derived from a T_i plasmid of *A. tumefaciens* (See, e.g., U.S. Patent Nos. 4,536,475, 4,693,977, 4,886,937, and 5,501,967; and European Patent EP 0 122 791) or a R_i plasmid of *A. rhizogenes*. Additional plant transformation vectors include, for example and without limitation, those described by Herrera-Estrella *et al.* (1983) Nature 303:209-13; Bevan *et al.* (1983), *supra*; Klee *et al.* (1985) Bio/Technol. 3:637-42; and in European Patent EP 0 120 516, and those derived from any of the foregoing. Other bacteria, such as *Sinorhizobium*, *Rhizobium*, and *Mesorhizobium*, that naturally interact with plants can be modified to mediate gene transfer to a number of diverse plants. These plant-associated symbiotic bacteria can be made competent for gene transfer by acquisition of both a disarmed T_i plasmid and a suitable binary vector.

The Nucleic Acid of Interest

The polynucleotide donor sequences for targeted insertion into a maize genomic locus typically range in length from about 10 to about 5,000 nucleotides. However, nucleotides substantially longer, up to 20,000 nucleotides can be used, including sequences of about 5, 6, 7, 8, 9, 10, 11 and 12 Kb in length. Additionally, donor sequences can comprise a vector molecule containing sequences that are not homologous to the replaced region. In one embodiment the nucleic acid of interest will include one or more regions that share homology with the targeted genomic loci. Generally, the homologous region(s) of the nucleic acid sequence of interest will have at least 50% sequence identity to a genomic sequence with which

recombination is desired. In certain embodiments, the homologous region(s) of the nucleic acid of interest shares 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 99.9% sequence identity with sequences located in the targeted genomic locus. However, any value between 1% and 100% sequence identity can be present, depending upon the length of the nucleic acid of interest.

5 A nucleic acid of interest can contain several, discontinuous regions of sequence sharing relatively high sequence identity to cellular chromatin. For example, for targeted insertion of sequences not normally present in a targeted genomic locus, the unique sequences can be present in a donor nucleic acid molecule and flanked by regions of sequences that share a relatively high sequence identity to a sequence present in the targeted genomic locus.

10 A nucleic acid of interest can also be inserted into a targeted genomic locus to serve as a reservoir for later use. For example, a first nucleic acid sequence comprising sequences homologous to a nongenic region of the maize genome, but containing a nucleic acid of interest (optionally encoding a ZFN under the control of an inducible promoter), may be inserted in a targeted genomic locus. Next, a second nucleic acid sequence is introduced into the cell to
15 induce the insertion of a DNA of interest into an optimal nongenic maize genomic locus. Either the first nucleic acid sequence comprises a ZFNs specific to the optimal nongenic maize genomic locus and the second nucleic acid sequence comprises the DNA sequence of interest, or vice versa. In one embodiment the ZFN will cleave both the optimal nongenic maize genomic locus and the nucleic acid of interest. The resulting double stranded break in the
20 genome can then become the integration site for the nucleic acid of interest released from the optimal genomic locus. Alternatively, expression of a ZFN already located in the genome can be induced after introduction of the DNA of interest to induce a double stranded break in the genome that can then become the integration site for the introduced nucleic acid of interest. In this way, the efficiency of targeted integration of a DNA of interest at any region of interest
25 may be improved since the method does not rely on simultaneous uptake of both the nucleic acids encoding the ZFNs and the DNA of interest.

A nucleic acid of interest can also be inserted into an optimal nongenic maize genomic locus to serve as a target site for subsequent insertions. For example, a nucleic acid of interest comprised of DNA sequences that contain recognition sites for additional ZFN designs may be
30 inserted into the locus. Subsequently, additional ZFN designs may be generated and expressed in cells such that the original nucleic acid of interest is cleaved and modified by repair or homologous recombination. In this way, reiterative integrations of nucleic acid of interests may occur at the optimal nongenic maize genomic locus.

Exemplary exogenous sequences that can be inserted into an optimal nongenic maize genomic locus include, but are not limited to, any polypeptide coding sequence (e.g., cDNAs), promoter, enhancer and other regulatory sequences (e.g., interfering RNA sequences, shRNA expression cassettes, epitope tags, marker genes, cleavage enzyme recognition sites and various types of expression constructs. Such sequences can be readily obtained using standard molecular biological techniques (cloning, synthesis, etc.) and/or are commercially available.

To express ZFNs, sequences encoding the fusion proteins are typically subcloned into an expression vector that contains a promoter to direct transcription. Suitable prokaryotic and eukaryotic promoters are well known in the art and described, e.g., in Sambrook et al., Molecular Cloning, A Laboratory Manual (2nd ed. 1989; 3rd ed., 2001); Kriegler, Gene Transfer and Expression: A Laboratory Manual (1990); and Current Protocols in Molecular Biology (Ausubel et al., supra. Bacterial expression systems for expressing the ZFNs are available in, e.g., *E. coli*, *Bacillus* sp., and *Salmonella* (Palva et al., *Gene* 22:229-235 (1983)). Kits for such expression systems are commercially available. Eukaryotic expression systems for mammalian cells, yeast, and insect cells are well known by those of skill in the art and are also commercially available.

The particular expression vector used to transport the genetic material into the cell is selected with regard to the intended use of the fusion proteins, e.g., expression in plants, animals, bacteria, fungus, protozoa, etc. (see expression vectors described below). Standard bacterial and animal expression vectors are known in the art and are described in detail, for example, U.S. Patent Publication 20050064474A1 and International Patent Publications WO05/084190, WO05/014791 and WO03/080809.

Standard transfection methods can be used to produce bacterial, mammalian, yeast or insect cell lines that express large quantities of protein, which can then be purified using standard techniques (see, e.g., Colley et al., *J. Biol. Chem.* 264:17619-17622 (1989); Guide to Protein Purification, in *Methods in Enzymology*, vol. 182 (Deutscher, ed., 1990)). Transformation of eukaryotic and prokaryotic cells are performed according to standard techniques (see, e.g., Morrison, *J. Bact.* 132:349-351 (1977); Clark-Curtiss & Curtiss, *Methods in Enzymology* 101:347-362 (Wu et al., eds., 1983)).

The disclosed methods and compositions can be used to insert polynucleotide donor sequences into a predetermined location such as one of the optimal nongenic maize genomic loci. This is useful inasmuch as expression of an introduced transgene into the maize genome depends critically on its integration site. Accordingly, genes encoding herbicide tolerance,

insect resistance, nutrients, antibiotics or therapeutic molecules can be inserted, by targeted recombination.

In one embodiment the nucleic acid of interest is combined or “stacked” with gene encoding sequences that provide additional resistance or tolerance to glyphosate or another herbicide, and/or provides resistance to select insects or diseases and/or nutritional enhancements, and/or improved agronomic characteristics, and/or proteins or other products useful in feed, food, industrial, pharmaceutical or other uses. The “stacking” of two or more nucleic acid sequences of interest within a plant genome can be accomplished, for example, via conventional plant breeding using two or more events, transformation of a plant with a construct which contains the sequences of interest, re-transformation of a transgenic plant, or addition of new traits through targeted integration via homologous recombination.

Such polynucleotide donor nucleotide sequences of interest include, but are not limited to, those examples provided below:

1. Genes or Coding Sequence (e.g. iRNA) That Confer Resistance to Pests or Disease

(A) Plant Disease Resistance Genes. Plant defenses are often activated by specific interaction between the product of a disease resistance gene (R) in the plant and the product of a corresponding avirulence (Avr) gene in the pathogen. A plant variety can be transformed with cloned resistance gene to engineer plants that are resistant to specific pathogen strains. Examples of such genes include, the tomato Cf-9 gene for resistance to *Cladosporium fulvum* (Jones et al., 1994 Science 266:789), tomato Pto gene, which encodes a protein kinase, for resistance to *Pseudomonas syringae* pv. tomato (Martin et al., 1993 Science 262:1432), and *Arabidopsis* RSSP2 gene for resistance to *Pseudomonas syringae* (Mindrinos et al., 1994 Cell 78:1089).

(B) A *Bacillus thuringiensis* protein, a derivative thereof or a synthetic polypeptide modeled thereon, such as, a nucleotide sequence of a Bt δ -endotoxin gene (Geiser et al., 1986 Gene 48:109), and a vegetative insecticidal (VIP) gene (see, e.g., Estruch et al. (1996) Proc. Natl. Acad. Sci. 93:5389-94). Moreover, DNA molecules encoding δ -endotoxin genes can be purchased from American Type Culture Collection (Rockville, Md.), under ATCC accession numbers 40098, 67136, 31995 and 31998.

(C) A lectin, such as, nucleotide sequences of several *Clivia miniata* mannose-binding lectin genes (Van Damme et al., 1994 Plant Molec. Biol. 24:825).

(D) A vitamin binding protein, such as avidin and avidin homologs which are useful as larvicides against insect pests. See U.S. Pat. No. 5,659,026.

(E) An enzyme inhibitor, e.g., a protease inhibitor or an amylase inhibitor. Examples of such genes include a rice cysteine proteinase inhibitor (Abe et al., 1987 J. Biol. Chem. 262:16793), a tobacco proteinase inhibitor I (Huub et al., 1993 Plant Molec. Biol. 21:985), and an α -amylase inhibitor (Sumitani et al., 1993 Biosci. Biotech. Biochem. 57:1243).

(F) An insect-specific hormone or pheromone such as an ecdysteroid and juvenile hormone a variant thereof, a mimetic based thereon, or an antagonist or agonist thereof, such as baculovirus expression of cloned juvenile hormone esterase, an inactivator of juvenile hormone (Hammock et al., 1990 Nature 344:458).

(G) An insect-specific peptide or neuropeptide which, upon expression, disrupts the physiology of the affected pest (J. Biol. Chem. 269:9). Examples of such genes include an insect diuretic hormone receptor (Regan, 1994), an allostatin identified in *Diploptera punctata* (Pratt, 1989), and insect-specific, paralytic neurotoxins (U.S. Pat. No. 5,266,361).

(H) An insect-specific venom produced in nature by a snake, a wasp, etc., such as a scorpion insectotoxic peptide (Pang, 1992 Gene 116:165).

(I) An enzyme responsible for a hyperaccumulation of monoterpene, a sesquiterpene, a steroid, hydroxamic acid, a phenylpropanoid derivative or another non-protein molecule with insecticidal activity.

(J) An enzyme involved in the modification, including the post-translational modification, of a biologically active molecule; for example, glycolytic enzyme, a proteolytic enzyme, a lipolytic enzyme, a nuclease, a cyclase, a transaminase, an esterase, a hydrolase, a phosphatase, a kinase, a phosphorylase, a polymerase, an elastase, a chitinase and a glucanase, whether natural or synthetic. Examples of such genes include, a callas gene (PCT published application WO93/02197), chitinase-encoding sequences (which can be obtained, for example, from the ATCC under accession numbers 3999637 and 67152), tobacco hookworm chitinase (Kramer et al., 1993 Insect Molec. Biol. 23:691), and parsley ubi4-2 polyubiquitin gene (Kawalleck et al., 1993 Plant Molec. Biol. 21:673).

(K) A molecule that stimulates signal transduction. Examples of such molecules include nucleotide sequences for mung bean calmodulin cDNA clones (Botella et al., 1994 Plant Molec. Biol. 24:757) and a nucleotide sequence of a maize calmodulin cDNA clone (Griess et al., 1994 Plant Physiol. 104:1467).

(L) A hydrophobic moment peptide. See U.S. Pat. Nos. 5,659,026 and 5,607,914; the latter teaches synthetic antimicrobial peptides that confer disease resistance.

(M) A membrane permease, a channel former or a channel blocker, such as a cecropin- β lytic peptide analog (Jaynes et al., 1993 Plant Sci. 89:43) which renders transgenic tobacco
5 plants resistant to *Pseudomonas solanacearum*.

(N) A viral-invasive protein or a complex toxin derived therefrom. For example, the accumulation of viral coat proteins in transformed plant cells imparts resistance to viral infection and/or disease development effected by the virus from which the coat protein gene is derived, as well as by related viruses. Coat protein-mediated resistance has been conferred upon
10 transformed plants against alfalfa mosaic virus, cucumber mosaic virus, tobacco streak virus, potato virus X, potato virus Y, tobacco etch virus, tobacco rattle virus and tobacco mosaic virus. See, for example, Beachy et al. (1990) Ann. Rev. Phytopathol. 28:451.

(O) An insect-specific antibody or an immunotoxin derived therefrom. Thus, an antibody targeted to a critical metabolic function in the insect gut would inactivate an affected
15 enzyme, killing the insect. For example, Taylor et al. (1994) Abstract #497, Seventh Int'l. Symposium on Molecular Plant-Microbe Interactions shows enzymatic inactivation in transgenic tobacco via production of single-chain antibody fragments.

(P) A virus-specific antibody. See, for example, Tavladoraki et al. (1993) Nature 266:469, which shows that transgenic plants expressing recombinant antibody genes are
20 protected from virus attack.

(Q) A developmental-arrestive protein produced in nature by a pathogen or a parasite. Thus, fungal endo α -1,4-D polygalacturonases facilitate fungal colonization and plant nutrient release by solubilizing plant cell wall homo- α -1,4-D-galacturonase (Lamb et al., 1992) Bio/Technology 10:1436. The cloning and characterization of a gene which encodes a bean
25 endopolygalacturonase-inhibiting protein is described by Toubart et al. (1992 Plant J. 2:367).

(R) A developmental-arrestive protein produced in nature by a plant, such as the barley ribosome-inactivating gene that provides an increased resistance to fungal disease (Longemann et al., 1992). Bio/Technology 10:3305.

(S) RNA interference, in which an RNA molecule is used to inhibit expression of a
30 target gene. An RNA molecule in one example is partially or fully double stranded, which triggers a silencing response, resulting in cleavage of dsRNA into small interfering RNAs, which are then incorporated into a targeting complex that destroys homologous mRNAs. See, e.g., Fire et al., US Patent 6,506,559; Graham et al. 6,573,099.

2. Genes That Confer Resistance to a Herbicide

(A) Genes encoding resistance or tolerance to a herbicide that inhibits the growing point or meristem, such as an imidazalinone, sulfonanilide or sulfonylurea herbicide. Exemplary
5 genes in this category code for mutant acetolactate synthase (ALS) (Lee et al., 1988 EMBOJ. 7:1241) also known as acetohydroxyacid synthase (AHAS) enzyme (Miki et al., 1990 Theor. Appl. Genet. 80:449).

(B) One or more additional genes encoding resistance or tolerance to glyphosate imparted by mutant EPSP synthase and *aroA* genes, or through metabolic inactivation by genes
10 such as DGT-28, 2mEPSPS, GAT (glyphosate acetyltransferase) or GOX (glyphosate oxidase) and other phosphono compounds such as glufosinate (*pat*, *bar*, and *dsm-2* genes), and aryloxyphenoxypropionic acids and cyclohexanediones (ACCase inhibitor encoding genes). See, for example, U.S. Pat. No. 4,940,835, which discloses the nucleotide sequence of a form of EPSP which can confer glyphosate resistance. A DNA molecule encoding a mutant *aroA* gene
15 can be obtained under ATCC Accession Number 39256, and the nucleotide sequence of the mutant gene is disclosed in U.S. Pat. No. 4,769,061. European patent application No. 0 333 033 and U.S. Pat. No. 4,975,374 disclose nucleotide sequences of glutamine synthetase genes which confer resistance to herbicides such as L-phosphinothricin. The nucleotide sequence of a phosphinothricinacetyl-transferase gene is provided in European application No. 0 242 246. De
20 Greef et al. (1989) Bio/Technology 7:61 describes the production of transgenic plants that express chimeric *bar* genes coding for phosphinothricin acetyl transferase activity. Exemplary of genes conferring resistance to aryloxyphenoxypropionic acids and cyclohexanediones, such as sethoxydim and haloxyfop, are the *Accl-S1*, *Accl-S2* and *Accl-S3* genes described by Marshall et al. (1992) Theor. Appl. Genet. 83:435.

(C) Genes encoding resistance or tolerance to a herbicide that inhibits photosynthesis, such as a triazine (*psbA* and *gs+* genes) and a benzonitrile (nitrilase gene). Przibilla et al. (1991) Plant Cell 3:169 describe the use of plasmids encoding mutant *psbA* genes to transform *Chlamydomonas*. Nucleotide sequences for nitrilase genes are disclosed in U.S. Pat. No. 4,810,648, and DNA molecules containing these genes are available under ATCC accession
30 numbers 53435, 67441 and 67442. Cloning and expression of DNA coding for a glutathione S-transferase is described by Hayes et al. (1992) Biochem. J. 285:173.

(D) Genes encoding resistance or tolerance to a herbicide that bind to hydroxyphenylpyruvate dioxygenases (HPPD), enzymes which catalyze the reaction in which

para-hydroxyphenylpyruvate (HPP) is transformed into homogentisate. This includes herbicides such as isoxazoles (EP418175, EP470856, EP487352, EP527036, EP560482, EP682659, U.S. Pat. No. 5,424,276), in particular isoxaflutole, which is a selective herbicide for maize, diketone nitriles (EP496630, EP496631), in particular 2-cyano-3-cyclopropyl-1-(2-SO₂CH₃-4-
 5 CF₃ phenyl)propane-1,3-dione and 2-cyano-3-cyclopropyl-1-(2-SO₂CH₃-4-2,3Cl₂phenyl)propane-1,3-dione, triketones (EP625505, EP625508, U.S. Pat. No. 5,506,195), in particular sulcotrione, and pyrazolinates. A gene that produces an overabundance of HPPD in plants can provide tolerance or resistance to such herbicides, including, for example, genes described in U.S. Patent Nos. 6,268,549 and 6,245,968 and U.S. Patent Application, Publication
 10 No. 20030066102.

(E) Genes encoding resistance or tolerance to phenoxy auxin herbicides, such as 2,4-dichlorophenoxyacetic acid (2,4-D) and which may also confer resistance or tolerance to aryloxyphenoxypropionate (AOPP) herbicides. Examples of such genes include the α -ketoglutarate-dependent dioxygenase enzyme (aad-1) gene, described in U.S. Patent No.
 15 7,838,733.

(F) Genes encoding resistance or tolerance to phenoxy auxin herbicides, such as 2,4-dichlorophenoxyacetic acid (2,4-D) and which may also confer resistance or tolerance to pyridyloxy auxin herbicides, such as fluroxypyr or triclopyr. Examples of such genes include the α -ketoglutarate-dependent dioxygenase enzyme gene (aad-12), described in WO
 20 2007/053482 A2.

(G) Genes encoding resistance or tolerance to dicamba (see, e.g., U.S. Patent Publication No. 20030135879).

(H) Genes providing resistance or tolerance to herbicides that inhibit protoporphyrinogen oxidase (PPO) (see U.S. Pat. No. 5,767,373).

(I) Genes providing resistance or tolerance to triazine herbicides (such as atrazine) and urea derivatives (such as diuron) herbicides which bind to core proteins of photosystem II reaction centers (PS II) (See Brussian et al., (1989) EMBO J. 1989, 8(4): 1237-1245).

3. Genes That Confer or Contribute to a Value-Added Trait

(A) Modified fatty acid metabolism, for example, by transforming maize or Brassica with an antisense gene or stearoyl-ACP desaturase to increase stearic acid content of the plant (Knultzon et al., 1992) Proc. Nat. Acad. Sci. USA 89:2624.

(B) Decreased phytate content

(1) Introduction of a phytase-encoding gene, such as the *Aspergillus niger* phytase gene (Van Hartingsveldt et al., 1993 Gene 127:87), enhances breakdown of phytate, adding more free phosphate to the transformed plant.

(2) A gene could be introduced that reduces phytate content. In maize, this, for example, could be accomplished by cloning and then reintroducing DNA associated with the single allele which is responsible for maize mutants characterized by low levels of phytic acid (Raboy et al., 1990 Maydica 35:383).

(C) Modified carbohydrate composition effected, for example, by transforming plants with a gene coding for an enzyme that alters the branching pattern of starch. Examples of such enzymes include, *Streptococcus mucus* fructosyltransferase gene (Shiroza et al., 1988) J. Bacteriol. 170:810, *Bacillus subtilis* levansucrase gene (Steinmetz et al., 1985 Mol. Gen. Genel. 200:220), *Bacillus licheniformis* α -amylase (Pen et al., 1992 Bio/Technology 10:292), tomato invertase genes (Elliot et al., 1993), barley amylase gene (Sogaard et al., 1993 J. Biol. Chem. 268:22480), and maize endosperm starch branching enzyme II (Fisher et al., 1993 Plant Physiol. 102:10450).

III. Recombinant Constructs

As disclosed herein the present disclosure provides recombinant genomic sequences comprising an optimal nongenic maize genomic sequence of at least 1 Kb and a DNA of interest, wherein the inserted DNA of interest is inserted into said nongenic sequence. In one embodiment the DNA of interest is an analytical domain, a gene or coding sequence (e.g. iRNA) that confers resistance to pests or disease, genes that confer resistance to a herbicide or genes that confer or contribute to a value-added trait, and the optimal nongenic maize genomic sequence comprises 1, 2, 3, 4, 5, 6, 7, or 8 of the following characteristics:

- a. the nongenic sequence is about 1 Kb to about 8.3 Kb in length and does not contain a methylated polynucleotide;
- b. the nongenic sequence exhibits a 0.00041 to 62.42 cM/Mb rate of recombination within the maize genome;
- c. the nongenic sequence exhibits a 0 to 0.962 level of nucleosome occupancy of the maize genome;
- d. the nongenic sequence shares less than 40% sequence identity with any other sequence contained in the maize genome;

e. the nongenic sequence has a relative location value from 0.00373 to 0.99908 ratio of genomic distance from a maize chromosomal centromere;

f. the nongenic sequence has a guanine/cytosine percent content range of 25.17 to 68.3%;

5 g. the nongenic sequence is located proximally to an genic sequence, comprising a known or predicted maize coding sequence within 40 Kb of contiguous genomic DNA comprising the native nongenic sequence; and,

h. the nongenic sequence is located in a 1 Mb region of maize genomic sequence that comprises at least a second nongenic sequence. In one embodiment the optimal nongenic
10 maize genomic sequence is further characterized as having a genic region comprising 1 to 9 known or predicted maize coding sequence within 40 Kb of contiguous genomic DNA comprising the native nongenic sequence. In one embodiment the optimal nongenic maize locus is selected from a loci of cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 2, 3, 4, 5, 6, 7, 8, 9, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32.

15 IV. Transgenic Plants

Transgenic plants comprising the recombinant optimal nongenic maize loci are also provided in accordance with one embodiment of the present disclosure. Such transgenic plants can be prepared using techniques known to those skilled in the art.

20 A transformed maize cell, callus, tissue or plant may be identified and isolated by selecting or screening the engineered plant material for traits encoded by the marker genes present on the transforming DNA. For instance, selection can be performed by growing the engineered plant material on media containing an inhibitory amount of the antibiotic or herbicide to which the transforming gene construct confers resistance. Further, transformed
25 cells can also be identified by screening for the activities of any visible marker genes (e.g., the yellow fluorescence protein, green fluorescence protein, red fluorescence protein, beta-glucuronidase, luciferase, B or C1 genes) that may be present on the recombinant nucleic acid constructs. Such selection and screening methodologies are well known to those skilled in the art.

30 Physical and biochemical methods also may be used to identify plant or plant cell transformants containing inserted gene constructs. These methods include but are not limited to: 1) Southern analysis or PCR amplification for detecting and determining the structure of the recombinant DNA insert; 2) Northern blot, S1 RNase protection, primer-extension or reverse

transcriptase-PCR amplification for detecting and examining RNA transcripts of the gene constructs; 3) enzymatic assays for detecting enzyme or ribozyme activity, where such gene products are encoded by the gene construct; 4) protein gel electrophoresis, Western blot techniques, immunoprecipitation, or enzyme-linked immunoassays (ELISA), where the gene construct products are proteins. Additional techniques, such as *in situ* hybridization, enzyme staining, and immunostaining, also may be used to detect the presence or expression of the recombinant construct in specific plant organs and tissues. The methods for doing all these assays are well known to those skilled in the art.

Effects of gene manipulation using the methods disclosed herein can be observed by, for example, Northern blots of the RNA (e.g., mRNA) isolated from the tissues of interest. Typically, if the mRNA is present or the amount of mRNA has increased, it can be assumed that the corresponding transgene is being expressed. Other methods of measuring gene and/or encoded polypeptide activity can be used. Different types of enzymatic assays can be used, depending on the substrate used and the method of detecting the increase or decrease of a reaction product or by-product. In addition, the levels of polypeptide expressed can be measured immunochemically, i.e., ELISA, RIA, EIA and other antibody based assays well known to those of skill in the art, such as by electrophoretic detection assays (either with staining or western blotting). As one non-limiting example, the detection of the AAD-1 (aryloxyalkanoate dioxygenase; see WO 2005/107437) and PAT (phosphinothricin-N-acetyltransferase (PAT)) proteins using an ELISA assay is described in U.S. Patent Publication No. 20090093366 which is herein incorporated by reference in its entirety. The transgene may be selectively expressed in some tissues of the plant or at some developmental stages, or the transgene may be expressed in substantially all plant tissues, substantially along its entire life cycle. However, any combinatorial expression mode is also applicable.

One of skill in the art will recognize that after the exogenous polynucleotide donor sequence is stably incorporated in transgenic plants and confirmed to be operable, it can be introduced into other plants by sexual crossing. Any of a number of standard breeding techniques can be used, depending upon the species to be crossed.

The present disclosure also encompasses seeds of the transgenic plants described above wherein the seed has the transgene or gene construct. The present disclosure further encompasses the progeny, clones, cell lines or cells of the transgenic plants described above wherein the progeny, clone, cell line or cell has the transgene or gene construct inserted into an optimal genomic loci.

Transformed plant cells which are produced by any of the above transformation techniques can be cultured to regenerate a whole plant which possesses the transformed genotype and thus the desired phenotype. Such regeneration techniques rely on manipulation of certain phytohormones in a tissue culture growth medium, typically relying on a biocide and/or herbicide marker which has been introduced together with the desired nucleotide sequences. Plant regeneration from cultured protoplasts is described in Evans, et al., "Protoplasts Isolation and Culture" in Handbook of Plant Cell Culture, pp. 124-176, Macmillian Publishing Company, New York, 1983; and Binding, Regeneration of Plants, Plant Protoplasts, pp. 21-73, CRC Press, Boca Raton, 1985. Regeneration can also be obtained from plant callus, explants, organs, pollens, embryos or parts thereof. Such regeneration techniques are described generally in Klee et al. (1987) Ann. Rev. of Plant Phys. 38:467-486.

A transgenic plant or plant material comprising a nucleotide sequence encoding a polypeptide may in some embodiments exhibit one or more of the following characteristics: expression of the polypeptide in a cell of the plant; expression of a portion of the polypeptide in a plastid of a cell of the plant; import of the polypeptide from the cytosol of a cell of the plant into a plastid of the cell; plastid-specific expression of the polypeptide in a cell of the plant; and/or localization of the polypeptide in a cell of the plant. Such a plant may additionally have one or more desirable traits other than expression of the encoded polypeptide. Such traits may include, for example: resistance to insects, other pests, and disease-causing agents; tolerances to herbicides; enhanced stability, yield, or shelf-life; environmental tolerances; pharmaceutical production; industrial product production; and nutritional enhancements.

In accordance with one embodiment a transgenic maize protoplast cell is provided comprising a recombinant optimal nongenic maize locus. More particularly, a maize protoplast plant cell is provided comprising a DNA of interest inserted into an optimal nongenic maize genomic loci of the maize protoplast cell, wherein said nongenic maize genomic loci is about 1 Kb to about 8.3 Kb in length and lacks any methylated nucleotides. In one embodiment the transgenic maize protoplast cell comprises a DNA of interest inserted into the optimal nongenic maize genomic locus wherein the DNA of interest comprises an analytical domain, and/or an open reading frame. In one embodiment the inserted DNA of interest encodes a peptide and in a further embodiment the DNA of interest comprises at least one gene expression cassette comprising a transgene.

In accordance with one embodiment a transgenic maize plant, maize plant part, or maize plant cell is provided comprising a recombinant optimal nongenic maize locus. More

particularly, a maize plant, maize plant part, or maize plant cell is provided comprising a DNA of interest inserted into an optimal nongenic maize genomic loci of the maize plant, maize plant part, or maize plant cell, wherein said nongenic maize genomic loci is about 1 Kb to about 8.5 Kb in length and lacks any methylated nucleotides. In one embodiment the transgenic maize plant, maize plant part, or maize plant cell comprises a DNA of interest inserted into the optimal nongenic maize genomic locus wherein the DNA of interest comprises an analytical domain, and/or an open reading frame. In one embodiment the inserted DNA of interest encodes a peptide and in a further embodiment the DNA of interest comprises at least one gene expression cassette comprising a transgene.

In accordance with embodiment 1 a recombinant sequence is provided wherein, said recombinant sequence comprises a nucleic acid sequence of at least 1 Kb and having at least 90%, 95% or 99% sequence identity with a nongenic sequence selected from the group consisting of loci_137693_G1 (SEQ ID NO:387), loci_265551_G1 (SEQ ID NO:463), loci_128078_G1 (SEQ ID NO:560), loci_168286_G1 (SEQ ID NO:573), loci_3733_G1 (SEQ ID NO:1268), loci_203075_G1 (SEQ ID NO:2030), loci_232484_G1 (SEQ ID NO:2053), loci_136086_G1 (SEQ ID NO:4425), loci_203704_G1 (SEQ ID NO:2033), loci_127268_G1 (SEQ ID NO:2709), loci_204637_G1 (SEQ ID NO:2731), loci_291068_G1 (SEQ ID NO:3230), loci_232222_G1 (SEQ ID NO:3357), loci_43577_G1 (SEQ ID NO:3428), loci_204726_G1 (SEQ ID NO:424), loci_232228_G1 (SEQ ID NO: 4529) and a DNA of interest, wherein the DNA of interest is inserted into said nongenic sequence to produce said recombinant sequence. In accordance with embodiment 2 a recombinant sequence of embodiment 1 is provided wherein said DNA of interest is inserted proximal to a zinc finger target site specific to the nongenic sequence, and more particularly a zinc finger target site of Table 8. In accordance with embodiment 3 a recombinant sequence of embodiment 1 is provided, wherein said DNA of interest is inserted between a pair of zinc finger target sites specific to the nongenic sequence, and more particularly a pair of zinc finger target sites selected from Table 8. In accordance with one embodiment a recombinant sequence is provided wherein, said recombinant sequence consists of a nucleic acid sequence of at least 1 Kb and having 100% sequence identity with a sequence present in a nongenic sequence selected from the group consisting of loci_137693_G1 (SEQ ID NO:387), loci_265551_G1 (SEQ ID NO:463), loci_128078_G1 (SEQ ID NO:560), loci_168286_G1 (SEQ ID NO:573), loci_3733_G1 (SEQ ID NO:1268), loci_203075_G1 (SEQ ID NO:2030), loci_232484_G1 (SEQ ID NO:2053), loci_136086_G1 (SEQ ID NO:4425), loci_203704_G1 (SEQ ID

NO:2033), loci_127268_G1 (SEQ ID NO:2709), loci_204637_G1 (SEQ ID NO:2731),
 loci_291068_G1 (SEQ ID NO:3230), loci_232222_G1 (SEQ ID NO:3357),
 loci_43577_G1 (SEQ ID NO:3428), loci_204726_G1 (SEQ ID NO:424), loci_232228_G1
 (SEQ ID NO: 4529) and a DNA of interest, wherein the DNA of interest is inserted into said
 5 nongenic sequence to produce said recombinant sequence.

In accordance with embodiment 4 a recombinant sequence of any one of embodiments
 1, 2 or 3 is provided wherein said DNA of interest comprises an analytical domain. In
 accordance with embodiment 5 a recombinant sequence of any one of embodiments 1, 2 or 3 is
 provided wherein said DNA of interest does not encode a peptide. In accordance with
 10 embodiment 6 a recombinant sequence of any one of embodiments 1, 2 or 3 is provided
 wherein said DNA of interest encodes a peptide. In accordance with embodiment 7 a
 recombinant sequence of aembodiment 6 is provided wherein said DNA of interest comprises a
 gene expression cassette comprising an insecticidal resistance gene, herbicide tolerance gene,
 nitrogen use efficiency gene, water use efficiency gene, nutritional quality gene, DNA binding
 15 gene, and selectable marker gene. In accordance with embodiment 8 a recombinant sequence
 of any one of embodiments 1-7 is provided wherein said DNA of interest comprises two or
 more gene expression cassettes. In accordance with embodiment 9 a recombinant sequence of
 embodiment 8 is provided wherein two or more of said nongenic sequences each comprise an
 inserted DNA of interest to produce two or more recombinant sequences wherein the two or
 20 more recombinant sequences are located on a same chromosome. In accordance with
 embodiment 10 a recombinant sequence of any one of embodiments 1-9 is provided wherein
 said DNA of interest and/or said nongenic sequence are modified during insertion of said DNA
 of interest into said nongenic sequence. In accordance with embodiment 11 a maize plant,
 maize plant part, or maize plant cell is provided comprising a recombinant sequence of any one
 25 of embodiments 1-10. In accordance with embodiment 12 a method of making a transgenic
 plant cell comprising a DNA of interest is provided wherein the method comprises selecting a
 target nongenic maize genomic locus having at least 90%, 95% or 99% sequence identity from
 the group consisting of loci_137693_G1 (SEQ ID NO:387), loci_265551_G1 (SEQ ID
 NO:463), loci_128078_G1 (SEQ ID NO:560), loci_168286_G1 (SEQ ID NO:573),
 30 loci_3733_G1 (SEQ ID NO:1268), loci_203075_G1 (SEQ ID NO:2030), loci_232484_G1
 (SEQ ID NO:2053), loci_136086_G1 (SEQ ID NO:4425), loci_203704_G1 (SEQ ID
 NO:2033), loci_127268_G1 (SEQ ID NO:2709), loci_204637_G1 (SEQ ID NO:2731),
 loci_291068_G1 (SEQ ID NO:3230), loci_232222_G1 (SEQ ID NO:3357), loci_43577_G1

(SEQ ID NO:3428), loci_204726_G1 (SEQ ID NO:424), loci_232228_G1 (SEQ ID NO: 4529), selecting a site specific nuclease that specifically binds and cleaves said target nongenic maize genomic locus, optionally one selected from Table 8, introducing said site specific nuclease into a maize plant cell, introducing the DNA of interest into the plant cell, inserting the DNA of interest into said target nongenic maize genomic loci, and selecting transgenic plant cells comprising the DNA of interest targeted to said nongenic locus. In accordance with embodiment 18 a method of making a transgenic plant cell of embodiment 12 wherein said site specific nuclease is selected from the group consisting of a zinc finger nuclease, a CRISPR nuclease, a TALEN, a homing endonuclease or a meganuclease. In accordance with embodiment 19 a method of making a transgenic plant cell of embodiment 12 or 18 wherein said DNA of interest is integrated within said nongenic locus via a homology directed repair integration method. In accordance with embodiment 20 a method of making a transgenic plant cell of embodiment 12 or 18 wherein said DNA of interest is integrated within said nongenic locus via a non-homologous end joining integration method. In accordance with embodiment 21 a method of making a transgenic plant cell of embodiment 12, 18, 19 or 20 wherein two or more of said DNA of interest are inserted into two or more of said target nongenic maize genomic loci, optionally wherein the two or more of said target nongenic maize genomic loci are located on a same chromosome.

In accordance with embodiment 1 a purified nongenic maize sequence of at least 1 Kb and having at least 90%, 95% or 99% sequence identity with a nongenic sequence selected from the group consisting of loci_137693_G1 (SEQ ID NO:387), loci_265551_G1 (SEQ ID NO:463), loci_128078_G1 (SEQ ID NO:560), loci_168286_G1 (SEQ ID NO:573), loci_3733_G1 (SEQ ID NO:1268), loci_203075_G1 (SEQ ID NO:2030), loci_232484_G1 (SEQ ID NO:2053), loci_136086_G1 (SEQ ID NO:4425), loci_203704_G1 (SEQ ID NO:2033), loci_127268_G1 (SEQ ID NO:2709), loci_204637_G1 (SEQ ID NO:2731), loci_291068_G1 (SEQ ID NO:3230), loci_232222_G1 (SEQ ID NO:3357), loci_43577_G1 (SEQ ID NO:3428), loci_204726_G1 (SEQ ID NO:424), loci_232228_G1 (SEQ ID NO: 4529) is provided. In accordance with one embodiment a purified nongenic maize sequence is provided wherein, said sequence consists of a nucleic acid sequence of at least 1 Kb and having 100% sequence identity with a sequence present in a nongenic sequence selected from the group consisting of loci_137693_G1 (SEQ ID NO:387), loci_265551_G1 (SEQ ID NO:463), loci_128078_G1 (SEQ ID NO:560), loci_168286_G1 (SEQ ID NO:573), loci_3733_G1 (SEQ ID NO:1268), loci_203075_G1 (SEQ ID NO:2030), loci_232484_G1 (SEQ ID NO:2053),

loci_136086_G1 (SEQ ID NO:4425), loci_203704_G1 (SEQ ID NO:2033), loci_127268_G1 (SEQ ID NO:2709), loci_204637_G1 (SEQ ID NO:2731), loci_291068_G1 (SEQ ID NO:3230), loci_232222_G1 (SEQ ID NO:3357), loci_43577_G1 (SEQ ID NO:3428), loci_204726_G1 (SEQ ID NO:424), loci_232228_G1 (SEQ ID NO: 4529)

EXAMPLES

Example 1: Identification of Targetable Genomic Loci in *Zea mays*

The *Zea mays* genome was screened with a bioinformatics approach using specific criteria to select optimal genomic loci for targeting of a polynucleotide donor. The specific criteria used for selecting the genomic loci were developed using considerations for optimal expression of a transgene within the plant genome, considerations for optimal binding of genomic DNA by a site specific DNA-binding protein, and transgenic plant product development requirements. In order to identify and select the genomic loci, genomic and epigenomic datasets of the *Zea mays* genome were scanned using a bioinformatics approach. Screening genomic and epigenomic datasets resulted in select loci which met the following criteria: 1) hypomethylated and greater than 1 Kb in length; 2) targetable *via* site specific nuclease-mediated integration of a polynucleotide donor; 3) agronomically neutral or non-genic; 4) regions from which an integrated transgene can be expressed; and 5) regions with recombination within/around the locus. Accordingly, a total of 5,286 genomic loci (SEQ ID NO:1 – SEQ ID NO:5286) were identified using these specific criteria. The specific criteria are further described in detail below.

Hypomethylation

The *Zea mays* genome was scanned to select optimal genomic loci larger than 1 Kb that were DNA hypomethylated. Genome-wide DNA methylation levels of shoot and root tissue isolated from *Zea mays* c.v. B73 were surveyed via a bioinformatics method using IlluminaTM/SolexaTM 1G parallel sequencing data. The data were generated from genomic DNA isolated from the above described *Zea mays* plant tissues according to the protocol specified in Wang *et al.*, (2009) Genome-Wide and Organ-Specific Landscapes of Epigenetic Modifications and Their Relationships to mRNA and Small RNA Transcriptomes in Maize. *Plant Cell* 21(4): 1053–1069). These data are available at the NCBI Genbank, Accession No; GEO:GSE15286. The raw sequencing reads were collected and mapped to the *Zea mays* c.v.

B73 reference genome using the Bismark™ mapping software as described in Krueger F, Andrews SR (2011) Bismark: a flexible aligner and methylation caller for Bisulfite-Seq applications. *Bioinformatics* 27: 1571–1572).

The methylation level for each cytosine base in the genome was calculated as a percentage of the number of methylated reads mapping a particular cytosine base location to the total number of reads mapping to that location. The following hypothetical explains how methylation levels were calculated for each base within the *Zea mays* genome. For example, consider that there is a cytosine base at position 100 in chromosome 1 of the *Zea mays* c.v. B73 reference sequence. If there are a total of 20 reads mapped to cytosine base at position 100, and 10 of these reads are methylated, then the methylation level for the cytosine base at position 100 in chromosome 1 is estimated to be 50%. Accordingly, a profile of the methylation level for all of the genomic DNA base pairs obtained from the root and shoot tissue of *Zea mays* was calculated. The reads that could not be correctly mapped to unique locations in the *Zea mays* genome matched repetitive sequences that are widespread in the *Zea mays* genome, and are known in the art to be predominantly methylated.

Using the above described protocol, the methylation levels for the *Zea mays* c.v. B73 genome were measured. As such, regions of the *Zea mays* genome containing methylated reads indicated that these regions of the *Zea mays* genome were methylated. Conversely, the regions of the *Zea mays* genome that were absent of methylated reads indicated these regions of the *Zea mays* genome were non-methylated. The regions of the *Zea mays* genome from the shoot and root tissues that were non-methylated and did not contain any methylated reads are considered as “hypomethylated” regions. To make the root and shoot methylation profiles available for visualization, wiggle plots (<http://useast.ensembl.org/info/website/upload/wig.html>) were generated for each of the *Zea mays* c.v. B73 chromosomes. A screen-shot sample of a wiggle plot for the DNA methylation profile of root and shoot tissues obtained from *Zea mays* c.v. B73 chromosome number 1 is shown in Figure 1.

The methylation profiles established for the *Zea mays* c.v. B73 root and shoot tissues, as described above, were combined into a consensus methylation profile and used to identify hypomethylated regions in the *Zea mays* c.v. B73 genome. The resulting *Zea mays* genomic consensus methylation profile was scanned to identify genomic locations without evidence of methylation, i.e. does not contain mapped methylated reads. Stretches of genomic DNA longer than 100 bp that were hypomethylated were identified. The specific length of each of these hypomethylated regions was calculated by determining the total number of base pairs between

two genomic regions that showed evidence of methylation. Table 1 summarizes the identified hypomethylated regions. In addition, a distribution of the lengths of the hypomethylated regions of the *Zea mays* c.v. B73 genome is shown in Figure 2.

5 Table 1. Hypomethylation profile of *Zea mays* c.v. B73 genome.

Total <i>Zea mays</i> c.v. B73 genome size	~2.1 Gb
Total combined length of hypomethylated region	~663 Mb (31.5% of the <i>Zea mays</i> c.v. B73 genome)
Number of hypomethylated regions above 100 Bp	1,564,310
Number of hypomethylated regions above 1 Kb	130,917
Number of hypomethylated regions above 2 Kb	47,045
Number of hypomethylated regions above 10 Kb	206
Minimum length of hypomethylated region	100 Bp
Maximum length of hypomethylated region	90,202 Bp

These hypomethylated regions of the *Zea mays* c.v. B73 genome were further characterized to identify and select specific genomic loci as the methylation free context of these regions indicated the presence of open chromatin. As such, all subsequent analyses were
 10 conducted on the identified hypomethylated regions.

Targetability

The hypomethylated sites identified in the *Zea mays* c.v. B73 were further analyzed to determine which sites were targetable *via* site specific nuclease-mediated integration of a
 15 polynucleotide donor. The *Zea mays* genome is known in the art to contain long stretches of highly repetitive DNA that are methylated and have high levels of sequence duplication. Annotation information of known repetitive regions in the *Zea mays* genome was collected from the Maize Genome Database (available at <http://www.maizegdb.org/>, and Lawrence, CJ et al (2008) MaizeGDB: The Maize Model Organism Database for Basic, Translational, and
 20 Applied Research. Int J Plant Genomics. 2008:496957).

Accordingly, the hypomethylated sites identified above were screened to remove any sites that aligned with known repetitive regions annotated on the maize genome. The remaining hypomethylated sites that passed this first screen were subsequently scanned using a BLAST™ based homology search of a maize genomic database *via* the NCBI BLAST™ software (version

2.2.23) run using default parameter settings (Stephen F. Altschul *et al* (1997) Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Res.* 25:3389-3402). As a result of the BLAST™ screen, any hypomethylated sites that had significant matches elsewhere in the genome, with sequence alignment coverage of over 40%,
5 were removed from further analyses.

Agronomically Neutral or Nongenetic

The hypomethylated sites identified in the *Zea mays* c.v. B73 were further analyzed to determine which sites were agronomically neutral or nongenetic. As such, the hypomethylated
10 sites described above were screened to remove any sites that overlapped or contained any known or predicted endogenous *Zea mays* c.v. B73 coding sequences. For this purpose, annotation data of known genes and mapping information of expressed sequence tag (EST) data were collected from Maize Genomic Database (available at www.maizegdb.org and Monaco, M., et al., Maize Metabolic Network Construction and Transcriptome Analysis. doi:10.3835/plantgenome2012.09.0025; Posted online 23 Jan. 2013). Any genomic region
15 immediately 2 Kb upstream and 1 Kb downstream to an open reading frame were also considered. These upstream and downstream regions may contain known or unknown conserved regulatory elements that are essential for gene function. The hypomethylated sites previously described above were analyzed for the presence of the known genes (including the 2
20 Kb upstream and 1 Kb downstream regions) and ESTs. Any hypomethylated sites that aligned with or overlapped with known genes (including the 2 Kb upstream and 1 Kb downstream regions) or ESTs were removed from downstream analysis.

Expression

The hypomethylated sites identified in the *Zea mays* c.v. B73 were further analyzed to determine which sites were within proximity to an expressed maize gene. The transcript level
25 expression of *Zea mays* genes was measured by analyzing transcriptome profiling data generated from *Zea mays* c.v. B73 root and shoot tissues using RNAseq™ technology as described in Wang *et al.*, (2009) Genome-Wide and Organ-Specific Landscapes of Epigenetic
30 Modifications and Their Relationships to mRNA and Small RNA Transcriptomes in Maize. *Plant Cell.* 21(4): 1053–1069. For each hypomethylated site, an analysis was completed to identify any annotated genes present within a 40 Kb region in proximity of the hypomethylated site, and an average expression level of the annotated gene(s) located in proximity to the

hypomethylated site. Hypomethylated sites located greater than 40 Kb from an annotated gene with a non-zero average expression level were determined to not be proximal to an expressed *Zea mays* gene and were removed from further analyses.

5 Recombination

The hypomethylated sites identified in the *Zea mays* c.v. B73 were further analyzed to determine which sites had evidence of recombination and could facilitate introgression of the optimal genomic loci into other lines of *Zea mays* via conventional breeding. Diverse *Zea mays* genotypes are routinely crossed during conventional breeding to develop new and improved *Zea mays* lines containing traits of agronomic interest. As such, agronomic traits that are introgressed into optimal genomic loci within a *Zea mays* line via plant-mediated transformation of a transgene should be capable of further being introgressed into other *Zea mays* lines, especially elite lines, via meiotic recombination during conventional plant breeding. The hypomethylated sites described above were screened to identify and select sites that possessed some level of meiotic recombination. Any hypomethylated sites that were present within chromosomal regions characterized as recombination “cold-spots” were identified and removed. In *Zea mays*, these cold spots were defined using a high resolution marker dataset generated from multiple mapping populations. (Jafar Mammadov, Wei Chen, Anastasia Chueva, Karthik Muthuraman, Ruihua Ren, David Meyer, and Siva Kumpatla. 2011. Distribution of Recombinant Frequencies across the Maize Genome. 52nd Annual Maize Genetics Conference).

The meiotic recombination frequencies between any pair of *Zea mays* genomic markers across a chromosome were calculated based on the ratio of the genetic distance between markers (in centimorgan (cM)) to the physical distance between the markers (in megabases (Mb)). For example, if the genetic distance between a pair of markers was 1 cM, and the physical distance between the same pair of markers was 2 Mb, then the calculated recombination frequency was determined to be 0.5 cM/Mb. For each hypomethylated site identified above, a pair of markers at least 1 Mb apart was chosen and the recombination frequency was calculated. Deployment of this method was used to calculate the recombination frequency of the hypomethylated sites. Any hypomethylated sites with a recombination frequency of 0.00041 cM/Mb were identified and removed from further analysis. The remaining hypomethylated regions comprising a recombination frequency greater than 0.00041 cM/Mb were selected for further analysis.

Identification of Optimal Genomic Loci

Application of the selection criteria described above resulted in the identification of a total of 52,885 optimal genomic loci from the *Zea mays* genome. Table 2 summarizes the lengths of the identified optimal genomic loci. These optimal genomic loci possess the following characteristics: 1) hypomethylated genomic loci greater than 1Kb in length; 2) genomic loci that are targetable *via* site specific nuclease-mediated integration of a polynucleotide donor; 3) genomic loci that are agronomically neutral or nongenic; 4) genomic loci from which a transgene can be expressed; and 5) evidence of recombination within the genomic loci. Of all of the optimal genomic loci described in Table 2, only the optimal genomic loci that were greater than 1 Kb were further analyzed and utilized for targeting of a donor polynucleotide sequence. The sequences of these optimal genomic loci are disclosed as SEQ ID NO:1 – SEQ ID NO:5,286. Collectively, these optimal genomic loci are locations within the *Zea mays* genome that can be targeted with a donor polynucleotide sequence, as further demonstrated herein below.

Table 2. Lists the size range of optimal genomic loci identified in the *Zea mays* genome that are hypomethylated, show evidence of recombination, targetable, agronomically neutral or nongenic, and are in proximity to an expressed endogenous gene.

Number of optimal genomic loci larger than 100 Bp	52,885
Number of optimal genomic loci larger than 1 Kb	5,286
Number of optimal genomic loci larger than 2 Kb	770
Number of optimal genomic loci larger than 4 Kb	16

Example 2: F-Distribution and Principal Component Analysis to Cluster Optimal Genomic Loci From *Zea mays*

The 5,286 identified optimal genomic loci (SEQ ID NO: 1-SEQ ID NO: 5,286) were further analyzed using the F-distribution and Principal Component Analysis statistical methods to define a representative population and clusters for grouping of the optimal genomic loci.

F-Distribution Analysis

The identified 5,286 optimal genomic loci were statistically analyzed using a continuous probability distribution statistical analysis. As an embodiment of the continuous probability

distribution statistical analysis, an F-distribution test was completed to determine a representative number of optimal genomic loci. The F-distribution test analysis was completed using equations and methods known by those with skill in the art. For more guidance, the F-distribution test analysis as described in K.M Remund, D. Dixon, DL. Wright and LR. Holden.

5 Statistical considerations in seed purity testing for transgenic traits. *Seed Science Research* (2001) 11, 101–119, herein incorporated by reference, is a non-limiting example of an F-distribution test. The F-distribution test assumes random sampling of the optimal genomic loci, so that any non-valid loci are evenly distributed across the 5,286 optimal genomic loci, and that the number of optimal genomic loci sampled is 10% or less of the total population of 5,286
10 optimal genomic loci.

The F-distribution analysis indicated that 72 of the 5,286 optimal genomic loci provided a representative number of the 5,286 optimal genomic loci, at a 95% confidence level. Accordingly, the F-distribution analysis showed that if 72 optimal genomic loci were tested and all were targetable with a donor polynucleotide sequence, then these results would indicate that
15 96% or more of the 5,286 optimal genomic loci are positive at the 95% confidence level. The best estimate of validating the total percentage of the 5,286 optimal genomic loci would be if 100% of the 72 tested optimal genomic loci were targetable. Accordingly, 96% is actually the lower bound of the true percent validated at the 95% confidence level. This lower bound is based on the 0.95 quantile of the F-distribution, for the 95% confidence level. (Remund K,
20 Dixon D, Wright D, and Holden L. Statistical considerations in seed purity testing for transgenic traits. *Seed Science Research* (2001) 11, 101–119).

Principal Component Analysis

Next, a Principal Component Analysis (PCA) statistical method was completed to further
25 assess and visualize similarities and differences of the data set comprising the 5,286 identified optimal genomic loci to enable sampling of diverse loci for targeting validation. The PCA involves a mathematical algorithm that transforms a larger number of correlated variables into a smaller number of uncorrelated variables called principal components.

The PCA was completed on the 5,286 identified optimal genomic loci by generating a set of
30 calculable features or attributes that could be used to describe the 5,286 identified optimal genomic loci. Each feature is numerically calculable and is defined specifically to capture the genomic and epigenomic context of the 5,286 identified optimal genomic loci. A set of 10

features for each *Zea mays* optimal genomic loci was identified and are described in greater detail below.

1. Length of the optimal genomic loci

- a. The length of the optimal genomic loci in this data set ranged from a minimum of 1,000 Bp to a maximum of 8,267 Bp.

2. Recombination frequency in a 1 MB region around the optimal genomic loci

- a. In maize, recombination frequency for a chromosomal location was defined using an internal high resolution marker dataset generated from multiple mapping populations (Jafar Mammadov, Wei Chen, Anastasia Chueva, Karthik Muthuraman, Ruihua Ren, David Meyer, and Siva Kumpatla. 2011. Distribution of Recombinant Frequencies across the Maize Genome. 52nd Annual Maize Genetics Conference).

- b. Recombination frequencies between any pairs of markers across the chromosome were calculated based on the ratio of the genetic distance between markers (in centimorgan (cM)) to the physical distance between the markers (in Mb). For example, if the genetic distance between a pair of markers is 1 cM and the physical distance between the same pairs of markers is 2 Mb, the calculated recombination frequency is 0.5 cM/Mb. For each optimal genomic loci, a pair of markers at least 1 Mb apart was chosen and the recombination frequency was calculated in this manner. These recombination values ranged from a minimum of 0.00041 cM/Mb to a maximum of 62.42 cM/Mb.

3. Level of optimal genomic loci sequence uniqueness

- a. For each optimal genomic loci, the nucleotide sequence of the optimal genomic loci was scanned against the *Zea mays* c.v. B73 genome using a BLAST™ based homology search using the NCBI BLAST™ software (version 2.2.23) run using the default parameter settings (Stephen F. Altschul et al (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402). As these optimal genomic loci sequences are identified from the *Zea mays* c.v. B73 genome, the first BLAST™ hit identified through this search represents the *Zea mays* c.v. B73 sequence itself. The second BLAST™ hit for each optimal genomic loci sequence was identified and the alignment coverage (represented as the percent of the optimal genomic loci covered by the BLAST™ hit) of the hit was used as a measure of

uniqueness of the optimal genomic loci sequence within the *Zea mays* genome. These alignment coverage values for the second BLAST™ hit ranged from a minimum of 0% to a maximum of 39.98% sequence identity. Any sequences that aligned at higher levels of sequence identity were not considered.

4. Distance from the optimal genomic loci to the closest gene in its neighborhood

- a. Gene annotation information and the location of known genes in the *Zea mays* genome were extracted from Maize Genome Database (available at, www.maizgdb.org and Monaco, M., et al., Maize Metabolic Network Construction and Transcriptome Analysis. doi:10.3835/plantgenome2012.09.0025; Posted online 23 Jan. 2013). For each optimal genomic loci, the closest annotated gene, considering both upstream and downstream locations, was identified and the distance between the optimal genomic loci sequence and the gene was measured (in Bp). For example, if a optimal genomic locus is located in chromosome 1 from position 500 to position 1500, and the closest gene to this optimal genomic locus is located in chromosome 1 from position 2000 to position 3000, the distance from the optimal genomic loci to this closest gene is calculated to be 500 Bp. These values for all 5,286 of the optimal genomic loci dataset ranged from a minimum of 1001 Bp to a maximum of 34,809 Bp.

5. GC % in the optimal genomic loci sequence

- a. For each optimal genomic locus, the nucleotide sequence was analyzed to estimate the number of Guanine and Cytosine bases present. This count was represented as a percentage of the sequence length of each optimal genomic locus and provides a measure for GC%. These GC% values for the maize optimal genomic loci dataset range from 25.17% to 68.3%.

6. Number of genes in a 40 Kb neighborhood around the optimal genomic loci sequence

- a. Gene annotation information and the location of known genes in the *Zea mays* c.v. B73 genome were extracted from Maize Genome Database. For each of the 5,286 optimal genomic loci sequence, a 40 Kb window around the optimal genomic loci sequence was defined and the number of annotated genes with locations overlapping this window was counted. These values ranged from a minimum of 1 gene to a maximum of 9 genes within the 40 Kb neighborhood.

7. Average gene expression in a 40 Kb neighborhood around the optimal genomic loci

a. Transcript level expression of maize genes was measured by analyzing available transcriptome profiling data generated from *Zea mays* c.v. B73 root and shoot tissues using RNAseq™ technology (Mortazavi, A. *et al.*, Mapping and quantifying mammalian transcriptomes by RNA-Seq. *Nat. Methods*. 5, 621–628 (2008); Wang *et al.*, Genome-Wide and Organ-Specific Landscapes of Epigenetic Modifications and Their Relationships to mRNA and Small RNA Transcriptomes in Maize. *Plant Cell*. 2009 April; 21(4): 1053–1069). Gene annotation information and the location of known genes in the *Zea mays* c.v. B73 genome were extracted from Maize Genome Database For each optimal genomic locus, annotated genes within the *Zea mays* c.v. B73 genome that were present in a 40 Kb neighborhood around the optimal genomic loci were identified. Expression levels for each of the genes were extracted from the transcriptome profiles described in the above referenced citations and an average gene expression level was calculated. Expression values of all genes within the genome of *Zea mays* vary greatly. The minimum expression value is 0 and the maximum expression value is 2511.397, with a mean expression value of 18.489 and a median expression value of 3.604. The average expression values for all of the 5,286 optimal genomic loci dataset ranged from a minimum of 0.00369 to a maximum of 2233.06.

8. Level of nucleosome occupancy around the optimal genomic loci

a. Understanding the level of nucleosome occupancy for a particular nucleotide sequence provides information about chromosomal functions and the genomic context of the sequence. The NuPoP™ statistical package was used to predict the nucleosome occupancy and the most probable nucleosome positioning map for any size of genomic sequences (Xi, L., Fondufe-Mittendorf, Y., Xia, L., Flatow, J., Widom, J. and Wang, J.-P., Predicting nucleosome positioning using a duration Hidden Markov Model, *BMC Bioinformatics*, 2010, doi:10.1186/1471-2105-11-346.). For each of the 5,286 optimal genomic loci, the nucleotide sequence was submitted for analysis with the NuPoP™ software and a nucleosome occupancy score was calculated. These nucleosome occupancy scores for the maize optimal genomic loci dataset ranged from a minimum of 0 to a maximum of 0.962.

9. Relative location within the chromosome (proximity to centromere)

a. A centromere is a region on a chromosome that joins two sister chromatids. The portions of a chromosome on either side of the centromere are known as chromosomal arms. Genomic locations of centromeres on all 10 Maize chromosomes were identified in the published *Zea mays* c.v. B73 reference sequence (Schnable, P., *et al.*, (2009) The B73 maize genome: complexity, diversity and dynamics. *Science*, 326(5956): 1112-1115). Information on the position of the centromere in each of the *Zea mays* chromosomes and the lengths of the chromosome arms was extracted from Maize Genome Database. For each optimal genomic locus, the genomic distance from the optimal genomic locus sequence to the centromere of the chromosome that it is located on, is measured (in Bp). The relative location of optimal genomic loci within the chromosome is represented as the ratio of its genomic distance to the centromere relative to the length of the specific chromosomal arm that it lies on. These relative location values for the maize optimal genomic loci dataset ranged from a minimum of 0.00373 to a maximum of 0.99908 ratio of genomic distance.

10. Number of optimal genomic loci in a 1 Mb region

a. For each optimal genomic loci, a 1 Mb genomic window around the optimal genomic loci location was defined and the number of other, additional optimal genomic loci present within or overlapping this region were calculated, including the optimal genomic loci under consideration. The number of optimal genomic loci in a 1 Mb ranged from a minimum of 1 to a maximum of 22.

All of the 5,286 optimal genomic loci were analyzed using the features and attributes described above. The results or values for the score of the features and attributes of each optimal genomic locus are further described in Table 3 (herein incorporated by reference as a separate electronic filing). The resulting dataset was used in the PCA statistical method to cluster the 5,286 identified optimal genomic loci into clusters. During the clustering process, after estimating the “p” principle components of the optimal genomic loci, the assignment of the optimal genomic loci to one of the 32 clusters proceeded in the “p” dimensional Euclidean space. Each of the “p” axes was divided into “k” intervals. Optimal genomic loci assigned to the same interval were grouped together to form clusters. Using this analysis, each PCA axis was divided into two intervals, which was chosen based on *a priori* information regarding the number of clusters required for experimental validation. All analysis and the visualization of the

resulting clusters were carried out with the Molecular Operating Environment™ (MOE) software from Chemical Computing Group Inc. (Montreal, Quebec, Canada).

The PCA approach was used to cluster the set of 5,286 identified optimal genomic loci into 32 distinct clusters based on their feature values, described above. During the PCA process, five principal components (PC) were generated, with the top three PCs containing about 90% of the total variation in the dataset (Table 4). These three PCAs were used to graphically represent the 32 clusters in a three dimensional plot (Figure 3). After the clustering process, was completed, one representative optimal genomic locus was chosen from each cluster. This was performed by choosing a select optimal genomic locus, within each cluster, that was closest to the centroid of that cluster (Table 4). The chromosomal locations of the 32 representative optimal genomic loci are uniformly distributed among the 10 maize chromosomes and are not biased toward any particular genomic location, as shown in Figure 4.

Table 4. Description of the 32 maize representative optimal genomic loci identified from the PCA

Optimal Genomic Loci Name	Genomic Location	Length (Bp)	Cluster Number	SEQ ID NO:
optimal_loci_59517_G1	chr2:43352132..43353146	1015	1	1
optimal_loci_159525_G1	chr4:172518643..172519712	1070	2	199
optimal_loci_9811_G1	chr1:52159463..52161841	2379	3	365
optimal_loci_7507_G1	chr1:39334848..39337271	2424	4	543
optimal_loci_178978_G1	chr5:35776311..35777560	1250	5	687
optimal_loci_285621_G1	chr8:118321357..118322528	1172	6	875
optimal_loci_221721_G1	chr6:91309097..91311722	2626	7	1089
optimal_loci_83937_G1	chr2:192746622..192748862	2241	8	1233
optimal_loci_37146_G1	chr1:223833176..223834563	1388	9	1369
optimal_loci_156393_G1	chr4:154313884..154315253	1370	10	1571
optimal_loci_343678_G1	chr10:113837795..113839503	1709	11	1795
optimal_loci_60209_G1	chr2:47513705..47515145	1441	12	1980
optimal_loci_282323_G1	chr8:100763204..100764398	1195	13	2171
optimal_loci_64542_G1	chr2:72203716..72205045	1330	14	2349
optimal_loci_162531_G1	chr4:189896984..189899332	2349	15	2557
optimal_loci_337001_G1	chr10:77188319..77190007	1689	16	2693
optimal_loci_66202_G1	chr2:83483805..83484909	1105	17	2855
optimal_loci_185454_G1	chr5:80270170..80271254	1085	18	3004
optimal_loci_239863_G1	chr7:14997553..14999296	1744	19	3151
optimal_loci_257541_G1	chr7:125978470..125980969	2500	20	3289
optimal_loci_217939_G1	chr6:67227678..67228708	1031	21	3455
optimal_loci_326869_G1	chr10:12348441..12349499	1059	22	3586
optimal_loci_31710_G1	chr1:194939396..194943360	3965	23	3731
optimal_loci_81941_G1	chr2:181418576..181421181	2606	24	3849
optimal_loci_198387_G1	chr5:164712378..164713567	1190	25	3981
optimal_loci_197372_G1	chr5:158680601..158681681	1081	26	4192

optimal_loci_106202_G1	chr3:85647138..85648635	1498	27	4401
optimal_loci_232228_G1	chr6:144719567..144723469	3903	28	4529
optimal_loci_244324_G1	chr7:40299412..40300584	1173	29	4646
optimal_loci_157315_G1	chr4:158710709..158711983	1275	30	4836
optimal_loci_137489_G1	chr4:29898267..29899725	1459	31	5046
optimal_loci_31764_G1	chr1:195178584..195182163	3580	32	5162

Final Selection of 72 Genomic Loci for Targeting of a Polynucleotide Donor Polynucleotide Sequence

A total of 72 genomic loci were identified and selected for targeting with a donor polynucleotide sequence from the 5,286 genomic loci that were clustered within 32 distinct clusters. For each of the 32 clusters, a representative genomic locus (32 representative genomic loci that were closest to the centroid of that cluster as described above in Table 4) and an additional genomic locus within each cluster were chosen. The additional optimal genomic loci were selected by first screening all of the 5,286 selected optimal genomic sequences against a whole genome database consisting of genomic DNA sequence data for both *Zea mays* c.v. Hi-II (targeting screening line) and *Zea mays* c.v. B104 (transformation line) to determine the coverage (how many optimal genomic loci were present in both genomes) and percentage of sequence identity in the genome from both lines. The additional optimal genomic loci with 100% coverage (the entire sequence length of the optimal loci aligned between both genomes) and 100% identity in both the Hi-II and B104 genomic databases were selected for targeting validation (Figure 5). Comparatively, a small number of the representative genomic loci had sequence identity that was less than 100% coverage and identity in both the Hi-II and B104 genomic database (Figure 5). Other criteria such as genomic loci size, extent of uniqueness, GC% content and chromosomal distribution of the optimal genomic loci were also taken into consideration in selecting the additional optimal genomic loci. The chromosomal location of the 72 selected optimal genomic loci and the specific genomic configuration of each *Zea mays* optimal genomic loci are shown in Figure 6 and Table 5, respectively.

Table 5. Description of the maize selected optimal genomic loci chosen for targeting validation.

From these optimal genomic loci listed in this table, 72 maize optimal genomic loci are representative of the identified total of 5,286 maize selected optimal genomic loci.

Optimal Genomic Loci Name	Genomic Location	Length (bp)	Cluster Number	SEQ ID NO:
optimal_loci_59517_G1	chr2:43352132..43353146	1015	1	1
optimal_loci_25001_G1	chr1:151371224..151372260	1037	1	100

optimal_loci_112632_G1	chr3:128098856..128100257	1402	2	203
optimal_loci_28905_G1	chr1:177037718..177038919	1202	2	295
optimal_loci_129164_G1	chr3:221246027..221247542	1516	3	384
optimal_loci_204726_G1	chr5:200665730..200670667	4938	3	424
optimal_loci_2425_G1	chr1:12810845..12814490	3646	3	451
optimal_loci_122036_G1	chr3:184608166..184609697	1532	4	547
optimal_loci_5735_G1	chr1:29190279..29192844	2566	4	671
optimal_loci_178978_G1	chr5:35776311..35777560	1250	5	687
optimal_loci_288388_G1	chr8:133290442..133291481	1040	5	781
optimal_loci_60310_G1	chr2:47967092..47968271	1180	5	843
optimal_loci_285621_G1	chr8:118321357..118322528	1172	6	875
optimal_loci_243330_G1	chr7:34630402..34631577	1176	6	967
optimal_loci_127038_G1	chr3:210603611..210605198	1588	7	1107
optimal_loci_262784_G1	chr7:155767046..155769049	2004	7	1147
optimal_loci_344662_G1	chr10:119131667..119133955	2289	7	1190
optimal_loci_153894_G1	chr4:139979597..139981225	1629	8	1252
optimal_loci_28771_G1	chr1:176062139..176063611	1473	8	1300
optimal_loci_1098_G1	chr1:5582601..5583834	1234	9	1371
optimal_loci_97772_G1	chr3:30209253..30210607	1355	9	1569
optimal_loci_156393_G1	chr4:154313884..154315253	1370	10	1571
optimal_loci_236662_G1	chr6:165975716..165977010	1295	10	1663
optimal_loci_139485_G1	chr4:42804231..42805751	1521	11	1822
optimal_loci_301175_G1	chr9:20325171..20326621	1451	11	1906
optimal_loci_152337_G1	chr4:130033092..130035481	2390	12	2003
optimal_loci_202616_G1	chr5:188822901..188824814	1914	12	2027
optimal_loci_203704_G1	chr5:194836270..194840217	3948	12	2033
optimal_loci_282323_G1	chr8:100763204..100764398	1195	13	2171
optimal_loci_262782_G1	chr7:155759080..155760097	1018	13	2256
optimal_loci_64542_G1	chr2:72203716..72205045	1330	14	2349
optimal_loci_236455_G1	chr6:164795991..164797027	1037	14	2428
optimal_loci_162531_G1	chr4:189896984..189899332	2349	15	2557
optimal_loci_301774_G1	chr9:23468085..23470278	2194	15	2632
optimal_loci_344663_G1	chr10:119143167..119144795	1629	15	2649
optimal_loci_337001_G1	chr10:77188319..77190007	1689	16	2693
optimal_loci_204637_G1	chr5:200298202..200301414	3213	16	2731
optimal_loci_238100_G1	chr7:4899227..4900708	1482	16	2753
optimal_loci_66202_G1	chr2:83483805..83484909	1105	17	2855
optimal_loci_264359_G1	chr7:163504241..163505487	1247	17	2934
optimal_loci_282653_G1	chr8:102704765..102705924	1160	18	3086
optimal_loci_80282_G1	chr2:173420834..173421870	1037	18	3139
optimal_loci_291068_G1	chr8:148277606..148279985	2380	19	3230
optimal_loci_56395_G1	chr2:24801482..24803132	1651	19	3270
optimal_loci_200497_G1	chr5:176879526..176881345	1820	20	3334
optimal_loci_232222_G1	chr6:144700575..144702126	1552	20	3357

optimal_loci_43577_G1	chr1:256469704..256472666	2963	20	3428
optimal_loci_5607_G1	chr1:28613065..28615113	2049	20	3435
optimal_loci_114664_G1	chr3:140106950..140108061	1112	21	3457
optimal_loci_228254_G1	chr6:126085629..126086823	1195	21	3497
optimal_loci_120993_G1	chr3:179419306..179420357	1052	22	3593
optimal_loci_53137_G1	chr2:7304197..7305496	1300	22	3702
optimal_loci_31710_G1	chr1:194939396..194943360	3965	23	3731
optimal_loci_344664_G1	chr10:119144946..119146850	1905	23	3815
optimal_loci_81941_G1	chr2:181418576..181421181	2606	24	3849
optimal_loci_321514_G1	chr9:140776147..140777584	1438	24	3939
optimal_loci_198387_G1	chr5:164712378..164713567	1190	25	3981
optimal_loci_301180_G1	chr9:20328932..20330129	1198	25	4113
optimal_loci_197372_G1	chr5:158680601..158681681	1081	26	4192
optimal_loci_348776_G1	chr10:142097590..142098803	1214	26	4350
optimal_loci_244439_G1	chr7:41068791..41070248	1458	27	4458
optimal_loci_348258_G1	chr10:139297032..139298517	1486	27	4487
optimal_loci_232228_G1	chr6:144719567..144723469	3903	28	4529
optimal_loci_322501_G1	chr9:146078534..146080201	1668	28	4610
optimal_loci_244324_G1	chr7:40299412..40300584	1173	29	4646
optimal_loci_97232_G1	chr3:27463016..27464143	1128	29	4832
optimal_loci_157315_G1	chr4:158710709..158711983	1275	30	4836
optimal_loci_282499_G1	chr8:101771408..101772767	1360	30	4953
optimal_loci_155031_G1	chr4:146991391..146993137	1747	31	5060
optimal_loci_301773_G1	chr9:23465509..23467762	2254	31	5110
optimal_loci_283161_G1	chr8:105321958..105323571	1614	32	5213
optimal_loci_55524_G1	chr2:20099003..20100485	1483	32	5264
optimal_loci_127268_G1	chr3:211767898..211770046	2149	16	2709
optimal_loci_136086_G1	chr4:22531506..22534989	3484	27	4425
optimal_loci_232484_G1	chr6:146122164..146125580	3417	12	2053
optimal_loci_203075_G1	chr5:191370802..191374627	3826	12	2030
optimal_loci_3733_G1	chr1:19232372..19235997	3626	11	1923
optimal_loci_168286_G1	chr4:219987223..219990695	3473	4	573
optimal_loci_128078_G1	chr3:215482594..215485640	3047	4	560
optimal_loci_265551_G1	chr7:170127188..170130734	3547	3	463
optimal_loci_137693_G1	chr4:31118968..31122359	3392	3	387

A large suite of 5,286 genomic locations have been identified in the *Zea mays* genome as optimal genomic loci for targeting with a donor polynucleotide sequence using precision genome engineering technologies. A statistical analysis approach was deployed to group the 5,286 selected genomic loci into 32 clusters with similar genomic contexts, and to identify a subset of 72 selected genomic loci representative of the set of 5,286 selected genomic loci. The 72 representative loci were validated as optimal genomic loci via targeting with a donor

polynucleotide sequence. By performing the PCA statistical analysis for the numerical values generated for the ten sets of features or attributes that are described above, the ten features or attributes were computed into PCA components of fewer dimensions. As such, PCA components were reduced into five dimensions that are representative of the ten features or attributes described above (Table 6). Each PCA component is equivalent to a combination of the ten features or attributes described above. From these PCA components comprising five dimensions, as computed using the PCA statistical analysis, the 32 clusters were determined.

14764-231316

Table 6. The five PCA components (PCA1, PCA2, PCA3, PCA4, and PCA5) that define each of the 32 clusters and the sequences (SEQ ID NO:1 –SEQ ID NO:5286) which make up each cluster. These five dimensions are representative of the ten features or attributes described above that were used to identify the optimal genomic loci. The minimum (Min), mean, median and maximum (Max) values for each PCA component are provided.

	Cluster1 (SEQ ID NO:1 -- SEQ ID NO:198)	Cluster2 (SEQ ID NO:199 -- SEQ ID NO:364)	Cluster3 (SEQ ID NO:365 -- SEQ ID NO:542)	Cluster4 (SEQ ID NO: 543-- SEQ ID NO:686)	Cluster5 (SEQ ID NO:687- - SEQ ID NO:874)	Cluster6 (SEQ ID NO:875 - - SEQ ID NO:1088)	Cluster7 (SEQ ID NO:1089 -- SEQ ID NO:1232)	Cluster8 (SEQ ID NO:1233 -- SEQ ID NO:1368)	Cluster9 (SEQ ID NO:1369 -- SEQ ID NO:1570)	(Cluster1 0 SEQ ID NO:1571 -- SEQ ID NO:1794 NO:1799)	Cluster1 1 (SEQ ID NO: 1795 -- SEQ ID NO:1979)	Cluster1 2 (SEQ ID NO: 1980 -- SEQ ID NO:2170)	Cluster1 3 (SEQ ID NO: 2171-- SEQ ID NO:2348)
Min	- 0.38899	- 0.93177	- 0.39537	- 0.93241	- 0.39582	-0.93174	-0.38719	-0.93217	-0.38101	-0.93175	-0.39194	-0.93253	-0.38415
Mean	0.73994	0.70291	0.79790	- 0.72366	0.69609	-0.70419	0.75999	-0.69832	0.79994	-0.71434	0.77029	-0.73093	0.65514
Media n	0.44473	- 0.72051	0.58197	- 0.72065	0.41229	-0.72032	0.46869	-0.71729	0.54692	0.34742	0.34742	-0.72075	0.31035
Max	3.01665	0.40085	3.06313	0.40153	3.82376	-0.40276	3.00728	-0.40162	4.26043	-0.41456	3.07238	-0.402	3.05451
Min	0.20045	0.21100	- 9.82023	- 5.15632	0.20059	0.23336	-4.04364	-4.90205	0.20494	0.20506	-5.36888	-6.75555	0.20683
Mean	0.60795	0.65168	- 0.77754	- 0.94886	0.62733	0.64049	-0.7257	-0.69802	0.61334	0.63953	-1.0031	-1.01406	0.61808
Media n	0.61604	0.69582	-0.4007	0.60703	0.65472	0.66268	-0.5115	-0.48357	0.64270	0.67324	-0.52447	-0.66079	0.63948
PCA 2 Max	0.94121	0.95060	0.18831	0.19363	0.93384	0.95102	0.19471	0.19361	0.95002	0.95666	0.19786	0.19368	0.95017
Min	-	-	-	-	-0.3145	-0.32531	-0.30392	-0.31372	-0.19958	-0.19843	-0.19868	-0.19755	-0.31583
Mean	0.25154	0.34875	0.15307	0.23056	-	-	-	-0.25128	0.24465	0.25742	0.12111	0.22983	-0.2653
Media n	-	-	-	-	0.26578	-0.28236	-0.2537	-0.26577	-0.02402	-0.02638	-0.05745	-0.02841	-0.26895
PCA 3 Max	6.48111	34.9050	11.2455	10.6752	-	-0.20094	-0.20105	-0.20248	5.73918	11.2077	3.38454	16.9224	-0.20086

14764-232316

PCA 4	Min	-	0.39542	-	0.39731	-	0.39369	-	0.39886	-	0.37619	-	0.37126	-	0.39716	-	0.39684	-	1.25027	-	1.22084	-	1.21449	-	1.13853	-	1.24332
	Mean	2	1.03065	2	0.94334	3	0.83983	3	0.72857	8	1.08865	8	1.12548	8	0.83798	8	0.86737	9	-0.881	-	0.83045	-	-0.8525	-	0.80304	-	0.87789
	Median	1	0.95657	6	0.84329	6	0.66454	6	0.33413	1	1.02571	9	1.06296	9	0.49167	7	0.59831	6	0.87578	-	0.82491	-	0.84403	-	0.81514	-	0.89279
	Max	2.82969		2.82634	2	2.89030	2	2.84848	4	2.87596	7	2.89113	7	2.86978	5	2.79200	3	0.41074	-	0.40079	-	0.43247	-	0.41111	-	-0.4172	
PCA 5	Min	-	0.19722	-	0.19899	-	0.18939	-	-0.1958	-	-0.1959	-	-0.1976	-	0.19078	-	0.19095	-	0.19058	-	0.18616	-	0.19615	-	0.18815	-	-0.196
	Mean	6	0.69288	1	0.75726	3	0.64203	5	0.69849	8	0.68265	4	0.69397	9	0.66165	5	0.61872	5	0.84803	-	0.77689	3	0.82206	2	0.79153	-	0.82428
	Median	4	0.53791	4	0.60913	4	0.43872	4	0.58786	2	0.50032	1	0.51461	3	0.45756	2	0.43232	4	0.77586	-	0.59967	6	0.80215	4	0.73028	-	0.79593
	Max	2.93832	2	4.20543	5	2.76582	4	2.80897	3	4.14041	7	2.99552	4	3.44651	9	2.71729	3	2.76030	5	2.59351	8	2.35178	4	2.94705	7	2.67123	

14764-232316

	Cluster14 (SEQ ID NO: 2349 -- SEQ ID NO:2556)	Cluster15 (SEQ ID NO: 2557-- SEQ ID NO:2692)	Cluster16 (SEQ ID NO: 2693 -- SEQ ID NO:2854)	Cluster17 (SEQ ID NO: 2854-- SEQ ID NO:3003)	Cluster18 (SEQ ID NO: 3004-- SEQ ID NO:3150)	Cluster19 (SEQ ID NO: 3151-- SEQ ID NO:3288)	Cluster20 (SEQ ID NO: 3289-- SEQ ID NO:3455)	Cluster21 (SEQ ID NO: 3456-- SEQ ID NO:3585)	Cluster22 (SEQ ID NO: 3586-- SEQ ID NO:3730)
	Min	-1.03449	-0.3984	-0.93226	-0.4	-0.93176	-0.3845	-0.39456	-0.93174
	Mean	-0.70636	0.519692	-0.72131	0.788093	-0.72141	0.822434	0.648476	-0.71986
	Median	-0.72054	0.149839	-0.72068	0.474147	-0.72052	0.469551	0.373243	-0.72054
PCA1	Max	-0.40125	2.973061	-0.4106	3.076914	-0.4042	3.022389	2.902287	-0.41693
	Min	0.206354	-4.6237	-4.17636	0.201471	0.200304	-12.4583	0.202767	0.202637
	Mean	0.613673	-0.71726	-0.89472	0.585603	0.656596	-0.99953	0.618663	0.60694
	Median	0.642803	-0.38947	-0.58265	0.600619	0.671923	-0.69949	0.650056	0.588239
PCA2	Max	0.955582	0.178297	0.199158	0.947875	0.957912	0.189554	0.949085	0.95292
	Min	-0.3256	-0.30535	-0.31509	-0.19941	-0.19977	-0.19819	-0.31601	-0.32437
	Mean	-0.27114	-0.2528	-0.26165	0.635893	0.335092	0.188191	-0.27138	-0.27931
	Median	-0.27173	-0.25626	-0.26456	-0.04339	0.008014	-0.04381	-0.27672	-0.29129
PCA3	Max	-0.20023	-0.20007	-0.20018	34.91703	8.740083	7.182482	-0.20023	-0.20086
	Min	-1.17361	-1.13483	-1.21844	-0.39205	-0.38758	-0.39849	-0.36964	-0.38206
	Mean	-0.85262	-0.83671	-0.8048	0.614565	0.833197	0.600433	0.646062	0.758589
	Median	-0.87973	-0.86109	-0.8269	0.451215	0.567642	0.449885	0.523269	0.57825
PCA4	Max	-0.4226	-0.43388	-0.41083	2.809658	3.04613	2.884778	2.6186	2.974322
	Min	-0.19829	-0.19924	-0.19297	-1.79801	-2.53365	-2.6192	-2.6779	-2.62344
	Mean	0.810572	0.736591	0.728155	-0.72144	-0.84754	-0.80889	-0.72856	-0.70873
	Median	0.764994	0.693731	0.657955	-0.72833	-0.77132	-0.70957	-0.59442	-0.57736
PCA5	Max	2.416623	2.278981	2.616655	-0.20335	-0.20762	-0.20218	-0.20116	-0.20382

14764-232316

		Cluster23 (SEQ ID NO: 3731 -- SEQ ID NO:3848)	Cluster24 (SEQ ID NO: 3849-- SEQ ID NO:3980)	Cluster25 (SEQ ID NO: 3981-- SEQ ID NO:4191)	Cluster26 (SEQ ID NO: 4192-- SEQ ID NO:4400)	Cluster27 (SEQ ID NO: 4401-- SEQ ID NO:4528)	Cluster28 (SEQ ID NO: 4529-- SEQ ID NO:4645)	Cluster29 (SEQ ID NO: 4646-- SEQ ID NO:4835)	Cluster30 (SEQ ID NO: 4836-- SEQ ID NO:5045)	Cluster31 (SEQ ID NO: 5046-- SEQ ID NO:5161)	Cluster32 (SEQ ID NO:5162 -- SEQ ID NO:5286)
	Min	-0.39968	-0.93205	-0.38484	-0.93175	-0.36299	-0.93202	-0.39541	-0.93174	-0.38676	-0.93219
	Mean	0.569528	-0.7112	0.89369	-0.71148	0.847871	-0.6997	0.733638	-0.71468	0.713562	-0.72235
	Median	0.307897	-0.71444	0.656779	-0.7205	0.473467	-0.71199	0.522102	-0.72051	0.378272	-0.72062
PCA1	Max	2.76172	-0.40915	3.044789	-0.40213	6.206739	-0.40329	2.997077	-0.40188	2.942702	-0.40344
	Min	-4.50821	-4.32937	0.205796	0.217611	-3.95614	-4.39001	0.203336	0.213622	-3.27891	-4.31097
	Mean	-0.777	-0.77438	0.615151	0.627195	-0.58233	-0.66813	0.642413	0.668567	-0.54379	-0.6389
	Median	-0.41811	-0.59493	0.63135	0.641379	-0.23895	-0.27959	0.691753	0.727605	-0.27039	-0.39873
PCA2	Max	0.196954	0.180603	0.941307	0.956251	0.199442	0.199682	0.947101	0.955864	0.197573	0.197193
	Min	-0.30606	-0.31336	-0.19852	-0.19834	-0.19909	-0.19493	-0.31606	-0.32335	-0.30162	-0.31598
	Mean	-0.25642	-0.26736	0.171006	0.21757	0.20907	0.183239	-0.26663	-0.28001	-0.25672	-0.27043
	Median	-0.26139	-0.27169	-0.03015	-0.02662	-0.03223	-0.06903	-0.27011	-0.28811	-0.25858	-0.27998
PCA3	Max	-0.20052	-0.20409	4.462448	7.171082	7.193004	6.524651	-0.20077	-0.20004	-0.20218	-0.20128
	Min	-0.39748	-0.39925	-0.7756	-0.74818	-0.78247	-0.75487	-0.79614	-0.74639	-0.78065	-0.74365
	Mean	0.668717	0.649507	-0.63225	-0.6052	-0.61175	-0.59977	-0.62563	-0.61235	-0.62339	-0.59687
	Median	0.41274	0.413211	-0.63785	-0.61495	-0.61728	-0.60438	-0.63223	-0.61292	-0.63546	-0.6038
PCA4	Max	2.854384	2.911189	-0.40047	-0.40417	-0.40476	-0.41372	-0.41488	-0.40099	-0.40756	-0.40546
	Min	-2.18571	-2.49096	-2.21238	-2.21096	-2.21537	-2.20254	-2.39722	-2.17311	-2.11438	-2.35552
	Mean	-0.85226	-0.79404	-0.8952	-0.956	-0.91416	-0.91719	-0.96664	-0.96062	-0.95439	-0.98418
	Median	-0.79315	-0.76484	-0.83735	-0.91891	-0.92024	-0.83148	-0.90166	-0.94788	-0.90938	-0.885
PCA5	Max	-0.20566	-0.20015	-0.20978	-0.20039	-0.22084	-0.20408	-0.2077	-0.21493	-0.20199	-0.22725

Example 3: Design of Zinc Fingers to Bind Genomic Loci in *Zea mays*

Zinc finger proteins directed against the identified DNA sequences of the representative genomic loci were designed as previously described. *See, e.g., Urnov et al., (2005) Nature* 435:646-551. Exemplary target sequence and recognition helices are shown in Table 7 (recognition helix regions designs) and Table 8 (target sites). In Table 8, nucleotides in the target site that are contacted by the ZFP recognition helices are indicated in uppercase letters and non-contacted nucleotides are indicated in lowercase. Zinc Finger Nuclease (ZFN) target sites were designed for all of the previously described 72 selected genomic loci. Numerous ZFP designs were developed and tested to identify the fingers which bound with the highest level of efficiency with 72 different representative genomic loci target sites which were identified and selected in *Zea mays* as described above. The specific ZFP recognition helices (Table 7) which bound with the highest level of efficiency to the zinc finger recognition sequences were used for targeting and integration of a donor sequence within the *Zea mays* genome.

Table 7. zinc finger designs for the *Zea mays* selected genomic loci (N/A indicates “not applicable”). It should be noted that the ZFP recognition helices that are identified with an asterisk (*) were designed for targeting and integration of a donor sequence, but the completion of donor integration within these genomic loci has not been completed.

pDAB Number	ZFP Number	F1	F2	F3	F4	F5	F6
111879	111879 ZFN5	SEQ ID NO:5287 QSGDL TR	SEQ ID NO:5288 RKDQL VA	SEQ ID NO:5289 RSDDL T	SEQ ID NO:5290 TSSNRK T	SEQ ID NO:5291 RSDTLS E	SEQ ID NO:5292 ARSTR N
	111879 ZFN7	SEQ ID NO:5293 RSDSL V	SEQ ID NO:5294 DRSNR KT	SEQ ID NO:5295 QSSHL R	SEQ ID NO:5296 RSDAL AR	SEQ ID NO:5297 RSDDL R	SEQ ID NO:5298 DPSAL K
111885	111885 ZFN1	SEQ ID NO:5299 RSDNLS Q	SEQ ID NO:5300 ASNDR KK	SEQ ID NO:5301 ERGTL AR	SEQ ID NO:5302 RSDHLS R	SEQ ID NO:5303 ERGTL AR	SEQ ID NO:5304 QSGHLS R
	111885 ZFN2	SEQ ID NO:5305 RSANL AR	SEQ ID NO:5306 DRSDLS R	SEQ ID NO:5307 RSDTLS Q	SEQ ID NO:5308 RSADLS R	SEQ ID NO:5309 DRSNLS R	SEQ ID NO:5310 NSRNLR N

117404	SIG115 737_31v 1	SEQ ID NO:5311 RSDSLS V	SEQ ID NO:5312 DRSHL AR	SEQ ID NO:5313 DRSNLS R	SEQ ID NO:5314 RRSDL KR	SEQ ID NO:5315 RSDTLS E	SEQ ID NO:5316 QNATRIN
	SIG115 737_32v 1	SEQ ID NO:5317 QSGSLT R	SEQ ID NO:5318 QSGDL TR	SEQ ID NO:5319 RSDVLS E	SEQ ID NO:5320 TRNGL KY	N/A	N/A
117408	SIG120 523_11v 1	SEQ ID NO:5321 RSDNLS R	SEQ ID NO:5322 DNSNR KT	SEQ ID NO:5323 QNAHR KT	SEQ ID NO:5324 QKATRI T	SEQ ID NO:5325 DRSHLT R	SEQ ID NO:5326 RSDDRK K
	SIG120 523_12v 1	SEQ ID NO:5327 ASKTRT N	SEQ ID NO:5328 QSGSLT R	SEQ ID NO:5329 LRHHL TR	SEQ ID NO:5330 QSAHL KA	N/A	N/A
117400	SIG115 246_5	SEQ ID NO:5331 QSGDL TR	SEQ ID NO:5332 ASHNL RT	SEQ ID NO:5333 DRSNLT R	SEQ ID NO:5334 QSSDLS R	SEQ ID NO:5335 DAGNR NK	N/A
	SIG115 246_6	SEQ ID NO:5336 DRSDLS R	SEQ ID NO:5337 RSDNLT R	SEQ ID NO:5338 DRSHLS R	SEQ ID NO:5339 TSGNLT R	SEQ ID NO:5340 QSSDLS R	N/A
117402	SIG115 636_1v1	SEQ ID NO:5341 QSSDLS R	SEQ ID NO:5342 HRSTR NR	SEQ ID NO:5343 RSDDL T	SEQ ID NO:5344 DRSNL KA	SEQ ID NO:5345 DRSHLT R	SEQ ID NO:5346 QRSTLKS
	SIG115 636_2v1	SEQ ID NO:5347 RSDALS R	SEQ ID NO:5348 RSDDL T	SEQ ID NO:5349 DRSHLT R	SEQ ID NO:5350 TSSNRK T	SEQ ID NO:5351 RSDTLS E	SEQ ID NO:5352 DRSHLA R
117406	SIG120 417_11v 1	SEQ ID NO:5353 DRSAR TR	SEQ ID NO:5354 QSGHLS R	SEQ ID NO:5355 QSGNL AR	SEQ ID NO:5356 RSDVLS T	SEQ ID NO:5357 RYAYL TS	SEQ ID NO:5358 RRWTLV G
	SIG120 417_12v 1	SEQ ID NO:5359 RSDNLS Q	SEQ ID NO:5360 ASNDR KK	SEQ ID NO:5361 QSGDL TR	SEQ ID NO:5362 LKDTL RR	SEQ ID NO:5363 QSGNL AR	N/A
117411	SIG120 621_15v 1	SEQ ID NO:5364 QSGDL TR	SEQ ID NO:5365 MQNYL SR	SEQ ID NO:5366 RSDHLS E	SEQ ID NO:5367 QNANR KT	SEQ ID NO:5368 RSADLT R	N/A
	SIG120 621_16v 1	SEQ ID NO:5369 RSDNLS E	SEQ ID NO:5370 QSANR TK	SEQ ID NO:5371 RSDALS R	SEQ ID NO:5372 DRSAL AR	SEQ ID NO:5373 RSDHLS E	SEQ ID NO:5374 DSQNRIK

117413	SIG120 78_11v1	SEQ ID NO:5375 QSGDL TR	SEQ ID NO:5376 DKGNL TK	SEQ ID NO:5377 RSADLT R	SEQ ID NO:5378 DRSHL AR	SEQ ID NO:5379 RSDTLS E	SEQ ID NO:5380 DRSNRK T
	SIG120 78_12v1	SEQ ID NO:5381 DRSNLS R	SEQ ID NO:5382 LRQDL KR	SEQ ID NO:5383 RSDHLS E	SEQ ID NO:5384 DRSAL AR	SEQ ID NO:5385 DRSALS R	SEQ ID NO:5386 NRRGRW S
117429	SIG157 315_1v1	SEQ ID NO:5387 RPYTLR L	SEQ ID NO:5388 HRSSLR R	SEQ ID NO:5389 RSDSLL R	SEQ ID NO:5390 WLSSL A	SEQ ID NO:5391 QSGDL TR	SEQ ID NO:5392 DRSHLA R
	SIG157 315_2v1	SEQ ID NO:5393 DRSNLS R	SEQ ID NO:5394 LKQHL NE	SEQ ID NO:5395 LRHHL TR	SEQ ID NO:5396 QSGNL HV	SEQ ID NO:5397 TSGHLS R	N/A
124802		SEQ ID NO:5495 QSSDLS R	SEQ ID NO:5496 QSGNL AR	SEQ ID NO:5497 DRSNR TT	SEQ ID NO:5498 DNSNRI K	N/A	N/A
		SEQ ID NO:5499 QSSDLS R	SEQ ID NO:5500 RTDAL RG	SEQ ID NO:5501 RSDHLS E	SEQ ID NO:5502 SYRSR WG	SEQ ID NO:5503 DRSAL AR	N/A
121900	SIGPPL 05_1	SEQ ID NO:5504 RSDTLS E	SEQ ID NO:5505 QSGDL TR	SEQ ID NO:5506 TSGNLT R	SEQ ID NO:5507 DRSAL AR	N/A	N/A
	SIGPPL 05_2	SEQ ID NO:5508 RSDSLS V	SEQ ID NO:5509 QSGDL TR	SEQ ID NO:5510 DRSNLS R	SEQ ID NO:5511 RQDSRS Q	SEQ ID NO:5512 RSDHLS A	SEQ ID NO:5513 QHGLA S
124810	SIGPPL 06_9	SEQ ID NO:5514 RSANL AR	SEQ ID NO:5515 RSDHLT T	SEQ ID NO:5516 RSANL AR	SEQ ID NO:5517 TNQNR T	N/A	N/A
	SIGPPL 06_10	SEQ ID NO:5518 QSGNL AR	SEQ ID NO:5519 QSNQL AV	SEQ ID NO:5520 QNAHR KT	SEQ ID NO:5521 RSDDL K	SEQ ID NO:5522 RSDTR KT	N/A
121902	SIGPPL 07_1	SEQ ID NO:5523 QSSHLT R	SEQ ID NO:5524 QSSDLT R	SEQ ID NO:5525 RSDDL R	SEQ ID NO:5526 QSSDL R	SEQ ID NO:5527 TSGSL R	SEQ ID NO:5528 TSSNRA V
	SIGPPL 07_2	SEQ ID NO:5529 RSDHLS R	SEQ ID NO:5530 DRSAR NS	SEQ ID NO:5531 RSDTLS E	SEQ ID NO:5532 SRCWR RK	N/A	N/A

123802	ZmPPL 18SIG_ 5	SEQ ID NO:5533 TSGNLT R	SEQ ID NO:5534 LKQML AV	SEQ ID NO:5535 QSSNLA R	SEQ ID NO:5536 RSDNLT R	SEQ ID NO:5537 RSDNLS T	SEQ ID NO:5538 QSGHLS R
	ZmPPL 18SIG_ 6	SEQ ID NO:5539 RSDNL AR	SEQ ID NO:5540 QKKDR SY	SEQ ID NO:5541 RSDVLS R	SEQ ID NO:5542 DSRDR KN	N/A	N/A
123805	ZmSIG PPL19_ 1	SEQ ID NO:5543 RSAHLS R	SEQ ID NO:5544 QSANR TK	SEQ ID NO:5545 QSSDLS R	SEQ ID NO:5546 QSSDLS R	SEQ ID NO:5547 QWSTR KR	N/A
	ZmSIG PPL19_ 2	SEQ ID NO:5548 QSSDLS R	SEQ ID NO:5549 QSAHR KN	SEQ ID NO:5550 RSDNLS T	SEQ ID NO:5551 DSSTRK T	SEQ ID NO:5552 RSDHLS R	SEQ ID NO:5553 DRSNRK T
121992	ZmPPL 20v2_ 1	SEQ ID NO:5554 QSSDLS R	SEQ ID NO:5555 QAGNL SK	SEQ ID NO:5556 DRSNLS R	SEQ ID NO:5557 LKQHL TR	N/A	N/A
	ZmPPL 20v2_ 2	SEQ ID NO:5558 DRSNLS R	SEQ ID NO:5559 QSGDL TR	SEQ ID NO:5560 QSSDLS R	SEQ ID NO:5561 QAGNL SK	SEQ ID NO:5562 QNAHR KT	N/A
118643	SIGPPL 09_ 1	SEQ ID NO:5563 RSDHLS Q	SEQ ID NO:5564 QNAHRI T	SEQ ID NO:5565 RSDDL T	SEQ ID NO:5566 QRSTLS S	SEQ ID NO:5567 TSGNLT R	SEQ ID NO:5568 DRSNLT R
	SIGPPL 09_ 2	SEQ ID NO:5569 TSGNLT R	SEQ ID NO:5570 RSDDL T	SEQ ID NO:5571 QSGDL TR	SEQ ID NO:5572 MQNYL SR	SEQ ID NO:5573 QSGNL AR	SEQ ID NO:5574 DQSGLA H
118648	SIGPPL 10_ 5	SEQ ID NO:5575 rsdnlst	SEQ ID NO:5576 drsalr	SEQ ID NO:5577 lkqhltr	SEQ ID NO:5578 rrddlrm	SEQ ID NO:5579 rsddltr	SEQ ID NO:5580 drsnlka
	SIGPPL 10_ 6	SEQ ID NO:5581 rsdtlse	SEQ ID NO:5582 qsgdltr	SEQ ID NO:5583 qsgdltr	SEQ ID NO:5584 drsvlrr	SEQ ID NO:5585 rsdnlar	SEQ ID NO:5586 drsnltr
118650	SIGPPL 21_ 1	SEQ ID NO:5587 DRSHLT R	SEQ ID NO:5588 QSGDL TR	SEQ ID NO:5589 QSGDL TR	SEQ ID NO:5590 RSDNLS E	SEQ ID NO:5591 KRGNR AK	N/A
	SIGPPL 21_ 2	SEQ ID NO:5592 ERGTL AR	SEQ ID NO:5593 RSDAL AR	SEQ ID NO:5594 RSDALS R	SEQ ID NO:5595 DRSAL AR	SEQ ID NO:5596 ERGTL AR	SEQ ID NO:5597 DRSALA R
118654	SIGPPL 22_ 3	SEQ ID NO:5598 QSSDLS R	SEQ ID NO:5599 RSDHLS R	SEQ ID NO:5600 RSDTLS Q	SEQ ID NO:5601 QKATRI T	SEQ ID NO:5602 RSDAL AR	N/A
	SIGPPL 22_ 4	SEQ ID NO:5603 RSDNLS V	SEQ ID NO:5604 DRSHL AR	SEQ ID NO:5605 RSDTLS R	SEQ ID NO:5606 QSADR TK	SEQ ID NO:5607 TSGHLS R	N/A
118656	SIGPPL 23_ 1	SEQ ID NO:5608	SEQ ID NO:5609	SEQ ID NO:5610	SEQ ID NO:5611	SEQ ID NO:5612	SEQ ID NO:5613

		QRSNL VR	DRSHL AR	RSDTLS E	RMYTL SK	DRSALS R	RSDDLT R
	SIGPPL 23_2	SEQ ID NO:5614 RSDALT Q	SEQ ID NO:5615 DRSDLS R	SEQ ID NO:5616 RRTDL RR	SEQ ID NO:5617 RSDNL AR	SEQ ID NO:5618 QRSPLP A	N/A
118659	SIGPPL 24_4	SEQ ID NO:5619 RSDSLS A	SEQ ID NO:5620 QNAHR KT	SEQ ID NO:5621 ERGTL AR	SEQ ID NO:5622 RSDNLT R	SEQ ID NO:5623 TSGNLT R	SEQ ID NO:5624 QRSHLS D
	SIGPPL 24_3	SEQ ID NO:5625 QSGDL TR	SEQ ID NO:5626 QRSNL NI	SEQ ID NO:5627 RSDNL AR	SEQ ID NO:5628 DRSVL HR	SEQ ID NO:5629 DRSDLS R	SEQ ID NO:5630 RQDTLR S
118660	SIGPPL 25_2	SEQ ID NO:5631 RSDALS R	SEQ ID NO:5632 QSGSLT R	SEQ ID NO:5633 RSDALS V	SEQ ID NO:5634 DSSHRT R	SEQ ID NO:5635 QSGDL TR	SEQ ID NO:5636 QSGHLS R
	SIGPPL 25_1	SEQ ID NO:5637 RSDNL AR	SEQ ID NO:5638 HRNTL LG	SEQ ID NO:5639 TSGSL R	SEQ ID NO:5640 RSDHLT T	SEQ ID NO:5641 QSGDL TR	SEQ ID NO:5642 RPYTLRL
118767	SIGPPL 26_1	SEQ ID NO : 5643 RSADLT R	SEQ ID NO : 5644 RSDAL AR	SEQ ID NO : 5645 RSDTLS Q	SEQ ID NO : 5646 RSDDR KK	SEQ ID NO : 5647 TSGSL R	N/A
	SIGPPL 26_2	SEQ ID NO : 5648 RSDTLS A	SEQ ID NO : 5649 RSADR KK	SEQ ID NO : 5650 QRSNL VR	SEQ ID NO : 5651 DRSHL AR	SEQ ID NO : 5652 RSDALS V	N/A
118769	SIGPPL 27_1	SEQ ID NO : 5653 DRSNLS R	SEQ ID NO : 5654 QSGNL AR	SEQ ID NO : 5655 RSDHLT Q	SEQ ID NO : 5656 QSGDL TR	SEQ ID NO : 5657 LRHQL KS	N/A
	SIGPPL 27_2	SEQ ID NO : 5658 RSADLT R	SEQ ID NO : 5659 QSGDL TR	SEQ ID NO : 5660 DRSHLS R	SEQ ID NO : 5661 TSGNLT R	SEQ ID NO : 5662 RSDHLS A	SEQ ID NO : 5663 TTRYRN R
118663	SIGPPL 28_1	SEQ ID NO : 5664 QSSDLS R	SEQ ID NO : 5665 QSGSLT R	SEQ ID NO : 5666 QSGHLS R	SEQ ID NO : 5667 TSGNLT R	SEQ ID NO : 5668 QSGHLS R	N/A
	SIGPPL 28_2	SEQ ID NO : 5669 QSGNL AR	SEQ ID NO : 5670 DISNRS K	SEQ ID NO : 5671 DRSDLS R	SEQ ID NO : 5672 RRTDL RR	SEQ ID NO : 5673 TSGSLT R	N/A
118668	SIGPPL 29_5	SEQ ID NO : 5674 DRSHLS	SEQ ID NO : 5675 TSGNLT	SEQ ID NO : 5676 DRSNLS	SEQ ID NO : 5677 FPGSRT	SEQ ID NO : 5678 RNDDR	N/A

		R	R	R	R	KK	
	SIGPPL 29_6	SEQ ID NO : 5679 TSGSLS R	SEQ ID NO : 5680 QLNNL KT	SEQ ID NO : 5681 RSDVLS T	SEQ ID NO : 5682 ASGNL LN	SEQ ID NO : 5683 RSDNLS R	SEQ ID NO : 5684 DNSNRK T
118669	SIGPPL 30_1	SEQ ID NO : 5685 RSDTLS Q	SEQ ID NO : 5686 ASANR TK	SEQ ID NO : 5687 QSSNLA R	SEQ ID NO : 5688 DSSDR KK	SEQ ID NO : 5689 RSDHLS T	SEQ ID NO : 5690 QSGHLS R
	SIGPPL 30_2	SEQ ID NO : 5691 RSDHLS A	SEQ ID NO : 5692 SYWSR TV	SEQ ID NO : 5693 DRSALS R	SEQ ID NO : 5694 DRSHL AR	SEQ ID NO : 5695 RSDNLT R	N/A
118670	SIGPPL 31_1	SEQ ID NO : 5696 DRSDLS R	SEQ ID NO : 5697 DRSNR NK	SEQ ID NO : 5698 RSDVLS E	SEQ ID NO : 5699 RNFSLT M	SEQ ID NO : 5700 RSDAL AR	N/A
	SIGPPL 31_2	SEQ ID NO : 5701 QSGAL AR	SEQ ID NO : 5702 QSSDLS R	SEQ ID NO : 5703 RRDILH Q	SEQ ID NO : 5704 RSADLT R	SEQ ID NO : 5705 QSGDL TR	N/A
118673	SIGPPL 32_5	SEQ ID NO : 5706 QSGAL AR	SEQ ID NO : 5707 DRSNLS R	SEQ ID NO : 5708 LKQHL TR	SEQ ID NO : 5709 RSDNLS T	SEQ ID NO : 5710 RSDHLS R	N/A
	SIGPPL 32_6	SEQ ID NO : 5711 QSSDLS R	SEQ ID NO : 5712 HRSNL NK	SEQ ID NO : 5713 DRSNLS R	SEQ ID NO : 5714 DASNL RQ	SEQ ID NO : 5715 TSSNLS R	N/A
118674	SIGPPL 33_1	SEQ ID NO : 5716 RSDSLL R	SEQ ID NO : 5717 CREYR GK	SEQ ID NO : 5718 TSGHLS R	SEQ ID NO : 5719 RSDVLS A	SEQ ID NO : 5720 RNDHRI N	NA
	SIGPPL 33_2	SEQ ID NO : 5721 QSGSLT R	SEQ ID NO : 5722 RSDNL RE	SEQ ID NO : 5723 QSGSLT R	SEQ ID NO : 5724 RLDNR TA	SEQ ID NO : 5725 RSDVLS N	SEQ ID NO : 5726 DRSTRIT

118676	SIGPPL 34_1	SEQ ID NO : 5727 RSDSL R	SEQ ID NO : 5728 WLSSL A	SEQ ID NO : 5729 ERGTL AR	SEQ ID NO : 5730 TSGSLT R	SEQ ID NO : 5731 RSDTLS E	SEQ ID NO : 5732 QSGHLS R
	SIGPPL 34_2	SEQ ID NO : 5733 QSGNL AR	SEQ ID NO : 5734 DISNRS K	SEQ ID NO : 5735 RSDHLS R	SEQ ID NO : 5736 HRYHR LS	N/A	N/A
118677	SIGPPL 35_1	SEQ ID NO : 5737 QSGSLT R	SEQ ID NO : 5738 DRSHL AR	SEQ ID NO : 5739 DRSALS R	SEQ ID NO : 5740 RSDAL AR	SEQ ID NO : 5741 QSSDLS R	SEQ ID NO : 5742 HKYHLR S
	SIGPPL 35_2	SEQ ID NO : 5743 RSDHLS E	SEQ ID NO : 5744 RKDARI T	SEQ ID NO : 5745 ERGTL AR	SEQ ID NO : 5746 RSDALT Q	SEQ ID NO : 5747 DRSHLT R	SEQ ID NO : 5748 RSDHLTT
118680	SIGPPL 36_1	SEQ ID NO : 5749 TSGSL R	SEQ ID NO : 5750 QMHHL KT	SEQ ID NO : 5751 TSSNLS R	SEQ ID NO : 5752 QSGAL AR	SEQ ID NO : 5753 RSDDLT R	N/A
	SIGPPL 36_2	SEQ ID NO : 5754 DRSALS R	SEQ ID NO : 5755 RSDHLS R	SEQ ID NO : 5756 DRSAR TR	SEQ ID NO : 5757 QSGHLS R	SEQ ID NO : 5758 RSDHLS E	SEQ ID NO : 5759 ARSTR N
118683	SIGPPL 37_1	SEQ ID NO : 5760 RSANL AR	SEQ ID NO : 5761 RNDDR KK	SEQ ID NO : 5762 DRSHLT R	SEQ ID NO : 5763 DRSNLT R	N/A	N/A
	SIGPPL 37_2	SEQ ID NO : 5764 TSGSL R	SEQ ID NO : 5765 DSSDR KK	SEQ ID NO : 5766 QSGDL TR	SEQ ID NO : 5767 DRSHLT R	SEQ ID NO : 5768 DRSHL AR	N/A
118685	SIGPPL 38_1	SEQ ID NO : 5769 RSDHLS A	SEQ ID NO : 5770 TKSNRT K	SEQ ID NO : 5771 DRSNLT R	SEQ ID NO : 5772 RSDDL R	SEQ ID NO : 5773 QKSSLR T	N/A
	SIGPPL 38_2	SEQ ID NO : 5774 RREDLI T	SEQ ID NO : 5775 TSSNLS R	SEQ ID NO : 5776 DRSALS R	SEQ ID NO : 5777 RSDDR KT	SEQ ID NO : 5778 RSDTLS E	SEQ ID NO : 5779 HRRSRW G

123833	ZmSIG PPL39_ 1	SEQ ID NO: 5780 RSDNLS A	SEQ ID NO: 5781 RNNDR KT	SEQ ID NO: 5782 QSGDL TR	SEQ ID NO: 5783 RSDDL T R	SEQ ID NO: 5784 QSSDLS R	SEQ ID NO: 5785 HKYHLR S
	ZmSIG PPL39_ 2	SEQ ID NO: 5786 TNQNRI T	SEQ ID NO: 5787 HRSSLR R	SEQ ID NO: 5788 DSSTRK T	SEQ ID NO: 5789 QSATRT K	SEQ ID NO: 5790 QSSDLS R	SEQ ID NO: 5791 HRKSLSR
118771	SIGPPL 40_1	SEQ ID NO : 5792 QSSDLS R	SEQ ID NO : 5793 QSTHR NA	SEQ ID NO : 5794 RSDHLT Q	SEQ ID NO : 5795 DRSDLS R	SEQ ID NO : 5796 RSDNLT R	N/A
	SIGPPL 40_2	SEQ ID NO : 5797 QSGDL TR	SEQ ID NO : 5798 DRSHLT R	SEQ ID NO : 5799 QSGSLT R	SEQ ID NO : 5800 DRSNLS R	SEQ ID NO : 5801 QSGNL AR	N/A
121943	ZmSIG PPL41_ 7	SEQ ID NO: 5802 DRSALS R	SEQ ID NO: 5803 RSDALT Q	SEQ ID NO: 5804 RSDSL R	SEQ ID NO: 5805 RSDALT Q	SEQ ID NO: 5806 RSDNLS T	SEQ ID NO: 5807 DNSNRIN
	ZmSIG PPL41_ 8	SEQ ID NO: 5808 RSDNLS T	SEQ ID NO: 5809 RSDNR TK	SEQ ID NO: 5810 RSDVLS T	SEQ ID NO: 5811 WSSSR AA	SEQ ID NO: 5812 QSGSLT R	SEQ ID NO: 5813 TSSNRKT
121946	ZmSIG PPL42_ 7	SEQ ID NO: 5814 QSSHLT R	SEQ ID NO: 5815 RSDALT Q	SEQ ID NO: 5816 ERGTL AR	SEQ ID NO: 5817 RNDDR KK	N/A	N/A
	ZmSIG PPL42_ 8	SEQ ID NO: 5818 QSGSLT R	SEQ ID NO: 5819 TSSNRK T	SEQ ID NO: 5820 RSDNLS V	SEQ ID NO: 5821 QNANRI T	SEQ ID NO: 5822 ERGTL AR	SEQ ID NO: 5823 RSDDL T R
121949	ZmSIG PPL43_ 3	SEQ ID NO: 5824 RSDNLS E	SEQ ID NO: 5825 RHSALS A	SEQ ID NO: 5826 QSSDLS R	SEQ ID NO: 5827 QSYNR FV	SEQ ID NO: 5828 ERGTL AR	SEQ ID NO: 5829 TSGSLTR
	ZmSIG PPL43_ 4	SEQ ID NO: 5830 ERGTL AR	SEQ ID NO: 5831 RSDDL T R	SEQ ID NO: 5832 RSDHLS E	SEQ ID NO: 5833 RNQHR KN	SEQ ID NO: 5834 DRSHL AR	N/A

121952	ZmSIG PPL44_ 1	SEQ ID NO: 5835 QSGNL AR	SEQ ID NO: 5836 QGANLI K	SEQ ID NO: 5837 RSDSLS V	SEQ ID NO: 5838 DRSDLS R	SEQ ID NO: 5839 QSGHLS R	N/A
	ZmSIG PPL44_ 2	SEQ ID NO: 5840 TSGSLS R	SEQ ID NO: 5841 QSGSLT R	SEQ ID NO: 5842 RSAHLS R	SEQ ID NO: 5843 RSDALS T	SEQ ID NO: 5844 DRSTRT K	N/A
121959	ZmSIG PPL45_ 7	SEQ ID NO: 5845 RSDDL K	SEQ ID NO: 5846 QSATRT K	SEQ ID NO: 5847 RSDALT Q	SEQ ID NO: 5848 DRSHLT R	SEQ ID NO: 5849 TSSNRK T	N/A
	ZmSIG PPL45_ 8	SEQ ID NO: 5850 DRSALS R	SEQ ID NO: 5851 TSSNRK T	SEQ ID NO: 5852 RSADLT R	SEQ ID NO: 5853 RSDDL R	SEQ ID NO: 5854 RSDVLS T	SEQ ID NO: 5855 DCRNRW R
121963	ZmSIG PPL46_ 7	SEQ ID NO: 5856 QSSDLS R	SEQ ID NO: 5857 QSGSLT R	SEQ ID NO: 5858 QSSDLS R	SEQ ID NO: 5859 RSDNLS T	SEQ ID NO: 5860 RSDNR TK	N/A
	ZmSIG PPL46_ 8	SEQ ID NO: 5861 QSSDLS R	SEQ ID NO: 5862 AASNR SK	SEQ ID NO: 5863 DRSHLS R	SEQ ID NO: 5864 DRSHL AR	SEQ ID NO: 5865 RSDTLS A	SEQ ID NO: 5866 RSADRK K
121971	ZmSIG PPL48_ 7	SEQ ID NO: 5867 RSDNLS T	SEQ ID NO: 5868 DRSNR KT	SEQ ID NO: 5869 RSDAL AR	SEQ ID NO: 5870 RSDNLS T	SEQ ID NO: 5871 DRSAL AR	N/A
	ZmSIG PPL48_ 8	SEQ ID NO: 5872 DRSDLS R	SEQ ID NO: 5873 DRSNR NK	SEQ ID NO: 5874 QSSDLS R	SEQ ID NO: 5875 WRSSL RQ	SEQ ID NO: 5876 RSDHLS Q	SEQ ID NO: 5877 TRSPLTT
121972	ZmSIG PPL49_ 1	SEQ ID NO: 5878 TRDHLS T	SEQ ID NO: 5879 RSDAR TN	SEQ ID NO: 5880 RSDHLS E	SEQ ID NO: 5881 QSNHR KT	SEQ ID NO: 5882 RSDAL AR	N/A
	ZmSIG PPL49_ 2	SEQ ID NO: 5883 ERGTL AR	SEQ ID NO: 5884 RSDALT Q	SEQ ID NO: 5885 RSDSLS V	SEQ ID NO: 5886 DRSAL AR	SEQ ID NO: 5887 QSSNLA R	SEQ ID NO: 5888 QSADRT K

124097	ZmSIG PPL50_ 5	SEQ ID NO: 5889 RSDHLS A	SEQ ID NO: 5890 QSGDL TR	SEQ ID NO: 5891 QSSDLS R	SEQ ID NO: 5892 RSDNL AR	SEQ ID NO: 5893 FREGLY K	N/A
	ZmSIG PPL50_ 6	SEQ ID NO: 5894 TSGNLT R	SEQ ID NO: 5895 LKQML AV	SEQ ID NO: 5896 ERGTL AR	SEQ ID NO: 5897 RSDHLS R	SEQ ID NO: 5898 QSSHLT R	SEQ ID NO: 5899 QSSDLTR
123818	ZmPPL 51_7	SEQ ID NO: 5900 RSDTLS E	SEQ ID NO: 5901 HRRSR WG	SEQ ID NO: 5902 RSDDL V	SEQ ID NO: 5903 TSSNRT K	N/A	N/A
	ZmPPL 51_8	SEQ ID NO: 5904 RSDTLS Q	SEQ ID NO: 5905 QRDHRI K	SEQ ID NO: 5906 DRSNLS R	SEQ ID NO: 5907 TSGNLT R	SEQ ID NO: 5908 RSDSL R	SEQ ID NO: 5909 WLSSL A
118705	SIGPPL 52_5	SEQ ID NO : 5910 DRSNLS R	SEQ ID NO : 5911 LRQNLI M	SEQ ID NO : 5912 QNAHR KT	SEQ ID NO : 5913 QSGAL AR	SEQ ID NO : 5914 QSGHLS R	N/A
	SIGPPL 52_6	SEQ ID NO : 5915 QSGNL AR	SEQ ID NO : 5916 LAYDR RK	SEQ ID NO : 5917 RSDVLS E	SEQ ID NO : 5918 RNFSLT M	SEQ ID NO : 5919 RSADLT R	SEQ ID NO : 5920 DSSDRK K
118711	SIGPPL 54_5	SEQ ID NO : 5921 RSDNL AR	SEQ ID NO : 5922 DQSYR RT	SEQ ID NO : 5923 RSDNLS E	SEQ ID NO : 5924 TSSNRK T	N/A	N/A
	SIGPPL 54_6	SEQ ID NO : 5925 TSGSL R	SEQ ID NO : 5926 RKELL S	SEQ ID NO : 5927 RPYTL L	SEQ ID NO : 5928 HRSSL R	SEQ ID NO : 5929 DRSTR K	SEQ ID NO : 5930 RSDYLA K
118718	ZmSIG PPL57_ 1	SEQ ID NO : 5931 QSSDLS R	SEQ ID NO : 5932 QSTHR NA	SEQ ID NO : 5933 RSADLT R	SEQ ID NO : 5934 RSDDL R	SEQ ID NO : 5935 DRSNLS R	SEQ ID NO : 5936 QSGNLA R
	ZmSIG PPL57_ 2	SEQ ID NO : 5937 QSGHL AR	SEQ ID NO : 5938 DRSHL AR	SEQ ID NO : 5939 RSANL AR	SEQ ID NO : 5940 QSANR TK	SEQ ID NO : 5941 RSDHLT Q	N/A

118722	ZmSIG PPL58_ 3	SEQ ID NO: 5942 QSSDLS R	SEQ ID NO: 5943 RSDHLT Q	SEQ ID NO: 5944 DRSAL AR	SEQ ID NO: 5945 RSDYL AK	SEQ ID NO: 5946 QSGDL TR	N/A
	ZmSIG PPL58_ 4	SEQ ID NO: 5947 RSDNLS Q	SEQ ID NO: 5948 QRQHR KT	SEQ ID NO: 5949 DQSNL RA	SEQ ID NO: 5950 RPYTLR L	SEQ ID NO: 5951 QSSNLA R	SEQ ID NO: 5952 RSDNLTT
118726	SIGPPL 59_5	SEQ ID NO : 5953 QSGHL AR	SEQ ID NO : 5954 QRVAL QA	SEQ ID NO : 5955 ERGTL AR	SEQ ID NO : 5956 QSGDL TR	SEQ ID NO : 5957 RSDDL T	N/A
	SIGPPL 59_6	SEQ ID NO : 5958 QSSDLS R	SEQ ID NO : 5959 HRSNL NK	SEQ ID NO : 5960 RSADLT R	SEQ ID NO : 5961 TNQNR I	SEQ ID NO : 5962 RSDAL AR	N/A
118728	ZmSIG PPL60_ 3	SEQ ID NO : 5963 DSSALI N	SEQ ID NO : 5964 TSSNLS R	SEQ ID NO : 5965 RSDHLS R	SEQ ID NO : 5966 YGWYR HK	SEQ ID NO : 5967 TSGHLS R	SEQ ID NO : 5968 RSDNLT R
	ZmSIG PPL60_ 4	SEQ ID NO : 5969 QSGHL AR	SEQ ID NO : 5970 QRTNL VE	SEQ ID NO : 5971 DRSTRT K	SEQ ID NO : 5972 QSGNL HV	SEQ ID NO : 5973 RSDHLT Q	N/A
118732	SIGPPL 61_5	SEQ ID NO : 5974 RSDNLS T	SEQ ID NO : 5975 RSDNR TK	SEQ ID NO : 5976 RSDNL AR	SEQ ID NO : 5977 QKVN L	SEQ ID NO : 5978 QSGAL AR	N/A
	SIGPPL 61_6	SEQ ID NO : 5979 QSGDL TR	SEQ ID NO : 5980 TQGYL RK	SEQ ID NO : 5981 RSDNL AR	SEQ ID NO : 5982 DSSGLT H	SEQ ID NO : 5983 RNDDR KK	N/A
118733	ZmSIG PPL62_ 1	SEQ ID NO : 5984 DRSDLS R	SEQ ID NO : 5985 RRDYL RT	SEQ ID NO : 5986 RSDTLS E	SEQ ID NO : 5987 NNRDR TK	SEQ ID NO : 5988 RSDTLS E	SEQ ID NO : 5989 QSGDLT R
	ZmSIG PPL62_ 2	SEQ ID NO : 5990 QSSDLS R	SEQ ID NO : 5991 QSTHR NA	SEQ ID NO : 5992 RSDDL S	SEQ ID NO : 5993 RSDAL AR	N/A	N/A

118735	SIGPPL 62_5	SEQ ID NO : 5994 RSANL AR	SEQ ID NO : 5995 RSDDL T	SEQ ID NO : 5996 RSDALS T	SEQ ID NO : 5997 DRSTR K	SEQ ID NO : 5998 QSGNL AR	SEQ ID NO : 5999 QSTPLFA
	SIGPPL 62_6	SEQ ID NO : 6000 QSGHL AR	SEQ ID NO : 6001 ERIALV R	SEQ ID NO : 6002 RSDHLS E	SEQ ID NO : 6003 RSAHLS R	SEQ ID NO : 6004 RSDNLS V	N/A
118739	ZmSIG PPL64_ 1	SEQ ID NO : 6005 RSDTLS E	SEQ ID NO : 6006 QSHNR TK	SEQ ID NO : 6007 DRSHLT R	SEQ ID NO : 6008 DRSAL AR	SEQ ID NO : 6009 TSGSLT R	N/A
	ZmSIG PPL64_ 2	SEQ ID NO : 6010 LRHHL TR	SEQ ID NO : 6011 QSYAR TL	SEQ ID NO : 6012 RSDNLS T	SEQ ID NO : 6013 RSDDL R	SEQ ID NO : 6014 RSAHLS R	SEQ ID NO : 6015 RSDNLT R
118742	SIGPPL 65_1	SEQ ID NO : 6016 RSDDL K	SEQ ID NO : 6017 DRSNR KT	SEQ ID NO : 6018 DRSNLS R	SEQ ID NO : 6019 QRTHL RD	SEQ ID NO : 6020 QSGHLS R	N/A
	SIGPPL 65_2	SEQ ID NO : 6021 QSSDLS R	SEQ ID NO : 6022 QSGNR TT	SEQ ID NO : 6023 DRSNLT R	SEQ ID NO : 6024 QSGHL AR	SEQ ID NO : 6025 QRTNL VE	N/A
118745	ZmSIG PPL66_ 1	SEQ ID NO : 6026 QSGDL TR	SEQ ID NO : 6027 RRDPLI N	SEQ ID NO : 6028 QSGDL TR	SEQ ID NO : 6029 RSDSLS R	SEQ ID NO : 6030 DKSNRI K	N/A
	ZmSIG PPL66_ 2	SEQ ID NO : 6031 QSSDLS R	SEQ ID NO : 6032 QSGDL TR	SEQ ID NO : 6033 QSSDLS R	SEQ ID NO : 6034 TSGNLT R	SEQ ID NO : 6035 QTSDR NK	N/A
124081	ZmSIG PPL67_ 3	SEQ ID NO : 6036 QSGSLT R	SEQ ID NO : 6037 RNDDR KK	SEQ ID NO : 6038 RSDSLS A	SEQ ID NO : 6039 QNAHR KT	SEQ ID NO : 6040 QNAHR KT	N/A
	ZmSIG PPL67_ 4	SEQ ID NO : 6041 QSGDL TR	SEQ ID NO : 6042 DKGNL TK	SEQ ID NO : 6043 QSSDLS R	SEQ ID NO : 6044 QSAHR KN	SEQ ID NO : 6045 QSSDLS R	N/A

125361		SEQ ID NO: 6046 RSDALS R	SEQ ID NO: 6047 QSGSLT R	SEQ ID NO: 6048 QSGSLT R	SEQ ID NO: 6049 QSGSLT R	SEQ ID NO: 6050 TSGHLS R	SEQ ID NO: 6051 DRSHLA R
		SEQ ID NO: 6052 QSGDL TR	SEQ ID NO: 6053 RSDHLS R	SEQ ID NO: 6054 RSDHLS T	SEQ ID NO: 6055 RSDHLS R	N/A	N/A
118753	SIGPPL 69_5	SEQ ID NO : 6056 QSSDLS R	SEQ ID NO : 6057 RSDYL RK	SEQ ID NO : 6058 QSGDL TR	SEQ ID NO : 6059 LRQTL NS	SEQ ID NO : 6060 QSGHLS R	N/A
	SIGPPL 69_6	SEQ ID NO : 6061 RSDTLS V	SEQ ID NO : 6062 DNSTRI K	SEQ ID NO : 6063 RSDNLS T	SEQ ID NO : 6064 DNSNRI N	SEQ ID NO : 6065 TSSNLS R	N/A
124878		SEQ ID NO: 6066 RSDVLS A	SEQ ID NO: 6067 QNATRI N	SEQ ID NO: 6068 RSDVLS E	SEQ ID NO: 6069 QSGNL AR	SEQ ID NO: 6070 RSDNLS V	N/A
		SEQ ID NO: 6071 QSADR TK	SEQ ID NO: 6072 DRSNLT R	SEQ ID NO: 6073 RSDNLS E	SEQ ID NO: 6074 KRCNL RC	N/A	N/A
123829	ZmSIG PPL71_ 5	SEQ ID NO: 6075 DRSNLS R	SEQ ID NO: 6076 DSSAR NT	SEQ ID NO: 6077 TSGNLT R	SEQ ID NO: 6078 DRSNLT R	SEQ ID NO: 6079 DRSNLS R	SEQ ID NO: 6080 QRSNLD S
	ZmSIG PPL71_ 6	SEQ ID NO: 6081 QSGNL AR	SEQ ID NO: 6082 QKVNR AG	SEQ ID NO: 6083 RSDNLS V	SEQ ID NO: 6084 QRNHR TT	SEQ ID NO: 6085 QKATRI T	N/A
118761	ZmSIG PPL72_ 3	SEQ ID NO : 6086 QSGAL AR	SEQ ID NO : 6087 LRHNL RA	SEQ ID NO : 6088 DRSTRT K	SEQ ID NO : 6089 HRSAR KR	SEQ ID NO : 6090 RSDHLS E	SEQ ID NO : 6091 TSSDRTK
	ZmSIG PPL72_ 4	SEQ ID NO : 6092 RSDSLS R	SEQ ID NO : 6093 DKSNRI K	SEQ ID NO : 6094 RSDDL T R	SEQ ID NO : 6095 DRSHLT R	SEQ ID NO : 6096 DRSNLT R	N/A

121904	SIGPPL 74_1	SEQ ID NO : 6097 RSDNLS T	SEQ ID NO : 6098 RQWSL RI	SEQ ID NO : 6099 TSGHLS R	SEQ ID NO : 6100 QSSDLS R	SEQ ID NO : 6101 RSDDL T R	N/A
	SIGPPL 74_2	SEQ ID NO : 6102 RSANL AR	SEQ ID NO : 6103 RLDNR TA	SEQ ID NO : 6104 QSGHL AR	SEQ ID NO : 6105 DSSNRE A	N/A	N/A
121905	ZmSIG PPL75_ 1	SEQ ID NO : 6106 RSDALS R	SEQ ID NO : 6107 RSDNLT R	SEQ ID NO : 6108 RSADLT R	SEQ ID NO : 6109 RSDNLT R	N/A	N/A
	ZmSIG PPL75_ 2	SEQ ID NO : 6110 RSDNLS V	SEQ ID NO : 6111 RSDTRT E	SEQ ID NO : 6112 TSGSLS R	SEQ ID NO : 6113 QSGNL AR	SEQ ID NO : 6114 RSADLT R	N/A
121917	SIGPPL 76_2	SEQ ID NO : 6115 TSGSLS R	SEQ ID NO : 6116 RSDHLT T	SEQ ID NO : 6117 RSDDL T R	SEQ ID NO : 6118 QRSTLS S	SEQ ID NO : 6119 ERGTL AR	SEQ ID NO : 6120 QSGHLS R
	SIGPPL 76_1	SEQ ID NO : 6121 RSDHLS Q	SEQ ID NO : 6122 DNASRI R	SEQ ID NO : 6123 RSDNLS T	SEQ ID NO : 6124 AQWTR AC	SEQ ID NO : 6125 RSDHLS E	SEQ ID NO : 6126 DKANRT R
121918	ZmSIG PPL77_ 2	SEQ ID NO : 6127 QSSDLS R	SEQ ID NO : 6128 LRHNL RA	SEQ ID NO : 6129 RSDTLS T	SEQ ID NO : 6130 DRSSRI K	N/A	N/A
	ZmSIG PPL77_ 1	SEQ ID NO : 6131 QSGAL AR	SEQ ID NO : 6132 RSDNLT R	SEQ ID NO : 6133 RSDNLS T	SEQ ID NO : 6134 DRSNLT R	SEQ ID NO : 6135 DRSDLS R	SEQ ID NO : 6136 DSSTRRR
121909	SIGPPL 78_1	SEQ ID NO : 6137 DRSAL AR	SEQ ID NO : 6138 DRSALS R	SEQ ID NO : 6139 DRSHL AR	SEQ ID NO : 6140 RSDNLS T	SEQ ID NO : 6141 RSDAR AN	N/A
	SIGPPL 78_2	SEQ ID NO : 6142 RSDHLS T	SEQ ID NO : 6143 DSSNRI K	SEQ ID NO : 6144 QSGAL AR	SEQ ID NO : 6145 RSDDL T R	SEQ ID NO : 6146 QSGSLT R	N/A

121912	SIGPPL 79_1	SEQ ID NO: 6147 DRSHLS R	SEQ ID NO: 6148 DRSHL AR	SEQ ID NO: 6149 QSSDLS R	SEQ ID NO: 6150 QSGDL TR	SEQ ID NO: 6151 RSDNLS E	SEQ ID NO: 6152 HSNARK T
	SIGPPL 79_2	SEQ ID NO: 6153 RSDALS V	SEQ ID NO: 6154 DSSHRT R	SEQ ID NO: 6155 QSGDL TR	SEQ ID NO: 6156 ASHNL RT	SEQ ID NO: 6157 RSDHLS T	SEQ ID NO: 6158 TSANLSR
121981	ZmSIG PPL80_ 3	SEQ ID NO: 6159 DRSDLS R	SEQ ID NO: 6160 DRSNLT R	SEQ ID NO: 6161 RSDSLL R	SEQ ID NO: 6162 RLDWL PM	SEQ ID NO: 6163 RSADLT R	SEQ ID NO: 6164 TSGNLTR
	ZmSIG PPL80_ 4	SEQ ID NO: 6165 RSDNLS Q	SEQ ID NO: 6166 DRSNR TK	SEQ ID NO: 6167 DSSDR KK	SEQ ID NO: 6168 RSDHLS E	SEQ ID NO: 6169 QSASR KN	N/A
124091	ZmSIG PPL81_ 3	SEQ ID NO: 6170 RSDVLS T	SEQ ID NO: 6171 STAALS Y	SEQ ID NO: 6172 QSANR TT	SEQ ID NO: 6173 QNAHR KT	SEQ ID NO: 6174 QSSDLS R	N/A
	ZmSIG PPL81_ 4	SEQ ID NO: 6175 QRNHR TT	SEQ ID NO: 6176 DRSNLT R	SEQ ID NO: 6177 TSGNLT R	SEQ ID NO: 6178 QSNQL RQ	SEQ ID NO: 6179 RSDALT Q	N/A
127268*		SEQ ID NO: 6620 DRSAL AR	SEQ ID NO: 6621 DYYGR HG	SEQ ID NO: 6622 DRSHL AR	SEQ ID NO: 6623 YRSSLK E	SEQ ID NO: 6624 TSGNLT R	N/A
		SEQ ID NO: 6625 HHHVL VQ	SEQ ID NO: 6626 QNATR TK	SEQ ID NO: 6627 DRSTR K	SEQ ID NO: 6628 RRDNL HS	SEQ ID NO: 6629 QKATR TT	SEQ ID NO: 6630 HRSSLRR
120993*		SEQ ID NO: 6631 QSSDLS R	SEQ ID NO: 6632 QWSTR KR	SEQ ID NO: 6633 RSDVLS E	SEQ ID NO: 6634 QTVHR NS	SEQ ID NO: 6635 RSDTLS E	SEQ ID NO: 6636 FRGSLT W
		SEQ ID NO: 6637 RSDNLS T	SEQ ID NO: 6638 RSTHRT Q	SEQ ID NO: 6639 RSDNLS V	SEQ ID NO: 6640 QKATRI N	SEQ ID NO: 6641 DRSNLT R	N/A

228254*		SEQ ID NO: 6642 QSGNL AR	SEQ ID NO: 6643 CRQNL AN	SEQ ID NO: 6644 DRSNLS R	SEQ ID NO: 6645 DGRNL RH	SEQ ID NO: 6646 RSDHLS T	SEQ ID NO: 6647 RSDNLT R
		SEQ ID NO: 6648 DRSNR TT	SEQ ID NO: 6649 QNATRI N	SEQ ID NO: 6650 QSGNL AR	SEQ ID NO: 6651 HKLSLS I	SEQ ID NO: 6652 DRSDLS R	SEQ ID NO: 6653 YRSNLV R
200497*		SEQ ID NO: 6654 DRSALS R	SEQ ID NO: 6655 QSGSLT R	SEQ ID NO: 6656 RSDNLT R	SEQ ID NO: 6657 RQDCL SL	SEQ ID NO: 6658 RNDNR KT	N/A
		SEQ ID NO: 6659 QSGNL AR	SEQ ID NO: 6660 DQSG AH	SEQ ID NO: 6661 QSANR TK	SEQ ID NO: 6662 DRSDLS R	SEQ ID NO: 6663 RSHHL KA	N/A
66202*		SEQ ID NO: 6664 QSGNL AR	SEQ ID NO: 6665 QSGSLT R	SEQ ID NO: 6666 DRSALS R	SEQ ID NO: 6667 QSGSLT R	SEQ ID NO: 6668 QSGNL AR	N/A
		SEQ ID NO: 6669 QSGNL AR	SEQ ID NO: 6670 WRISLA A	SEQ ID NO: 6671 RSDNLS E	SEQ ID NO: 6672 RSQHR KT	SEQ ID NO: 6673 QSSDLS R	N/A
5607*		SEQ ID NO: 6674 RSANL AR	SEQ ID NO: 6675 RSDHLT T	SEQ ID NO: 6676 RSDNLS E	SEQ ID NO: 6677 DRSHL AR	SEQ ID NO: 6678 QSAHR KN	SEQ ID NO: 6679 LKHHLT D
		SEQ ID NO: 6680 TSGNLT R	SEQ ID NO: 6681 DRSNLT R	SEQ ID NO: 6682 RSDNLS Q	SEQ ID NO: 6683 RKADR TK	SEQ ID NO: 6684 TSGNLT R	SEQ ID NO: 6685 DSSNLAT

Table 8. Zinc finger target site of *Zea mays* selected genomic loci

Locus ID	Name	pDAB Number	ZFP Number and Binding Site (5'→3')	SEQ ID NO:
optimal loci_ 204637	OGL1	111879	111879ZFN5:ctACTCCGTATGCGAA GGCAcg	5398
			111879ZFN7: taTTCGCGGTGGGACACTTGat	5399
optimal_loci_20 4726	OGL2	111885	111885ZFN1: ccGGAGCCGGGGCCTCCCAGgc	5400
			111885ZFN2: atCGCGACGCGACGcGACGAGac	5401

optimal_loci_15 6393	OGL 12	117404	SIG115737_31v1: TGCATGCGCAGTA	5402
			SIG115737_32v1: ACACCGGCGCACGGCACG	5403
optimal_loci_19 8387	OGL 15	117408	SIG120523_11v1: AGAGGTGTAACC	5404
			SIG120523_12v1: TCGGGCACAAGAAACGAG	5405
optimal_loci_31 710	OGL 08	117400	SIG115246_5: TACGCTGACAATGCA	5406
			SIG115246_6: CCAGCTGATGGAGAGGAC	5407
optimal_loci_64 542	OGL 11	117402	SIG115636_1v1: AGAGCAGGCGAG	5408
			SIG115636_2v1: AGCAAAGTGAGTAGTT	5409
optimal_loci_19 7372	OGL14	117406	SIG120417_11v1: TGGATGGAAGGAATC	5410
			SIG120417_12v1: GAAGCTACATCCCAG	5411
optimal_loci_23 2228	OGL 16	117411	SIG120621_15v1: TACGCGCAACGGAACGCA	5412
			SIG120621_16v1: CACCGGTGTCGTGTAACAG	5413
optimal_loci_28 5621	OGL17	117413	SIG12078_11v1: CCCGGACGACGCCGAG	5414
			SIG12078_12v1: GACATGGCACGCGCATCGAG	5415
optimal_loci_15 7315	OGL 13	117429	SIG157315_1v1: GCATGTGTGGTTTTG	5416
			SIG157315_2v1: GGTCAAGGTAGTGAC	5417
optimal_loci_43 577	OGL04	124802	ZFN_binding_1: AGCTTCAATAGTA	6180
			ZFN_binding_2: GTCTTCCGGTTGGCT	6181
optimal_loci_30 1774	OGL05	121900	ZFN_binding_3: GTCGATGCACCG	6182
			ZFN_binding_4: CTAAGGATGGACGCAGTG	6183
optimal_loci_23 2222	OGL06	124810	ZFN_binding_5: CATGAGAGGGAT	6184
			ZFN_binding_6: ATGTCGTAGAAAAGAA	6185
optimal_loci_20 3704	OGL07	121902	ZFN_binding_7: CATGTTCGCTGCGGCTGGA	6186
			ZFN_binding_8: AGTCCGCTCGGG	6187
optimal_loci_59 517	OGL09	118643	ZFN_binding_9: GACGATCTAGCGAGAAGG	6188
			ZFN_binding_10: ATCGAAGAACGCAGCGGAT	6189
optimal_loci_25 001	OGL10	118648	ZFN_binding_12: CACGCGCCGGGTGTCTAG	6190
			ZFN_binding_13: GACGAGCACCGCCCCACCG	6191

optimal_loci_11 2632	OGL18	123802	ZFN_binding_14: CGGGTACTGGGAAAGGAG	6192
			ZFN_binding_15: GAGCGTCCTGATTGACATG	6193
optimal_loci_28 905	OGL19	123805	ZFN_binding_16: ACGGTGCATCAAGCTTAAG	6194
			ZFN_binding_17: CAAGGGACCTAGTGAGCT	6195
optimal_loci_12 9164	OGL20	121992	ZFN_binding_18: GGTGACTAAGCT	6196
			ZFN_binding_19: AGATAAGCTGCAGAC	6197
optimal_loci_24 25	OGL21	118650	ZFN_binding_20: GAGCAGGCAGGCAGGC	6198
			ZFN_binding_21: GTCGTCGTCGTGCGTGGCC	6199
optimal_loci_12 2036	OGL22	118654	ZFN_binding_22: GTGGCAACGGGGGCT	6200
			ZFN_binding_23: GGTTCAGCGGGCTAG	6201
optimal_loci_57 35	OGL23	118656	ZFN_binding_24: GCGGTCTTGCCGGGCGAA	6202
			ZFN_binding_25: CTAGAGGCGCCCATG	6203
optimal_loci_17 8978	OGL24	118659	ZFN_binding_26: ACGGACAGCCGAGAAAGCA	6204
			ZFN_binding_27: CGAGATCGAGGCCAGATCG	6205
optimal_loci_28 8388	OGL25	118660	ZFN_binding_28: TTGCCATGGGTTATTGAG	6206
			ZFN_binding_29: GGAGCATGGCCAGGTAGTG	6207
optimal_loci_60 310	OGL26	118767	ZFN_binding_30: CCAGTTCGACGAGTGGCG	6208
			ZFN_binding_31: GGCCTGGGCGAACGCCGCCG	6209
optimal_loci_24 3330	OGL27	118769	ZFN_binding_32: AGTGCAAGGGAAGAC	6210
			ZFN_binding_33: AGGAGGGATGGAGCAGCG	6211
optimal_loci_12 7038	OGL28	118663	ZFN_binding_34: GGAGATAGGAGTAGCT	6212
			ZFN_binding_35: GTTGCGCCCTACGAA	6213
optimal_loci_26 2784	OGL29	118668	ZFN_binding_36: TCGGTTGACCGATGGC	6214
			ZFN_binding_37: AACGAGCCATATGCAAGTT	6215
optimal_loci_34 4662	OGL30	118669	ZFN_binding_38: GGATGGCTCCGAATGATATG	6216
			ZFN_binding_39: GAGGGCGTCTTGAGG	6217

optimal_loci_15 3894	OGL31	118670	ZFN_binding_40: GTGTTGCTGTACGAC	6218
			ZFN_binding_41: GCAGCGAACGGCTGTA	6219
optimal_loci_28 771	OGL32	118673	ZFN_binding_42: GGGTAGGGGTGACGTA	6220
			ZFN_binding_43: GATCACGACATATCCA	6221
optimal_loci_10 98	OGL33	118674	ZFN_binding_44: TGGGTGGGTTTGC GTG	6222
			ZFN_binding_45: CCCATGCAGGTAAAGGTA	6223
optimal_loci_97 772	OGL34	118676	ZFN_binding_46: GGACTGGGTGCCTGTGTG	6224
			ZFN_binding_47: CGTGGGTACGAA	6225
optimal_loci_23 6662	OGL35	118677	ZFN_binding_48: CGTGCTGTGGTCTGGCGTA	6226
			ZFN_binding_49: TGGGGCTATGGCCATGGGG	6227
optimal_loci_13 9485	OGL36	118680	ZFN_binding_50: GCGGTACGATAGTGTT	6228
			ZFN_binding_51: ACTCGGGGAGTCGGGGTC	6229
optimal_loci_30 1175	OGL37	118683	ZFN_binding_52: GACGGATCGGAG	6230
			ZFN_binding_53: GGCGGATGCATCCGTT	6231
optimal_loci_15 2337	OGL38	118685	ZFN_binding_54: ATAGCGGACCGATCGG	6232
			ZFN_binding_55: ATCCCGGCCGGTCGATTCG	6233
optimal_loci_20 2616	OGL39	123833	ZFN_binding_56: cgtgcttgcggcaccgcag	6234
			ZFN_binding_57: gccgctgcaccgctcat	6235
optimal_loci_28 2323	OGL40	118771	ZFN_binding_58: GAGGACAGGCGAGCT	6236
			ZFN_binding_59: GAAGACGTAGGCGCA	6237
optimal_loci_26 2782	OGL41	121943	ZFN_binding_60: CACAAGATGGTGATGGTC	6238
			ZFN_binding_61: CATGTATGTATGTAGTAG	6239
optimal_loci_23 6455	OGL42	121946	ZFN_binding_62: TCGGCCATGGGA	6240
			ZFN_binding_63: GCGGCCAAAAGCATGTA	6241
optimal_loci_16 2531	OGL43	121949	ZFN_binding_64: GGTGCCAAAGCCATGCAG	6242
			ZFN_binding_65: GGCTGGCGGGCGGCC	6243

optimal_loci_34 4663	OGL44	121952	ZFN_binding_66: GGAGACTCGATAAGAA	6244
			ZFN_binding_67: GCCATGTGGGGTAGTT	6245
optimal_loci_33 7001	OGL45	121959	ZFN_binding_68: CATGGCATGGCATCG	6246
			ZFN_binding_69: CACATGCGCGGCGCATGTC	6247
optimal_loci_23 8100	OGL46	121963	ZFN_binding_70: TAGTAGGCTAGTAGCT	6248
			ZFN_binding_71: ACGCCGCGGCGGCTTGCCT	6249
optimal_loci_26 4359	OGL48	121971	ZFN_binding_72: ATCTAGGTGCAACTAG	6250
optimal_loci_28 2653	OGL49	121972	ZFN_binding_73: GTGAAACGGATGTGT	6251
			ZFN_binding_74: TCAGAATATCATGATGGCC	6252
optimal_loci_80 282	OGL50	124097	ZFN_binding_75: TGCGAGCGCTGCATGG	6253
			ZFN_binding_76: GCTGGAGGGGCAATGAT	6254
optimal_loci_29 1068	OGL51	123818	ZFN_binding_77: TATCCGATCCCG	6255
			ZFN_binding_78: TGTGTGGATGACGAAACG	6256
optimal_loci_56 395	OGL52	118705	ZFN_binding_79: GGAGTAAGAAATGAC	6257
			ZFN_binding_80: TCCGCGTTGCTGTCTGAA	6258
optimal_loci_11 4664	OGL54	118711	ZFN_binding_81: TATCAGCTCGAG	6259
			ZFN_binding_82: TAGACCTGTTTTGATGGTT	6260
optimal_loci_53 137	OGL57	118718	ZFN_binding_83: GAAGACGGCGGCGAGAGCT	6261
			ZFN_binding_84: AGGGAAGAGAGGAGGA	6262
optimal_loci_34 4664	OGL58	118722	ZFN_binding_85: GCACAGATCAGGGCT	6263
			ZFN_binding_86: AAGGATTTGCACAGACAG	6264
optimal_loci_81 941	OGL59	118726	ZFN_binding_87: GCGGCAGCCATAGGA	6265
			ZFN_binding_88: GTGCATGCGTATCCA	6266
optimal_loci_32 1514	OGL60	118728	ZFN_binding_89: GAGGGTCTTGGGGTGATATC	6267
			ZFN_binding_90: AGGAAAGCCCAAGGA	6268
optimal_loci_30 1180	OGL61	118732	ZFN_binding_91: GTACAAGAGTAGTAG	6269
			ZFN_binding_92: TCGATCGAGGGCGCA	6270
optimal_loci_34	OGL62	118733	ZFN_binding_93:	6271

8776			CCACCGTCTCCGTAGGCC	
			ZFN_binding_94: GTGTCGAGAGCT	6272
optimal_loci_24 4439	OGL63	118735	ZFN_binding_95: ATAGAAAACCATGGCGGAG	6273
			ZFN_binding_96: AAGGGGCGGCAACGGA	6274
optimal_loci_34 8258	OGL64	118739	ZFN_binding_97: GTTGTCTGGATAACCG	6275
			ZFN_binding_98: GAGGGGGAGTAGCTAGGT	6276
optimal_loci_32 2501	OGL65	118742	ZFN_binding_99: GGACGAGACCAAATCG	6277
			ZFN_binding_100: CAAGGAGACAAAGCT	6278
optimal_loci_24 4324	OGL66	118745	ZFN_binding_101: TACGTGGCAATTGGCA	6279
			ZFN_binding_102: TCAGATGCTGCAGCT	6280
optimal_loci_97 232	OGL67	124081	ZFN_binding_103: AGAAGATCGATCGGTA	6281
			ZFN_binding_104: GCTTGAGCTCACGCA	6282
optimal_loci_28 2499	OGL68	125361	ZFN_binding_105: CACTACTACTACTACCGCC	6283
			ZFN_binding_106: GGGTGGGGGGGCA	6284
optimal_loci_15 5031	OGL69	118753	ZFN_binding_107: GGACCTACAATAGGCA	6285
			ZFN_binding_108: GATCACAAGACCAAG	6286
optimal_loci_30 1773	OGL70	124878	ZFN_binding_109: CATTGTCAGTTCCTT	6287
			ZFN_binding_110: CAGCAGGACTCT	6288
optimal_loci_28 3161	OGL71	123829	ZFN_binding_111: AAGACAGACGATGTC	6289
			ZFN_binding_112: ACAAAAAAGCAAGAA	6290
optimal_loci_55 524	OGL72	118761	ZFN_binding_113: TCACGGTGTTACCCATGTA	6291
			ZFN_binding_114: GACGGATGCGTACGTG	6292
optimal_loci_12 7268	OGL73	124086	ZFN_binding_131: GTTGTTATTCAAACA	6293
			ZFN_binding_132: CACAAGTAATGTGGA	6294
optimal_loci_13 7693	OGL74	121904	ZFN_binding_115: GCGGCTGGTTTGCAG	6295
			ZFN_binding_116: CACGGACAGGAG	6296

optimal_loci_26 5551	OGL75	121905	ZFN_binding_117: GAGGCGGAGGTG	6297
			ZFN_binding_118: AGGGCGGAAGTTACGGAG	6298
optimal_loci_12 8078	OGL76	121917	ZFN_binding_119: GGAGCCCCCAGCGTGGGTT	6299
			ZFN_binding_120: GACCGGTCAGTAGGTCAAG	6300
optimal_loci_16 8286	OGL77	121918	ZFN_binding_121: TTCACGTCATGCT	6301
			ZFN_binding_122: GCCGACGACTAGGAGGTA	6302
optimal_loci_37 33	OGL78	121909	ZFN_binding_123: CTGTAGGGCGTCGTC	6303
			ZFN_binding_124: GTAGCGGTACTACTGG	6304
optimal_loci_20 3075	OGL79	121912	ZFN_binding_125: ATCCAGGCAGCTGGCGGC	6305
			ZFN_binding_126: GATTGGAATGCAGGCCCG	6306
optimal_loci_23 2484	OGL80	121981	ZFN_binding_127: GATGCGTCTGGTGTGACGAC	6307
			ZFN_binding_128: ACACAGTCCTACTAG	6308
optimal_loci_13 6086	OGL81	124091	ZFN_binding_129: GCTCGAAACTTATG	6309
			ZFN_binding_130: ATGAAAGATGACCGA	6310
optimal_loci_22 8254	OGL55	n/a	TTCATGGTTGTTACCACTCatnnnatG ATCCCTTTGAAGTAAAC	6686
optimal_loci_66 202	OGL47	n/a	TTCTACGATTACTTctannctGCTAGT CAGATTGAA	6687
optimal_loci_12 0993	OGL56	n/a	TGATGCAAGGTGGCGTAAAggnngg GACATAAAGAGGCAG	6688
optimal_loci_20 0497	OGL53	n/a	GATTACCTCCACCTTttnnctAGGCC TAATATCGAA	6689
optimal_loci_56 07	OGL03	n/a	ATCCCTCTATCCTTCACGaanngaAA CGATCTCGAAGGACGAT	6690

The *Zea mays* representative genomic loci zinc finger designs were incorporated into zinc finger expression vectors encoding a protein having at least one finger with a CCHC structure. See, U.S. Patent Publication No. 2008/0182332. In particular, the last finger in each protein had a CCHC backbone for the recognition helix. The non-canonical zinc finger-encoding sequences were fused to the nuclease domain of the type IIS restriction enzyme *FokI* (amino acids 384-579 of the sequence of Wah *et al.*, (1998) Proc. Natl. Acad. Sci. USA 95:10564-10569) via a four amino acid ZC linker and an *opaque-2* nuclear localization signal derived from *Zea mays* to form zinc-finger nucleases (ZFNs). See, U.S. Patent No. 7,888,121.

Zinc fingers for the various functional domains were selected for *in vivo* use. Of the numerous ZFNs that were designed, produced and tested to bind to the putative genomic target site, the

ZFNs described in Table 8 above were identified as having *in vivo* activity and were characterized as being capable of efficiently binding and cleaving the unique *Zea mays* genomic polynucleotide target sites *in planta*.

5 ZFN Construct Assembly

Plasmid vectors containing ZFN gene expression constructs, which were identified as previously described, were designed and completed using skills and techniques commonly known in the art (*see*, for example, Ausubel or Maniatis). Each ZFN-encoding sequence was fused to a sequence encoding an *opaque-2* nuclear localization signal (Maddaloni *et al.*, (1989) 10 Nuc. Acids Res. 17:7532), that was positioned upstream of the zinc finger nuclease. The non-canonical zinc finger-encoding sequences were fused to the nuclease domain of the type IIS restriction enzyme FokI (amino acids 384-579 of the sequence of Wah *et al.* (1998) Proc. Natl. Acad. Sci. USA 95:10564-10569). Expression of the fusion proteins was driven by the strong constitutive promoter from the *Zea mays* Ubiquitin gene, (which includes the 5' untranslated 15 region (UTR) (Toki *et al.*, (1992) Plant Physiology 100;1503-07). The expression cassette also included the 3' UTR (comprising the transcriptional terminator and polyadenylation site) from the *Zea mays* peroxidase 5 gene (Per5) gene (US Patent Publication No. 2004/0158887). The self-hydrolyzing 2A encoding the nucleotide sequence from *Thosea asigna* virus (Szymczak *et al.*, (2004) Nat Biotechnol. 22:760-760) was added between the two Zinc Finger Nuclease 20 fusion proteins that were cloned into the construct.

The plasmid vectors were assembled using the IN-FUSION™ Advantage Technology (Clontech, Mountain View, CA). Restriction endonucleases were obtained from New England BioLabs (Ipswich, MA) and T4 DNA Ligase (Invitrogen, Carlsbad, CA) was used for DNA ligation. Plasmid preparations were performed using NUCLEOSPIN® Plasmid Kit (Macherey- 25 Nagel Inc., Bethlehem, PA) or the Plasmid Midi Kit (Qiagen) following the instructions of the suppliers. DNA fragments were isolated using QIAQUICK GEL EXTRACTION KIT™ (Qiagen) after agarose tris-acetate gel electrophoresis. Colonies of all ligation reactions were initially screened by restriction digestion of miniprep DNA. Plasmid DNA of selected clones was sequenced by a commercial sequencing vendor (Eurofins MWG Operon, Huntsville, AL). 30 Sequence data were assembled and analyzed using the SEQUENCHER™ software (Gene Codes Corp., Ann Arbor, MI).

Plasmids were constructed and confirmed via restriction enzyme digestion and via DNA sequencing.

35 Zinc Finger Cloning Via Automated Workflow

A subset of Zinc Finger Nuclease vectors were cloned via an automated DNA construction pipeline. Overall, the automated pipeline resulted in vector constructions with identical ZFN architecture as described previously. Each Zinc Finger monomer, which confers the DNA binding specificity of the ZFN, were divided into 2-3 unique sequences at a KPF amino acid motif. Both the 5' and 3' ends of the ZFN fragments were modified with inclusion of a BsaI recognition site (GGTCTCN) and derived overhangs. Overhangs were distributed such that a 6-8 part assembly would only result in the desired full length expression clone. Modified DNA fragments were synthesized *de novo* (Synthetic Genomics Incorporated, La Jolla, CA). A single maize backbone, pDAB118791 was used in all of the maize ZFN builds. It contained the ZmUbi1 promoter and the Opaque2 NLS as well as the FokI domain and the ZmPer5 3'UTR. Cloned in between the Opaque 2 NLS and the FokI domain was a BsaI flanked SacB gene from *Bacillus subtilis*. When putative ligation events were plated on Sucrose containing media, the SacB cassette acts as a negative selection agent reducing or eliminating vector backbone contamination. A second part repeatedly utilized in all builds was pDAB117462. This vector contains the first monomer FokI domain, the t2A stutter sequence, and the 2nd monomer Opaque2 NLS all flanked by BsaI sites.

Using these materials as as the ZFN DNA parts library, a Freedom Evo 150 (TECAN, Männedorf, Switzerland) manipulated the addition of 75-100ng of each DNA plasmid or synthesized fragment from 2D bar coded tubes into a PCR plate (ThermoFisher, Waltham, MA). BsaI (NEB, Ipswich, MA) and T4 DNA ligase (NEB, Ipswich, MA) supplemented with Bovine Serum Albumin protein (NEB, Ipswich, MA) and T4 DNA Ligase Buffer (NEB, Ipswich, MA) were added to the reaction. Reactions were cycled (25X) with incubations for 3 minutes at 37°C and 4 minutes at 16°C C1000 Touch Thermo Cycler (BioRad, Hercules CA). Ligated material was transformed and screened in Top10 cells (Life Technologies Carlsbad, CA) by hand or using a Qpix460 colony picker and LabChip GX (Perkin Elmer, Waltham, MA). Correctly digesting colonies were sequence confirmed provided to plant transformation.

Universal Donor Construct Assembly

To support rapid testing of a large number of target loci, a novel, flexible universal donor system sequence was designed and constructed. The universal donor polynucleotide sequence was compatible with high throughput vector construction methodologies and analysis. The universal donor system was composed of at least three modular domains: a variable ZFN binding domain, a non-variable analytical and user defined features domain, and a simple plasmid backbone for vector scale up. The non-variable universal donor polynucleotide sequence was common to all donors and permits design of a finite set of assays that can be used

across all of the *Zea mays* target sites thus providing uniformity in targeting assessment and reducing analytical cycle times. The modular nature of these domains allowed for high throughput donor assembly. Additionally, the universal donor polynucleotide sequence has other unique features aimed at simplifying downstream analysis and enhancing the interpretation of results. It contains asymmetric restriction site sequence that allows the digestion of PCR products into diagnostically predicted sizes. Sequences comprising secondary structures that were expected to be problematic in PCR amplification were removed. The universal donor polynucleotide sequence is small in size (less than 3.0 Kb). Finally, the universal donor polynucleotide sequence was built upon the high copy pUC19 backbone that allows a large amount of test DNA to be bulked in a timely fashion.

As an embodiment, an example plasmid comprising a universal donor polynucleotide sequence is provided as SEQ ID NO:5418 and Figure 7. In an additional embodiment, a universal donor polynucleotide sequence is provided as: pDAB11846, SEQ ID NO:5419, Figure 15; pDAB117415, SEQ ID NO:5420, Figure 16; pDAB117416, SEQ ID NO:5421, Figure 17; pDAB117417, SEQ ID NO:5422, Figure 18; pDAB117419, SEQ ID NO:5423, Figure 19; pDAB117434, SEQ ID NO:5424, Figure 20; pDAB117418, SEQ ID NO:5425, Figure 21; pDAB117420, SEQ ID NO:5426, Figure 22; and, pDAB117421, SEQ ID NO:5427, Figure 23. In another embodiment, additional sequences comprising the universal donor polynucleotide sequence with functionally expressing coding sequence or nonfunctional (promoterless) expressing coding sequences can be constructed.

In another embodiment, the universal donor polynucleotide sequence is a small 2-3 Kb modular donor system delivered as a plasmid. This is a minimal donor, comprising any number of ZFN binding sites, a short 100-150 bp template region referred to as "DNA X" or "UZI Sequence" (SEQ ID NO:5428) that carries restriction sites and DNA sequences for primer design or coding sequences, and a simple plasmid backbone (Figure 8). The entire plasmid was inserted through NHEJ following DNA double strand breaks at the appropriate ZFN binding site; the ZFN binding sites can be incorporated tandemly. This embodiment of a universal donor polynucleotide sequence was most suitable for rapid screening of target sites and ZFNs, and sequences that were difficult to amplify are minimized in the donor.

In a further embodiment the universal donor polynucleotide sequence was made up of at least 4 modules and carries ZFN binding sites, homology arms, DNA X with either just the approximately 100 bp analytical piece or coding sequences. This embodiment of the universal donor polynucleotide sequence was suitable for interrogating HDR mediated gene insertion at a variety of target sites, with several ZFNs (Figure 9).

The universal donor polynucleotide sequence can be used with all targeting molecules with defined DNA binding domains, with two modes of targeted donor insertion (NHEJ/HDR). As such, when the universal donor polynucleotide sequence was co-delivered with the appropriate ZFN expression construct, the donor vector and the maize genome was cut in one specific location dictated by the binding of the particular ZFN. Once linearized, the donor can be incorporated into the genome by NHEJ or HDR. The different analytical considerations in the vector design can then be exploited to determine the Zinc Finger which maximizes the efficient delivery of targeted integration. (Figure 10).

Example 4: *Zea mays* Transformation Procedures

Before delivery to *Zea mays* c.v. Hi-II protoplasts, plasmid DNA for each ZFN construct was prepared from cultures of *E. coli* using the PURE YIELD PLASMID MAXIPREP SYSTEM® (Promega Corporation, Madison, WI) or PLASMID MAXI KIT® (Qiagen, Valencia, CA) following the instructions of the suppliers.

Protoplast Isolation

Zea mays c.v. Hi-II suspension cells were maintained at a 3.5 day maintenance schedule, 4 mL packed cell volume (PCV) of cells were collected and transferred to 50 mL sterile conical tubes (Fisher Scientific) containing 20 mL of enzyme solution (0.6% PECTOLYASE™, 6% CELLULASE™ (“Onozuka” R10; Yakult Pharmaceuticals, Japan), 4 mM MES (pH 5.7), 0.6 M mannitol, 15 mM MgCl₂). The cultures were capped and wrapped in PARAFILM™ and placed on a platform rocker (Thermo Scientific, Vari Mix platform Rocker) at speed setting 10 for incubation for 16-18 hours at room temperature until protoplasts were released. Following incubation, a drop of cells was checked under microscope to check the quality of digestion and digested cells were filtered through 100 µm cell strainer, rinsed with 10 mL W5 media [2mM MES (pH5.7), 205 mM NaCl, 167 mM CaCl₂, 6.7mM KCl], followed by filtering through 70 µm and 40 µm cell strainers. The 100 µm and 40 µm strainer was rinsed with 10 mL W5 media. The filtered protoplasts along with rinsed media were collected in 50 mL centrifuge tube and final volume was approximately 40 mL. 8 mL of “Heavy Gradient solution” [500 mM sucrose, 1 mM CaCl₂, 5 mM MES (pH6.0)] was then slowly added to the bottom of the protoplast/enzyme solution, centrifuged in a centrifuge with a swing arm bucket rotor for 15 minutes at 300-350 x g. Following centrifugation, about 7-8 mL of protoplast band was removed, washed with 25 mL of W5, and centrifuged for 15 minutes at 180-200 x g. The protoplasts were then resuspended in 10 mLs of MMG solution [4 mM MES (pH 5.7), 0.6 M

mannitol, 15 mM MgCl₂]. Protoplasts were counted using a haemocytometer or flow cytometer and diluted to 1.67 million per mL using MMG.

Transformation of *Zea mays* c.v. HI-II Suspension Culture Derived Protoplasts Using PEG

Approximately 0.5 million protoplasts (300 µl in MMG solution) were transferred to 2 mL tubes, and mixed with 40 µl of DNA and incubated at room temperature for 5-10 minutes. Next, 300 µl of freshly prepared PEG solution [36% PEG 4000, 0.3 M mannitol, 0.4M CaCl₂] was added, and the mixture was incubate at room temperature 15-20 minutes with periodic mixing by inversion. After incubation, 1 ml of W5 wash was added slowly and mixed gently and protoplasts were pelleted by centrifugation at 180-200 x g for 15 minutes. The pellet was resuspended in 1 mL of WI media [4 mM MES (pH 5.7), 0.6 M mannitol, 20 mM KCl] and protoplast containing tube wrapped with aluminum foil and incubated in room temperature overnight for about 16 hours.

Transformation of ZFN and Donor

For each of the selected genomic loci of Table 5, the *Zea mays* protoplasts were transfected with a *yfp* gene expressing control, ZFN alone, donor alone and a mixture of ZFN and donor at 1:10 ratio (by weight). The total amount of DNA for transfection of 0.5 million protoplasts was 80 µg. All treatments were conducted in replicates of either 3 or 6. The *yfp* gene expressing control used was pDAB8393 (Figure 11) containing the *Zea mays* Ubiquitin 1 promoter – yellow fluorescent protein coding sequence – *Zea mays* Per5 3'UTR and the Rice Actin1 promoter – *pat* coding sequence – *Zea mays* lipase 3'UTR gene expression cassettes. To provide a consistent amount of total DNA per transfection, either salmon sperm or a plasmid containing the *yfp* gene was used as filler where necessary. In a typical targeting experiment, 4 µg of ZFN alone or with 36 µg of donor were transfected and appropriate amount of salmon sperm or pUC19 plasmid DNA was added to bring the overall amount of DNA to 80 µg. Inclusion of *yfp* gene expressing plasmid as filler allows assessment of transfection quality across multiple loci and replicate treatments.

Example 5: Cleavage of Genomic Loci in *Zea mays* via Zinc Finger Nuclease

ZFN transfected *Zea mays* c.v. Hi-II protoplasts were harvested 24 hours post-transfection, by centrifugation at 1600 rpm in 2 ml EPPENDORF™ tubes and the supernatant was completely removed. Genomic DNA was extracted from protoplast pellets using the QIAGEN PLANT DNA EXTRACTION KIT™ (Qiagen, Valencia, CA). The isolated DNA was resuspended in 50 µL of water and concentration was determined by NANODROP®

(Invitrogen, Grand Island, NY). The integrity of the DNA was estimated by running samples on 0.8% agarose gel electrophoresis. All samples were normalized (20-25 ng/ μ L) for PCR amplification to generate amplicons for sequencing (Illumina, Inc., San Diego, CA). Bar-coded PCR primers for amplifying regions encompassing each test ZFN recognition sequence from treated and control samples were designed and purchased from IDT (Coralville, IA, HPLC purified). Optimum amplification conditions were identified by gradient PCR using 0.2 μ M appropriate bar-coded primers, ACCUPRIME PFX SUPERMIX™ (Invitrogen, Carlsbad, CA) and 100 ng of template genomic DNA in a 23.5 μ L reaction. Cycling parameters were initial denaturation at 95°C (5 min) followed by 35 cycles of denaturation (95°C, 15 sec), annealing (55-72°C, 30 sec), extension (68°C, 1 min) and a final extension (68°C, 7 min). Amplification products were analyzed on 3.5% TAE agarose gels and appropriate annealing temperature for each primer combination was determined and used to amplify amplicons from control and ZFN treated samples as described above. All amplicons were purified on 3.5% agarose gels, eluted in water and concentrations were determined by NANODROP™. For Next Generation Sequencing, approximately 100 ng of PCR amplicon from the ZFN treated and corresponding maize protoplast controls were pooled together and sequenced using Illumina Next Generation Sequencing (NGS).

The cleavage activity of appropriate ZFNs at each *Zea mays* selected genomic loci were assayed. Short amplicons encompassing the ZFN cleavage sites were amplified from the genomic DNA and subjected to Illumina NGS from ZFN treated and control protoplasts. The ZFN induced cleavage or DNA double strand break was resolved by the cellular NHEJ repair pathway by insertion or deletion of nucleotides (indels) at the cleavage site and presence of indels at the cleavage site is thus a measure of ZFN activity and is determined by NGS. Cleavage activity of the target specific ZFNs was estimated as the number of sequences with indels per 1 million high quality sequences using NGS analysis software (Patent publication 2012-0173,153, data Analysis of DNA sequences) (Figure 12). Activities in the range of 5-100 fold over controls were observed for *Zea mays* selected genomic loci targets and were further confirmed by sequence alignments that showed a diverse footprint of indels at each ZFN cleavage site. This data suggests that the *Zea mays* selected genomic loci were amenable to cleavage by ZFNs. Differential activity at each target was reflective of its chromatin state and amenability to cleavage as well as the efficiency of expression of each ZFN.

Example 6: Rapid Targeting Analysis of the Integration of a Polynucleotide Donor

Validation of the targeting of the universal donor polynucleotide sequence within the *Zea mays* selected genomic loci targets via non-homologous end joining (NHEJ) mediated

donor insertion, was performed using a semi-throughput protoplast based Rapid Testing Analysis method. For each *Zea mays* selected genomic loci target, 3-6 ZFN designs were tested and targeting was assessed by measuring ZFN mediated cleavage by Next Generation Sequencing methods (Figure 12) and donor insertion by junctional in-out PCR (Figure 13). *Zea* 5 *mays* selected genomic loci that were positive in both assays were identified as a targetable locus.

ZFN Donor Insertion Rapid Testing Analysis

To determine if a *Zea mays* selected genomic loci target can be targeted for donor 10 insertion, a ZFN construct and universal donor polynucleotide construct were co-delivered to maize protoplasts which were incubated for 24 hours before the genomic DNA was extracted for analysis. If the expressed ZFN was able to cut the target binding site both at the *Zea mays* selected genomic loci target and in the donor, the linearized donor would then be inserted into the cleaved target site in the maize genome via the non-homologous end joining (NHEJ) 15 pathway. Confirmation of targeted integration at the *Zea mays* selected genomic loci target was completed based on an “In-Out” PCR strategy, where an “In” primer recognizes sequence at the native optimal genomic loci and an “Out” primer binds to sequence within the donor DNA. The primers were designed in a way that only when the donor DNA was inserted at the *Zea mays* selected genomic loci target, would the PCR assay produce an amplification product with the 20 expected size. The In-Out PCR assay was performed at both the 5’- and 3’-ends of the insertion junction. The primers used for the analysis of integrated polynucleotide donor sequences are provided in Table 9.

ZFN Donor insertion at Target Loci using nested “In-Out” PCR

25 All PCR amplifications were conducted using a TAKARA EX TAQ HS™ kit (Clontech, Mountain View, CA). The first In-Out PCR was carried out in 20 µL final reaction volume that contains 1X TAKARA EX TAQ HS™ buffer, 0.2 mM dNTPs, 0.2 µM “Out” primer (Table 9), 0.05 µM “In” primer (designed from the universal donor cassette described above), 0.75 unit of TAKARA EX TAQ HS™ polymerase, and 10 ng extracted maize 30 protoplast DNA. The reaction was then carried out using a PCR program that consisted of 94 °C for 2 min, 20 cycles of 98 °C for 12 sec and 68 °C for 2 min, followed by 72 °C for 10 min and held at 4 °C. Final PCR products were run on an agarose gel along with 1KB PLUS DNA LADDER™ (Life Technologies , Grand Island, NY) for visualization.

The nested In-Out PCR was conducted in 20 µL final reaction volume that contained 1X 35 TAKARA EX TAQ HS™ buffer, 0.2 mM dNTPs, 0.2 µM “Out” primer (Table 9), 0.1 µM

“In” primer (designed from the universal donor cassette described above, Table 10), 0.75 unit of TAKARA EX TAQ HS™ polymerase, and 1 µL of the first PCR product. The reaction was then carried out using a PCR program that consisted of 94 °C for 2 min, 31 cycles of 98 °C for 12 sec, 66 °C for 30 sec and 68 °C for 45 sec, followed by 72 °C for 10 min and held at 4 °C.

- 5 Final PCR products were run on an agarose gel along with 1KB PLUS DNA LADDER™ (Life Technologies, Grand Island, NY) for visualization.

Table 9. List of all “Out” primers for nested In-Out PCR analysis of optimal genomic loci.

OGL1	First PCR	5'-end	APL02-5PriF1	SEQ ID NO:5430 CGCCACAAATCTGAACCAGCA
			Spec-PriR1	SEQ ID NO:5431 CCACGATCGACATTGATCTGGCTA
		3'-end	APL02-3PriR1	SEQ ID NO:5432 GCGACATATCAGGCCAACAGG
			Uzi-PriF1	SEQ ID NO:5433 GGGATATGTGTCCTACCGTATCAGG
	Nest PCR	5'-end	APL02-5nstPriF1	SEQ ID NO:5434 CCAGCATAACAGTTAGGGCCCA
			Spec-nstPriR1	SEQ ID NO:5435 GTTGCCTTGGTAGGTCCAGC
		3'-end	APL02-3nstPriR1	SEQ ID NO:5436 CGAAAACTCAGCATGCGGGAA
			Uzi-nstPriF1	SEQ ID NO:5437 GAGCCATCAGTCCAACACTGC
OGL2	First PCR	5'-end	APL01-5PriF1	SEQ ID NO:5438 ACAGGCGTACAGCAACACCA
		3'-end	APL01-3PriR1	SEQ ID NO:5439 GACCCTATGGTGTGGATCCCA
	Nest PCR	5'-end	APL01-5nstPriF1	SEQ ID NO:5440 CGGGAGCTAGGCAACAAATCG
		3'-end	APL01-3nstPriR1	SEQ ID NO:5441 TCTGACTAAACGGGTGGATGCTG
OGL8	First PCR	5'-end	OGL08-5nstPriF2	SEQ ID NO:5442 CGGATCAGTTGATTCGCTCACTTTCA
		3'-end	OGL08-3PriR	SEQ ID NO:5443 GCCGAAAAGCAGCAACTGGAA
	Nest PCR	5'-end	OGL08-5nstPriF	SEQ ID NO:6619 GATTGCTACGCAGACCGCCTA
		3'-end	OGL08-3nstPriR	SEQ ID NO:5444 CACTATTCCTCCGGCATGCAG

OGL11	First PCR	5'-end	OGL11-5PriF	SEQ ID NO:5445 TGACCTATTGATCGGTCGGCTC
		3'-end	OGL11-3PriR2	SEQ ID NO:5446 TGCCTTGAATCTCAGGGATGCA
	Nest PCR	5'-end	OGL11-5nstPriF	SEQ ID NO:5447 GCCGAAGCTAACTAGCGGACA
		3'-end	OGL11-3nstPriR2	SEQ ID NO:5448 CATGGAGTAGCAGCTGTGCTG
OGL12	First PCR	5'-end	OGL12-5PriF	SEQ ID NO:5449 GAAAAGCAGTCACCGGCTCTG
		3'-end	OGL12-3PriR	SEQ ID NO:5450 CCATGGACATGAATTCGGCACG
	Nest PCR	5'-end	OGL12-5nstPriF	SEQ ID NO:5451 CTTTTCACCCACGGAGCAGAC
		3'-end	OGL12-3nstPriR	SEQ ID NO:5452 GCTAGCAAACTTTGAAGCTCGCTC
OGL13	First PCR	5'-end	OGL13-5PriF	SEQ ID NO:5453 GAGGTCCCTTACGGGTCATCG
		3'-end	OGL13-3PriR	SEQ ID NO:5454 ACCAGGTCTATCTTGCGCAGAC
	Nest PCR	5'-end	OGL13-5nstPriF	SEQ ID NO:5455 AATAGCGTGGTCGGGTCCTAG
		3'-end	OGL13-3nstPriR	SEQ ID NO:5456 ACGAACGATCCAAGGTGCAGT
OGL14	First PCR	5'-end	OGL14-5PriF	SEQ ID NO:5457 TAGAGACGAGGACTCTGGGCT
		3'-end	OGL14-3PriR	SEQ ID NO:5458 AAGTCCAACATGGGCACAACC
	Nest PCR	5'-end	OGL14-5nstPriF	SEQ ID NO:5459 CCTCGTTAAGGGTGCAGGTTG
		3'-end	OGL14-3nstPriR	SEQ ID NO:5460 CCAAGTCAGCTTCTAAGCCATCAAAC
OGL15	First PCR	5'-end	OGL15-5PriF	SEQ ID NO:5461 AACCCTAGACTTCTGCCTGGTG
		3'-end	OGL15-3PriR	SEQ ID NO:5462 GCTCACTTACGAGCAGATCCCA
	Nest PCR	5'-end	OGL15-5nstPriF	SEQ ID NO:5463 GGTGCACGCATGTTCTCATGT
		3'-end	OGL15-3nstPriR	SEQ ID NO:5464 TGTTTACCGCAGCCATGCTTG
OGL16	First PCR	5'-end	OGL16-5PriF	SEQ ID NO:5465 GTTGTATACGGCATCCATCCGCT
		3'-end	OGL16-3PriR	SEQ ID NO:5466 GAATGAACTGGTGGTCTGCTCC
	Nest PCR	5'-end	OGL16-5nstPriF	SEQ ID NO:5467 CCGACGAGGTACAAGTAGCAGG
		3'-end	OGL16-3nstPriR	SEQ ID NO:5468 CCCGTAGTCCAGATTCTTGTTGGT

OGL17	First PCR	5'-end	OGL17-5PriF	SEQ ID NO:5469 GTCGTTTGTTCGGAAGGGGAG
		3'-end	OGL17-3PriR	SEQ ID NO:5470 CGTAGTTGTCCGGCATGTCCT
	Nest PCR	5'-end	OGL17-5nstPriF	SEQ ID NO:5471 TGTATCCCTTCGGTGAGCACG
		3'-end	OGL17-3nstPriR	SEQ ID NO:5472 TGAATCGACTCGCTGACAGGTG
OGL04	First PCR	5'-end	OGL04-5PriF	SEQ ID NO: 6311 CAACCAGAAACGTCCTGCACTG
			Spec-PriR1	SEQ ID NO: 6312 CCACGATCGACATTGATCTGGCTA
		3'-end	OGL04-3PriR	SEQ ID NO: 6313 AAATCCAAGCCACGTACGCAC
			UnivDonor-3PriF1	SEQ ID NO: 6314 GTTTCATCAAGCCTTACGGTCACC
	Nest PCR	5'-end	OGL04-5nstPriF	SEQ ID NO: 6315 ACACCAATTGCCCATTGCGCA
			Spec-nstPriR2	SEQ ID NO: 6316 GCTGGCGATGAGCGAAATGTAG
		3'-end	OGL04-3nstPriR	SEQ ID NO: 6317 TTGGTTAGCAGCACGGATGGA
			UnivDonor-3PriF2	SEQ ID NO: 6318 CAGCAACGTCGGTTCGAGATG
OGL05	First PCR	5'-end	OGL05-1-5PriF	SEQ ID NO: 6319 ATGCCACTTTCGAAGAGAGGACG
		3'-end	OGL05-1-3PriR2	SEQ ID NO: 6320 CATCTCCAACGTCATCGGCAC
	Nest PCR	5'-end	OGL05-1-5nstPriF	SEQ ID NO: 6321 GGGAAACAGATTTCGTCAGCTTGC
		3'-end	OGL05-1-3nstPriR	SEQ ID NO: 6322 GCCTATCCAGTGGCGGATACA
OGL06	First PCR	5'-end	OGL06-5PriF	SEQ ID NO: 6323 CTTGCTCTACAACTCTGCCCCA
			Spec-PriR1	SEQ ID NO: 6324 CCACGATCGACATTGATCTGGCTA
		3'-end	OGL06-3PriR	SEQ ID NO: 6325 AGTCGGTACCTGCAAGCTACG
			UnivDonor-3PriF1	SEQ ID NO: 6326 GTTTCATCAAGCCTTACGGTCACC
	Nest PCR	5'-end	OGL06-5nstPriF	SEQ ID NO: 6327 TGGATTTGAGGCCAACTGCAC
			Spec-nstPriR2	SEQ ID NO: 6328 GCTGGCGATGAGCGAAATGTAG
		3'-end	OGL06-3nstPriR	SEQ ID NO: 6329 TCTGCATTGTTGGGATCGACCA
			UnivDonor-3PriF2	SEQ ID NO: 6330 CAGCAACGTCGGTTCGAGATG

OGL07	First PCR	5'-end	OGL07-1-5nstPriF	SEQ ID NO: 6331 ACGATCGCAGGTTATCCTCGC
		3'-end	OGL07-1-3PriR	SEQ ID NO: 6332 CTTGTCTGGTTGCTGTGTGGAC
	Nest PCR	5'-end	OGL07-1-5nstPriF	SEQ ID NO: 6333 AACACGGATGGCCTGCAATG
		3'-end	OGL07-1-3nstPriR	SEQ ID NO: 6334 GCATGGGCGTACGTCACTTG
OGL09	First PCR	5'-end	OGL09-5PriF	SEQ ID NO: 6335 ACCCAGAATCTCTGGTTCCGT
		3'-end	OGL09-3PriR	SEQ ID NO: 6336 CAGGAAGCTCTGCATCTGCG
	Nest PCR	5'-end	OGL09-5nstPriF	SEQ ID NO: 6337 AGTCTTTGATGTAAACGTCTTGCCCT
		3'-end	OGL09-3nstPriR	SEQ ID NO: 6338 GCATGGAAACACCAGGTCTGA
OGL10	First PCR	5'-end	OGL10-5PriF	SEQ ID NO: 6339 GCAGCGAATAGGAATGCGAGAC
		3'-end	OGL10-3PriR	SEQ ID NO: 6340 TAACCTTGTTTCGCTGACTCCC
	Nest PCR	5'-end	OGL10-5nstPriF	SEQ ID NO: 6341 CTTCTTCTACCTACACGCACCAG
		3'-end	OGL10-3nstPriR	SEQ ID NO: 6342 GATCCGTTTCCTCACTCTCGC
OGL18	First PCR	5'-end	OGL18-5PriF	SEQ ID NO: 6343 AGGTGAATCTTCCGTGGCTGT
		3'-end	OGL18-3PriR	SEQ ID NO: 6344 CCATAATCAGTGTGACTGGTGGCT
	Nest PCR	5'-end	OGL18-5nstPriF	SEQ ID NO: 6345 CGGATCTAAGGTGCCCTGTCT
		3'-end	OGL18-3nstPriR	SEQ ID NO: 6346 GTCTAGCTCATGGAAGTGGGAGG
OGL19	First PCR	5'-end	OGL19-5PriF	SEQ ID NO: 6347 GACTTCTAAGCCCCAAGGCCTA
		3'-end	OGL19-3PriR2	SEQ ID NO: 6348 AGATCTTTTGGCTCCCTCTCACC
	Nest PCR	5'-end	OGL19-5nstPriF	SEQ ID NO: 6349 GTGCTTCGAGGGCTCAAGGTA
		3'-end	OGL19-3nstPriR2	SEQ ID NO: 6350 ATTGCTCACCCCATCCCCTT
OGL20	First PCR	5'-end	OGL20-5PriF	SEQ ID NO: 6351 GGCTATGACCCGGACACTACC
		3'-end	OGL20-3PriR	SEQ ID NO: 6352 CAGTTGGGCGTCAAGTTAGTTCAG
	Nest PCR	5'-end	OGL20-5nstPriF	SEQ ID NO: 6353 AAGTCCACAAGGATCTGACCACG
		3'-end	OGL20-3nstPriR	SEQ ID NO: 6354 TGAAACTTTGGTTCAGTCTGCTCG

OGL21	First PCR	5'-end	OGL21-5PriF	SEQ ID NO: 6355 TATGTCCAAGCCACGAGAAGC
		3'-end	OGL21-3PriR	SEQ ID NO: 6356 ACTGCAGGTACTACTGGTACGC
	Nest PCR	5'-end	OGL21-5nstPriF	SEQ ID NO: 6357 GCTACAGTATAGCAGGAGCAGC
		3'-end	OGL21-3nstPriR	SEQ ID NO: 6358 GTCCTACTATACGCTGCCGC
OGL22	First PCR	5'-end	OGL22-5PriF	SEQ ID NO: 6359 CAATCCTTCTGAGCTGCACCG
		3'-end	OGL22-3PriR	SEQ ID NO: 6360 GGTGTCAATGACCTCACGAGC
	Nest PCR	5'-end	OGL22-5nstPriF	SEQ ID NO: 6361 CCGTACCAAACAGGCAAGCAG
		3'-end	OGL22-3nstPriR	SEQ ID NO: 6362 GATCGCCCATATGCTTGGATTAC
OGL23	First PCR	5'-end	OGL23-5PriF	SEQ ID NO: 6363 GGATTAGGACGGCTGACTGGT
		3'-end	OGL23-3PriR	SEQ ID NO: 6364 GTTGCTTTGTTTGC GTGCTCC
	Nest PCR	5'-end	OGL23-5nstPriF	SEQ ID NO: 6365 TTAAAGTGCTAGCTGACTGACCGA
		3'-end	OGL23-3nstPriR	SEQ ID NO: 6366 GGCCCATGCCTTAGGTTGAC
OGL24	First PCR	5'-end	OGL24-5PriF	SEQ ID NO: 6367 ACTGAGACTGGGAGTCTGGGA
		3'-end	OGL24-3PriR	SEQ ID NO: 6368 CGCCGTCCGACTGTTATTACC
	Nest PCR	5'-end	OGL24-5nstPriF	SEQ ID NO: 6369 CTTCGGCCTTGGATTGGATCAC
		3'-end	OGL24-3nstPriR	SEQ ID NO: 6370 ACAACGCAGATCCCTAGAATCCA
OGL25	First PCR	5'-end	OGL25-5PriF	SEQ ID NO: 6371 GGGATCTCTTGTACCAAATCAGC
		3'-end	OGL25-3PriR	SEQ ID NO: 6372 TTGACAGTGAGACATGGGAGTACC
	Nest PCR	5'-end	OGL25-5nstPriF	SEQ ID NO: 6373 TGCCTGCATTGCATCGATCTG
		3'-end	OGL25-3nstPriR	SEQ ID NO: 6374 AGTACCCACTGTCACTGCACG
OGL26	First PCR	5'-end	OGL26-5PriF	SEQ ID NO: 6375 ATCTTCACCAAGTATCCCACACCT
		3'-end	OGL26-3PriR2	SEQ ID NO: 6376 GCTGTGTAGTATCGTCGAAGGCT
	Nest PCR	5'-end	OGL26-5nstPriF	SEQ ID NO: 6377 TCAAACCTCACCTGATGTATCGCT
		3'-end	OGL26-3nstPriR2	SEQ ID NO: 6378 CGAACCTCCAATTTATCGGCAATCG

OGL27	First PCR	5'-end	OGL27-5PriF	SEQ ID NO: 6379 AAGTCCCTAGAGCCCTCATGC
		3'-end	OGL27-3PriR	SEQ ID NO: 6380 GAGAGTTAGGAGGGAGCATGGC
	Nest PCR	5'-end	OGL27-5nstPriF	SEQ ID NO: 6381 GTGTCCGAGATAGGTCGTGTCC
		3'-end	OGL27-3nstPriR	SEQ ID NO: 6382 TTGAACTTGGGCATGAGTGGGA
OGL28	First PCR	5'-end	OGL28-5PriF	SEQ ID NO: 6383 GTCGGCTGTGCGTTATGAGAC
		3'-end	OGL28-3PriR	SEQ ID NO: 6384 GATTAATCGGTTATCGGTGGACGC
	Nest PCR	5'-end	OGL28-5nstPriF	SEQ ID NO: 6385 ACGGACAGATCACAGATCGGG
		3'-end	OGL28-3nstPriR	SEQ ID NO: 6386 CCTTAATCCGGTTTGGTGAACCC
OGL29	First PCR	5'-end	OGL29-5PriF	SEQ ID NO: 6387 GCTTACACCGATGCAGGGGTA
		3'-end	OGL29-3PriR	SEQ ID NO: 6388 GGTTGACATCGGAATTCGTGCC
	Nest PCR	5'-end	OGL29-5nstPriF	SEQ ID NO: 6389 TGAAAGAGAGCGGCCCAACTAC
		3'-end	OGL29-3nstPriR	SEQ ID NO: 6390 TTAATGCTGGCCTCTCCTGCA
OGL30	First PCR	5'-end	OGL30-5PriF	SEQ ID NO: 6391 ATGAAGAGCACCAGCTACCCC
		3'-end	OGL30-3PriR	SEQ ID NO: 6392 GGAAGATGGAACCACATGCCC
	Nest PCR	5'-end	OGL30-5nstPriF	SEQ ID NO: 6393 GGCTACAAAACCCAAGAGGGG
		3'-end	OGL30-3nstPriR	SEQ ID NO: 6394 CCCTTTCATGCAACGATCAGGC
OGL31	First PCR	5'-end	OGL31-5PriF	SEQ ID NO: 6395 TGTTCAAGTTGGTAAGTCGTCGCT
		3'-end	OGL31-3PriR	SEQ ID NO: 6396 GTTCTTGAGAGTGATTGTCGGC
	Nest PCR	5'-end	OGL31-5nstPriF	SEQ ID NO: 6397 CTTCACCTCAAGGGAAGCAAGC
		3'-end	OGL31-3nstPriR	SEQ ID NO: 6398 GGTGAACTGAGCTGGAATTGG
OGL32	First PCR	5'-end	OGL32-5PriF	SEQ ID NO: 6399 GATCCACAACCACATTCAACAAGGT
		3'-end	OGL32-3PriR	SEQ ID NO: 6400 TGATCAAAGTAGAGGCCTGATGACG
	Nest PCR	5'-end	OGL32-5nstPriF	SEQ ID NO: 6401 GGACAAATGACATGTAACCCACTCC
		3'-end	OGL32-3nstPriR	SEQ ID NO: 6402 ATGACGACAGCGTGTTTGTGG

OGL33	First PCR	5'-end	OGL33-5PriF	SEQ ID NO: 6403 AGCTCCACTTCCAGTAGTCCTG
		3'-end	OGL33-3PriR	SEQ ID NO: 6404 CGGATAGCGTCCACAAACGAG
	Nest PCR	5'-end	OGL33-5nstPriF	SEQ ID NO: 6405 AATCATGCGGCTGTCGAAAGG
		3'-end	OGL33-3nstPriR	SEQ ID NO: 6406 GCGATAAGAAAGCATCCTGCGG
OGL34	First PCR	5'-end	OGL34-5PriF	SEQ ID NO: 6407 ACTGTACCACCGAAAGACGACC
		3'-end	OGL34-3PriR	SEQ ID NO: 6408 CCCGTCTCACTGTGGATCTATGTC
	Nest PCR	5'-end	OGL34-5nstPriF	SEQ ID NO: 6409 AAAGACGACCAAACAGTCCTGC
		3'-end	OGL34-3nstPriR	SEQ ID NO: 6410 GAGTCAACGTGTCAGTGTCCACC
OGL35	First PCR	5'-end	OGL35-5PriF	SEQ ID NO: 6411 AGGTGTAGTCCTGCTCTGTCTG
		3'-end	OGL35-3PriR	SEQ ID NO: 6412 AACTGAAGACACTGACGACATCCA
	Nest PCR	5'-end	OGL35-5nstPriF	SEQ ID NO: 6413 TAGGGCGCTAGGCATGTACTC
		3'-end	OGL35-3nstPriR	SEQ ID NO: 6414 GTGGCCTTCTAGGTACACTAGGG
OGL36	First PCR	5'-end	OGL36-5PriF	SEQ ID NO: 6415 GCAACCAACTTTGTCGGATGCT
		3'-end	OGL36-3PriR	SEQ ID NO: 6416 AAAGCTCACCTCACAGCACGA
	Nest PCR	5'-end	OGL36-5nstPriF	SEQ ID NO: 6417 TCATAGATTTTCGCGTGGTTGAACTG
		3'-end	OGL36-3nstPriR	SEQ ID NO: 6418 ACTCTGCAGCCATGAATTCCAC
OGL37	First PCR	5'-end	OGL37-5PriF	SEQ ID NO: 6419 GAGAAACCGAGGGATCGGAACA
		3'-end	OGL37-3PriR	SEQ ID NO: 6420 ACATGTACGTGTGCGAGAGTCG
	Nest PCR	5'-end	OGL37-5nstPriF	SEQ ID NO: 6421 AGTACGACTGGAATCCAACGCG
		3'-end	OGL37-3nstPriR	SEQ ID NO: 6422 CTCTCCCTAGCTCGACGCTTG
OGL38	First PCR	5'-end	OGL38-5PriF	SEQ ID NO: 6423 GTAGCACTGCACCGTTCATGC
		3'-end	OGL38-3PriR	SEQ ID NO: 6424 ACTCTCCTTCCCTCGACGGTA
	Nest PCR	5'-end	OGL38-5nstPriF	SEQ ID NO: 6425 AGGAGATGAAGGCTTTGTCCCC
		3'-end	OGL38-3nstPriR	SEQ ID NO: 6426 GCAAACCTGCATGGTTGATGC

OGL39	First PCR	5'-end	OGL39-5PriF	SEQ ID NO: 6427 TTGGGTTTGTGCACCACACTC
		3'-end	OGL39-3PriR	SEQ ID NO: 6428 GCTTCTGGAAAAACGCCAGCA
	Nest PCR	5'-end	OGL39-5nstPriF	SEQ ID NO: 6429 ATTCCTTGCCTCCGTACGAA
		3'-end	OGL39-3nstPriR	SEQ ID NO: 6430 CTTTGCATTGCAGGCACGGTTA
OGL40	First PCR	5'-end	OGL40-5PriF	SEQ ID NO: 6431 CCGAGGTAAATCCACAGGCG
		3'-end	OGL40-3PriR	SEQ ID NO: 6432 GCGCATTTCTTGCCCTCAAA
	Nest PCR	5'-end	OGL40-5nstPriF	SEQ ID NO: 6433 GTTACAGGTACGACAGCAGC
		3'-end	OGL40-3nstPriR	SEQ ID NO: 6434 TACGTTGCCACCAAAAGAGCC
OGL41	First PCR	5'-end	OGL41-5PriF	SEQ ID NO: 6435 AGCAGGCTACTGTGGTCAGG
		3'-end	OGL41-3PriR	SEQ ID NO: 6436 CGATTGCATACAGCAGGTGCC
	Nest PCR	5'-end	OGL41-5nstPriF	SEQ ID NO: 6437 GGCAGGTTTTGAAGGACCCC
		3'-end	OGL41-3nstPriR	SEQ ID NO: 6438 ACGAGCAATGCAGTGAAGGGT
OGL42	First PCR	5'-end	OGL42-5PriF	SEQ ID NO: 6439 TGAGAACGAAACCCGTCAAGCA
		3'-end	OGL42-3PriR	SEQ ID NO: 6440 CACGTCGATCAAACGGCGAG
	Nest PCR	5'-end	OGL42-5nstPriF	SEQ ID NO: 6441 CGTCAAGCATGCAGAAAGGCT
		3'-end	OGL42-3nstPriR	SEQ ID NO: 6442 CCCCTAATCCGCACCGTGTA
OGL43	First PCR	5'-end	OGL43-5PriF	SEQ ID NO: 6443 CCTGTTCTTCTCCCGAATGC
		3'-end	OGL43-3PriR	SEQ ID NO: 6444 GGTACAAAGTGAAAAGGGCCGG
	Nest PCR	5'-end	OGL43-5nstPriF	SEQ ID NO: 6445 GTGCAATCAAGCCTTGCCCAT
		3'-end	OGL43-3nstPriR	SEQ ID NO: 6446 GAAGTGATGGTCCCTGCCAC
OGL44	First PCR	5'-end	OGL44-5PriF	SEQ ID NO: 6447 GGCTCTAACACATGGTGAGGC
		3'-end	OGL44-3PriR	SEQ ID NO: 6448 AATCATGGTCCTAGTTGTAGCCCC
	Nest PCR	5'-end	OGL44-5nstPriF	SEQ ID NO: 6449 ACTAGGATGAGGGAGCCAATGG
		3'-end	OGL44-3nstPriR	SEQ ID NO: 6450 CTATGGAGATGCCTCCCACCAT

OGL45	First PCR	5'-end	OGL45-5PriF	SEQ ID NO: 6451 GAAGAGCTCGGCATCGGAGAT
		3'-end	OGL45-3PriR	SEQ ID NO: 6452 TCCCAAAACGAACTGTGTGCG
	Nest PCR	5'-end	OGL45-5nstPriF	SEQ ID NO: 6453 TGGCTAGAGCGACCTTGTTTCG
		3'-end	OGL45-3nstPriR	SEQ ID NO: 6454 TCGAGATCAGGCATCCACACC
OGL46	First PCR	5'-end	OGL46-5PriF	SEQ ID NO: 6455 CCAAAGTATTTGGTGGGATTCTCGC
		3'-end	OGL46-3PriR	SEQ ID NO: 6456 CTGCAACAAGTGAAAAGCGCC
	Nest PCR	5'-end	OGL46-5nstPriF	SEQ ID NO: 6457 GGATTCTCGCTTTTTCCCACCAAG
		3'-end	OGL46-3nstPriR	SEQ ID NO: 6458 TACATCGATCCAGCTCGTGCTG
OGL47	First PCR	5'-end	OGL47-5PriF	SEQ ID NO: 6459 CGGAACACTAAAACGGGGACATG
			Spec-PriR1	SEQ ID NO: 6460 CCACGATCGACATTGATCTGGCTA
		3'-end	OGL47-3PriR	SEQ ID NO: 6461 TCTTCCTGGCAAGCACTAGGAAC
			UnivDonor-3PriF1	SEQ ID NO: 6462 GTTTCATCAAGCCTTACGGTCACC
	Nest PCR	5'-end	OGL47-5nstPriF	SEQ ID NO: 6463 ACCGAGTAAGGGCTTGTTTCGG
			Spec-nstPriR2	SEQ ID NO: 6464 GCTGGCGATGAGCGAAATGTAG
		3'-end	OGL47-3nstPriR	SEQ ID NO: 6465 TCTCCAGCAACCCCTAGATGC
			UnivDonor-3PriF2	SEQ ID NO: 6466 CAGCAACGTCGGTTCGAGATG
OGL48	First PCR	5'-end	OGL48-5PriF	SEQ ID NO: 6467 GCAGTGACACTATAGCCACGTGT
		3'-end	OGL48-3PriR	SEQ ID NO: 6468 GCCCAATCAATTGTCCCTGGAC
	Nest PCR	5'-end	OGL48-5nstPriF	SEQ ID NO: 6469 TGCTACCCAATGGTGTGGACTT
		3'-end	OGL48-3nstPriR	SEQ ID NO: 6470 AATGCCCATTTCGGTTGAACCC
OGL49	First PCR	5'-end	OGL49-5PriF	SEQ ID NO: 6471 TCTGATGATCGGGTTGAGGCC
		3'-end	OGL49-3PriR	SEQ ID NO: 6472 CCTCCGGAATCATTTCCTGTTG
	Nest PCR	5'-end	OGL49-5nstPriF	SEQ ID NO: 6473 GTGCTGATCTGGTTGTGGGTC
		3'-end	OGL49-3nstPriR	SEQ ID NO: 6474 CGGAACAATTCTGGGCACAA

OGL50	First PCR	5'-end	OGL50-5PriF	SEQ ID NO: 6475 AGCTATGGTTAACGGGAATGCCA
			Spec-PriR1	SEQ ID NO: 6476 CCACGATCGACATTGATCTGGCTA
		3'-end	OGL50-3PriR	SEQ ID NO: 6477 TCTAGCGAGAGGTGGTCAGGT
			UnivDonor-3PriF1	SEQ ID NO: 6478 GTTTCATCAAGCCTTACGGTCACC
	Nest PCR	5'-end	OGL50-5nstPriF	SEQ ID NO: 6479 GCTGAAATTGCTGCATCATGGC
			Spec-nstPriR1	SEQ ID NO: 6480 GTTGCCTTGGTAGGTCCAGC
		3'-end	OGL50-3nstPriR	SEQ ID NO: 6481 AGCTGCTACATCTGTGGTCGG
			UnivDonor-3PriF2	SEQ ID NO: 6482 CAGCAACGTCGGTTCGAGATG
OGL51	First PCR	5'-end	OGL51-5PriF	SEQ ID NO: 6483 CCTTCACAGTACTTGAACGTGCTGCA
		3'-end	OGL51-3PriR	SEQ ID NO: 6484 CACTCACATGGTGCGTTCCG
	Nest PCR	5'-end	OGL51-5nstPriF	SEQ ID NO: 6485 TGTATGCCTCGTCATCGAGGG
		3'-end	OGL51-3nstPriR	SEQ ID NO: 6486 AGGGGAATGACCAGGAGCAG
OGL52	First PCR	5'-end	OGL52-5PriF	SEQ ID NO: 6487 TCACGTACTGACCACAGAACACC
		3'-end	OGL52-3PriR	SEQ ID NO: 6488 GAATATGCTCCACGCGCATCTC
	Nest PCR	5'-end	OGL52-5nstPriF	SEQ ID NO: 6489 GCTGACTCTAAAACCGCCTTGTG
		3'-end	OGL52-3nstPriR	SEQ ID NO: 6490 GATCCGGCTTGTTCGCTTGAC
OGL53	First PCR	5'-end	OGL53-5PriF	SEQ ID NO: 6491 AACCATAGTGGCTCGCCAGT
		3'-end	OGL53-3PriR	SEQ ID NO: 6492 AATCGCACTAGGTCAGCATGGT
	Nest PCR	5'-end	OGL53-5nstPriF	SEQ ID NO: 6493 GATCATGTCTAGCCTCCAACCA
		3'-end	OGL53-3nstPriR	SEQ ID NO: 6494 GTGAAGACTCGAGCTTGGCCT
OGL54	First PCR	5'-end	OGL54-5PriF2	SEQ ID NO: 6495 CAACAAGCTGGTTTGCAGGGT
		3'-end	OGL54-3PriR	SEQ ID NO: 6496 TAACCCCTTAGAGATGCACATGC
	Nest PCR	5'-end	OGL54-5nstPriF2	SEQ ID NO: 6497 ACCCAGCAAATTGGACGATCT
		3'-end	OGL54-3nstPriR	SEQ ID NO: 6498 TAGATCGATGAAACCGGTCGATGTG

OGL55	First PCR	5'-end	OGL55-5PriF	SEQ ID NO: 6499 GACCAACCATTGTTGCCCT
		3'-end	OGL55-3PriR	SEQ ID NO: 6500 CACGTCTTTGTAGCGACTGTCCA
	Nest PCR	5'-end	OGL55-5nstPriF	SEQ ID NO: 6501 TCCGAAAACTCAAGCATGCCC
		3'-end	OGL55-3nstPriR	SEQ ID NO: 6502 GTGGTGAACCTCCCTCTAGACCC
OGL56	First PCR	5'-end	OGL56-5PriF2	SEQ ID NO: 6503 TGGAAAAACGTAGATGTGCTTGCC
		3'-end	OGL56-3PriR2	SEQ ID NO: 6504 CAAGCTCTTTGATCGTGGTTGACG
	Nest PCR	5'-end	OGL56-5nstPriF2	SEQ ID NO: 6505 GCAGTAAACCTAGTGATGCTGCCT
		3'-end	OGL56-3nstPriR2	SEQ ID NO: 6506 ATGCTTGGTCAACGTGCCAC
OGL57	First PCR	5'-end	OGL57-5PriF2	SEQ ID NO: 6507 CGGTGAATGCAAGCTGGATCAC
		3'-end	OGL57-3PriR2	SEQ ID NO: 6508 GCACTTGTGCTATCCGCCAG
	Nest PCR	5'-end	OGL57-5nstPriF2	SEQ ID NO: 6509 CTTTGGTGGCGGAGATCAGG
		3'-end	OGL57-3nstPriR2	SEQ ID NO: 6510 TGGAGGAGGAAATCTCTGCTATTCGT
OGL58	First PCR	5'-end	OGL58-5PriF	SEQ ID NO: 6511 ACAGTGGACTCCCTCGCAAG
		3'-end	OGL58-3PriR2	SEQ ID NO: 6512 GTAAGCTTCCTCGACACCTCCA
	Nest PCR	5'-end	OGL58-5nstPriF	SEQ ID NO: 6513 TCTGAAGCACAGTTTAGCCGCA
		3'-end	OGL58-3nstPriR2	SEQ ID NO: 6514 GTGGTTATCTGTAGCTTGAGCACTGA
OGL59	First PCR	5'-end	OGL59-5PriF2	SEQ ID NO: 6515 TGTGTTTCCTTCTCCATGCACCT
		3'-end	OGL59-3PriR2	SEQ ID NO: 6516 CCTTGTCACGGAGACTCTCGG
	Nest PCR	5'-end	OGL59-5nstPriF2	SEQ ID NO: 6517 TCACATGCCTCAACTGGAGCA
		3'-end	OGL59-3nstPriR2	SEQ ID NO: 6518 TGGAAGGGCAAACTGAGCC
OGL60	First PCR	5'-end	OGL60-5PriF	SEQ ID NO: 6519 GCGACCTTTTCATTGTTGGAGTAGG
		3'-end	OGL60-3PriR	SEQ ID NO: 6520 TACCACACCATCGAGCCGTC
	Nest PCR	5'-end	OGL60-5nstPriF	SEQ ID NO: 6521 ACGATTCAGTAGGTAGGGTGCCT
		3'-end	OGL60-3nstPriR	SEQ ID NO: 6522 ACCCATTTTCGAGCTGCCTGT

OGL61	First PCR	5'-end	OGL61-5PriF	SEQ ID NO: 6523 CCATGCAGATGTCTGAGGCAAC
		3'-end	OGL61-3PriR	SEQ ID NO: 6524 TACTGCCTTCTGAACCGTCGG
	Nest PCR	5'-end	OGL61-5nstPriF	SEQ ID NO: 6525 TGTTTAGCTACATCCACGGGCAT
		3'-end	OGL61-3nstPriR	SEQ ID NO: 6526 ACTGCAATGACAAGGCACATCC
OGL62	First PCR	5'-end	OGL62-5PriF	SEQ ID NO: 6527 GCACGTCGTTAGTGATCGAGCT
		3'-end	OGL62-3PriR	SEQ ID NO: 6528 GTTGTCAACGAAGCCCGTCTAATTG
	Nest PCR	5'-end	OGL62-5nstPriF	SEQ ID NO: 6529 CCTGCAGTTAACGCAGACGTG
		3'-end	OGL62-3nstPriR	SEQ ID NO: 6530 CTAGACCGTACTATTGTGCTGTGAAG
OGL63	First PCR	5'-end	OGL63-5PriF	SEQ ID NO: 6531 TCCTTACTGGCCCCTAGTCCA
		3'-end	OGL63-3PriR	SEQ ID NO: 6532 CTCCCACGAGCGACTAGCTAC
	Nest PCR	5'-end	OGL63-5nstPriF	SEQ ID NO: 6533 TGCAACTATGGACTTGGCCACA
		3'-end	OGL63-3nstPriR	SEQ ID NO: 6534 CCTCACGAATAAAAGCACCCCC
OGL64	First PCR	5'-end	OGL64-5PriF	SEQ ID NO: 6535 AGTCTACGTGGCATAACAACCC
		3'-end	OGL64-3PriR	SEQ ID NO: 6536 GAAACTTGGACCTTGCTGTCTGG
	Nest PCR	5'-end	OGL64-5nstPriF	SEQ ID NO: 6537 AGGTCTCGAACAACCTCCCTATGC
		3'-end	OGL64-3nstPriR	SEQ ID NO: 6538 CCATTCCATGAAGACCGACTCCA
OGL65	First PCR	5'-end	OGL65-5PriF	SEQ ID NO: 6539 ACCAAATCCGTTTGCTTTACCG
		3'-end	OGL65-3PriR	SEQ ID NO: 6540 CTCTGACAGATACCACGTTCGCT
	Nest PCR	5'-end	OGL65-5nstPriF	SEQ ID NO: 6541 CACCGTTTCACGAAGCTGCA
		3'-end	OGL65-3nstPriR	SEQ ID NO: 6542 ACCGAAATCTGCGCGCTAGTT
OGL66	First PCR	5'-end	OGL66-5PriF	SEQ ID NO: 6543 ACAGAAGAGGTTGCGGAGTAACG
		3'-end	OGL66-3PriR	SEQ ID NO: 6544 AAACAAAATCGTATCGCCGAGCAG
	Nest PCR	5'-end	OGL66-5nstPriF	SEQ ID NO: 6545 TACTTGACCGGCCTCTACCT
		3'-end	OGL66-3nstPriR	SEQ ID NO: 6546 AACCTTGCAACAGCCCCAAAT

OGL67	First PCR	5'-end	OGL67-5PriF	SEQ ID NO: 6547 AGGTAATACCACTGAGCCGAC
			Spec-PriR1	SEQ ID NO: 6548 CCACGATCGACATTGATCTGGCTA
		3'-end	OGL67-3PriR	SEQ ID NO: 6549 CACTCTGTACTGGGAGAGGG
			UnivDonor-3PriF1	SEQ ID NO: 6550 GTTTCATCAAGCCTTACGGTCACC
	Nest PCR	5'-end	OGL67-5nstPriF	SEQ ID NO: 6551 ATAATGCAGCGCTTGCAGAT
			Spec-nstPriR2	SEQ ID NO: 6552 GCTGGCGATGAGCGAAATGTAG
		3'-end	OGL67-3nstPriR	SEQ ID NO: 6553 CTCAATTCCATGTGCAACCAAAC
			UnivDonor-3PriF2	SEQ ID NO: 6554 CAGCAACGTCGGTTCGAGATG
OGL68	First PCR	5'-end	OGL68-5PriF	SEQ ID NO: 6555 GTGGTGATACCGTCGTCTCTCC
		3'-end	OGL68-3PriR	SEQ ID NO: 6556 CACTTTGTCCCTGCTCGGTTC
	Nest PCR	5'-end	OGL68-5nstPriF	SEQ ID NO: 6557 GAAACAAGCCATTGATTGTGCCCA
		3'-end	OGL68-3nstPriR	SEQ ID NO: 6558 GTCGACTCACAACGCTTCCC
OGL69	First PCR	5'-end	OGL69-5PriF	SEQ ID NO: 6559 AGTACAACACTGAGACGTGGGC
		3'-end	OGL69-3PriR	SEQ ID NO: 6560 ACTAGGATTGCTAGGGAGCACGAA
	Nest PCR	5'-end	OGL69-5nstPriF	SEQ ID NO: 6561 AGATTGCAGGGCACTTGAGGT
		3'-end	OGL69-3nstPriR	SEQ ID NO: 6562 ACAGGATTACAAGCCCAAACCCA
OGL70	First PCR	5'-end	OGL70-5PriF	SEQ ID NO: 6563 TTCTTCAGGCGGCATCGCATA
			Spec-PriR1	SEQ ID NO: 6564 CCACGATCGACATTGATCTGGCTA
		3'-end	OGL70-3PriR	SEQ ID NO: 6565 TAGTAGCCGACAATGTGGCCC
			UnivDonor-3PriF1	SEQ ID NO: 6566 GTTTCATCAAGCCTTACGGTCACC
	Nest PCR	5'-end	OGL70-5nstPriF	SEQ ID NO: 6567 CGCTCAGGAAATCCTTGATGCC
			Spec-nstPriR2	SEQ ID NO: 6568 GCTGGCGATGAGCGAAATGTAG
		3'-end	OGL70-3nstPriR	SEQ ID NO: 6569 GTGAACGACGGCAACAAGCT
			UnivDonor-3PriF2	SEQ ID NO: 6570 CAGCAACGTCGGTTCGAGATG

OGL71	First PCR	5'-end	OGL71-5PriF	SEQ ID NO: 6571 GAGGTCCCTTACGGGTCATCG
		3'-end	OGL71-3PriR	SEQ ID NO: 6572 ACCAGGTCTATCTTGCGCAGAC
	Nest PCR	5'-end	OGL71-5nstPriF	SEQ ID NO: 6573 AATAGCGTGGTCGGGTCCTAG
		3'-end	OGL71-3nstPriR	SEQ ID NO: 6574 ACGAACGATCCAAGGTGCAGT
OGL72	First PCR	5'-end	OGL72-5PriF	SEQ ID NO: 6575 CCAATGGACGACAGCGGTTAG
		3'-end	OGL72-3PriR	SEQ ID NO: 6576 ACGAGAACAAGCCACTCTTGCT
	Nest PCR	5'-end	OGL72-5nstPriF	SEQ ID NO: 6577 CAACCGGAGAACGGATAGCCT
		3'-end	OGL72-3nstPriR	SEQ ID NO: 6578 TGAAGATTTCCCTACCGTCGCC
OGL73	First PCR	5'-end	OGL73-5PriF1	SEQ ID NO: 6579 AGTACTGGGGACGTTACCCG
		3'-end	OGL73-3PriR1	SEQ ID NO: 6580 CGACAAGAACCCGGTACATGC
	Nest PCR	5'-end	OGL73-5PriF2	SEQ ID NO: 6581 AGAGCTGAAACTGATCGCGGT
		3'-end	OGL73-3PriR2	SEQ ID NO: 6582 GACAGAGTCCGATCCCTGCT
OGL74	First PCR	5'-end	OGL74-5PriF	SEQ ID NO: 6583 GCCACACGGATTTTGCGTATCA
		3'-end	OGL74-3PriR	SEQ ID NO: 6584 CTTTTGTCGGTCCTGCCACTG
	Nest PCR	5'-end	OGL74-5nstPriF	SEQ ID NO: 6585 AGCAACGTAGGGTCACGGAC
		3'-end	OGL74-3nstPriR	SEQ ID NO: 6586 GAGGAGTCTTCGATGCCACGA
OGL75	First PCR	5'-end	OGL75-5PriF	SEQ ID NO: 6587 GAAAGCACCAGGTCGTATCTTGC
		3'-end	OGL75-3PriR	SEQ ID NO: 6588 CGCACAATCTTCGCTTCAAACCA
	Nest PCR	5'-end	OGL75-5nstPriF	SEQ ID NO: 6589 GCATTGCTCTTCAGGAGGTACGT
		3'-end	OGL75-3nstPriR	SEQ ID NO: 6590 CAGCTGTGCAAGTCCGACTG
OGL76	First PCR	5'-end	OGL76-5PriF	SEQ ID NO: 6591 TCTCCATACCTGCACTGGGTG
		3'-end	OGL76-3PriR	SEQ ID NO: 6592 ACGTGCTCTCAGCAACATCCA
	Nest PCR	5'-end	OGL76-5nstPriF	SEQ ID NO: 6593 CGTCCAAACAGGCTAGACAGC
		3'-end	OGL76-3nstPriR	SEQ ID NO: 6594 TGCCTTTTGCGTCAACGGTG

OGL77	First PCR	5'-end	OGL77-5PriF	SEQ ID NO: 6595 CCATCCAGATCGCGGTTGTC
		3'-end	OGL77-3PriR	SEQ ID NO: 6596 TACGAGTTCACGCCATTGCGT
	Nest PCR	5'-end	OGL77-5nstPriF	SEQ ID NO: 6597 GTCTCCTCTTTGACGGTTGCG
		3'-end	OGL77-3nstPriR	SEQ ID NO: 6598 TCGATCCACACTCGCATGCA
OGL78	First PCR	5'-end	OGL78-5PriF	SEQ ID NO: 6599 GTGGACCAGTGTAAGCCCCG
		3'-end	OGL78-3PriR	SEQ ID NO: 6600 TCCCTAGTGCCAGGACCTGA
	Nest PCR	5'-end	OGL78-5nstPriF	SEQ ID NO: 6601 ACACCAAATGTCCGGTAGCGA
		3'-end	OGL78-3nstPriR	SEQ ID NO: 6602 CGACGATTCTCCATTGGCCG
OGL79	First PCR	5'-end	OGL79-5PriF	SEQ ID NO: 6603 GCTAGAAACGCTGAACAGCAGC
		3'-end	OGL79-3PriR	SEQ ID NO: 6604 CGGGTTTAGAATCCACAAGCCG
	Nest PCR	5'-end	OGL79-5nstPriF	SEQ ID NO: 6605 GACAAAAGCTGCCATCAACGCT
		3'-end	OGL79-3nstPriR	SEQ ID NO: 6606 CCCGATATGGACAGGTCAGCT
OGL80	First PCR	5'-end	OGL80-5PriF	SEQ ID NO: 6607 AAAGGCGACACACACCTTTGC
		3'-end	OGL80-3PriR	SEQ ID NO: 6608 AGACAGCCATCCTCACTCGC
	Nest PCR	5'-end	OGL80-5nstPriF	SEQ ID NO: 6609 TTTGGTGCAGAGGCCGAGAA
		3'-end	OGL80-3nstPriR	SEQ ID NO: 6610 AAGTAGCCAGGCAGACAACCA
OGL81	First PCR	5'-end	OGL81-5PriF	SEQ ID NO: 6611 CTAGGCAGGGTGGCATGAAAG
			Spec-PriR1	SEQ ID NO: 6612 CCACGATCGACATTGATCTGGCTA
		3'-end	OGL81-3PriR	SEQ ID NO: 6613 ACCATCAGAGGTTGTGAAGGCA
			UnivDonor-3PriF	SEQ ID NO: 6614 CAAATCCCCACTAAGCGCTCGG
	Nest PCR	5'-end	OGL81-5nstPriF	SEQ ID NO: 6615 AAGGGCAACTTCATGGTTCAACC
			Spec-nstPriR1	SEQ ID NO: 6616 GTTGCCTTGGTAGGTCCAGC
		3'-end	OGL81-3nstPriR	SEQ ID NO: 6617 ACCAGTAAATCCACAACCCATGGT
			UnivDonor-3nstPriF	SEQ ID NO: 6618 GTAAAGGTGAGCAGAGGCACG

OGL03	First PCR	5'-end	OGL03-5PriF	SEQ ID NO: 6691 TATATGGTGGCCAATGGACGATGG
		3'-end	OGL03-3PriR	SEQ ID NO: 6692 CCACAGGAGCAAGCAGTGAC
	Nest PCR	5'-end	OGL03-5nstPriF	SEQ ID NO: 6693 CGCATCTTTGGGGGTAGTGG
		3'-end	OGL03-3nstPriR	SEQ ID NO: 6694 AGTACCCAGTTGGTCTCGCC

Table 10. List of all “In” primers for nested In-Out PCR analysis of optimal genomic loci.

All Reactions	First PCR	5'-end	Spec-PriR1	SEQ ID NO:5473 CCACGATCGACATTGATCTGGCTA
		3'-end	Uzi-PriF1	SEQ ID NO:5474 GGGATATGTGTCCTACCGTATCAGG
	Nest PCR	5'-end	Spec-nstPriR1	SEQ ID NO:5475 GTTGCCTTGGTAGGTCCAGC
		3'-end	Uzi-nstPriF1	SEQ ID NO:5476 GAGCCATCAGTCCAACACTGC

Table 11. Primers for ZFN cleavage activity.

OGL 1	Control/ZFN 111879	SEQ ID NO:5477 TGGCACTAATCTCACC GGCT
		SEQ ID NO:5478 AGTCTTAGAAGTACGCTACCGT
OGL 2	Control/ZFN 111885	SEQ ID NO:5479 TACTTGGCTTCGGCGGCGA
		SEQ ID NO:5480 GGGTGACTTTTACGCGTCTCG
OGL 11	Control/ZFN 117402	SEQ ID NO:5481 GGTCACGACGCATGGCCTAA
		SEQ ID NO:5482 AGGATGCATGGATCACC GTC
OGL 12	Control/ZFN 117404	SEQ ID NO:5483 GCTCTGTTGTGCAGCCGTAC
		SEQ ID NO:5484 CGTTGCAGATACCACAGTGTAC
OGL 13	Control/ZFN 117429	SEQ ID NO:5485 GCTAGTAGCTGTTTACACGGCGTCT
		SEQ ID NO:5486 AGGTCGAGACAACCAAGTAGAG
OGL 14	Control/ZFN 117406	SEQ ID NO:5487 ACAGGACATCGAGCTTGCAT
		SEQ ID NO:5488 CAGAAGAAAGGCATCAACTCATG

OGL 15	Control/ZFN 117408	SEQ ID NO:5489 CTCTTTCACCTCTACTTTTACTTCAG
		SEQ ID NO:5490 ATTGAACCGTTGTCAAAGCCA
OGL 16	Control/ZFN 117411	SEQ ID NO:5491 CACAGCGTCAGGGCGGTAAC
		SEQ ID NO:5492 GGCACGCACCTGTCACTGAC
OGL 17	Control/ZFN 117413	SEQ ID NO:5493 GTACGCGCCCGGGAACCTCCT
		SEQ ID NO:5494 CCTGCGGCCACGTGCATCT

Deployment of the In-Out PCR assay in a protoplast targeting system was particularly challenging as large amounts of the plasmid DNA was used for transfection, and the large amount of DNA remains in the protoplast targeting system and was subsequently extracted along with cellular genomic DNA. The residual plasmid DNA may dilute the relative concentration of the genomic DNA and reduce the overall sensitivity of detection and can also be a significant cause of non-specific, aberrant PCR reactions. ZFN induced NHEJ-based donor insertion typically occurs in either a forward or a reverse orientation. In-Out PCR analysis of DNA for the forward orientation insertion often exhibited false positive bands, possibly due to shared regions of homology around the ZFN binding site in the target and donor that could result in priming and extension of unintegrated donor DNA during the amplification process. False positives were not seen in analyses that probed for reverse orientation insertion products and therefore all targeted donor integration analysis was carried out to interrogate reverse donor insertion in the RTA. In order to further increase specificity and reduce background, a nested PCR strategy was also employed. The nested PCR strategy used a second PCR amplification reaction that amplified a shorter region within the first amplification product of the first PCR reaction. Use of asymmetric amounts of “in” and “out” primers optimized the junctional PCR further for rapid targeting analysis at selected genomic loci.

The In-Out PCR analysis results were visualized on an agarose gel. For all *Zea mays* selected genomic loci of Table 12, “ZFN + donor treatments” produced a near expected sized band at the 5’ and 3’ ends. Control ZFN or donor alone treatments were negative in the PCR suggesting that the method was specifically scoring for donor integration at the target site of at least 72 of the optimal nongenic maize genomic loci. All treatments were conducted in replicates of 3-6 and presence of the anticipated PCR product in multiple replicates (≥ 2 at both ends) was used to confirm targeting. Donor insertion through NHEJ often produces lower intensity side products that were generated due to processing of linearized ends at the target

and/or donor ZFN sites. In addition, it was observed that different ZFNs resulted in different levels of efficiency for targeted integration, with some of the ZFNs producing consistently high levels of donor integration, some ZFNs producing less consistent levels of donor integration, and other ZFNs resulting in no integration. Overall, for each of the *Zea mays* selected genomic loci targets that were tested, targeted integration was demonstrated within the *Zea mays* representative genomic loci targets by one or more ZFNs, which confirms that each of these loci were targetable. Furthermore, each of the *Zea mays* selected genomic loci targets was suitable for precision gene transformation. The validation of these *Zea mays* selected genomic loci targets was repeated multiple times with similar results every time, thus confirming the reproducibility of the validation process which includes plasmid design and construct, protoplast transformation, sample processing, and sample analysis.

Conclusion

The donor plasmid and one ZFN designed to specifically cleave a *Zea mays* selected genomic loci targets were transfected into *Zea mays* c.v. Hi-II protoplasts and cells were harvested 24 hours later. Analysis of the genomic DNA isolated from control, ZFN treated and ZFN with donor treated protoplasts by in-out junctional PCR showed targeted insertion of the universal donor polynucleotide as a result of genomic DNA cleavage by the ZFNs (Table 12). These studies show that the universal donor polynucleotide system can be used to assess targeting at endogenous sites and for screening candidate ZFNs. Finally, the protoplast based Rapid Targeting Analysis and the novel universal donor polynucleotide sequence systems provide a rapid avenue for screening genomic targets and ZFNs for precision genome engineering efforts in plants. The methods can be extended to assess site specific cleavage and donor insertion at genomic targets in any system of interest using any nuclease that introduces DNA double or single strand breaks.

Table 12. Illustrates the results of the integration of a universal donor polynucleotide sequence within the *Zea mays* selected genomic loci targets. As indicated by the * below, donor insertion within OGL73 was only confirmed by a PCR reaction of the 5' junction sequence.

Name	ID	Location	Cluster Assignment	ZFN (pDAB#)	Donor (pDAB#)	Targetable Locus (Y/N)
OGL01	optimal_loci_204637_G1	chr5:200298202..200301414	16	111879	111845	Y
OGL02	optimal_loci_204726_G1	chr5:200665730..200670667	03	111885	111846	Y
OGL0	optimal_loci_*	chr1:19493939	23	117400	117415	Y

8	31710	6..194943360				
OGL1 1	optimal_loci_ 64542	chr2:72203716 ..72205045	14	117402	117416	Y
OGL1 2	optimal_loci_ 156393	chr4:15431388 4..154315253	10	117404	117417	Y
OGL1 5	preffered_loci_ 198387	chr5:16471237 8..164713567	25	117408	117419	Y
OGL1 3	optimal_loci_ 157315	chr4:15871070 9..158711983	30	117429	117434	Y
OGL1 4	optimal_loci_ 197372	chr5:15868060 1..158681681	26	117406	117418	Y
OGL1 6	optimal_loci_ 232228	chr6:14471956 7..144723469	28	117411	117420	Y
OGL1 7	optimal_loci_ 285621	chr8:11832135 7..118322528	06	117413	117421	Y
OGL0 4	optimal_loci_ 43577	chr1:25646970 4..256472666	20	124802	124812	Y
OGL0 5	optimal_loci_ 301774	chr9:23468085 ..23470278	15	121900	121926	Y
OGL0 6	optimal_loci_ 232222	chr6:14470057 5..144702126	20	124810	124813	Y
OGL0 7	optimal_loci_ 203704	chr5:19483627 0..194840217	12	121902	121930	Y
OGL0 9	optimal_loci_ 59517	chr2:43352132 ..43353146	1	118643	118697	Y
OGL1 0	optimal_loci_ 25001	chr1:15137122 4..151372260	1	118648	118686	Y
OGL1 8	optimal_loci_ 112632	chr3:12809885 6..128100257	2	123802	123810	Y
OGL1 9	optimal_loci_ 28905	chr1:17703771 8..177038919	2	123805	123809	Y
OGL2 0	optimal_loci_ 129164	chr3:22124602 7..221247542	3	121992	123808	Y
OGL2 1	optimal_loci_ 2425	chr1:12810845 ..12814490	3	118650	118697	Y
OGL2 2	optimal_loci_ 122036	chr3:18460816 6..184609697	4	118654	118688	Y
OGL2 3	optimal_loci_ 5735	chr1:29190279 ..29192844	4	118656	118689	Y
OGL2 4	optimal_loci_ 178978	chr5:35776311 ..35777560	5	118659	118690	Y
OGL2 5	optimal_loci_ 288388	chr8:13329044 2..133291481	5	118660	118697	Y
OGL2 6	optimal_loci_ 60310	chr2:47967092 ..47968271	5	118767	118787	Y
OGL2 7	optimal_loci_ 243330	chr7:34630402 ..34631577	6	118769	118787	Y

OGL2 8	optimal_loci_ 127038	chr3:21060361 1..210605198	7	118663	118697	Y
OGL2 9	optimal_loci_ 262784	chr7:15576704 6..155769049	7	118668	118691	Y
OGL3 0	optimal_loci_ 344662	chr10:1191316 67..119133955	7	118669	118692	Y
OGL3 1	optimal_loci_ 153894	chr4:13997959 7..139981225	8	118670	118693	Y
OGL3 2	optimal_loci_ 28771	chr1:17606213 9..176063611	8	118673	118694	Y
OGL3 3	optimal_loci_ 1098	chr1:5582601.. 5583834	9	118674	118695	Y
OGL3 4	optimal_loci_ 97772	chr3:30209253 ..30210607	9	118676	118696	Y
OGL3 5	optimal_loci_ 236662	chr6:16597571 6..165977010	10	118677	118697	Y
OGL3 6	optimal_loci_ 139485	chr4:42804231 ..42805751	11	118680	118697	Y
OGL3 7	optimal_loci_ 301175	chr9:20325171 ..20326621	11	118683	118764	Y
OGL3 8	optimal_loci_ 152337	chr4:13003309 2..130035481	12	118685	118765	Y
OGL3 9	optimal_loci_ 202616	chr5:18882290 1..188824814	12	123833	123809	Y
OGL4 0	optimal_loci_ 282323	chr8:10076320 4..100764398	13	118771	118787	Y
OGL4 1	optimal_loci_ 262782	chr7:15575908 0..155760097	13	121943	121983	Y
OGL4 2	optimal_loci_ 236455	chr6:16479599 1..164797027	14	121946	121984	Y
OGL4 3	optimal_loci_ 162531	chr4:18989698 4..189899332	15	121949	121985	Y
OGL4 4	optimal_loci_ 344663	chr10:1191431 67..119144795	15	121952	121986	Y
OGL4 5	optimal_loci_ 337001	chr10:7718831 9..77190007	16	121959	121987	Y
OGL4 6	optimal_loci_ 238100	chr7:4899227.. 4900708	16	121963	121988	Y
OGL4 8	optimal_loci_ 264359	chr7:16350424 1..163505487	17	121971	121990	Y
OGL4 9	optimal_loci_ 282653	chr8:10270476 5..102705924	18	121972	121991	Y
OGL5 0	optimal_loci_ 80282	chr2:17342083 4..173421870	18	124097	124295	Y
OGL5 1	optimal_loci_ 291068	chr8:14827760 6..148279985	19	123818	123831	Y
OGL5 2	optimal_loci_ 56395	chr2:24801482 ..24803132	19	118705	121201	Y
OGL5 4	optimal_loci_ 114664	chr3:14010695 0..140108061	21	118711	118792	Y
OGL5	optimal_loci_ chr2:7304197..		22	118718	118794	Y

7	53137	7305496				
OGL5 8	optimal_loci_ 344664	chr10:1191449 46..119146850	23	118722	121208	Y
OGL5 9	optimal_loci_ 81941	chr2:18141857 6..181421181	24	118726	121209	Y
OGL6 0	optimal_loci_ 321514	chr9:14077614 7..140777584	24	118728	121210	Y
OGL6 1	optimal_loci_ 301180	chr9:20328932 ..20330129	25	118732	121211	Y
OGL6 2	optimal_loci_ 348776	chr10:1420975 90..142098803	26	118733	121212	Y
OGL6 3	optimal_loci_ 244439	chr7:41068791 ..41070248	27	118735	118795	Y
OGL6 4	optimal_loci_ 348258	chr10:1392970 32..139298517	27	118739	121214	Y
OGL6 5	optimal_loci_ 322501	chr9:14607853 4..146080201	28	118742	121215	Y
OGL6 6	optimal_loci_ 244324	chr7:40299412 ..40300584	29	118745	121216	Y
OGL6 7	optimal_loci_ 97232	chr3:27463016 ..27464143	29	124081	124866	Y
OGL6 8	optimal_loci_ 282499	chr8:10177140 8..101772767	30	125361	125366	Y
OGL6 9	optimal_loci_ 155031	chr4:14699139 1..146993137	31	118753	121218	Y
OGL7 0	optimal_loci_ 301773	chr9:23465509 ..23467762	31	124878	123880	Y
OGL7 1	optimal_loci_ 283161	chr8:10532195 8..105323571	32	123829	123832	Y
OGL7 2	optimal_loci_ 55524	chr2:20099003 ..20100485	32	118761	121221	Y
OGL 73	optimal_loci_ 127268	chr3:21176789 8..211770046	16	124086	124298	Y*
OGL7 4	optimal_loci_ 137693	chr4:31118968 ..31122359	3	121904	121927	Y
OGL7 5	optimal_loci_ 265551	chr7:17012718 8..170130734	3	121905	121927	Y
OGL7 6	optimal_loci_ 128078	chr3:21548259 4..215485640	4	121917	121927	Y
OGL7 7	optimal_loci_ 168286	chr4:21998722 3..219990695	4	121918	121928	Y
OGL7 8	optimal_loci_ 3733	chr1:19232372 ..19235997	11	121909	121930	Y
OGL7 9	optimal_loci_ 203075	chr5:19137080 2..191374627	12	121912	121929	Y
OGL8 0	optimal_loci_ 232484	chr6:14612216 4..146125580	12	121981	121936	Y
OGL8 1	optimal_loci_ 136086	chr4:22531506 ..22534989	27	124091	124298	Y

Example 7: Expression of Polynucleotide Donor Sequence within the Genomic Loci of *Zea mays*

Randomly integrated maize transformation events were generated by transformation with the pDAB105817 and pEPS1027 plasmids containing the *aad-1* transgene, described in U.S. Patent No. 7,838,733. (Figure 14). Large numbers of events were produced and 1,027 stable events were analyzed to determine if any of the events contained a randomly integrated transgene within the *Zea mays* selected genomic loci targets via a genome flanking analysis method as described in U.S. Patent Application No. 2012/0258867. As such, the chromosomal location of the integrated transgene in 223 events was mapped within the *Zea mays* genome. The data, Table 13, indicated that the chromosomal location of the integrated transgenes demonstrated integration within hypomethylated regions (45-73%) and in transcriptional units (promoter/gene/3'UTR) downstream of at least 1 Kb areas (60%).

Table 13. Genomic and epigenomic context of the 1027 mapped events.

	No. events mapped with high confidence	No. events mapped with low confidence	No. of total number of events
Count	107	116	223
100 bp hypomethylated regions	102	61	163
2kb hypomethylated regions	68	27	95
Gene body	45	26	71
Upstream 2kb	32	11	43
Downstream 1kb	16	3	19
Repeat	9	62	71
Total genic/repeat	88	98	186

The mapped events were further analyzed using the optimal locus predictive criteria described in Examples 1 and 2 (hypomethylated regions, unique regions, nongenic, non-repeat, proximal to genes in a 40 Kb neighborhood, evidence of active expression in roots/shoots, evidence of recombination) and several randomly integrated events were identified within the *Zea mays* selected genomic loci targets (Table 14). For example, targeting within the *Zea mays* selected genomic loci targets optimal_loci_232222 and optimal_loci_127268 have been demonstrated using Rapid Testing Analysis and by *in planta* targeting, respectively.

The average length of the experimental *Zea mays* selected genomic loci targets were approximately 1 Kb and varying degrees of *aad-1* expression was observed at each of the *Zea mays* selected genomic loci targets (Table 14). The average *aad-1* expression analysis was

conducted at the T₁ plant transformation stage via a real-time PCR analysis of isolated transgenic leaf material. As such, random integration events within the *Zea mays* genome were capable of expressing a transgene within the experimental *Zea mays* selected genomic loci targets.

5

Table 14. Expression of the *aad-1* transgene in randomly integrated within the optimal genomic loci. The Location, Length and RNA expression for the *aad-1* marker gene at the locus are shown.

Event ID	Optimal Genomic Loci Name	SEQ ID NO:	Location	Length	AAD1 RNA Expression Avg T/R
G3_PL2863_1027-nstPri3	optimal_loci_43565	655	chr1:256293759..256295777	2018	22.687
H4_PL2783_1027-nstPri3	optimal_loci_164397	4552	chr4:199185401..199186813	1413	32.825
B6_PL2955_1027-nstPri3	optimal_loci_232222	3357	chr6:144700575..144702126	1553	3.1805
E7_PL3018_1027-nstPri3	optimal_loci_125749	19	chr3:204456962..204458140	1179	0.5185
E4_PL2955_1027-nstPri3	optimal_loci_7953	1777	chr1:41279823..41280909	1087	4.0805
A7_PL2746_1027-nstPri3	optimal_loci_205643	2037	chr5:205773760..205775465	1705	1.3761
F4_PL2978_1027-nstPri3	optimal_loci_201819	2726	chr5:184470152..184471958	1807	0.56075
B8_PL2955_1027-nstPri3	optimal_loci_42519	1929	chr1:250905847..250908881	3035	0.4591
B104/pDAB105817{1}015.001-1	optimal_loci_127268	2709	chr3:211,767,898..211,770,046	2149	1.54

10 Example 8: Optimal Nongenic Maize Genomic Loci for Transgene Integration

A suite of optimal nongenic maize genomic loci were identified from the 5,286 optimal nongenic maize genomic loci to select multiple loci for site specific targeting of gene expression cassettes and to generate stacks of gene expression cassettes. The following criteria were used to filter the pool of optimal nongenic maize genomic loci and select a suite of optimal nongenic maize genomic loci:

15

- 1) Greater than 3 Kb in length. The optimal nongenic maize genomic loci can be targeted with the integration of at least two sets of gene expression cassettes.
- 2) Recombination frequency of 0.5 to 1.0, which is less than the average recombination frequency of the identified 5,286 optimal nongenic maize genomic loci (average recombination frequency is about 2.0).
- 3) Greater than average expression of endogenous genes within 40 Kb of the identified 5,286 optimal nongenic maize genomic loci. Average expression of genes within a 40 Kb region in root and shoot tissues is greater than 6.30, which is the 48th percentile of all optimal nongenic maize genomic loci.
- 4) Sequence coverage and sequence identity of greater than 90% between *Zea mays* c.v. B104 and *Zea mays* c.v. Hi-II.

Each of the above described criteria were applied to select a suite of optimal nongenic maize genomic loci. Fig. 24 provides three illustrative diagrams of the criteria, and how the selected optimal nongenic maize genomic loci compared in relation to other loci. Nine optimal nongenic maize genomic loci (optimal_loci_137693_G1, optimal_loci_265551_G1, optimal_loci_128078_G1, optimal_loci_168286_G1, optimal_loci_3733_G1, optimal_loci_203075_G1, optimal_loci_232484_G1, optimal_loci_136086_G1, and optimal_loci_203704_G1) that were at least 3 Kb in length were identified using this criteria. See Table 15. Additional optimal nongenic maize genomic loci were identified by reducing the size limitation to ≥ 2 Kb (optimal_loci_291068_G1, and optimal_loci_43577_G1), these loci were added to the suite of optimal nongenic maize genomic loci. Another set of optimal nongenic maize genomic loci were added to the suite of optimal nongenic maize genomic loci as there was evidence of expression of a randomly integrated transgene via *Agrobacterium* transformation at these sites (optimal_loci_232222_G1 and optimal_loci_127268_G1). The optimal_loci_204637_G1 and optimal_loci_204726_G1 genomic loci were added to the suite for their meiotic recombination unit features. In addition, optimal_loci_204637_G1 and optimal_loci_204726_G1 have been successfully targeted for integration of a donor polynucleotide. Likewise, optimal_loci_232228 was included in the suite as this optimal nongenic maize genomic loci has been successfully targeted for integration of a donor polynucleotide, and the length of the sequence is 3.9 Kb.

Next, all of the optimal nongenic maize genomic loci were characterized for distance to proximal genes and distance from centromere (Fig 25). The suite of select optimal nongenic loci are about 1-15 Kb away from proximal genes and are located towards the end of chromosomes (distance >0.70 from centromeres) (Table 16, Fig 25). Finally, interference by

quantitative trait loci was probed to fully characterize the suite of optimal nongenic maize genomic loci.

Table 15. Suite of optimal nongenic maize genomic loci.

OGL_ID	Location	Length	SEQ ID NO:
optimal_loci_203704_G1	chr5:194836270..194840217	3948	2033
optimal_loci_291068_G1	chr8:148277606..148279985	2380	3230
optimal_loci_43577_G1	chr1:256469704..256472666	2963	3428
optimal_loci_232222_G1	chr6:144700575..144702126	1552	3357
optimal_loci_204637_G1	chr5:200298202..200301414	3213	2731
optimal_loci_204726_G1	chr5:200665730..200670667	4938	424
optimal_loci_232228_G1	chr6:144719567..144723469	3902	4529
optimal_loci_127268_G1	chr3:211767898..211770046	2149	2709
optimal_loci_136086_G1	chr4:22531506..22534989	3484	4425
optimal_loci_232484_G1	chr6:146122164..146125580	3417	2053
optimal_loci_203075_G1	chr5:191370802..191374627	3826	2030
optimal_loci_3733_G1	chr1:19232372..19235997	3626	1923
optimal_loci_168286_G1	chr4:219987223..219990695	3473	573
optimal_loci_128078_G1	chr3:215482594..215485640	3047	560
optimal_loci_265551_G1	chr7:170127188..170130734	3547	463
optimal_loci_137693_G1	chr4:31118968..31122359	3392	387

5

Table 16: Optimal nongenic maize genomic loci characteristics.

OGL ID	Distance to closest gene	Distance to centromere
optimal_loci_137693_G1	4070	.70444101
optimal_loci_265551_G1	9252	.94191056
optimal_loci_128078_G1	2491	.87326872
optimal_loci_168286_G1	1710	.84128147
optimal_loci_3733_G1	14910	.856875
optimal_loci_203075_G1	1001	.75612998
optimal_loci_232484_G1	1001	.80656755
optimal_loci_136086_G1	4381	.7859925

optimal_loci_203704_G1	2001	.788019
optimal_loci_127268_G1	2758	.84500724
optimal_loci_204637_G1	2874	.83827931
optimal_loci_291068_G1	4243	.77879798
optimal_loci_232222_G1	2832	.79463887
optimal_loci_43577_G1	2001	.73018748
optimal_loci_204726_G1	11370	.84166127

The optimal nongenic maize genomic loci that are selected using the above described criteria are validated by integrating a gene expression construct that contains selectable/reportable markers. This gene expression cassette is stably integrated into maize plants via genomic targeting using a site specific nuclease. The targeted optimal nongenic maize genomic loci that are produced and contain an expressable transgene are analyzed to identify single copy events that contain a full length integrated gene expression cassette. The expression profiles of the optimal nongenic maize genomic loci are analyzed via qRT-PCR, Western blot, ELISA, LC-MS MS, and other known RNA or protein detection methods over multiple plant generations (e.g., T₁ and T₂ generations). In addition, the effect of the transgene expression cassette integration within the optimal nongenic maize genomic loci on neighboring gene expression is assayed. Finally, the effect of the transgene expression cassette integration within the optimal nongenic maize genomic loci on agronomic properties of maize plants is assayed.

TABLE 3

OGL ID	Length of the OGL	Recombination	Level of OGL uniqueness	Distance from the	GC% in the OGL sequence	Number of	Average gene expression in a 40kb neighborhood around the OGL	Level of	Relative location within the chromosome (proximity to centromere)	Number of OGLs in a 1Mb region around the OGL
		frequency in a 1MB region around the OGL		OGL to the closest gene in its neighborhood		genes in a 40kb neighborhood around the OGL		Nucleosome occupancy around the OGL		
optimal_loci_141_G1	1151	1.762917	19.72	10615	39.53	3	0.994628114	0.247	0.995110469	4
optimal_loci_144_G1	1629	1.762917	0	12985	50.58	3	0.994628114	0.5	0.995059769	4
optimal_loci_168_G1	1078	1.61634	0	3093	47.3	4	20.09560715	0.514	0.992690193	4
optimal_loci_195_G1	1028	0.982617	22.37	1001	38.61	1	11.29280113	0.215	0.99229317	4
optimal_loci_444_G1	2593	0.544453	35.75	3651	35.48	1	1.556021429	0.134	0.982865573	2
optimal_loci_445_G1	1330	0.544453	10.6	1249	36.39	1	1.556021429	0.3	0.982847701	2
optimal_loci_535_G1	3121	1.93197	5.31	1001	49.05	3	11.12779061	0.481	0.978366615	5
optimal_loci_557_G1	1067	2.481339	0	15992	42.36	1	5.776709427	0.248	0.977298936	6
optimal_loci_625_G1	1014	3.355066	0	1001	38.46	3	5.876923554	0.293	0.975005915	6
optimal_loci_628_G1	1222	3.373899	0	3314	50.4	3	5.876923554	0.354	0.974898973	6
optimal_loci_638_G1	2038	3.27174	2.36	4972	49.31	2	1.383591852	0.41	0.974701719	6
optimal_loci_650_G1	2412	3.2379	0	7154	55.3	1	10.90270876	0.731	0.974398058	5
optimal_loci_827_G1	2368	2.89912	0	4237	50.8	2	0.077566736	0.607	0.966860052	11
optimal_loci_856_G1	1067	2.704681	0	2086	48.92	1	3.231810412	0.412	0.966178497	13
optimal_loci_857_G1	2350	3.352892	0	1001	37.7	1	3.231810412	0.062	0.966125952	13
optimal_loci_858_G1	1387	3.368528	0	3960	37.05	1	3.231810412	0.05	0.966111101	14
optimal_loci_861_G1	1387	3.33734	0	7121	43.47	1	3.231810412	0.469	0.966087582	14
optimal_loci_877_G1	3205	3.441965	3.65	1001	52.38	2	33.88506673	0.579	0.965772954	15
optimal_loci_897_G1	1158	4.28108	5.79	2359	39.03	3	1.600327134	0.213	0.964815848	16
optimal_loci_899_G1	1474	4.28108	34.26	4878	38.67	3	1.600327134	0.31	0.964794754	16
optimal_loci_908_G1	1103	4.28108	0	8527	44.42	5	3.743287562	0.278	0.96473151	16
optimal_loci_913_G1	1224	4.28108	2.37	4275	61.27	4	4.232624355	0.712	0.964699874	16
optimal_loci_919_G1	1318	4.108832	18.59	1001	49.92	5	21.47846729	0.363	0.964606317	16
optimal_loci_978_G1	1448	3.157154	0	2001	45.64	4	20.05751478	0.212	0.962951637	16
optimal_loci_984_G1	1106	3.157154	0	2403	63.65	7	8.932988157	0.709	0.962745454	16
optimal_loci_989_G1	3508	3.300461	0	6547	51.65	1	19.79392737	0.407	0.962365774	17
optimal_loci_994_G1	1212	3.565712	0	13086	34.24	1	19.79392737	0.222	0.962334204	15

optimal_loci_1024_G1	1050	3.347472	9.81	19468	41.71	1	2.961478685	0.505	0.96112401	17
optimal_loci_1044_G1	1107	3.158041	0	2007	53.38	4	17.64968313	0.419	0.96024474	12
optimal_loci_1075_G1	3104	2.67965	0	3955	40.14	3	26.94552083	0.344	0.958885841	10
optimal_loci_1077_G1	1705	2.67965	5.92	2001	37.3	3	26.94552083	0.108	0.958863557	10
optimal_loci_1079_G1	2033	2.67965	5.41	1489	50.46	3	26.94552083	0.459	0.95881003	10
optimal_loci_1098_G1	1234	2.780217	0	5231	55.42	1	182.626325	0.598	0.958453616	9
optimal_loci_1122_G1	2962	2.696832	0	3710	55.7	4	4.474779038	0.653	0.957965521	9
optimal_loci_1125_G1	1704	2.680075	0	1200	49.06	3	3.864097548	0.412	0.957927961	9
optimal_loci_1197_G1	2597	2.298471	1.27	4150	37.54	1	3.679516793	0.225	0.954839903	7
optimal_loci_1209_G1	1017	2.881375	0	2525	50.83	4	18.96083651	0.3	0.954027946	4
optimal_loci_1214_G1	1249	2.881375	23.22	6647	44.91	3	25.28111535	0.293	0.953965506	4
optimal_loci_1217_G1	2597	2.881375	37.66	1065	36.23	5	22.98794007	0.161	0.953747619	4
optimal_loci_1314_G1	1046	2.343475	11.09	2022	35.94	1	3.060076745	0.251	0.949548118	5
optimal_loci_1317_G1	1241	2.343475	2.74	11102	48.83	2	16.41305621	0.359	0.949420074	5
optimal_loci_1354_G1	1009	2.643982	36.27	1001	40.93	2	4.348145791	0.141	0.947555476	8
optimal_loci_1362_G1	1062	2.596837	23.54	2359	47.92	4	5.518672085	0.322	0.947371443	9
optimal_loci_1379_G1	1060	3.237749	30.09	4561	36.88	1	2.90843939	0.21	0.94591093	10
optimal_loci_1382_G1	1442	3.237749	4.3	1273	38.97	3	14.10824565	0.219	0.945642693	8
optimal_loci_1416_G1	1141	3.092295	0	19833	36.8	1	31.58293622	0.001	0.944723534	8
optimal_loci_1438_G1	1216	2.654868	4.28	2650	38.81	1	1.139784848	0.136	0.944236436	9
optimal_loci_1450_G1	1069	3.283236	0	2151	38.54	4	7.840503628	0.2	0.943760751	11
optimal_loci_1479_G1	2891	3.220867	7.96	4010	38.11	2	22.53145908	0.187	0.942632403	10
optimal_loci_1531_G1	1251	4.483067	0	1023	38.68	2	2.555363414	0.142	0.940787976	8
optimal_loci_1553_G1	1011	4.516747	0	10028	43.71	3	8.666855182	0.347	0.940327597	7
optimal_loci_1554_G1	1584	4.516747	0	8405	38.25	3	8.666855182	0.202	0.940315521	7
optimal_loci_1564_G1	1139	4.516747	0	1631	52.58	4	6.506181351	0.451	0.940210491	7
optimal_loci_1651_G1	1381	4.848085	7.17	2001	40.91	3	6.720707876	0.225	0.937086049	5
optimal_loci_1760_G1	1045	1.456051	0	1001	42.67	2	18.94302616	0.19	0.933249204	5
optimal_loci_1771_G1	1041	1.529016	0	1001	48.89	5	13.52108314	0.512	0.93262619	5
optimal_loci_1811_G1	1288	1.72731	2.72	3252	47.67	1	1.982319031	0.429	0.931385938	5
optimal_loci_1812_G1	1845	1.72731	6.18	4573	41.08	1	1.982319031	0.352	0.931371964	5
optimal_loci_1814_G1	1140	1.72731	0	10063	41.84	1	1.982319031	0.062	0.931336362	5
optimal_loci_1901_G1	1128	2.994309	30.94	2001	37.94	1	9.687699471	0.271	0.926265179	2

optimal_loci_1912_G1	1013	5.111349	0	10771	43.92	1	24.69651467	0.164	0.925429144	2
optimal_loci_1993_G1	1676	5.237859	8.65	7115	51.96	1	72.13759189	0.686	0.921616629	14
optimal_loci_2003_G1	1110	3.665929	0	1731	39.81	3	18.46241818	0.161	0.921264405	14
optimal_loci_2014_G1	1425	4.072832	0	6394	50.38	1	11.26133949	0.419	0.92062846	16
optimal_loci_2058_G1	1631	3.532103	36.73	2001	34.7	2	4.363429422	0.208	0.919506719	17
optimal_loci_2059_G1	1881	3.532103	6.17	1062	34.76	2	4.363429422	0.103	0.919461049	17
optimal_loci_2065_G1	1345	3.532103	8.03	6083	36.57	3	2.908952948	0.241	0.919356853	17
optimal_loci_2067_G1	2179	3.532103	39.7	1681	49.74	3	2.908952948	0.477	0.9193241	17
optimal_loci_2085_G1	1018	3.921883	0	2487	33.59	1	6.403415156	0	0.918921376	17
optimal_loci_2089_G1	1189	3.922634	0	2742	47.35	1	6.403415156	0.41	0.918855818	17
optimal_loci_2099_G1	1054	3.922634	16.22	2193	53.32	3	3.212324232	0.59	0.918392969	17
optimal_loci_2103_G1	1148	3.920215	0	2001	61.06	5	23.56310006	0.486	0.918337932	18
optimal_loci_2104_G1	1364	3.920588	0	1001	57.25	5	23.56310006	0.581	0.918327537	18
optimal_loci_2107_G1	1114	3.920043	0	3221	61.93	5	23.56310006	0.565	0.918279754	18
optimal_loci_2109_G1	1662	3.920043	8.97	2931	32	4	28.24187981	0.062	0.918254464	18
optimal_loci_2144_G1	1166	4.359676	0	1001	38.76	2	3.0407807	0.11	0.917151987	16
optimal_loci_2145_G1	1023	4.359676	18.38	2313	40.76	2	3.0407807	0.189	0.917143289	16
optimal_loci_2164_G1	1162	4.510942	0	6712	44.06	2	27.68671345	0.227	0.916511161	15
optimal_loci_2183_G1	1851	1.500135	0	1001	51.53	2	29.38735736	0.632	0.914627857	9
optimal_loci_2230_G1	1422	2.146715	5.66	2001	42.96	3	8.093391992	0.381	0.911043661	4
optimal_loci_2288_G1	1005	4.889778	0	2305	44.67	5	6.736261772	0.289	0.908244241	10
optimal_loci_2304_G1	1742	5.102126	15.44	5795	37.19	3	1.244801123	0.147	0.907607173	14
optimal_loci_2338_G1	1338	5.187835	0	6396	54.26	4	290.4975527	0.522	0.906932031	13
optimal_loci_2339_G1	1123	5.187835	0	4704	61.53	3	383.5718436	0.585	0.906919442	13
optimal_loci_2344_G1	1012	5.187835	18.97	1390	34.68	2	574.6776887	0.153	0.906810751	13
optimal_loci_2376_G1	1204	4.530283	11.46	2440	38.78	1	0.021097089	0.175	0.905817068	13
optimal_loci_2424_G1	1295	5.197383	11.89	11671	40.69	1	34.12760531	0.233	0.904683333	13
optimal_loci_2425_G1	3646	5.197383	7.3	7741	46.9	2	17.06380265	0.506	0.904654092	13
optimal_loci_2428_G1	1318	5.197383	22.15	5162	42.86	2	17.06380265	0.326	0.904634903	13
optimal_loci_2451_G1	1307	4.936769	3.52	5965	49.8	2	3.299835243	0.42	0.904289338	12
optimal_loci_2453_G1	1043	4.936769	0	7705	47.36	2	3.299835243	0.315	0.904278356	12
optimal_loci_2457_G1	2590	4.936769	1.39	14471	51.85	2	3.299835243	0.673	0.904216503	12
optimal_loci_2459_G1	1551	4.936769	0	17976	57.18	2	3.299835243	0.575	0.904198155	12

optimal_loci_2648_G1	1714	2.299355	1.63	8459	49.53	2	3.697785991	0.358	0.899100037	3
optimal_loci_2664_G1	1652	3.322662	0	3268	47.39	1	20.72616287	0.48	0.898213304	4
optimal_loci_2697_G1	1109	2.493383	0	2813	54.46	1	0.920413948	0.624	0.89555285	6
optimal_loci_2719_G1	1346	1.867214	0	2001	38.93	1	13.50480412	0.293	0.894613557	7
optimal_loci_2781_G1	2115	1.82215	38.49	2300	35.36	3	3.378126793	0.221	0.892923914	8
optimal_loci_2792_G1	1491	1.44159	0	3816	38.9	3	3.378126793	0.218	0.892839777	8
optimal_loci_2847_G1	1462	1.016508	15.18	5160	40.76	1	31.43259932	0.254	0.8917925	7
optimal_loci_2855_G1	2667	1.016508	23.55	5664	35.62	1	31.43259932	0.079	0.891671436	7
optimal_loci_2877_G1	1392	3.288193	0	1918	42.09	2	2.450275248	0.166	0.889786265	13
optimal_loci_2883_G1	1776	3.288193	0	7070	38.17	2	2.450275248	0.111	0.889745074	13
optimal_loci_2922_G1	3619	4.283331	1.08	2393	48.3	2	38.04877138	0.337	0.887788668	11
optimal_loci_2929_G1	1521	4.283331	0	12020	52.26	4	19.25151997	0.586	0.887720811	11
optimal_loci_2949_G1	1028	4.283331	2.72	2434	37.93	1	11.30966101	0	0.887354591	11
optimal_loci_2952_G1	1031	4.283331	0	4475	44.51	1	11.30966101	0.264	0.887339382	11
optimal_loci_2959_G1	2997	4.283331	2.54	10039	56.62	2	8.778257016	0.713	0.887211682	11
optimal_loci_2976_G1	1491	4.283331	20.19	4727	46.27	3	2.082284339	0.277	0.887070112	11
optimal_loci_2993_G1	2059	2.026961	0	4625	54.2	1	3.309036076	0.65	0.886335007	11
optimal_loci_3016_G1	1257	2.026961	5.09	6113	43.43	1	167.9691338	0.229	0.885810022	9
optimal_loci_3051_G1	1631	1.869173	0	2001	61.61	3	4.685791449	0.658	0.884523132	10
optimal_loci_3142_G1	2867	2.689704	0	1001	55.42	1	6.048693577	0.562	0.880941771	6
optimal_loci_3147_G1	1716	2.624457	0	2447	42.65	2	3.091999065	0.397	0.880622329	5
optimal_loci_3155_G1	1834	2.624457	0	1001	54.74	2	3.091999065	0.495	0.880482359	5
optimal_loci_3160_G1	1755	2.368372	12.99	6639	49.8	1	0.332283554	0.32	0.879972753	5
optimal_loci_3203_G1	1758	1.960224	0	12483	52.5	2	3.749654734	0.362	0.877596533	5
optimal_loci_3278_G1	1496	0.551557	0	13026	51	1	0.0978642	0.412	0.873491875	4
optimal_loci_3279_G1	1574	0.551557	32.47	11282	40.4	1	0.0978642	0.216	0.873478899	4
optimal_loci_3280_G1	1143	0.551557	10.5	9745	36.22	1	0.0978642	0.165	0.873467463	4
optimal_loci_3282_G1	2910	0.551557	0	6173	42.95	1	0.0978642	0.181	0.873440885	4
optimal_loci_3423_G1	1053	3.41382	13.01	4016	46.05	4	27.35019546	0.291	0.868773743	7
optimal_loci_3430_G1	2846	3.388195	0	2563	41.98	6	9.413705275	0.268	0.868409107	8
optimal_loci_3433_G1	1323	3.267962	26.46	4243	42.4	5	8.692940648	0.25	0.868375372	8
optimal_loci_3451_G1	2909	3.197778	0	2857	38.53	3	4.474422446	0.082	0.867166607	8
optimal_loci_3455_G1	2127	3.480523	0	1001	48.14	2	1.640208201	0.596	0.866900975	8

optimal_loci_3460_G1	1267	3.480523	0	4820	55.95	2	1.640208201	0.503	0.866878958	8
optimal_loci_3466_G1	1024	3.480523	29.79	10996	40.82	2	1.640208201	0.273	0.866834814	8
optimal_loci_3498_G1	1236	1.526293	0	12011	50.4	2	48.02506617	0.444	0.864756659	10
optimal_loci_3595_G1	1044	1.114121	2.68	5669	45.97	1	4.299051222	0.345	0.861429293	8
optimal_loci_3605_G1	2781	1.113712	1.26	7112	46.27	1	4.299051222	0.351	0.861291972	8
optimal_loci_3606_G1	1599	1.113712	0	9940	50.03	1	4.299051222	0.408	0.861279725	8
optimal_loci_3640_G1	1273	1.912519	0	8690	34.09	2	0.102629761	0.165	0.85994381	10
optimal_loci_3649_G1	1560	1.853888	0	2088	40.64	1	0.05280726	0.058	0.859407909	10
optimal_loci_3673_G1	1978	1.623379	14.56	15794	36.65	1	26.19342066	0.167	0.858940283	10
optimal_loci_3705_G1	1599	1.389297	7.44	2106	36.83	4	54.69216478	0.204	0.85791942	10
optimal_loci_3733_G1	3626	0.775751	3.17	14910	58.08	1	36.8970222	0.671	0.856875022	9
optimal_loci_3741_G1	2009	0.775751	10.65	2374	42.11	2	44.69442336	0.467	0.856714368	9
optimal_loci_3742_G1	1072	0.775751	4.2	2025	34.98	2	44.69442336	0.248	0.856702165	9
optimal_loci_3877_G1	1140	0.138883	4.47	18568	46.84	1	1.477141613	0.31	0.853698616	5
optimal_loci_3885_G1	4424	0.138883	0.63	11768	48.12	2	11.06380836	0.402	0.853562329	5
optimal_loci_3976_G1	1786	0.164675	0	1001	39.86	1	433.0851054	0.133	0.848080885	1
optimal_loci_4065_G1	1463	0.519426	0	12853	33.42	2	4.726553134	0.042	0.843643876	1
optimal_loci_4160_G1	3368	1.103192	25.24	3181	45.13	4	6.609911267	0.365	0.838576607	7
optimal_loci_4161_G1	1404	1.103192	0	5463	55.27	4	6.609911267	0.566	0.838564516	7
optimal_loci_4162_G1	3429	1.103192	0	2001	43.59	4	6.609911267	0.249	0.838538757	7
optimal_loci_4166_G1	1624	0.452612	0	2648	54.31	2	11.06033262	0.516	0.83843128	7
optimal_loci_4168_G1	2269	0.452612	15.91	2881	58.74	2	11.06033262	0.563	0.838407924	7
optimal_loci_4177_G1	1069	0.452612	0	13330	50.51	1	4.144796403	0.535	0.838268698	7
optimal_loci_4265_G1	1163	0.882696	0	17617	40.58	1	5.933948611	0.216	0.836213237	8
optimal_loci_4358_G1	1096	1.44233	0	1012	48.26	2	10.54192483	0.577	0.832606905	4
optimal_loci_4384_G1	2843	1.295085	14.03	1001	53.85	5	8.080097473	0.562	0.831568073	8
optimal_loci_4385_G1	1305	1.295085	22.38	1169	45.36	5	8.080097473	0.348	0.831445558	8
optimal_loci_4420_G1	1054	1.506298	30.08	2730	39.08	1	0.118320026	0.106	0.828481466	11
optimal_loci_4427_G1	1354	1.506298	0	7204	43.2	1	0.118320026	0.097	0.828445945	11
optimal_loci_4431_G1	1277	1.456949	36.18	17014	40.32	1	0.118320026	0.268	0.828373527	12
optimal_loci_4441_G1	1266	1.508054	14.53	7357	43.75	1	1.668752012	0.198	0.828102135	14
optimal_loci_4447_G1	3421	1.465072	0	2473	59.31	1	1.668752012	0.6	0.82799125	14
optimal_loci_4465_G1	1695	1.552655	12.33	6839	43.59	2	2.427661501	0.29	0.827363519	12

optimal_loci_4470_G1	2202	1.616642	0	3329	52.86	3	7.487953654	0.533	0.827154568	12
optimal_loci_4471_G1	2446	1.616642	0	5689	54.74	4	5.61596524	0.47	0.827135193	12
optimal_loci_4472_G1	1762	1.616642	0	5288	51.87	4	5.61596524	0.501	0.827114561	12
optimal_loci_4544_G1	1173	1.904105	0	1001	46.2	2	11.08252821	0.253	0.824683661	11
optimal_loci_4546_G1	1284	1.904105	8.41	3413	38.7	2	1.923620392	0.301	0.824559293	10
optimal_loci_4549_G1	1354	1.904105	2.22	1880	59.37	2	19.76041069	0.468	0.824483921	10
optimal_loci_4674_G1	1938	0.696321	32.04	5446	33.95	1	12.77974205	0.181	0.821090945	10
optimal_loci_4704_G1	1291	0.923729	15.03	15938	53.83	1	2.71856824	0.593	0.820004442	9
optimal_loci_4717_G1	1395	0.923729	4.01	3425	40.86	1	2.71856824	0.294	0.819911339	9
optimal_loci_4721_G1	1044	0.903937	0	3941	55.74	2	15.89171465	0.513	0.819841161	9
optimal_loci_4723_G1	1470	0.903937	29.46	5953	49.86	2	15.89171465	0.448	0.819823021	9
optimal_loci_4741_G1	1026	1.601481	0	7247	58.57	1	5.3050065	0.589	0.819187924	10
optimal_loci_4745_G1	1241	1.601481	2.5	2001	47.21	1	5.3050065	0.127	0.819148891	10
optimal_loci_4819_G1	2018	0.79928	0	2354	51.53	1	58.92282379	0.424	0.816424978	9
optimal_loci_4825_G1	1544	0.79928	2.53	3351	44.49	1	58.92282379	0.375	0.816351369	9
optimal_loci_4851_G1	1077	0.560723	0	1549	37.04	2	8.93256229	0.151	0.815923966	6
optimal_loci_4924_G1	1309	1.442388	29.03	6513	48.58	2	8.100071493	0.497	0.812589315	2
optimal_loci_5007_G1	1746	2.1117	3.38	3964	44.84	1	8.42162261	0.553	0.808649539	2
optimal_loci_5038_G1	1020	2.019556	37.84	2788	37.74	2	37.38301299	0.214	0.807980685	2
optimal_loci_5152_G1	1775	1.174499	14.65	5103	47.66	2	16.60562234	0.388	0.803231235	5
optimal_loci_5177_G1	2188	1.178051	6.63	3592	49.54	1	2.395997004	0.512	0.802288795	5
optimal_loci_5179_G1	1298	1.178051	4.01	2001	54.69	1	2.395997004	0.736	0.802276957	6
optimal_loci_5240_G1	1091	3.352873	17.42	1001	40.51	1	0.597701311	0.2	0.799770982	11
optimal_loci_5241_G1	1493	3.352873	0	2001	47.01	1	0.597701311	0.55	0.799724874	11
optimal_loci_5267_G1	1386	3.80779	32.18	1280	37.73	3	5.077399855	0.164	0.798548869	9
optimal_loci_5278_G1	1195	4.302836	0	3289	37.48	4	5.712146575	0.067	0.798448467	8
optimal_loci_5284_G1	2217	4.302836	3.43	2952	43.7	4	4.597249728	0.203	0.79830314	8
optimal_loci_5288_G1	1042	4.302836	33.3	4396	43.57	4	4.597249728	0.497	0.798275372	8
optimal_loci_5301_G1	1295	4.302836	0	10103	54.59	2	0.152942505	0.705	0.798072939	9
optimal_loci_5303_G1	1675	2.789403	0	12238	54.86	2	0.152942505	0.523	0.798054226	9
optimal_loci_5385_G1	1138	1.460982	0	1676	40.94	3	7.667374239	0.144	0.794390655	4
optimal_loci_5417_G1	1865	1.086419	23.65	13865	38.82	1	14.06932808	0.333	0.793004747	2
optimal_loci_5545_G1	2238	2.003561	30.12	13513	36.32	2	4.331342949	0.017	0.788677098	5

optimal_loci_5551_G1	1259	1.927181	0	8087	57.34	2	14.79025054	0.719	0.788244115	5
optimal_loci_5552_G1	1373	1.923923	0	9453	52.51	2	14.79025054	0.603	0.788233103	5
optimal_loci_5553_G1	1028	1.923185	0	11072	39.88	2	14.79025054	0.193	0.788223624	5
optimal_loci_5607_G1	2049	2.134787	7.13	2239	41.97	3	10.64286957	0.327	0.787089933	5
optimal_loci_5728_G1	1079	1.263874	21.96	17103	41.89	1	13.27024894	0.346	0.782920432	9
optimal_loci_5735_G1	2566	1.505242	10.48	3304	59.54	1	8.328344883	0.539	0.782791339	12
optimal_loci_5757_G1	1160	1.852207	0	6997	52.84	1	23.18619617	0.382	0.781304405	14
optimal_loci_5773_G1	1601	1.853432	5.5	3965	47.72	1	10.03717269	0.438	0.78034814	14
optimal_loci_5791_G1	1105	1.853432	0	5967	43.52	1	9.10231746	0.369	0.780128631	14
optimal_loci_5792_G1	1527	1.853432	1.83	7679	42.56	1	9.10231746	0.341	0.780112753	14
optimal_loci_5793_G1	1776	1.853432	0	9530	42.73	1	9.10231746	0.339	0.780097128	14
optimal_loci_5823_G1	1201	2.031953	15.99	10846	38.3	1	4.860147555	0.299	0.779225067	14
optimal_loci_5825_G1	2101	2.031953	0	8028	40.4	1	4.860147555	0.154	0.7792041	14
optimal_loci_5828_G1	1081	2.031953	0	3023	47.17	2	2.430073778	0.351	0.77916686	13
optimal_loci_5829_G1	1769	2.031953	0	1001	52.96	2	2.430073778	0.502	0.779151815	13
optimal_loci_5836_G1	1333	2.031953	0	4021	40.88	2	2.430073778	0.203	0.779066369	13
optimal_loci_5863_G1	1835	1.879968	2.89	1001	45.17	1	1.121452974	0.26	0.778332054	15
optimal_loci_5872_G1	1140	1.735365	26.23	10676	42.71	1	1.121452974	0.486	0.778265238	16
optimal_loci_5976_G1	1404	0.881883	0	5057	43.73	1	9.494875344	0.303	0.774918438	7
optimal_loci_5982_G1	2277	0.787433	11.73	2099	49.18	2	4.747437672	0.389	0.774818847	7
optimal_loci_5983_G1	3278	0.787433	6.71	2001	44.81	4	0.203608686	0.396	0.774668125	7
optimal_loci_5985_G1	1218	0.772606	14.04	1001	47.12	4	0.203608686	0.41	0.774587835	6
optimal_loci_6095_G1	2157	0.585779	0	2620	58.59	1	12.62016873	0.56	0.771691979	5
optimal_loci_6209_G1	2735	1.183263	0	2001	47.09	1	1.164561217	0.336	0.763595231	7
optimal_loci_6211_G1	1454	1.183263	0	5617	47.04	1	1.164561217	0.509	0.763577857	7
optimal_loci_6213_G1	1088	1.183263	38.24	8028	52.94	1	1.164561217	0.455	0.763562641	7
optimal_loci_6242_G1	1912	0.833339	13.55	5364	41.78	2	24.65985781	0.226	0.763006853	7
optimal_loci_6262_G1	1074	0.981536	17.69	7948	46.74	3	3.883493015	0.412	0.761816719	7
optimal_loci_6270_G1	1548	0.981536	21.19	2784	47.09	2	26.31429733	0.263	0.76131744	7
optimal_loci_6276_G1	1042	0.722503	0	2907	44.33	2	26.31429733	0.273	0.761175655	7
optimal_loci_6366_G1	3067	0.405366	10.53	11153	42.22	2	0.014956037	0.303	0.757040677	4
optimal_loci_6381_G1	1663	0.641973	1.92	1138	46.9	1	4.699691557	0.341	0.756287507	4
optimal_loci_6388_G1	1589	0.641973	0	6403	52.04	1	4.699691557	0.49	0.75620744	5

optimal_loci_6422_G1	1012	1.630877	0	10308	42.09	2	6.757920618	0.368	0.75438378	9
optimal_loci_6456_G1	1403	2.19278	4.35	5882	38.63	1	25.13022052	0.31	0.752519144	7
optimal_loci_6470_G1	1153	2.19278	0	7451	53.77	1	25.13022052	0.443	0.752386771	6
optimal_loci_6475_G1	1593	2.19278	0	17468	52.85	1	25.13022052	0.471	0.752308966	6
optimal_loci_6510_G1	1363	2.858521	0	2163	50.84	3	40.33504934	0.563	0.751276942	8
optimal_loci_6518_G1	1006	2.858521	0	3668	32.1	3	5.256160573	0.09	0.751092753	8
optimal_loci_6602_G1	2225	0.795966	1.26	5798	44.67	3	8.348114403	0.372	0.748197455	7
optimal_loci_6603_G1	2842	0.795966	0	8056	53.06	3	8.348114403	0.413	0.748176064	7
optimal_loci_6638_G1	1278	0.020253	28.95	3637	39.67	1	0.539972941	0.251	0.745829122	6
optimal_loci_6665_G1	1430	0.039099	0	17932	43	1	19.33029757	0.428	0.744835618	6
optimal_loci_6666_G1	1662	0.039099	8.06	16237	43.5	1	19.33029757	0.205	0.744823006	6
optimal_loci_6733_G1	1909	0.037927	31.48	1001	45.2	3	13.40717925	0.18	0.742432247	11
optimal_loci_6775_G1	1497	0.035611	1.73	10124	46.49	1	3.664276091	0.332	0.740986451	10
optimal_loci_6793_G1	1449	0.027553	4	10655	38.37	1	11.2783208	0.12	0.740137909	10
optimal_loci_6803_G1	1758	0.027553	0	1001	48	1	11.2783208	0.332	0.740066079	10
optimal_loci_6804_G1	1056	0.027553	2.65	2001	60.98	3	5.87411037	0.634	0.739962262	10
optimal_loci_6805_G1	2123	0.027553	13.19	3090	44.41	4	15.39489093	0.491	0.73994622	10
optimal_loci_6806_G1	1860	0.027553	0	2588	46.12	4	15.39489093	0.391	0.739930067	10
optimal_loci_6808_G1	2047	0.027553	0	1529	56.03	4	15.39489093	0.599	0.739869598	10
optimal_loci_6841_G1	1634	0.147935	0	2001	50.73	1	3.893134174	0.45	0.738003393	10
optimal_loci_6855_G1	2940	0.164609	4.69	1591	43.8	2	10.04898499	0.43	0.737809978	10
optimal_loci_6908_G1	1551	0.305043	2.06	11561	41.39	2	10.0811258	0.141	0.735138832	7
optimal_loci_6925_G1	3060	0.361468	12.09	1564	48.23	4	81.86403318	0.389	0.733919464	5
optimal_loci_6932_G1	1269	0.338669	2.6	1001	33.72	2	1.667651035	0.189	0.733508936	5
optimal_loci_6935_G1	1049	0.321296	0	4872	38.41	1	12.7941427	0.211	0.73301439	6
optimal_loci_6937_G1	1228	0.321296	0	2933	40.96	1	12.7941427	0.266	0.732999963	6
optimal_loci_7054_G1	1154	0.158738	0	6727	45.66	1	0.426403384	0.461	0.729496823	3
optimal_loci_7187_G1	1224	0.167022	12.99	1001	52.61	1	13.50603816	0.347	0.723205766	1
optimal_loci_7267_G1	2239	0.080736	0	3470	50.15	2	0.298799073	0.508	0.7194041	3
optimal_loci_7355_G1	1394	0.250544	29.41	2413	37.01	2	77.70132465	0.07	0.716261086	6
optimal_loci_7374_G1	1035	0.254727	19.81	6582	49.46	1	3.202976028	0.574	0.715678065	6
optimal_loci_7375_G1	1052	0.254727	4.18	8023	38.87	1	3.202976028	0.385	0.715667217	5
optimal_loci_7377_G1	1071	0.261707	0	10287	32.39	1	3.202976028	0.074	0.715650231	5

optimal_loci_7392_G1	1225	0.22112	17.96	4088	47.42	2	6.865646723	0.44	0.714816689	5
optimal_loci_7456_G1	3017	0.370803	1.56	2360	48.06	5	22.30375504	0.429	0.71081006	5
optimal_loci_7478_G1	3146	0.35259	6.33	19653	51.39	1	4.048418853	0.429	0.709699323	5
optimal_loci_7483_G1	1282	0.304701	0	2182	41.1	1	74.44689501	0.38	0.708948229	5
optimal_loci_7497_G1	3090	0.310757	2.04	4537	48.83	1	6.750339546	0.394	0.707913638	6
optimal_loci_7507_G1	2424	0.314481	8.25	1001	52.22	1	46.36409035	0.455	0.707311972	9
optimal_loci_7567_G1	1129	0.808359	35.96	3061	42.24	5	3.102203808	0.399	0.704217202	15
optimal_loci_7575_G1	1040	0.947362	0	7538	30.86	3	0.067674625	0.054	0.704113824	14
optimal_loci_7578_G1	1572	0.947362	4.9	10215	40.13	3	0.067674625	0.127	0.704089948	14
optimal_loci_7580_G1	1449	0.918583	0	2793	37.47	3	3.054008388	0.213	0.703998199	14
optimal_loci_7602_G1	1287	0.800491	2.25	3973	37.99	2	26.65034815	0.164	0.703123571	15
optimal_loci_7606_G1	2098	1.002903	1.53	1200	53.81	2	26.65034815	0.566	0.703102939	15
optimal_loci_7610_G1	1513	0.972441	2.41	3483	49.1	2	28.05284615	0.314	0.702940067	15
optimal_loci_7677_G1	1252	0.99883	0	8994	34.42	1	0.211480263	0.175	0.701049747	18
optimal_loci_7686_G1	1247	0.99883	0	8326	36.08	2	59.37279745	0.182	0.700864531	18
optimal_loci_7692_G1	1353	0.952613	4.58	1018	54.1	1	118.5341146	0.513	0.70067657	18
optimal_loci_7697_G1	2816	0.952613	4.19	4664	51.63	1	118.5341146	0.574	0.700638557	18
optimal_loci_7699_G1	1149	0.963644	0	15554	56.48	1	118.5341146	0.599	0.700569933	18
optimal_loci_7700_G1	1386	0.964257	36	16736	54.47	1	118.5341146	0.293	0.700559375	18
optimal_loci_7723_G1	1110	0.895844	0	16500	55.49	1	61.7595277	0.563	0.699414509	15
optimal_loci_7724_G1	1200	0.895844	0	15242	46.25	1	61.7595277	0.293	0.699405149	15
optimal_loci_7748_G1	2022	0.433691	0	10649	53.21	2	51.75286618	0.533	0.699125856	12
optimal_loci_7782_G1	2090	0.433691	1.96	7101	38.56	1	2.018493798	0.363	0.698208735	12
optimal_loci_7783_G1	1587	0.433691	0	5431	49.84	1	2.018493798	0.432	0.69819631	12
optimal_loci_7857_G1	1006	0.541515	21.37	14925	43.33	1	10.03648326	0.134	0.695698862	11
optimal_loci_7937_G1	1138	0.451276	26.1	5405	38.92	4	4.807646079	0.09	0.693245915	6
optimal_loci_7943_G1	1327	0.442126	37.91	3883	46.11	2	9.605093478	0.386	0.693110551	6
optimal_loci_7946_G1	1382	0.442126	13.89	6290	47.53	2	9.605093478	0.532	0.693092232	6
optimal_loci_7953_G1	1087	0.43103	0	1001	52.16	2	14.9380337	0.647	0.692850379	6
optimal_loci_7969_G1	1374	0.274538	2.24	1027	39.88	1	0.024135834	0.261	0.692143571	7
optimal_loci_8053_G1	3731	0.086922	12.38	8538	34.95	2	11.78786692	0.121	0.688422083	4
optimal_loci_8076_G1	1768	0.149979	9.9	7124	34.1	2	9.527129738	0.079	0.687275603	5
optimal_loci_8113_G1	1301	0.225157	2.15	3242	45.11	2	23.15317428	0.342	0.686299933	5

optimal_loci_8127_G1	1216	0.229819	33.06	3906	44.98	2	4.024261264	0.351	0.683981347	6
optimal_loci_8131_G1	1220	0.229819	4.51	1001	48.03	2	4.024261264	0.333	0.683927225	6
optimal_loci_8190_G1	1533	0.974755	9.2	2346	36.13	4	14.11393795	0.159	0.681128006	4
optimal_loci_8193_G1	1294	0.974755	5.33	5701	41.19	4	14.11393795	0.311	0.681051912	4
optimal_loci_8310_G1	1013	2.89445	32.58	2001	30.2	3	57.20028428	0.394	0.674914338	6
optimal_loci_8324_G1	1037	3.380917	0	2001	58.53	3	6.181965628	0.566	0.674326034	6
optimal_loci_8326_G1	1378	3.380917	2.76	3309	47.67	3	6.181965628	0.445	0.674313765	6
optimal_loci_8339_G1	1177	3.241783	13.25	1001	38.06	2	12.23483761	0.243	0.672789315	6
optimal_loci_8390_G1	1363	3.194924	21.32	4240	44.75	3	61.81035401	0.187	0.671368051	6
optimal_loci_8391_G1	1100	3.197226	0	5374	42.81	3	61.81035401	0.252	0.671346317	6
optimal_loci_8554_G1	1059	0.165947	0	9657	41.64	2	2.832105954	0.1	0.665644695	3
optimal_loci_8561_G1	1385	0.165947	0	1001	38.33	2	2.832105954	0.173	0.665520818	3
optimal_loci_8601_G1	1111	0.165947	27.9	6255	41.58	2	1.801908047	0.127	0.664243631	3
optimal_loci_8699_G1	1044	1.311307	0	1566	33.71	3	0.25473009	0.13	0.659628824	3
optimal_loci_8701_G1	1861	1.311307	14.4	1537	42.07	4	0.425871889	0.284	0.659611503	3
optimal_loci_8776_G1	1086	2.147955	20.99	4686	36.18	2	16.54547941	0.125	0.655957693	4
optimal_loci_8870_G1	3271	1.258413	3.12	1358	52.43	2	78.74086903	0.453	0.652632708	5
optimal_loci_8885_G1	1762	2.534411	0	3979	48.35	4	10.12537104	0.384	0.651423519	4
optimal_loci_8897_G1	2099	2.440985	8.81	1299	39.25	1	2.279378386	0.35	0.650859524	4
optimal_loci_8914_G1	1621	2.45419	5.74	2182	34.91	2	8.65879336	0.077	0.649259382	5
optimal_loci_8952_G1	1033	2.434861	7.84	4823	41.91	2	5.022829212	0.24	0.64680192	3
optimal_loci_9017_G1	1083	0.849213	0	2001	32.31	2	3.660893972	0.082	0.644152984	3
optimal_loci_9082_G1	1176	0.995597	0	2001	51.7	3	0.005946027	0.784	0.642027917	4
optimal_loci_9208_G1	1008	0.609865	0	1732	48.41	3	3.8697641	0.302	0.638858876	7
optimal_loci_9222_G1	4319	0.609865	4.49	2159	49.36	3	3.8697641	0.524	0.638758504	7
optimal_loci_9234_G1	1759	0.609865	1.78	14927	52.87	1	23.98721535	0.474	0.638076027	6
optimal_loci_9235_G1	2366	0.609865	0	7043	54.9	1	23.98721535	0.565	0.638017366	6
optimal_loci_9236_G1	1132	0.609865	0	5878	64.13	1	23.98721535	0.781	0.638008698	6
optimal_loci_9250_G1	1140	0.609865	8.51	2398	43.24	1	19.21761933	0.214	0.637696585	6
optimal_loci_9383_G1	2665	0.049255	33.21	14211	36.99	1	1.68076566	0	0.632602969	1
optimal_loci_9573_G1	2038	0.678551	36.41	2389	38.66	3	3.542859748	0.208	0.622865618	3
optimal_loci_9629_G1	1133	0.975742	25.51	3254	38.48	3	101.6829737	0.12	0.620483132	10
optimal_loci_9633_G1	1351	1.115086	24.35	1458	41.82	2	0.183978988	0.374	0.620227098	10

optimal_loci_9657_G1	1907	1.179086	34.77	3267	42.42	5	11.48966433	0.243	0.618302701	9
optimal_loci_9679_G1	1465	1.113368	12.15	4836	37.54	1	22.47996169	0.177	0.617610729	9
optimal_loci_9680_G1	1431	1.113368	0	3255	42.27	1	22.47996169	0.165	0.617598966	9
optimal_loci_9685_G1	1147	1.093941	5.84	2638	45.42	1	22.47996169	0.22	0.617529695	9
optimal_loci_9687_G1	2267	1.093941	1.81	4687	44.59	1	22.47996169	0.204	0.617506116	9
optimal_loci_9690_G1	1546	1.093941	0	9535	43.53	1	22.47996169	0.268	0.617475409	9
optimal_loci_9693_G1	1331	1.093941	0	12418	45.3	1	22.47996169	0.322	0.617455558	9
optimal_loci_9811_G1	2379	0.282427	24	3618	56.95	1	166.3398338	0.657	0.611891064	4
optimal_loci_9832_G1	1234	0.216784	24.47	2109	40.76	1	8.911102067	0.173	0.611181451	4
optimal_loci_9843_G1	1295	0.177754	0	7024	34.13	1	1.405568871	0.056	0.610570484	4
optimal_loci_9852_G1	1046	0.177754	0	1790	55.35	1	1.405568871	0.555	0.610471674	4
optimal_loci_9940_G1	2168	1.51479	2.68	2001	47.27	1	13.49658105	0.275	0.606208884	3
optimal_loci_10030_G1	2501	1.547849	0	6610	53.93	1	14.35755727	0.68	0.602566801	5
optimal_loci_10033_G1	2220	1.547849	2.34	2618	51.26	1	14.35755727	0.397	0.602537098	5
optimal_loci_10082_G1	1523	1.688913	2.69	2153	45.17	2	96.22956343	0.608	0.600955097	5
optimal_loci_10086_G1	1346	1.681541	14.26	13833	39.74	1	7.579623569	0.138	0.600809449	5
optimal_loci_10181_G1	1106	0.245467	0	1903	60.12	1	1.263847783	0.611	0.597229978	3
optimal_loci_10382_G1	1314	0.288465	24.96	2001	34.39	2	11.77748289	0.161	0.586984449	3
optimal_loci_10387_G1	1087	0.288465	2.76	5395	43.14	2	11.77748289	0.237	0.586960885	3
optimal_loci_10419_G1	1423	0.427579	0	3405	36.54	2	10.28984048	0.062	0.585220432	5
optimal_loci_10467_G1	1170	0.686121	7.01	4622	39.82	1	13.93766814	0.158	0.582823504	4
optimal_loci_10471_G1	1031	0.778282	29	1279	50.14	1	13.93766814	0.279	0.582742158	5
optimal_loci_10513_G1	1203	1.47036	0	3956	54.28	3	0.752553337	0.406	0.58093715	6
optimal_loci_10537_G1	1425	1.526092	3.09	2014	50.59	4	39.75724094	0.521	0.579014338	7
optimal_loci_10538_G1	1012	1.526092	0	4410	39.32	4	39.75724094	0.162	0.578999583	6
optimal_loci_10540_G1	1286	1.526092	0	5833	41.75	3	25.83468107	0.212	0.578986957	6
optimal_loci_10631_G1	1267	1.166018	0	1001	37.17	2	20.96832526	0.072	0.576656451	6
optimal_loci_10633_G1	1050	1.166018	0	3320	35.14	2	20.96832526	0.094	0.576640811	6
optimal_loci_10697_G1	2114	0.170467	31.6	5072	44.46	1	10.67453458	0.389	0.57398215	3
optimal_loci_10878_G1	3135	0.396549	0	19405	47.94	1	42.97263234	0.366	0.565080223	4
optimal_loci_10883_G1	1281	0.128737	31.46	14704	42.38	1	42.97263234	0.027	0.565045246	4
optimal_loci_10884_G1	1191	0.128737	3.53	12988	54.99	1	42.97263234	0.373	0.565032478	4
optimal_loci_10919_G1	1114	0.160994	0	1158	33.75	2	2.970274442	0.109	0.563071525	4

optimal_loci_11051_G1	1862	0.211163	7.95	2001	38.93	1	42.11417497	0.133	0.555336034	3
optimal_loci_11169_G1	1161	0.087237	9.47	2191	49.61	2	59.51880917	0.563	0.552508118	3
optimal_loci_11170_G1	1041	0.087237	0	1001	52.64	3	102.8048951	0.4	0.552449903	3
optimal_loci_11268_G1	1296	0.693545	14.04	16780	35.26	1	8.59812967	0.088	0.547812507	3
optimal_loci_11269_G1	1333	0.693545	18.6	18164	46.21	1	8.59812967	0.475	0.547801935	3
optimal_loci_11276_G1	1325	0.693545	0	3015	40.37	2	7.077168932	0.15	0.547063996	3
optimal_loci_11368_G1	1507	0.829076	5.57	1552	45.58	3	2.692167469	0.223	0.54140997	1
optimal_loci_11463_G1	1079	0.863703	19.83	13386	33.08	1	28.82793269	0.024	0.536018281	2
optimal_loci_11532_G1	1740	0.449025	9.37	3209	33.44	5	1.23357691	0.112	0.533509211	3
optimal_loci_11552_G1	1244	0.086722	0	8363	34.56	2	3.84932272	0.069	0.531993891	3
optimal_loci_11590_G1	1009	0.013247	30.13	3571	42.81	1	48.5510861	0.351	0.529728333	4
optimal_loci_11664_G1	1151	0.251496	5.08	5620	43.78	1	66.83366388	0.354	0.526490402	4
optimal_loci_11671_G1	1642	0.308453	7.31	12621	29.23	3	22.79587405	0.163	0.526311577	4
optimal_loci_11765_G1	2495	0.576848	5.49	2516	47.21	1	0.6208928	0.267	0.523158423	4
optimal_loci_11875_G1	1318	0.150668	33.84	5301	36.26	2	0.133971089	0.093	0.519706235	2
optimal_loci_12197_G1	1588	0.459055	6.93	9252	51.57	1	85.10926704	0.343	0.506563862	2
optimal_loci_12248_G1	1087	0.454063	8.65	1810	50.32	1	9.567827412	0.392	0.504583415	2
optimal_loci_12600_G1	1998	1.475944	0	3644	48.74	1	6.277971263	0.436	0.485893616	1
optimal_loci_12753_G1	1285	1.366417	23.35	15089	37.35	1	20.20422279	0.221	0.480166667	4
optimal_loci_12754_G1	1150	0.426581	0	13906	61.13	1	20.20422279	0.511	0.480157865	4
optimal_loci_12762_G1	1104	0.426581	6.25	1001	31.06	2	125.3939211	0.048	0.480016071	4
optimal_loci_12793_G1	2168	0.239027	20.2	14542	34.68	1	7.347597431	0.066	0.478118378	4
optimal_loci_12883_G1	1272	1.626637	0	4357	38.28	1	0.623568323	0.186	0.473829568	2
optimal_loci_12969_G1	1621	1.626637	0	3347	41.14	1	11.838924	0.164	0.471265625	3
optimal_loci_12998_G1	1599	2.292658	0	2490	34.02	1	38.34413298	0.068	0.470094509	3
optimal_loci_13066_G1	1112	1.636187	0	8206	37.67	2	6.087227098	0.047	0.467466652	2
optimal_loci_13288_G1	1294	0.503234	0	1001	44.97	1	5.360286943	0.363	0.458341131	1
optimal_loci_13456_G1	1335	0.127873	21.42	2001	45.24	1	85.6582528	0.573	0.449616369	1
optimal_loci_13557_G1	1862	0.268679	20.77	1880	39.09	2	5.842853262	0.243	0.444856109	3
optimal_loci_13558_G1	1073	0.268679	34.78	4846	38.02	2	5.842853262	0.168	0.444839911	3
optimal_loci_13570_G1	1543	0.262066	0	1023	44.58	1	8.974322515	0.288	0.444684881	3
optimal_loci_13679_G1	1142	0.236161	0	3361	36.51	1	21.24201486	0.093	0.439042783	2
optimal_loci_13754_G1	1290	0.389212	8.91	3477	37.9	1	15.33230619	0.243	0.436276868	4

optimal_loci_13800_G1	1267	0.613452	0	2001	53.43	1	4.831481253	0.584	0.434847545	3
optimal_loci_13860_G1	1005	0.84795	0	3348	47.76	1	0.290502133	0.458	0.432737121	4
optimal_loci_13931_G1	1005	0.977745	0	7644	44.77	1	26.31136074	0.263	0.430044635	3
optimal_loci_14015_G1	1276	0.985339	0	2001	53.6	2	0.417581768	0.579	0.426912783	4
optimal_loci_14034_G1	1973	1.055384	9.22	1806	66.34	1	14.32697457	0.718	0.426019918	3
optimal_loci_14037_G1	1246	1.055384	0	3013	55.21	1	14.32697457	0.618	0.42596407	3
optimal_loci_14380_G1	1540	0.013771	7.08	19750	46.81	1	12.40313901	0.199	0.410248862	1
optimal_loci_14600_G1	1212	0.742189	0	4476	53.21	2	20.38515676	0.416	0.401135335	4
optimal_loci_14629_G1	1052	0.681853	0	2001	53.61	3	1.722608898	0.528	0.399701503	4
optimal_loci_14644_G1	1118	0.839564	0	1001	38.81	1	0.43089278	0.123	0.399030149	4
optimal_loci_14679_G1	1251	0.960286	7.75	2325	37.41	1	0.039588839	0.216	0.398336228	4
optimal_loci_14823_G1	1590	0.697809	0	1001	28.8	2	3.898908238	0	0.393031704	2
optimal_loci_14838_G1	2168	0.656697	10.61	2361	36.76	2	6.494991498	0.276	0.39285378	2
optimal_loci_14898_G1	1211	0.048627	0	2001	39.3	1	29.29655873	0.153	0.388703683	4
optimal_loci_14904_G1	1881	0.048627	35.14	8297	41.67	1	29.29655873	0.193	0.388651853	4
optimal_loci_14955_G1	1577	0.223812	0	4607	40.13	2	16.89962509	0.158	0.385499926	5
optimal_loci_14956_G1	1175	0.223812	12.43	6261	39.48	2	16.89962509	0.213	0.38549061	5
optimal_loci_14988_G1	2958	0.311782	4.56	1407	36.78	2	5.676741968	0.032	0.384674769	3
optimal_loci_15098_G1	1743	0.205753	0	12748	39.75	1	44.91609922	0.234	0.379557173	2
optimal_loci_15153_G1	1254	0.331649	0	1232	36.04	1	0.141733571	0	0.37765971	3
optimal_loci_15227_G1	3089	0.205304	7.96	2292	39.43	2	0.907429188	0.142	0.374562574	2
optimal_loci_15388_G1	1425	0.197088	12.84	3497	36	1	15.19364142	0.176	0.368898869	2
optimal_loci_15412_G1	1231	0.231211	0	3609	59.22	2	14.57761848	0.933	0.367375298	2
optimal_loci_15538_G1	1353	0.126236	12.66	1147	39.61	1	20.94837083	0.153	0.36090096	2
optimal_loci_15558_G1	1313	0.136592	0	4246	35.49	2	9.926160535	0.168	0.360114018	2
optimal_loci_15623_G1	1589	0.211199	0	12631	38.82	2	16.23809566	0.172	0.355447865	1
optimal_loci_15703_G1	1196	0.53291	0	2585	37.54	2	1.826061235	0.092	0.351484993	1
optimal_loci_15794_G1	1188	0.431496	0	3209	42.5	2	1.436859446	0.206	0.346938088	2
optimal_loci_15828_G1	1431	0.681062	31.31	8865	31.23	1	2.869193659	0	0.345947418	3
optimal_loci_15895_G1	1965	0.992948	11.15	1015	50.43	2	121.9794617	0.569	0.342814576	4
optimal_loci_15961_G1	2313	0.708119	14.31	16781	42.84	1	34.86229561	0.296	0.341416882	4
optimal_loci_15964_G1	1218	0.710031	2.3	14701	36.94	1	34.86229561	0.278	0.341401406	4
optimal_loci_16030_G1	1224	0.012886	2.86	4903	37.82	1	222.1464292	0.112	0.338869985	3

optimal_loci_16396_G1	1193	1.449954	10.31	16231	39.06	1	5.198069065	0.287	0.323384516	3
optimal_loci_16432_G1	1092	1.813261	0	9410	44.87	1	36.75397262	0.254	0.321148006	4
optimal_loci_16436_G1	2481	1.9038	11.81	15462	55.5	1	36.75397262	0.552	0.320922805	4
optimal_loci_16479_G1	1376	0.421655	13.3	18684	51.3	1	15.30422394	0.453	0.319313415	7
optimal_loci_16534_G1	1407	0.391508	0	5755	35.6	2	7.947263678	0.4	0.317111868	5
optimal_loci_16535_G1	1966	0.391508	18.31	7343	35.7	2	7.947263678	0.035	0.317095893	5
optimal_loci_16548_G1	1163	0.391508	21.84	3472	61.65	1	20.17586161	0.682	0.316425967	5
optimal_loci_16549_G1	1486	0.391508	0	1867	53.23	1	20.17586161	0.515	0.316414025	5
optimal_loci_16717_G1	1455	0.271729	13.4	14900	33.05	2	17.11118907	0.067	0.309467813	6
optimal_loci_16718_G1	1556	0.271729	0	17533	41.96	2	17.11118907	0.29	0.30944747	6
optimal_loci_16730_G1	1231	0.263044	2.27	13281	35.98	1	0.041101011	0.169	0.309106473	6
optimal_loci_16738_G1	1273	0.263044	5.5	2001	33.22	1	0.041101011	0.119	0.308963475	6
optimal_loci_16769_G1	1789	0.268036	19.01	2546	37.84	1	2.249835338	0.219	0.307511362	6
optimal_loci_16772_G1	1503	0.268036	4.92	1953	46.37	1	2.249835338	0.315	0.307454576	6
optimal_loci_16922_G1	1405	0.260618	0	9579	39.78	2	1.211905099	0.086	0.301172054	1
optimal_loci_17413_G1	2121	0.445976	9.9	10418	49.59	1	1.142048288	0.345	0.28116125	1
optimal_loci_17536_G1	2176	0.136731	11.86	2333	40.21	1	4.081236377	0.186	0.274482768	1
optimal_loci_17645_G1	1133	0.143408	0	2001	38.57	2	4.145164277	0.194	0.268478199	2
optimal_loci_17718_G1	1048	0.136822	19.66	5471	40.17	1	24.64682834	0.329	0.265209673	2
optimal_loci_17930_G1	1451	0.135701	0	12579	57.2	2	5.861051041	0.677	0.256129174	1
optimal_loci_18343_G1	1181	0.288672	0	6351	42.25	2	9.952352183	0.239	0.239315744	1
optimal_loci_18450_G1	1422	0.305057	0	1540	48.52	1	9.206449522	0.385	0.234023415	1
optimal_loci_18698_G1	1018	0.179202	34.53	15902	37.03	1	1.330007457	0.199	0.221503698	1
optimal_loci_19015_G1	1207	0.177841	0	1001	38.77	2	20.86042949	0.287	0.204605089	3
optimal_loci_19073_G1	1507	0.175506	0	2001	48.1	2	17.32070507	0.499	0.202502195	3
optimal_loci_19093_G1	1168	0.014192	0	1001	40.06	2	6.09958815	0.154	0.201706853	3
optimal_loci_19848_G1	1141	0.087337	0	4304	33.3	1	0.058332362	0.177	0.16207122	1
optimal_loci_20568_G1	2974	0.02816	20.44	2057	39.81	2	0.365307593	0.207	0.12416814	2
optimal_loci_20623_G1	1030	0.049876	39.61	4179	65.63	1	1.471580223	0.528	0.121610275	2
optimal_loci_20899_G1	1110	0.022727	0	4149	44.23	1	8.028679239	0.49	0.109657478	2
optimal_loci_20910_G1	1580	0.020914	5.13	11397	47.4	1	8.028679239	0.425	0.109600052	2
optimal_loci_24242_G1	1166	0.214805	0	19512	37.65	1	7.713961533	0.114	0.070597055	1
optimal_loci_24777_G1	1106	0.042095	0	5252	54.52	2	3.639627836	0.881	0.091295098	2

optimal_loci_24784_G1	1008	0.040266	21.83	1620	37.5	1	13.86676006	0.107	0.091500695	2
optimal_loci_25001_G1	1037	0.042739	17.94	12602	58.72	1	93.27353588	0.738	0.098411885	1
optimal_loci_25099_G1	1541	0.046799	0	7039	42.95	1	5.509738271	0.222	0.102912813	2
optimal_loci_25102_G1	1717	0.037586	22.95	3593	38.78	1	9.295802385	0.093	0.103207383	2
optimal_loci_25470_G1	2068	0.031907	0	9843	50.43	1	5.339401699	0.566	0.116174846	1
optimal_loci_25586_G1	1404	0.081797	0	2228	58.61	2	27.87444258	0.582	0.121350768	2
optimal_loci_25653_G1	1707	0.151596	7.91	1001	41.41	2	2.144517122	0.222	0.12406936	2
optimal_loci_25737_G1	1153	0.149674	22.2	9400	40.32	2	1.605517346	0.426	0.127477865	3
optimal_loci_25738_G1	1555	0.149674	0	5028	42.57	2	1.605517346	0.366	0.12750173	3
optimal_loci_25741_G1	1057	0.149674	0	2624	37.74	2	1.605517346	0.034	0.127519175	3
optimal_loci_26001_G1	1481	0.157634	0	17075	43.14	1	14.03167646	0.172	0.138132707	3
optimal_loci_26033_G1	1013	0.157634	19.84	6218	45.8	1	2.600571215	0.486	0.13941615	3
optimal_loci_26052_G1	1017	0.157634	38.94	13422	41.88	1	79.94940496	0.194	0.140059031	3
optimal_loci_26311_G1	1027	0.091166	0	3318	56.76	2	0.018299609	0.538	0.151018687	2
optimal_loci_26347_G1	2243	0.079907	19.57	1903	40.57	1	0.078952173	0.222	0.153407861	5
optimal_loci_26389_G1	1373	0.093649	35.18	18640	51.05	1	1.071189135	0.534	0.154329774	5
optimal_loci_26395_G1	1566	0.093649	23.88	14750	45.91	1	1.071189135	0.378	0.154544719	5
optimal_loci_26433_G1	1642	0.089924	5.54	2701	50.66	1	3.802624659	0.544	0.15541021	5
optimal_loci_26476_G1	1339	0.092099	0	1636	57.28	2	6.164501178	0.558	0.156505355	4
optimal_loci_27175_G1	1132	0.056153	0	2682	38.07	2	132.8751096	0.052	0.178146951	4
optimal_loci_27178_G1	1174	0.056153	0	2398	46.33	2	132.8751096	0.26	0.178201371	4
optimal_loci_27184_G1	1077	0.056153	16.43	6506	47.35	2	132.8751096	0.462	0.178226066	4
optimal_loci_27185_G1	1362	0.056153	9.1	8297	33.7	1	265.4488881	0.081	0.178236832	4
optimal_loci_27258_G1	1409	0.119309	11.43	3290	32.71	2	64.22537745	0.177	0.182830472	1
optimal_loci_27955_G1	1180	0.586681	0	2597	41.61	1	25.45456244	0.24	0.213588637	1
optimal_loci_28113_G1	1494	0.305679	0	11530	44.04	1	34.98726783	0.341	0.219717941	1
optimal_loci_28294_G1	1216	0.549195	0	14238	30.09	2	0.016467518	0	0.227585789	1
optimal_loci_28517_G1	1347	0.949343	0	1313	49.51	3	8.510783271	0.335	0.236160177	3
optimal_loci_28538_G1	1921	0.817545	19.26	1673	36.23	2	2.683111723	0.07	0.236671634	3
optimal_loci_28560_G1	1705	0.695191	2.87	10160	45.63	1	0.02866405	0.327	0.23752354	4
optimal_loci_28627_G1	1345	0.309986	38.66	13192	37.32	1	0.609944317	0.108	0.24051556	2
optimal_loci_28700_G1	2659	0.674724	31.59	2791	34.37	1	10.97385632	0.12	0.244253009	3
optimal_loci_28732_G1	1030	0.868756	39.42	1001	33.39	1	3.777040016	0.122	0.245805949	3

optimal_loci_28771_G1	1473	1.001132	12.22	2869	44.39	3	4.514351346	0.332	0.246835698	3
optimal_loci_28905_G1	1202	0.310837	6.74	3085	43.67	4	132.9767715	0.228	0.252700169	1
optimal_loci_28998_G1	1859	0.675156	0	14439	45.88	1	0.971050988	0.444	0.256054777	1
optimal_loci_29158_G1	2344	0.590675	0	7037	41.63	1	1.206277533	0.204	0.260837899	3
optimal_loci_29179_G1	2139	0.590675	34.13	7485	40.62	3	1.833020781	0.319	0.261004441	3
optimal_loci_29180_G1	1970	0.590675	34.62	4810	40.25	3	1.833020781	0.122	0.261021537	3
optimal_loci_29352_G1	1434	0.85151	0	1765	46.37	2	8.704487768	0.334	0.267923253	4
optimal_loci_29395_G1	1449	1.153892	0	3180	48.3	1	0.349529177	0.369	0.269478628	4
optimal_loci_29396_G1	1031	1.153892	27.26	2091	39.57	1	0.349529177	0.161	0.269487687	4
optimal_loci_29415_G1	1161	0.940082	0	1785	53.05	1	0.17391138	0.661	0.270057736	4
optimal_loci_29513_G1	1119	1.621101	13.23	2472	46.38	2	3.602733112	0.127	0.273651274	1
optimal_loci_29843_G1	2204	1.141486	7.94	2764	36.11	2	1.179432428	0.04	0.286318942	4
optimal_loci_29860_G1	1222	1.295009	0	2075	42.55	1	102.5274595	0.249	0.287296033	4
optimal_loci_29871_G1	1347	1.353481	0	2560	54.86	3	4.939906671	0.586	0.287748441	4
optimal_loci_29890_G1	1008	0.857665	0	1118	42.65	2	2.992143939	0.214	0.289052298	4
optimal_loci_29982_G1	1025	1.228404	28.49	2950	42.43	2	13.06454895	0.101	0.293439595	3
optimal_loci_29984_G1	1301	1.228404	0	4507	44.04	2	13.06454895	0.327	0.293448955	3
optimal_loci_29988_G1	1223	1.228404	0	1001	36.71	2	17.96773761	0.213	0.293671672	3
optimal_loci_30074_G1	1030	0.093084	7.09	1854	59.02	3	0.013958382	0.551	0.298318752	2
optimal_loci_30076_G1	1033	0.094071	0	3093	47.14	3	0.013958382	0.486	0.298331081	2
optimal_loci_30421_G1	1153	0.277871	0	8259	58.45	1	0.416174054	0.504	0.3141474	3
optimal_loci_30422_G1	2412	0.277871	0	2001	36.15	1	0.416174054	0.157	0.31417745	3
optimal_loci_30432_G1	1444	0.277871	0	6728	57.89	3	4.805464672	0.613	0.314571357	3
optimal_loci_30584_G1	1359	2.837071	0	5107	44	2	16.851732	0.31	0.319249113	1
optimal_loci_30711_G1	2466	0.475893	5.03	1011	51.7	2	0.007854302	0.637	0.324023385	3
optimal_loci_30714_G1	2395	0.475801	1.29	1298	35.69	2	1.922277199	0.103	0.324190865	3
optimal_loci_30715_G1	2722	0.475801	1.43	3806	56.79	2	1.922277199	0.499	0.324205942	3
optimal_loci_30777_G1	1101	0.542932	0	2934	43.68	1	0.10264377	0.296	0.327522198	2
optimal_loci_30845_G1	2462	0.632445	0	2108	35.74	4	5.090210943	0.06	0.32936796	2
optimal_loci_31008_G1	1403	0.727193	16.46	5941	34.85	1	48.41586095	0.074	0.333512455	2
optimal_loci_31025_G1	1331	0.874186	0	11116	46.43	1	42.93358149	0.488	0.33383071	2
optimal_loci_31101_G1	1671	3.829776	37.94	14720	35.24	1	11.15668503	0.222	0.338310947	2
optimal_loci_31147_G1	1071	2.417029	31	9079	47.24	1	0.031099928	0.522	0.340414358	3

optimal_loci_31177_G1	2402	2.681721	0	2001	46	4	6.875760686	0.415	0.341824428	2
optimal_loci_31474_G1	1399	0.017106	0	2114	45.31	1	0.027202357	0.375	0.351369937	2
optimal_loci_31481_G1	1083	0.017106	0	1930	37.76	1	0.532444614	0.197	0.351606072	2
optimal_loci_31567_G1	1037	1.6267	0	1096	39.44	1	207.3989086	0.095	0.355992636	4
optimal_loci_31611_G1	1263	1.116997	0	3431	40.77	1	3.405537984	0.242	0.35742621	6
optimal_loci_31621_G1	1630	1.116997	33.93	1220	38.46	1	69.73762547	0.206	0.357600741	6
optimal_loci_31669_G1	2884	0.92146	1.11	7263	55.72	1	3.201549358	0.408	0.358782786	8
optimal_loci_31710_G1	3965	1.089961	4.19	4043	45.29	1	1.771070208	0.361	0.36031203	7
optimal_loci_31712_G1	1470	1.089961	0	8650	57.27	1	1.771070208	0.826	0.360339723	7
optimal_loci_31763_G1	1015	1.272812	0	7054	39.01	1	0.640332023	0.096	0.361740681	5
optimal_loci_31764_G1	3580	1.281486	1.45	2963	43.85	1	0.640332023	0.345	0.361749854	5
optimal_loci_31876_G1	1442	0.723993	39.67	16431	37.51	1	7.544476076	0.332	0.365464327	1
optimal_loci_31980_G1	1003	1.712125	0	2781	49.95	2	37.9822666	0.524	0.369303901	1
optimal_loci_32088_G1	1372	1.428143	2.84	4917	57.28	2	10.74347696	0.733	0.373086759	4
optimal_loci_32090_G1	1211	1.428143	0	3211	49.54	2	10.74347696	0.335	0.373098402	4
optimal_loci_32133_G1	2162	1.302793	0	1061	57.12	1	8.65402018	0.545	0.375038829	5
optimal_loci_32137_G1	1469	1.302793	0	4930	33.83	1	8.65402018	0.163	0.375062087	5
optimal_loci_32236_G1	1833	1.67013	11.35	1171	51.28	1	1.805231204	0.461	0.377479947	5
optimal_loci_32267_G1	1004	2.333205	0	18757	44.12	1	18.65471202	0.36	0.378630288	4
optimal_loci_32299_G1	1410	2.458319	0	3351	65.17	1	0.530054277	0.772	0.379900572	6
optimal_loci_32346_G1	1059	2.735521	0	3350	47.87	1	0.399254003	0.609	0.381587689	6
optimal_loci_32355_G1	1293	2.735521	5.03	6018	38.28	1	1.459995485	0.138	0.381919884	5
optimal_loci_32356_G1	1733	2.735521	9.23	4155	32.83	1	1.459995485	0.15	0.381928438	5
optimal_loci_32383_G1	1931	2.344027	0	2001	40.96	3	1.280595607	0.044	0.38318988	5
optimal_loci_32446_G1	3313	1.53928	2.69	2363	56.53	1	0.147158364	0.68	0.385163639	3
optimal_loci_32522_G1	1455	2.675096	0	1142	52.57	3	4.220543906	0.4	0.387720606	7
optimal_loci_32559_G1	1269	3.504185	33.88	2081	34.75	3	1.246949896	0.15	0.389280435	6
optimal_loci_32585_G1	1660	3.6962	21.02	6841	34.09	2	9.879981618	0.214	0.39009403	6
optimal_loci_32588_G1	2764	3.6962	7.27	2589	28.14	1	19.7153205	0.208	0.390112954	6
optimal_loci_32612_G1	2321	3.302941	11.16	3923	35.76	3	8.537009607	0.252	0.390700658	7
optimal_loci_32613_G1	1040	3.302941	0	2776	33.26	3	8.537009607	0.055	0.390715253	7
optimal_loci_32689_G1	1142	1.753269	3.42	1370	45.44	5	167.6740698	0.325	0.393672451	6
optimal_loci_32717_G1	2032	1.194649	1.48	1258	47.88	3	123.2244064	0.46	0.394526743	4

optimal_loci_32718_G1	1210	1.194649	3.64	2001	45.12	3	123.2244064	0.28	0.394574604	4
optimal_loci_32753_G1	1394	0.757841	0	1135	60.68	1	0.261670469	0.675	0.395897661	4
optimal_loci_32914_G1	1084	1.143933	0	2884	35.14	2	0.029804097	0.199	0.402473446	2
optimal_loci_32979_G1	1718	1.285847	0	2075	40.8	2	0.42220368	0.297	0.403683016	2
optimal_loci_33122_G1	1219	1.279387	9.27	2007	33.63	2	70.75309731	0.119	0.407376619	2
optimal_loci_33200_G1	1057	1.278198	37.84	1814	29.61	1	373.3248184	0.137	0.409771582	2
optimal_loci_33362_G1	1545	0.643607	0	1010	43.17	2	3.401348378	0.265	0.415148244	5
optimal_loci_33369_G1	1164	0.643607	0	8720	40.97	2	3.401348378	0.187	0.415289905	5
optimal_loci_33376_G1	1033	0.591395	0	8043	36.49	1	0.055590605	0.067	0.415373763	5
optimal_loci_33378_G1	1275	0.591395	0	5845	39.52	1	0.055590605	0.166	0.415385521	5
optimal_loci_33407_G1	1314	0.514096	20.09	1198	52.28	3	0.736769432	0.523	0.416311419	5
optimal_loci_33474_G1	1356	0.751941	0	5430	37.61	1	88.40504608	0.191	0.419644645	4
optimal_loci_33535_G1	1025	2.159286	0	2001	27.31	3	18.83449092	0.102	0.422138945	9
optimal_loci_33537_G1	1952	2.159286	0	4722	29.04	3	18.83449092	0.147	0.422199701	9
optimal_loci_33540_G1	2134	2.159286	6.14	1605	35.98	3	18.83449092	0.114	0.422217344	9
optimal_loci_33549_G1	1552	2.592519	4.7	1870	53.6	1	24.63228637	0.649	0.423018761	8
optimal_loci_33562_G1	1308	2.316275	0	2741	35.77	4	26.68843988	0.083	0.423232221	8
optimal_loci_33615_G1	1029	2.496314	9.62	1302	34.2	1	14.15407025	0.268	0.424967026	8
optimal_loci_33618_G1	1444	2.496314	0	18074	32.4	1	14.15407025	0.286	0.425067847	8
optimal_loci_33619_G1	1120	2.496314	6.25	19679	34.46	1	14.15407025	0.139	0.425077495	8
optimal_loci_33738_G1	1101	0.955856	21.07	6771	31.24	2	14.59843425	0.177	0.428313159	3
optimal_loci_33862_G1	1381	1.180457	0	1570	35.77	1	145.3979355	0.036	0.431277305	6
optimal_loci_33863_G1	1709	1.180457	5.68	3237	37.56	1	145.3979355	0.222	0.431287326	6
optimal_loci_33889_G1	1637	1.425026	0	14909	43.18	2	3.359795267	0.461	0.432057881	6
optimal_loci_33891_G1	1637	1.425026	8.31	13891	42.02	2	3.359795267	0.244	0.432081138	6
optimal_loci_33933_G1	2202	1.59982	21.66	11070	34.28	1	14.01488626	0.103	0.432945667	7
optimal_loci_34010_G1	1320	1.568224	5	17639	59.46	1	0.383289558	0.681	0.435040037	8
optimal_loci_34027_G1	1336	1.524119	0	1001	40.11	2	0.779873421	0.025	0.435896066	6
optimal_loci_34049_G1	2743	1.405693	10.28	11426	37.07	1	4.525121391	0.18	0.43656565	5
optimal_loci_34077_G1	1513	1.326727	4.56	8526	45.07	1	7.982081326	0.292	0.437151755	6
optimal_loci_34083_G1	2101	1.274837	11.14	13222	41.31	1	7.982081326	0.278	0.437179984	6
optimal_loci_34158_G1	1015	1.719899	13.3	1767	41.47	1	0.034681132	0.159	0.440037851	4
optimal_loci_34244_G1	1011	2.739201	0	1001	39.46	1	1.756839825	0.331	0.442387789	6

optimal_loci_34266_G1	1531	2.70804	0	2916	41.34	1	0.193086668	0.181	0.443202172	6
optimal_loci_34275_G1	1033	2.624463	22.65	8604	39.3	1	0.132240029	0.072	0.443459743	7
optimal_loci_34281_G1	1341	2.486544	11.56	15990	35.42	2	4.716430692	0.086	0.443505255	7
optimal_loci_34329_G1	1289	0.951483	0	3330	59.27	1	16.52860807	0.692	0.444653822	8
optimal_loci_34365_G1	1280	0.943908	0	1235	44.92	2	92.85965284	0.435	0.445568353	7
optimal_loci_34407_G1	1628	0.489412	15.79	2389	37.46	2	1.351940908	0.363	0.446259012	6
optimal_loci_34424_G1	1896	0.413033	3.27	2509	42.14	1	15.86641964	0.293	0.44664582	4
optimal_loci_34501_G1	1601	1.620245	0	7147	39.35	1	35.36206905	0.257	0.450823636	2
optimal_loci_34516_G1	1680	1.643348	18.57	15746	42.5	2	1.736695402	0.23	0.451316903	2
optimal_loci_34613_G1	1204	2.052535	39.78	1001	36.04	2	0.157130886	0.116	0.454733271	2
optimal_loci_34621_G1	2082	2.052535	0	2001	33.23	1	0.142059088	0.06	0.454869901	2
optimal_loci_34728_G1	1576	3.040325	6.85	2379	52.15	2	1.549711101	0.526	0.458392122	6
optimal_loci_34733_G1	1554	3.178244	5.98	5058	49.16	2	1.549711101	0.334	0.458519663	6
optimal_loci_34742_G1	1099	3.178244	17.83	2001	39.76	2	0.159684648	0.295	0.458871239	6
optimal_loci_34764_G1	1574	3.290561	0	13723	35.51	3	3.270681241	0.23	0.459396642	6
optimal_loci_34793_G1	1410	4.316681	16.17	1265	35.1	3	40.98119334	0.104	0.460028655	6
optimal_loci_34809_G1	1114	2.108106	18.04	1001	37.61	2	11.66453271	0.099	0.460919099	6
optimal_loci_34911_G1	1248	0.244455	9.94	10498	46.87	3	1.388755868	0.334	0.463949345	3
optimal_loci_34963_G1	1209	0.248974	20.51	4550	36.22	1	3.691022687	0.014	0.46602401	3
optimal_loci_34971_G1	1121	0.248974	0	3152	48.52	1	3.691022687	0.47	0.466089058	3
optimal_loci_35100_G1	1281	0.251682	10.69	12554	36.37	1	9.37104086	0.262	0.470182319	2
optimal_loci_35102_G1	1017	0.251682	0	9728	35.29	1	9.37104086	0.126	0.470200894	2
optimal_loci_35280_G1	1422	0.23893	0	1001	36	2	4.420620893	0.021	0.474380604	4
optimal_loci_35342_G1	1173	0.31547	10.49	1780	39.47	2	1.850515803	0	0.476714041	4
optimal_loci_35343_G1	1879	0.31547	0	1001	40.39	2	1.850515803	0.289	0.476721976	4
optimal_loci_35347_G1	1392	0.31547	0	15561	49.85	1	0.121348878	0.421	0.476838739	4
optimal_loci_35492_G1	1041	1.505486	8.36	7733	60.23	2	0.802353233	0.782	0.48077804	6
optimal_loci_35503_G1	1095	1.505486	3.01	1001	46.11	2	0.802353233	0.402	0.480844429	6
optimal_loci_35552_G1	1284	1.639781	2.49	7564	44	1	9.922660564	0.42	0.482072429	6
optimal_loci_35554_G1	1909	1.639781	0	4902	34.67	1	9.922660564	0.103	0.482084674	6
optimal_loci_35560_G1	1078	1.639781	0	1525	33.48	1	9.922660564	0.109	0.482165628	6
optimal_loci_35573_G1	1162	1.58813	0	8844	50.77	2	29.9606265	0.44	0.483004357	7
optimal_loci_35669_G1	1255	1.041556	0	3509	38.08	1	7.719766086	0.378	0.485522533	3

optimal_loci_35693_G1	1461	1.041484	0	8523	44.28	2	0.507412117	0.4	0.486295727	3
optimal_loci_35744_G1	1161	1.643741	0	11691	40.82	1	2.359631812	0.189	0.488638789	3
optimal_loci_35783_G1	1301	1.712803	15.91	6400	41.04	2	15.40632939	0.146	0.490358698	2
optimal_loci_36002_G1	1247	1.070158	15.96	10224	31.03	1	30.825439	0.116	0.49637835	1
optimal_loci_36257_G1	2470	0.338532	13.81	13177	41.25	1	11.16852243	0.197	0.503350013	2
optimal_loci_36329_G1	1495	0.081095	12.11	2001	33.97	1	25.81479381	0	0.50631651	2
optimal_loci_36469_G1	1378	0.135623	21.63	2308	37.3	3	0.051728594	0.109	0.511334125	1
optimal_loci_36579_G1	2720	0.020755	13.68	15196	40.58	2	18.86304296	0.253	0.515788375	1
optimal_loci_36750_G1	1450	0.046306	0	7165	27.24	2	8.48636671	0.071	0.52395853	1
optimal_loci_36922_G1	2678	0.047948	9.3	4557	39.24	4	5.234346336	0.218	0.528759078	5
optimal_loci_36925_G1	1512	0.047948	24.54	2638	47.08	2	9.102067797	0.351	0.528847167	5
optimal_loci_36927_G1	1911	0.047948	9.94	1004	56.77	1	3.041934378	0.788	0.528888663	5
optimal_loci_36962_G1	1571	0.043117	10.95	5093	42.01	1	13.50782875	0.311	0.530016426	5
optimal_loci_37020_G1	1933	0.041431	7.35	3086	49.81	3	12.75754871	0.403	0.530868415	7
optimal_loci_37120_G1	1399	0.042007	2.29	2023	45.53	3	26.77632139	0.48	0.533605305	9
optimal_loci_37130_G1	1095	0.042007	0	6685	44.1	4	20.08224104	0.14	0.533658084	9
optimal_loci_37143_G1	1039	0.041471	0	3035	52.06	2	11.86842862	0.255	0.533982825	8
optimal_loci_37146_G1	1388	0.041471	0	5960	55.11	2	11.86842862	0.459	0.534000408	8
optimal_loci_37213_G1	1476	0.047565	33.6	8092	37.33	2	5.45867098	0.143	0.535604053	12
optimal_loci_37214_G1	1784	0.047565	0	10508	58.01	2	5.45867098	0.738	0.535618577	12
optimal_loci_37226_G1	1017	0.042435	7.18	2001	58.6	2	13.20729905	0.605	0.536485685	12
optimal_loci_37229_G1	1796	0.042435	0	2264	49.44	2	13.20729905	0.354	0.536500394	12
optimal_loci_37244_G1	1453	0.022769	0	7555	36.95	2	118.5197406	0.107	0.537188216	9
optimal_loci_37254_G1	1071	0.031582	0	1801	34.64	2	26.6591814	0.081	0.537655665	12
optimal_loci_37265_G1	1408	0.031582	0	19964	46.73	1	43.78929631	0.346	0.537812607	12
optimal_loci_37282_G1	1375	0.032814	0	3287	38.03	2	40.94387679	0.307	0.538035324	12
optimal_loci_37332_G1	1662	0.022753	21.78	7980	35.07	4	5.991041923	0.153	0.539518961	8
optimal_loci_37353_G1	1635	0.011131	0	2440	41.52	1	21.06248367	0.272	0.540542644	7
optimal_loci_37354_G1	1023	0.011131	11.53	4256	48.97	1	21.06248367	0.359	0.540553561	7
optimal_loci_37357_G1	1604	0.011131	17.46	6410	54.86	1	21.06248367	0.505	0.540566509	7
optimal_loci_37448_G1	1310	0.011755	32.6	1471	36.48	3	20.22803232	0.135	0.543953368	2
optimal_loci_37539_G1	1791	0.012138	36.29	4399	45.72	3	6.003119083	0.358	0.546321767	3
optimal_loci_37653_G1	1232	0.01105	0	5754	40.42	1	17.12564684	0.308	0.548730676	2

optimal_loci_37808_G1	2218	0.021931	1.85	3921	52.34	2	42.04979789	0.463	0.552620252	5
optimal_loci_37810_G1	1076	0.021931	0	7053	50.55	2	42.04979789	0.515	0.552639079	5
optimal_loci_37811_G1	1451	0.021931	31.36	8325	51.06	2	42.04979789	0.545	0.552646726	5
optimal_loci_37835_G1	1184	0.011016	18.5	6793	35.81	1	43.40441757	0	0.553134612	5
optimal_loci_37883_G1	1411	0.010133	0	1743	37.63	2	56.28981278	0.137	0.55452178	5
optimal_loci_38115_G1	1536	0.020538	0	7827	36.71	1	38.46925513	0.179	0.562859571	4
optimal_loci_38138_G1	1001	0.010263	2.8	5457	40.95	1	3.962197901	0.153	0.563412079	5
optimal_loci_38141_G1	1271	0.010263	0	3440	34.61	2	0.097195089	0.095	0.563514174	5
optimal_loci_38204_G1	1495	0.011144	19.33	14188	50.63	2	8.10058198	0.393	0.565617464	6
optimal_loci_38227_G1	1735	0.011185	5.94	5528	44.72	2	12.28356625	0.328	0.566140721	5
optimal_loci_38311_G1	2299	0.010551	28.93	2001	35.01	4	11.86236245	0.128	0.568443435	6
optimal_loci_38329_G1	2077	0.01038	0	13286	33.79	2	0.831093938	0.067	0.569219707	6
optimal_loci_38330_G1	1234	0.01038	0	10176	34.11	2	0.831093938	0.127	0.56924347	6
optimal_loci_38368_G1	1030	0.010871	12.33	4256	38.64	3	9.416628683	0.246	0.570496784	7
optimal_loci_38417_G1	1497	0.010915	13.83	1823	39.27	2	2.785489321	0.086	0.571824067	6
optimal_loci_38428_G1	1060	0.010915	0	5372	40.84	2	22.83153479	0.243	0.572111243	6
optimal_loci_38439_G1	1042	0.020421	0	2514	51.72	4	3.615578467	0.524	0.572414764	4
optimal_loci_38533_G1	2350	0.010637	4.98	5922	56.89	1	30.39933602	0.686	0.575826378	6
optimal_loci_38544_G1	1207	0.010516	0	15402	47.63	1	30.39933602	0.567	0.57604523	6
optimal_loci_38577_G1	2205	0.010739	18.19	11982	62.99	2	1.254710599	0.875	0.576698806	7
optimal_loci_38651_G1	1550	0.010804	0	2655	43.8	2	5.512293019	0.301	0.578221419	7
optimal_loci_38684_G1	1055	0.011007	38.96	1081	35.92	1	9.352040883	0.176	0.578770735	8
optimal_loci_38685_G1	1390	0.011007	8.71	2751	42.87	1	9.352040883	0.195	0.578780774	8
optimal_loci_38698_G1	1165	0.012718	0	2354	54.5	1	6.780366814	0.684	0.5793964	6
optimal_loci_38740_G1	1293	0.011218	0	1001	35.88	3	12.42923541	0.123	0.581429184	5
optimal_loci_38789_G1	1539	0.010461	0	2082	41.19	1	59.63375711	0.224	0.584194303	5
optimal_loci_38817_G1	1147	0.017311	15.17	3206	38.18	1	4.345671959	0.152	0.585129771	4
optimal_loci_38820_G1	1701	0.014741	0	6624	42.68	1	4.345671959	0.245	0.585150318	4
optimal_loci_38826_G1	1115	0.014728	0	5759	37.93	1	23.99582757	0.243	0.585459051	4
optimal_loci_39389_G1	2164	0.011215	0	4208	38.26	2	0.903331332	0.133	0.602261242	1
optimal_loci_39461_G1	1469	0.073066	19.33	9723	33.62	3	7.991863142	0.166	0.605288351	5
optimal_loci_39472_G1	1336	0.091352	0	3003	37.64	1	102.6979625	0.126	0.605705112	5
optimal_loci_39485_G1	1237	0.096669	10.11	18265	48.9	1	13.4144878	0.277	0.606021612	5

optimal_loci_39518_G1	1125	0.106745	38.22	1808	40.26	1	196.3550199	0.171	0.6066124	5
optimal_loci_39573_G1	1067	0.126416	31.21	2914	39.83	1	0.021563411	0.296	0.608276897	5
optimal_loci_39923_G1	1619	0.125685	0	1568	39.9	2	1.479774423	0.225	0.61819784	2
optimal_loci_39955_G1	1185	0.124238	16.79	2157	41.26	3	3.153743501	0.221	0.618925974	3
optimal_loci_40008_G1	1115	0.127756	16.14	2550	38.02	1	7.091183638	0.092	0.621247461	5
optimal_loci_40026_G1	1460	0.123737	0	17284	40.47	1	0.257897062	0.115	0.622284868	4
optimal_loci_40071_G1	1498	0.12672	1.94	16678	40.58	1	4.328615527	0.224	0.623564037	4
optimal_loci_40073_G1	1455	0.12672	0	3163	39.65	1	4.328615527	0.223	0.623645538	4
optimal_loci_40335_G1	1353	0.123959	6.95	13944	49.22	1	1.539871268	0.378	0.633575072	3
optimal_loci_40348_G1	1078	0.134478	0	1384	56.58	2	0.300141223	0.639	0.6339793	3
optimal_loci_40351_G1	2305	0.132312	13.36	2655	42.6	3	8.609533192	0.375	0.634075125	3
optimal_loci_40494_G1	1287	0.121562	11.81	2464	43.12	2	25.33516297	0.07	0.637158487	3
optimal_loci_40563_G1	2303	0.129085	34.3	13426	37.6	2	0.923387716	0.217	0.63863925	3
optimal_loci_40607_G1	2003	0.124026	0	2296	44.13	3	2.97025499	0.328	0.639404876	3
optimal_loci_40822_G1	1113	0.120201	26.24	5361	41.5	1	43.09493659	0.127	0.645767266	2
optimal_loci_40853_G1	1190	0.127634	16.39	7181	32.18	1	2.830939913	0.104	0.646613395	2
optimal_loci_40999_G1	1788	0.120181	26.51	19445	47.42	1	0.092012036	0.366	0.650389183	4
optimal_loci_41007_G1	1272	0.121568	22.01	1466	37.02	1	0.092012036	0.178	0.650500362	4
optimal_loci_41055_G1	1224	0.129981	0	13049	41.42	1	12.74694918	0.287	0.651983307	4
optimal_loci_41089_G1	1428	0.132868	2.17	1818	50.63	1	0.878592446	0.453	0.653144282	5
optimal_loci_41153_G1	1090	0.128244	17.71	3182	37.52	1	27.4205524	0.125	0.655634133	3
optimal_loci_41211_G1	1481	0.125354	18.03	16864	34.77	1	0.255224823	0.16	0.657047094	4
optimal_loci_41303_G1	1103	0.133704	26.65	2751	41.7	3	0.151527994	0.339	0.659811588	4
optimal_loci_41309_G1	2713	0.133704	0	2556	33.39	4	0.327095065	0.148	0.659829886	4
optimal_loci_41373_G1	1163	0.105546	0	3366	40.92	1	12.80366957	0.334	0.662252808	3
optimal_loci_41528_G1	1606	0.194042	8.16	1248	35.92	2	0.953358362	0.166	0.66654815	1
optimal_loci_41602_G1	1310	0.322306	34.12	2510	55.72	3	17.80938012	0.78	0.669732586	3
optimal_loci_41603_G1	1533	0.322306	0	4082	50.88	3	17.80938012	0.49	0.669742036	3
optimal_loci_41706_G1	3381	0.277069	5.44	2026	39.39	3	12.26782701	0.243	0.671330268	3
optimal_loci_41929_G1	1575	0.23197	35.81	1001	31.93	3	0.107351875	0.071	0.677839754	1
optimal_loci_42030_G1	1048	0.227921	4.39	1614	39.02	1	6.148692767	0.367	0.68117473	3
optimal_loci_42043_G1	1686	0.252662	4.69	4954	48.81	2	12.63470185	0.6	0.681775034	4
optimal_loci_42117_G1	1488	0.325201	13.84	16672	40.32	1	0.304045758	0.34	0.683439291	4

optimal_loci_42156_G1	1392	0.388006	19.47	3586	37.78	4	133.9429103	0.172	0.684492544	5
optimal_loci_42257_G1	2190	0.478012	1.37	2209	50.95	2	7.335890378	0.551	0.687129046	8
optimal_loci_42258_G1	2725	0.478012	10.06	1182	34.31	2	7.335890378	0.109	0.687244246	8
optimal_loci_42318_G1	1027	0.459481	0	16422	40.79	1	6.880570796	0.403	0.688013688	7
optimal_loci_42322_G1	1047	0.459481	7.55	19026	29.03	1	6.880570796	0.139	0.688029342	7
optimal_loci_42331_G1	1659	0.459481	0	5941	44.48	1	22.04663632	0.232	0.688458877	7
optimal_loci_42334_G1	1187	0.459481	0	3972	47	1	22.04663632	0.396	0.688473551	7
optimal_loci_42348_G1	2322	0.459481	24.16	7389	40.26	1	22.04663632	0.216	0.688566731	7
optimal_loci_42422_G1	1427	0.469494	22.49	1001	40.92	3	10.83981009	0.384	0.693082784	2
optimal_loci_42424_G1	1231	0.469494	7.8	6130	37.12	4	8.129857567	0.052	0.693158328	2
optimal_loci_42511_G1	1238	0.284795	0	10392	45.63	2	6.49517639	0.495	0.696567326	8
optimal_loci_42513_G1	2433	0.255022	24.37	2114	46.69	1	6.549363762	0.403	0.696634448	8
optimal_loci_42519_G1	3035	0.255022	2.57	10605	57	1	6.549363762	0.611	0.696741605	8
optimal_loci_42525_G1	3338	0.216044	4.43	16345	53.59	1	6.549363762	0.518	0.69677611	8
optimal_loci_42549_G1	1100	0.051707	0	3449	40.54	3	0.122983933	0.37	0.697956339	8
optimal_loci_42557_G1	1740	0.052122	0	2001	33.39	5	3.408329025	0.145	0.698222199	8
optimal_loci_42565_G1	1144	0.052122	0	5744	46.76	2	4.110483641	0.324	0.698326795	8
optimal_loci_42568_G1	1184	0.052122	6	8678	46.11	2	4.110483641	0.176	0.698344432	8
optimal_loci_42715_G1	2019	0.067087	2.82	1001	51.16	2	32.48269997	0.418	0.701715987	2
optimal_loci_42746_G1	2071	0.080751	0	1327	45	2	4.410838745	0.455	0.703261779	2
optimal_loci_42894_G1	1105	0.072917	0	2001	41.17	3	2.523936412	0.222	0.70807248	11
optimal_loci_42908_G1	1915	0.068263	0	2179	44.12	2	21.75325267	0.322	0.709386527	13
optimal_loci_42916_G1	1096	0.068263	23.27	12290	40.6	1	43.50650535	0.196	0.709521684	13
optimal_loci_42928_G1	1650	0.071258	12.91	2500	37.27	2	10.7869635	0.137	0.710004533	14
optimal_loci_42935_G1	1244	0.070595	0	10115	41.31	1	12.73828673	0.25	0.71020531	14
optimal_loci_42936_G1	1390	0.070595	0	11514	43.52	1	12.73828673	0.27	0.71021372	14
optimal_loci_42938_G1	1246	0.070595	0	13465	54.57	1	12.73828673	0.461	0.710225448	14
optimal_loci_42939_G1	1935	0.254944	1.55	15148	54.62	1	12.73828673	0.656	0.710235565	14
optimal_loci_42942_G1	1933	0.254944	0	18120	59.07	1	12.73828673	0.603	0.71025343	14
optimal_loci_42957_G1	1269	0.322781	0	5597	31.12	1	0.717340143	0.294	0.71053394	14
optimal_loci_42970_G1	2379	1.148495	1.18	6606	43.88	3	90.82787333	0.349	0.710910985	15
optimal_loci_42985_G1	1794	1.722318	7.8	3333	41.8	3	5.749727976	0.192	0.711174856	14
optimal_loci_42991_G1	1093	1.722318	35.04	1001	41.17	3	5.749727976	0.138	0.711203109	14

optimal_loci_43048_G1	1151	2.142868	0	1442	54.56	1	4.717441761	0.372	0.712979704	13
optimal_loci_43062_G1	1248	2.384845	13.14	1826	37.66	2	11.42099488	0.135	0.713926372	7
optimal_loci_43087_G1	1358	2.799876	0	1001	50.66	3	10.85324449	0.48	0.714787985	4
optimal_loci_43176_G1	1068	1.375542	0	10017	41.47	1	0.344752083	0.164	0.716924361	5
optimal_loci_43222_G1	1457	1.157691	0	4210	38.5	1	6.173596937	0.447	0.718496784	3
optimal_loci_43223_G1	1528	1.157691	0	2574	36.78	1	6.173596937	0.087	0.718506192	3
optimal_loci_43377_G1	1433	0.656363	2.02	4657	47.8	2	4.60541645	0.378	0.723338545	1
optimal_loci_43565_G1	2019	0.65504	12.18	1001	42.59	2	64.40155138	0.305	0.729129811	5
optimal_loci_43577_G1	2963	0.668	4.22	2001	41.3	2	23.65164825	0.275	0.730187464	5
optimal_loci_43588_G1	1957	0.668	9.61	1184	43.84	1	47.3032965	0.412	0.730313497	5
optimal_loci_43596_G1	1046	0.666618	28.78	1001	34.99	4	23.57172831	0.28	0.730759268	5
optimal_loci_43621_G1	1558	0.652872	0	1831	34.85	2	17.28827784	0.105	0.731312726	5
optimal_loci_43690_G1	2211	0.593102	1.27	4284	46.26	1	2.935578121	0.31	0.734455281	6
optimal_loci_43693_G1	1528	0.593102	13.42	1001	43.32	1	2.935578121	0.372	0.734479122	6
optimal_loci_43694_G1	1210	0.593102	0	2209	56.36	2	5.005302861	0.565	0.73452393	6
optimal_loci_43736_G1	1346	0.560757	19.61	2001	41.3	2	2.30376179	0.214	0.7353506	7
optimal_loci_43764_G1	1534	0.447093	16.23	3158	40.35	1	2.044480917	0.09	0.736153021	8
optimal_loci_43836_G1	1084	0.488914	0	18956	37.45	1	0.27844958	0.133	0.737405511	8
optimal_loci_43854_G1	1249	0.457521	10.97	5616	34.82	1	0.104886873	0.18	0.738052835	5
optimal_loci_43872_G1	1023	0.942828	16.72	18415	45.35	1	0.291919797	0.369	0.738522935	4
optimal_loci_44019_G1	2989	1.64676	1.07	8986	52.22	2	8.587489467	0.451	0.741766816	5
optimal_loci_44030_G1	1524	1.58402	34.51	3458	42.19	2	10.48811348	0.295	0.741998123	6
optimal_loci_44031_G1	1311	1.58402	0	2001	56.29	2	10.48811348	0.77	0.742008162	6
optimal_loci_44062_G1	1872	1.345734	0	2354	40.49	2	0.898694411	0.086	0.743253295	6
optimal_loci_44065_G1	1251	1.345734	0	2659	49.24	3	0.630076634	0.353	0.743301758	6
optimal_loci_44095_G1	1790	0.877385	15.92	11261	42.4	1	0.022806614	0.284	0.74484086	6
optimal_loci_44137_G1	2078	0.278092	1.64	2099	42.2	2	892.966274	0.221	0.747201433	2
optimal_loci_44307_G1	1508	0.275763	0	2182	50	3	8.614326952	0.456	0.752205162	4
optimal_loci_44345_G1	2080	0.282619	36.63	15520	43.26	1	0.28080591	0.264	0.753710565	4
optimal_loci_44363_G1	1406	0.281802	19.06	8741	42.53	2	0.007413835	0.343	0.754098412	5
optimal_loci_44370_G1	2255	0.27909	1.6	4536	37.87	1	46.16596044	0.253	0.754475319	5
optimal_loci_44445_G1	2017	0.280231	0	2946	53.79	2	23.88632052	0.615	0.757007609	3
optimal_loci_44515_G1	1104	0.273735	0	19740	53.44	1	1.008662484	0.615	0.761003109	2

optimal_loci_44531_G1	1802	0.273735	17.87	2107	42.28	1	1.008662484	0.343	0.76110491	2
optimal_loci_44624_G1	1088	0.507726	0	6972	35.11	3	4.044317824	0	0.764219765	6
optimal_loci_44633_G1	1351	0.507726	10.51	11800	39.82	4	5.918184654	0.134	0.764265445	6
optimal_loci_44635_G1	2227	0.507726	0	6761	38.48	4	5.918184654	0.252	0.76429047	6
optimal_loci_44637_G1	1283	0.507726	0	5057	37.1	3	7.608088452	0.132	0.764306388	6
optimal_loci_44649_G1	1199	0.604552	0	7911	61.05	2	10.05905981	0.743	0.764540202	6
optimal_loci_44702_G1	3478	1.693723	17.45	7107	32.43	3	1.567805588	0.038	0.766110046	7
optimal_loci_44776_G1	1093	2.486037	0	1001	38.51	1	3.794632305	0.091	0.769067844	3
optimal_loci_44900_G1	1196	1.060922	0	9846	43.56	1	8.624085709	0.152	0.772024224	6
optimal_loci_44930_G1	1082	0.278591	32.35	9382	37.33	1	4.998505875	0.081	0.773005805	5
optimal_loci_44932_G1	1291	0.278591	0	1330	31.13	1	4.998505875	0.091	0.773090005	5
optimal_loci_44933_G1	1539	0.278591	0	2666	58.67	1	4.998505875	0.638	0.773098036	5
optimal_loci_44937_G1	1022	0.210404	18.2	2809	36.88	2	16.14733189	0.25	0.773288942	5
optimal_loci_45046_G1	1017	0.804728	18.68	10268	38.15	4	35.59822147	0.095	0.776552792	2
optimal_loci_45047_G1	1196	0.804728	10.2	2001	39.04	2	67.08642708	0.245	0.776642871	2
optimal_loci_45163_G1	1175	0.819282	0	3045	38.89	2	0.590674639	0.11	0.781526404	3
optimal_loci_45176_G1	1106	0.816562	0	1079	48.64	1	5.907907829	0.51	0.783380251	7
optimal_loci_45202_G1	1758	0.822949	8.76	1631	55.46	3	2.620522113	0.539	0.784088872	8
optimal_loci_45222_G1	1095	0.827202	14.52	2457	49.31	1	0.164963239	0.312	0.784626279	7
optimal_loci_45300_G1	1058	0.827294	0	2521	39.13	1	0.077087726	0.137	0.785975251	10
optimal_loci_45301_G1	1194	0.827294	0	3791	36.59	1	0.077087726	0.143	0.785982885	10
optimal_loci_45306_G1	1313	0.827294	0	8383	45.62	1	0.077087726	0.189	0.786010489	10
optimal_loci_45338_G1	1990	0.651623	0	14278	41.95	1	8.21583554	0.152	0.786815056	9
optimal_loci_45355_G1	1281	0.604385	15.14	12990	31.77	1	8.801554564	0.067	0.787654836	7
optimal_loci_45356_G1	1164	0.604385	0	11743	37.02	1	8.801554564	0.223	0.787663036	7
optimal_loci_45372_G1	1414	0.604385	0	8899	43.7	1	16.77890815	0.212	0.787984362	7
optimal_loci_45565_G1	1043	0.315045	0	7915	40.26	3	17.99667492	0.182	0.79451487	2
optimal_loci_45568_G1	1091	0.315045	11.82	10658	42.8	3	17.99667492	0.141	0.794531359	2
optimal_loci_45689_G1	2257	2.007482	39.12	7376	34.82	2	4.966529074	0.02	0.798137299	3
optimal_loci_45708_G1	1697	1.998097	22.63	7382	53.74	5	22.04271925	0.6	0.798767779	3
optimal_loci_45724_G1	1958	2.365526	0	5724	42.49	3	6.419902163	0.347	0.798992691	3
optimal_loci_45895_G1	1378	1.683864	0	1001	51.52	5	1.801530429	0.459	0.805173818	5
optimal_loci_45908_G1	1083	1.53458	0	3157	51.43	3	72.09334655	0.317	0.805756491	5

optimal_loci_45914_G1	1077	1.582736	30.83	3796	29.34	1	0.17023875	0.171	0.805971255	5
optimal_loci_45923_G1	1208	1.754879	0	4284	38.65	3	13.47292565	0.164	0.806294584	5
optimal_loci_45926_G1	1036	1.754879	0	14979	39.18	1	6.068047254	0.235	0.806358874	6
optimal_loci_46021_G1	1109	0.78199	3.52	2026	44	1	3.796839463	0.203	0.809350474	4
optimal_loci_46065_G1	1272	0.780569	0	7615	52.2	2	4.767975353	0.408	0.81101669	3
optimal_loci_46100_G1	1591	0.777876	0	12030	33.75	1	6.807609606	0.091	0.812188834	4
optimal_loci_46166_G1	1353	3.423297	26.53	6152	38.95	1	3.32836282	0.129	0.81484001	12
optimal_loci_46181_G1	1165	4.161348	0	2195	47.98	2	7.765993228	0.339	0.815559355	11
optimal_loci_46189_G1	1125	4.161348	2.67	2535	57.06	1	12.52145275	0.538	0.815742446	11
optimal_loci_46194_G1	1297	4.161348	0	9979	39.7	3	7.804848121	0.373	0.815865545	11
optimal_loci_46197_G1	1418	4.161348	0	2955	41.81	2	5.446545805	0.248	0.815907041	11
optimal_loci_46198_G1	1921	4.161348	9.32	1001	35.5	2	5.446545805	0.119	0.815915763	11
optimal_loci_46248_G1	1193	3.933443	8.05	2375	39.89	2	32.49870162	0.164	0.817443618	11
optimal_loci_46249_G1	1052	3.933443	0	3849	36.02	1	18.14576221	0.174	0.817452479	11
optimal_loci_46253_G1	1407	3.933443	0	6257	55.01	1	18.14576221	0.523	0.817466954	11
optimal_loci_46254_G1	1145	3.933443	0	18686	46.81	1	18.14576221	0.234	0.817541668	11
optimal_loci_46255_G1	1016	3.933443	7.78	19985	33.07	1	18.14576221	0	0.817549477	11
optimal_loci_46388_G1	1682	0.881023	0	16795	62.24	1	15.31350877	0.79	0.822039422	8
optimal_loci_46391_G1	1636	0.90238	2.02	7355	46.21	1	15.31350877	0.335	0.822096445	8
optimal_loci_46393_G1	1011	0.90238	2.97	5775	54.3	1	15.31350877	0.385	0.8221097	8
optimal_loci_46397_G1	2739	0.90238	2.01	1880	45.05	1	15.31350877	0.367	0.822122726	8
optimal_loci_46400_G1	1102	0.90238	0	2109	34.57	1	15.31350877	0.117	0.822178132	8
optimal_loci_46407_G1	1041	0.924691	0	7920	51.2	1	15.31350877	0.241	0.822213064	8
optimal_loci_46437_G1	1201	0.087004	0	8483	63.11	1	1.579757796	0.707	0.822959291	11
optimal_loci_46475_G1	1754	1.511535	0	7096	39.9	3	2.663786472	0.155	0.823869578	12
optimal_loci_46525_G1	1369	1.511535	0	11190	53.54	1	16.99527685	0.438	0.825566278	7
optimal_loci_46528_G1	1947	1.511535	0	6107	57.98	1	16.99527685	0.703	0.825593358	7
optimal_loci_46530_G1	1506	1.511535	5.58	4192	55.51	1	16.99527685	0.549	0.825607521	7
optimal_loci_46549_G1	2043	0.529461	0	2126	41.01	2	0.297289372	0.178	0.826307203	7
optimal_loci_46575_G1	1397	0.328506	7.95	6034	36.36	1	4.558764601	0.068	0.82757162	6
optimal_loci_46626_G1	1171	0.073157	9.82	4438	35.09	1	86.1003095	0.061	0.829142167	11
optimal_loci_46676_G1	4012	2.877314	0	18501	48.37	1	0.123542338	0.346	0.830930641	10
optimal_loci_46677_G1	2428	2.877314	0	16040	52.67	1	0.123542338	0.589	0.830954956	10

optimal_loci_46695_G1	1731	2.614927	2.31	4019	46.79	3	3.493460345	0.313	0.83131416	10
optimal_loci_46699_G1	1213	2.614927	28.85	4356	41.22	4	7.332569366	0.099	0.831407491	10
optimal_loci_46709_G1	1367	2.614927	0	5435	58.52	2	9.424948215	0.647	0.831573204	10
optimal_loci_46714_G1	1691	2.614927	0	9426	37.61	2	9.424948215	0.372	0.831597195	10
optimal_loci_46718_G1	2208	2.444315	12.91	18749	44.42	1	8.202970758	0.371	0.831668062	10
optimal_loci_46721_G1	1355	2.396866	0	1617	49.96	2	4.101485379	0.348	0.831776174	10
optimal_loci_46788_G1	1655	2.338528	23.02	2764	42.83	2	41.83063057	0.304	0.833769368	10
optimal_loci_46848_G1	1376	0.436067	13.44	1001	32.84	1	414.1568129	0.102	0.835451887	2
optimal_loci_46940_G1	1031	1.87891	0	4330	35.59	3	46.7197077	0.14	0.839950399	4
optimal_loci_46941_G1	1365	1.87891	0	2723	37.8	3	46.7197077	0.205	0.839958051	4
optimal_loci_46998_G1	1078	2.168782	10.48	6739	37.01	2	12.60303637	0.047	0.841177828	4
optimal_loci_47037_G1	2241	2.620605	1.34	3428	54.97	4	17.04746781	0.558	0.841803566	4
optimal_loci_47108_G1	1896	1.114186	0	2947	41.82	1	0.690279491	0.186	0.845109573	3
optimal_loci_47122_G1	2643	1.060531	1.4	1486	48.05	4	10.55970398	0.608	0.845809874	3
optimal_loci_47175_G1	1278	1.116064	2.82	2001	43.42	1	13.09481191	0.355	0.848002287	3
optimal_loci_47311_G1	1311	1.303325	21.89	7270	35.85	2	0.014358178	0.179	0.854398431	2
optimal_loci_47351_G1	1793	0.893084	37.59	1001	37.08	1	19.13540217	0.042	0.856620462	2
optimal_loci_47449_G1	1015	1.791493	0	1001	60.39	1	10.31155776	0.526	0.860574677	6
optimal_loci_47452_G1	1128	1.783119	0	5385	40.42	3	9.145221663	0.129	0.860662333	6
optimal_loci_47492_G1	2626	2.06218	7.69	4540	43.86	2	0.028151276	0.359	0.862300976	9
optimal_loci_47494_G1	1030	2.06218	0	8422	47.96	2	0.028151276	0.465	0.862324312	9
optimal_loci_47509_G1	2454	2.06218	0	2887	46.98	3	3.836679401	0.447	0.862639002	9
optimal_loci_47530_G1	1065	1.918804	0	2258	39.62	5	0.623073558	0.227	0.863339904	9
optimal_loci_47553_G1	1103	1.856746	39.98	10401	41.25	2	1.353663953	0.356	0.863703929	9
optimal_loci_47608_G1	1674	1.661352	22.82	18493	36.37	1	0.286934489	0.064	0.864902949	9
optimal_loci_47612_G1	1037	1.661352	0	8908	49.75	2	0.778324442	0.775	0.864964397	9
optimal_loci_47676_G1	2617	1.620313	11.39	11905	42.83	2	32.94726837	0.402	0.866432818	6
optimal_loci_47683_G1	1021	1.637792	0	2483	31.53	2	6.360135489	0.233	0.866714645	6
optimal_loci_47727_G1	1270	1.705225	0	2001	36.85	2	12.74979429	0.132	0.868085377	7
optimal_loci_47808_G1	1222	1.671717	0	12465	56.46	1	0.04490182	0.596	0.870216848	9
optimal_loci_47812_G1	3787	1.664712	2.24	2001	49.3	1	0.04490182	0.439	0.870264331	9
optimal_loci_47844_G1	1184	1.597727	21.37	17296	45.86	2	0.942086964	0.372	0.870896681	9
optimal_loci_47856_G1	1251	1.59933	35.41	3143	39.56	4	29.50537105	0.214	0.871053178	9

optimal_loci_47886_G1	1565	1.510755	0	1766	42.55	1	12.01282596	0.337	0.87214221	8
optimal_loci_47941_G1	1177	1.52276	2.72	1001	47.15	3	3.267300779	0.438	0.872899005	8
optimal_loci_47943_G1	2129	1.52276	6.48	3343	44.66	3	3.267300779	0.464	0.872913475	8
optimal_loci_47945_G1	1146	1.52276	3.75	1509	49.82	3	3.267300779	0.253	0.872967702	9
optimal_loci_48009_G1	1586	2.25613	0	2538	54.85	2	91.28237473	0.632	0.875933189	4
optimal_loci_48075_G1	2018	3.373715	26.56	2001	38.94	2	10.56759909	0.248	0.878600998	6
optimal_loci_48077_G1	1019	3.407607	0	3303	34.05	2	10.56759909	0.119	0.878682505	6
optimal_loci_48100_G1	1324	3.77184	2.79	19805	37.38	1	28.24227248	0.211	0.879444379	8
optimal_loci_48108_G1	1843	4.11421	18.5	4066	49.7	2	14.45287721	0.393	0.879605548	8
optimal_loci_48110_G1	1169	4.13692	12.06	3025	39.52	2	14.45287721	0.153	0.879626683	8
optimal_loci_48236_G1	1280	3.797536	0	4686	47.26	1	3.448287524	0.368	0.881905683	7
optimal_loci_48242_G1	1544	3.797536	0	1297	31.21	1	3.448287524	0.08	0.881924468	7
optimal_loci_48250_G1	1067	3.797536	0	3654	43.2	2	0.35214668	0.291	0.882294997	7
optimal_loci_48267_G1	1787	3.797536	13.82	6968	43.25	1	1.639176957	0.186	0.882659827	4
optimal_loci_48569_G1	1146	1.342848	0	4737	39.87	2	2.371366536	0.133	0.888084441	4
optimal_loci_48648_G1	1109	1.588509	11.27	18385	48.51	1	0.51329719	0.441	0.890676087	5
optimal_loci_48666_G1	1760	1.593464	0	7942	37.72	3	0.171099063	0.033	0.890734949	5
optimal_loci_48702_G1	1248	1.690209	0	4735	45.11	3	2.484167723	0.342	0.891096197	5
optimal_loci_48707_G1	1043	1.580679	23.87	2622	34.99	2	12.89199134	0.094	0.89155529	4
optimal_loci_49154_G1	1527	1.50384	0	5363	41.06	3	19.20127254	0.234	0.902010629	4
optimal_loci_49165_G1	1846	1.50384	13.43	2001	38.35	2	4.880883076	0.255	0.902277037	4
optimal_loci_49167_G1	1276	1.50384	2.19	1001	45.29	3	21.83535609	0.457	0.90233204	4
optimal_loci_49242_G1	1150	1.419112	0	1793	52.26	3	31.12027534	0.433	0.904843123	4
optimal_loci_49365_G1	1891	2.497009	3.7	2383	37.96	1	1.159439349	0.343	0.909917833	6
optimal_loci_49369_G1	1967	2.497009	0	2001	51.7	1	3.609778819	0.54	0.910127885	6
optimal_loci_49374_G1	1477	2.610361	0	13763	36.83	1	38.72848162	0.243	0.910307051	6
optimal_loci_49377_G1	1467	1.234433	7.36	7930	45.39	1	38.72848162	0.381	0.910342175	6
optimal_loci_49382_G1	1346	1.254157	16.94	2368	46.58	1	72.77100016	0.344	0.910722207	7
optimal_loci_49383_G1	1043	1.254157	0	1001	38.25	1	72.77100016	0.131	0.910732246	7
optimal_loci_49478_G1	1582	3.023787	0	1480	56.38	3	0.696356737	0.549	0.913671434	5
optimal_loci_49498_G1	1609	3.023787	31.7	3521	36.17	1	0.0178318	0.166	0.914060898	3
optimal_loci_49508_G1	1021	2.669324	0	10019	34.28	1	92.57645231	0.09	0.91444622	4
optimal_loci_49562_G1	1063	2.377502	7.62	2001	47.22	2	18.70422843	0.765	0.917239454	5

optimal_loci_49574_G1	1369	1.682401	16.44	1001	42.51	4	25.7080339	0.203	0.918062169	4
optimal_loci_49589_G1	3521	1.682401	23.6	11020	41.09	4	25.6944679	0.301	0.918122396	4
optimal_loci_49631_G1	1379	1.978996	0	3158	45.97	1	10.18935518	0.301	0.919645598	4
optimal_loci_49835_G1	1020	4.145865	0	1259	38.52	2	23.93501364	0.047	0.92861714	3
optimal_loci_49842_G1	1001	4.145865	0	3911	46.95	2	0.823644744	0.508	0.928742685	3
optimal_loci_49881_G1	1458	3.872632	38.75	2001	50.68	3	6.238575429	0.6	0.930807088	5
optimal_loci_49914_G1	1099	3.476978	0	1083	44.22	2	29.83281941	0.243	0.9329745	3
optimal_loci_49945_G1	1301	3.514708	15.07	3841	39.73	3	25.77707063	0.214	0.933548902	3
optimal_loci_50154_G1	2164	0.924366	10.17	2703	37.84	2	1.440033809	0.251	0.941142912	2
optimal_loci_50185_G1	1621	1.867435	39.79	1844	42.68	1	37.91716483	0.228	0.942100513	2
optimal_loci_50284_G1	1202	2.639845	0	2138	58.65	2	86.05865655	0.504	0.94514348	2
optimal_loci_50325_G1	2498	2.647378	0	2224	43.75	2	58.99737208	0.262	0.946921975	3
optimal_loci_50411_G1	1443	3.466717	0	3349	30	3	14.36784538	0.084	0.949787067	6
optimal_loci_50422_G1	1241	3.694299	0	1001	35.93	4	13.13388217	0.051	0.950015075	5
optimal_loci_50469_G1	1322	3.787899	22.92	17631	59.53	1	2.90972745	0.725	0.951640823	10
optimal_loci_50479_G1	1338	3.787899	0	1664	48.43	1	2.90972745	0.243	0.951736709	10
optimal_loci_50493_G1	1364	3.824662	14.59	1001	50.21	2	0.208006933	0.504	0.95213091	10
optimal_loci_50519_G1	1368	1.564904	35.82	5416	31.65	2	8.417245698	0.019	0.953200436	10
optimal_loci_50537_G1	1164	1.53108	16.32	8961	34.27	1	16.8344914	0.201	0.953310412	11
optimal_loci_50542_G1	1780	1.514776	0	12197	34.77	2	6.785107205	0.135	0.953442408	11
optimal_loci_50545_G1	1545	1.514776	11.52	9869	35.79	2	6.785107205	0.136	0.953457815	11
optimal_loci_50552_G1	1378	1.493484	0	2001	61.82	5	47.51709342	0.615	0.953591247	11
optimal_loci_50587_G1	1372	1.627616	8.09	2033	36.88	2	1.088516103	0.242	0.955417598	8
optimal_loci_50590_G1	1872	1.627616	0	2001	43.21	2	1.088516103	0.258	0.95547539	8
optimal_loci_50607_G1	2418	0.813456	16	11473	46.98	1	30.18102701	0.391	0.956294161	7
optimal_loci_50700_G1	2670	3.455192	0	5857	52.92	2	24.75850342	0.496	0.959552103	3
optimal_loci_50719_G1	2353	5.036694	39.91	17471	34.84	1	2.279955811	0.104	0.959861028	3
optimal_loci_50734_G1	1056	5.656081	4.64	4175	38.44	2	260.2044072	0.138	0.960732332	4
optimal_loci_50820_G1	1421	5.966694	8.66	2121	43.84	3	15.86696549	0.33	0.963388599	3
optimal_loci_50830_G1	1152	6.326304	23	14946	35.5	1	1.294816529	0.086	0.964003756	3
optimal_loci_50926_G1	1338	3.689608	0	18878	37.96	1	10.24822372	0.102	0.966547715	3
optimal_loci_50941_G1	1460	3.787461	1.92	1288	57.05	3	2.036550004	0.839	0.967115028	2
optimal_loci_51075_G1	1262	1.398277	8.72	3607	41.12	5	16.50316479	0.21	0.973112667	3

optimal_loci_51101_G1	1587	1.203214	0	1521	51.29	2	124.7017819	0.413	0.973903847	3
optimal_loci_51120_G1	1275	1.17643	8.71	1291	32.62	3	1.551129348	0.143	0.974815949	4
optimal_loci_51178_G1	1551	0.024541	14.44	16615	35.65	1	24.71785478	0.055	0.977256622	2
optimal_loci_51281_G1	2038	3.011175	0	1555	46.61	2	3.984222476	0.344	0.981491804	1
optimal_loci_51361_G1	1227	3.943736	7.42	2001	35.69	1	19.1352505	0.092	0.984587939	3
optimal_loci_51379_G1	2820	5.521172	4.43	2001	52.55	5	7.515979922	0.481	0.985679514	6
optimal_loci_51380_G1	1141	5.521172	14.81	4836	36.1	5	7.515979922	0.183	0.985700542	6
optimal_loci_51472_G1	1168	4.334889	19.78	9696	38.44	2	28.66139134	0.07	0.988557417	5
optimal_loci_51473_G1	3705	4.334889	4.94	5706	34.3	2	28.66139134	0	0.988566151	5
optimal_loci_51482_G1	1459	4.373623	0	1001	48.32	2	28.66139134	0.462	0.988688697	5
optimal_loci_51589_G1	1535	2.087855	1.89	1343	42.08	2	0.102296968	0.224	0.992083233	4
optimal_loci_51591_G1	1328	2.087855	8.28	2153	35.09	2	0.102296968	0.235	0.992120581	4
optimal_loci_51640_G1	3185	1.584899	30.24	5346	34.5	1	0.043276121	0.148	0.993181161	4
optimal_loci_51655_G1	2123	1.373386	9.94	8302	39.04	1	15.54882446	0.317	0.993431837	4
optimal_loci_51796_G1	1030	0.861109	0	13338	40	1	1.805609138	0.195	0.998758486	2
optimal_loci_51803_G1	2073	0.821922	35.31	2001	37.53	1	1.805609138	0.173	0.998820366	2
optimal_loci_51949_G1	1469	1.03722	9.19	1074	48.33	1	6.169026665	0.445	0.991900183	1
optimal_loci_52050_G1	1339	5.086547	38.46	1897	43.46	6	6.84979128	0.353	0.982233036	8
optimal_loci_52052_G1	1960	5.086547	9.44	2087	48.16	6	7.382237087	0.315	0.981740527	8
optimal_loci_52090_G1	1258	4.505889	0	1001	40.06	6	13.78892165	0.3	0.977863832	12
optimal_loci_52101_G1	1224	4.804254	35.95	2104	37.99	6	16.19567036	0.283	0.977744489	12
optimal_loci_52103_G1	1522	4.804254	0	4201	54.46	3	8.264605947	0.524	0.977520431	12
optimal_loci_52106_G1	1353	4.804254	0	7441	41.98	4	7.714029043	0.412	0.977487374	12
optimal_loci_52113_G1	1469	4.804254	0	5873	45.94	5	7.370813452	0.328	0.977424607	12
optimal_loci_52122_G1	1150	5.108975	9.3	2976	48.52	4	12.29195057	0.551	0.977126986	12
optimal_loci_52177_G1	1665	5.69598	0	5368	56.63	2	7.082802302	0.595	0.975658267	10
optimal_loci_52178_G1	3135	5.69598	5.58	2200	53.07	3	4.856352542	0.518	0.975624166	10
optimal_loci_52226_G1	3116	5.101162	0	1689	47.65	4	17.43323222	0.423	0.973252788	10
optimal_loci_52227_G1	1213	5.101162	8.33	1080	52.51	4	17.43323222	0.524	0.973238224	10
optimal_loci_52292_G1	1297	4.258825	31.23	1542	37.77	3	3.720674455	0.134	0.967656534	2
optimal_loci_52299_G1	1300	4.258825	14.31	4177	43.61	3	3.720674455	0.432	0.967598837	2
optimal_loci_52420_G1	1118	4.033901	17.62	2822	40.6	4	60.28504566	0.341	0.961744198	9
optimal_loci_52424_G1	1725	4.026847	0	2001	59.88	4	60.28504566	0.717	0.961649699	9

optimal_loci_52428_G1	1511	4.170072	0	3159	43.01	6	16.18247655	0.162	0.961323832	9
optimal_loci_52429_G1	2598	4.170072	0	2001	52.5	6	16.18247655	0.514	0.96129395	9
optimal_loci_52477_G1	1177	3.697188	13.51	4604	36.78	3	2.030991102	0.086	0.95833986	19
optimal_loci_52480_G1	1671	3.697188	12.27	2001	47.63	3	2.030991102	0.349	0.958311841	19
optimal_loci_52483_G1	1363	3.697188	0	1647	34.48	3	2.030991102	0.159	0.958237481	19
optimal_loci_52490_G1	1228	3.697188	26.3	18900	37.37	1	22.67616371	0.102	0.957971981	19
optimal_loci_52503_G1	1207	3.59195	7.79	14076	46.14	2	88.93890884	0.301	0.957045716	19
optimal_loci_52560_G1	1083	3.911517	0	2625	34.53	1	0.352758048	0.223	0.954177621	15
optimal_loci_52564_G1	2031	3.911517	0	2489	57.8	1	0.352758048	0.516	0.954061141	15
optimal_loci_52566_G1	1757	3.911517	0	4949	41.26	1	0.352758048	0.23	0.95403761	15
optimal_loci_52571_G1	1129	3.911517	15.77	9384	37.11	2	58.28568418	0.109	0.953817718	15
optimal_loci_52572_G1	1131	3.911517	0	7877	46.68	2	58.28568418	0.445	0.953801496	15
optimal_loci_52573_G1	1535	3.911517	2.02	6247	54.65	2	58.28568418	0.668	0.95378395	15
optimal_loci_52574_G1	2346	3.911517	0	3790	51.61	2	58.28568418	0.529	0.953757503	15
optimal_loci_52583_G1	1701	3.82478	0	6628	50.61	3	38.85712279	0.365	0.95358747	15
optimal_loci_52584_G1	1055	3.82478	0	7556	41.99	3	38.85712279	0.319	0.95357409	15
optimal_loci_52598_G1	1704	3.82478	0	2001	53.11	4	3.771012079	0.384	0.953226738	15
optimal_loci_52706_G1	1136	5.979401	0	2919	44.71	4	44.39863695	0.375	0.945364855	11
optimal_loci_52707_G1	1219	5.974435	3.53	4491	38.63	4	44.39863695	0.194	0.94534704	12
optimal_loci_52709_G1	1975	5.974435	0	2952	47.44	6	29.94110848	0.415	0.945320764	12
optimal_loci_52751_G1	2197	6.28964	0	3485	49.84	2	20.26268253	0.501	0.943794316	13
optimal_loci_52758_G1	1176	6.28964	0	9604	47.44	3	41.40017581	0.382	0.943043186	13
optimal_loci_52791_G1	1056	6.162786	0	6351	64.01	2	2.824823706	0.962	0.940794316	13
optimal_loci_52798_G1	1217	6.335294	0	2893	54.23	2	2.824823706	0.649	0.940674822	15
optimal_loci_52810_G1	1119	6.235049	0	7917	47.54	2	2.249470894	0.643	0.940377503	15
optimal_loci_52815_G1	2415	6.202157	1.2	1851	48.19	2	21.11283371	0.416	0.940312207	15
optimal_loci_52817_G1	2133	6.175366	0	2001	61.65	3	27.10879548	0.724	0.940199903	15
optimal_loci_52821_G1	1092	6.175366	3.3	4089	60.16	3	27.10879548	0.67	0.94016268	15
optimal_loci_52826_G1	1334	6.21184	0	3099	41.67	2	40.66319322	0.487	0.939962422	14
optimal_loci_52843_G1	3646	6.160549	3.57	1001	55.89	1	2.553826385	0.649	0.938807417	14
optimal_loci_52875_G1	2458	5.959415	0	1920	50.85	4	2.295083449	0.515	0.935375178	14
optimal_loci_52877_G1	2479	5.955449	15.61	2680	56.75	5	1.844157538	0.448	0.935286243	14
optimal_loci_52953_G1	1113	3.285277	0	1181	61.18	4	10.62413854	0.715	0.933472745	9

optimal_loci_52956_G1	1255	3.285277	3.11	3325	54.26	5	8.499310829	0.664	0.933448138	9
optimal_loci_52962_G1	1219	3.286553	13.95	2001	52.83	5	8.499310829	0.488	0.933385113	8
optimal_loci_52963_G1	1757	3.278565	0	1001	47.75	4	10.62413854	0.339	0.933322013	8
optimal_loci_52977_G1	2306	2.964391	24.11	2727	34.99	2	2.536108118	0.04	0.931950872	8
optimal_loci_53026_G1	1302	4.301557	0	2834	59.83	3	0.022010351	0.808	0.929304015	6
optimal_loci_53126_G1	1965	3.922653	34.66	2907	43.05	5	4.095434433	0.333	0.922530818	2
optimal_loci_53137_G1	1300	3.87381	5.38	1001	42.53	4	4.476943704	0.265	0.921361722	2
optimal_loci_53270_G1	2226	0.497425	0	4777	43.26	1	0.878088261	0.126	0.914569795	2
optimal_loci_53276_G1	3200	0.497425	0	4849	57.21	2	3.758390701	0.688	0.91438592	2
optimal_loci_53423_G1	1168	4.824315	19.78	1490	48.45	6	28.49149737	0.454	0.904159451	13
optimal_loci_53430_G1	1576	4.49616	12.56	2182	55.32	1	0.98792547	0.61	0.903559429	17
optimal_loci_53432_G1	1273	4.49616	27.49	4463	34.72	1	0.98792547	0.129	0.903538138	17
optimal_loci_53446_G1	1824	6.056942	19.74	1024	43.42	1	4.884892144	0.289	0.902216932	18
optimal_loci_53447_G1	1201	6.170885	0	9956	52.95	2	50.85177139	0.46	0.902044844	19
optimal_loci_53448_G1	1030	6.170885	14.95	11796	40.58	2	50.85177139	0.4	0.902026878	20
optimal_loci_53452_G1	1148	6.170885	3.14	9771	39.8	2	50.85177139	0.178	0.901991927	20
optimal_loci_53478_G1	1162	6.586746	14.97	3325	49.05	2	59.1581833	0.432	0.900289171	20
optimal_loci_53483_G1	1641	6.586746	0	2001	42.35	2	59.1581833	0.25	0.900194672	20
optimal_loci_53484_G1	1627	6.586746	0	1001	49.53	2	59.1581833	0.343	0.900124435	20
optimal_loci_53517_G1	1147	5.478453	0	2001	55.79	2	57.10966723	0.323	0.899313563	20
optimal_loci_53522_G1	1214	5.464954	0	4677	56.42	2	57.10966723	0.655	0.899135264	20
optimal_loci_53524_G1	1989	5.464954	11.61	6926	53.69	2	57.10966723	0.616	0.899102713	20
optimal_loci_53532_G1	1133	4.904385	7.77	7903	45.27	3	2.885428278	0.467	0.898542325	19
optimal_loci_53537_G1	1278	4.904385	0	4914	42.87	4	2.84711135	0.389	0.898490549	19
optimal_loci_53539_G1	1112	4.904385	17.18	1135	50.44	4	2.84711135	0.354	0.898449871	19
optimal_loci_53540_G1	1098	4.904385	0	2001	39.98	3	2.917320105	0.248	0.898392659	19
optimal_loci_53548_G1	1452	4.734425	37.47	1001	47.1	5	6.448684145	0.365	0.897794155	17
optimal_loci_53574_G1	1443	4.107517	0	2748	46.7	2	2.907779761	0.359	0.896738837	17
optimal_loci_53577_G1	1560	4.107517	0	3841	59.16	5	1.868379855	0.685	0.896634403	16
optimal_loci_53666_G1	1101	1.510483	16.49	13165	42.77	1	9.86548846	0.341	0.892031055	6
optimal_loci_53693_G1	1272	2.987244	21.38	2001	38.36	5	6.946744596	0.152	0.888304618	6
optimal_loci_53706_G1	2077	4.773684	25.9	1001	40.1	4	49.37321906	0.162	0.887338934	6
optimal_loci_53712_G1	1095	4.773684	0	2001	52.87	5	11.64362889	0.277	0.886964263	6

optimal_loci_53765_G1	1716	4.029627	0	2414	43.47	4	6.579121202	0.455	0.885233638	5
optimal_loci_53783_G1	1551	3.864732	0	2163	49.51	2	12.5907944	0.425	0.883846857	5
optimal_loci_53949_G1	1486	2.700815	0	3340	56.19	2	8.693360798	0.705	0.875697976	9
optimal_loci_53950_G1	1635	2.700815	1.77	5327	43.36	2	8.693360798	0.454	0.875674984	9
optimal_loci_53955_G1	1284	2.813794	0	3168	51.47	2	5.345516719	0.483	0.87551282	9
optimal_loci_53958_G1	1192	2.818734	10.49	1715	47.65	2	4.753667676	0.4	0.875314887	9
optimal_loci_53964_G1	1310	2.818734	0	2001	52.74	2	4.753667676	0.364	0.875202121	9
optimal_loci_53972_G1	1387	2.893695	0	2001	44.7	1	6.848655211	0.26	0.874852691	9
optimal_loci_53976_G1	1792	3.082349	0	4426	57.81	2	3.444019853	0.568	0.874563509	11
optimal_loci_54002_G1	1214	4.588314	2.31	2445	44.97	3	3.268877018	0.463	0.873418493	13
optimal_loci_54009_G1	1042	4.588314	0	3669	39.73	3	3.268877018	0.265	0.873321819	13
optimal_loci_54062_G1	1454	4.249769	22.28	5478	51.03	2	21.53672793	0.492	0.869351141	9
optimal_loci_54064_G1	1037	4.249769	0	7525	57.66	1	43.07345586	0.567	0.869333595	9
optimal_loci_54073_G1	1633	4.538432	7.96	8044	48.86	3	7.348671915	0.406	0.868225038	9
optimal_loci_54083_G1	2104	4.538432	0	3035	32.36	4	8.778208177	0.225	0.868157104	9
optimal_loci_54088_G1	1648	5.105257	0	12046	38.95	3	4.355605654	0.141	0.867786276	7
optimal_loci_54128_G1	2594	3.18945	25.4	2806	37.74	2	1.694387174	0.104	0.863959064	11
optimal_loci_54138_G1	1938	3.18945	0	2719	45.04	2	157.3582378	0.404	0.863387169	9
optimal_loci_54146_G1	1669	1.37934	17.91	1001	58.29	1	2.091011194	0.398	0.862235296	9
optimal_loci_54149_G1	1670	1.37934	16.29	4049	35.98	1	2.091011194	0.171	0.862116233	9
optimal_loci_54151_G1	1316	1.522022	2.43	7006	44.6	1	2.091011194	0.388	0.862088213	9
optimal_loci_54212_G1	1158	1.877403	19.69	1909	44.55	2	0.234247621	0.239	0.858994112	13
optimal_loci_54245_G1	1592	1.491934	0	4753	53.64	5	8.074340409	0.424	0.856929279	14
optimal_loci_54249_G1	1036	1.491934	0	3860	35.13	6	7.352165517	0.15	0.856890312	14
optimal_loci_54250_G1	1367	1.491934	2.93	2074	45.13	6	7.352165517	0.353	0.856871087	14
optimal_loci_54304_G1	1233	1.968056	26.03	2047	36.57	3	5.077060852	0.213	0.855152777	11
optimal_loci_54314_G1	1628	1.743049	16.28	2001	58.66	1	42.94204063	0.635	0.854212723	11
optimal_loci_54319_G1	1152	1.743049	0	7159	59.37	1	42.94204063	0.558	0.854078105	11
optimal_loci_54320_G1	1359	1.743049	0	2809	41.28	1	100.8474336	0.432	0.853699763	11
optimal_loci_54326_G1	1082	1.997936	0	1532	50.64	2	3.394080109	0.591	0.853388127	12
optimal_loci_54332_G1	1734	1.997936	9.57	5266	36.1	3	2.262720073	0.122	0.853230721	12
optimal_loci_54353_G1	1696	1.86666	7.9	2317	37.85	2	21.48559525	0.301	0.852467944	13
optimal_loci_54404_G1	1107	0.90197	0	1001	45.52	1	2233.060052	0.283	0.848163079	12

optimal_loci_54407_G1	1279	0.90197	0	3657	35.18	1	2233.060052	0.11	0.848053746	12
optimal_loci_54422_G1	1081	0.596548	9.25	1001	41.99	2	39.35057751	0.227	0.847097481	11
optimal_loci_54427_G1	1619	0.810291	0	1001	56.7	3	88.81804522	0.64	0.846871604	10
optimal_loci_54429_G1	1106	0.810291	0	2114	54.97	3	88.81804522	0.507	0.846851399	10
optimal_loci_54437_G1	1794	0.895346	1.56	9496	46.98	1	56.04020913	0.326	0.8465331	10
optimal_loci_54439_G1	1129	0.895346	3.54	2001	48.89	1	56.04020913	0.253	0.846452422	10
optimal_loci_54453_G1	1757	0.974483	2.96	2963	58.45	3	1.42520307	0.65	0.84576718	10
optimal_loci_54463_G1	1056	0.928638	0	1001	44.6	3	24.65807769	0.339	0.844288364	11
optimal_loci_54490_G1	1620	0.90135	1.85	3604	43.76	2	1.582124616	0.28	0.842025694	13
optimal_loci_54534_G1	1004	0.948911	0	1240	35.55	5	0.373449385	0.082	0.839811163	9
optimal_loci_54574_G1	2392	0.894463	0	2392	47.24	2	0.828723327	0.538	0.838467589	14
optimal_loci_54581_G1	1515	0.894463	0	8204	35.57	2	0.828723327	0.078	0.838414467	14
optimal_loci_54590_G1	1335	0.894463	10.19	2111	45.84	2	0.828723327	0.247	0.83831606	14
optimal_loci_54602_G1	1352	1.001145	0	2946	47.55	4	19.26113011	0.506	0.837252002	15
optimal_loci_54628_G1	1813	0.733752	12.91	5493	42.8	1	2.8111154	0.225	0.835513821	14
optimal_loci_54629_G1	1466	0.733752	3.07	7414	52.11	1	2.8111154	0.334	0.835496878	14
optimal_loci_54662_G1	1704	2.10634	0	5794	46.83	2	4.705640944	0.399	0.833450215	15
optimal_loci_54663_G1	2038	2.10634	0	3723	55.05	2	4.705640944	0.568	0.833427922	15
optimal_loci_54664_G1	1098	2.10634	0	2514	53.64	2	4.705640944	0.507	0.833414909	15
optimal_loci_54665_G1	1412	2.10634	2.41	1001	44.47	2	4.705640944	0.287	0.833398622	15
optimal_loci_54666_G1	2402	2.10634	0	1001	50.74	2	4.705640944	0.404	0.833300721	16
optimal_loci_54669_G1	1537	2.10634	0	10631	39.55	2	4.705640944	0.133	0.833206372	16
optimal_loci_54700_G1	1020	2.033852	0	12708	31.66	2	9.498957249	0.121	0.832569397	13
optimal_loci_54741_G1	1184	3.10672	14.02	9885	47.38	2	11.12465416	0.38	0.829321281	11
optimal_loci_54742_G1	1201	3.095487	0	2001	29.3	5	14.50445146	0.191	0.829105188	11
optimal_loci_54763_G1	1038	2.825139	29.96	1966	45.56	5	18.65473284	0.315	0.827957212	8
optimal_loci_54788_G1	1232	2.416864	14.85	1336	41.88	2	3.510193903	0.34	0.825362067	14
optimal_loci_54829_G1	1747	2.996545	32.86	2368	33.37	1	0.537773747	0.121	0.823504607	16
optimal_loci_54847_G1	1893	2.725532	12.41	1259	48.38	3	27.02597468	0.403	0.82189887	17
optimal_loci_54857_G1	1319	2.597436	0	4386	64.82	1	27.34759026	0.651	0.820948418	18
optimal_loci_54858_G1	1609	2.597436	12.18	2744	38.59	2	15.2765972	0.092	0.820930743	18
optimal_loci_54859_G1	1097	2.597436	0	1001	45.48	2	15.2765972	0.235	0.820911981	18
optimal_loci_54861_G1	2768	2.597436	3.58	2882	48.8	3	12.70324067	0.524	0.820817051	18

optimal_loci_54863_G1	1721	2.597436	9.59	5731	36.25	3	12.70324067	0.06	0.820790904	18
optimal_loci_54865_G1	3154	2.597436	12.46	1400	54.66	3	12.70324067	0.528	0.820744284	18
optimal_loci_54867_G1	1043	2.534195	12.94	1001	47.07	2	8.169368741	0.543	0.820430635	18
optimal_loci_54868_G1	2807	2.534195	6.06	2077	34.16	1	8.782209866	0.117	0.820400065	18
optimal_loci_54878_G1	1527	2.509605	18.07	9504	48.59	1	3.62849279	0.313	0.81899958	18
optimal_loci_54899_G1	1000	2.500876	0	3279	37.7	1	0.984972012	0.136	0.818438568	19
optimal_loci_54900_G1	1798	2.500876	14.68	1397	45.38	1	0.984972012	0.446	0.81841831	19
optimal_loci_54903_G1	1004	2.500876	0	3940	50.59	1	0.984972012	0.714	0.818309699	19
optimal_loci_54920_G1	2119	2.633172	1.84	9493	50.49	1	22.06176365	0.565	0.81776662	18
optimal_loci_54924_G1	2441	2.633172	4.01	3897	52.47	1	22.06176365	0.457	0.817706383	18
optimal_loci_54949_G1	2345	2.623336	3.16	2190	53.9	1	24.25194469	0.489	0.816014833	19
optimal_loci_55003_G1	1627	2.28514	0	16758	51.87	1	6.428749981	0.759	0.814496168	12
optimal_loci_55026_G1	1011	1.685981	5.44	2225	37.09	2	94.0070788	0.075	0.81343296	11
optimal_loci_55050_G1	1147	1.744099	0	2298	39.66	3	6.142266627	0.294	0.811062433	6
optimal_loci_55062_G1	1130	1.744099	0	1112	46.1	2	11.91305991	0.353	0.810687147	7
optimal_loci_55098_G1	2098	1.814236	0	2001	48.23	2	1.138218329	0.477	0.809611733	7
optimal_loci_55154_G1	1113	0.505251	0	1434	36.11	1	8.284041069	0.108	0.805401981	7
optimal_loci_55164_G1	1445	0.495105	14.33	7566	37.71	2	362.8853448	0.155	0.80468916	6
optimal_loci_55197_G1	1193	0.642185	8.47	2001	38.64	2	18.48626573	0.156	0.803516695	7
optimal_loci_55225_G1	1416	1.356189	8.83	4569	39.83	1	5.081544148	0.246	0.802396362	7
optimal_loci_55227_G1	1744	1.356189	0	7116	40.53	1	5.081544148	0.366	0.802365414	7
optimal_loci_55290_G1	1191	0.918414	0	2316	48.11	1	9.91014601	0.452	0.798678493	6
optimal_loci_55312_G1	1148	0.97049	0	13245	46.86	2	9.396252486	0.379	0.798181087	6
optimal_loci_55390_G1	1637	1.424313	19.55	1001	48.8	2	60.35787855	0.508	0.793341292	5
optimal_loci_55413_G1	1545	1.64217	0	2001	47.18	2	2.87487977	0.385	0.791941184	3
optimal_loci_55415_G1	1469	1.369326	0	1460	43.36	2	0.671973682	0.17	0.791628525	3
optimal_loci_55485_G1	1067	2.658796	19.31	2096	42.83	1	1.300190612	0.458	0.784849569	16
optimal_loci_55492_G1	1247	3.687435	9.38	5358	38.97	2	0.967253093	0.263	0.784681141	16
optimal_loci_55493_G1	1179	3.687435	0	4146	48.85	2	0.967253093	0.393	0.784668095	16
optimal_loci_55494_G1	1804	3.687435	0	2126	52.66	2	0.967253093	0.491	0.784646351	16
optimal_loci_55495_G1	1024	3.687435	0	1001	55.76	2	0.967253093	0.634	0.784634241	16
optimal_loci_55499_G1	1139	3.687435	0	5992	39.33	1	0.634315574	0.152	0.784537492	16
optimal_loci_55502_G1	2219	3.687435	5.14	8044	48.35	1	0.634315574	0.472	0.784503778	16

optimal_loci_55524_G1	1483	2.961612	1.89	1753	42.68	3	0.994446883	0.254	0.7836331	18
optimal_loci_55527_G1	1067	2.961612	0	2628	39.45	4	0.745835162	0.196	0.783562304	18
optimal_loci_55528_G1	1027	2.796359	0	4115	51.7	4	0.745835162	0.659	0.783546728	18
optimal_loci_55529_G1	1895	2.796359	0	5175	51.55	4	0.745835162	0.618	0.783525974	18
optimal_loci_55530_G1	1271	2.796359	10.31	7103	44.92	4	0.745835162	0.192	0.783511938	18
optimal_loci_55531_G1	2569	2.796359	16.58	5493	36.78	4	0.745835162	0.203	0.783482842	18
optimal_loci_55532_G1	1266	2.796359	0	3953	29.3	4	0.745835162	0.081	0.783466265	18
optimal_loci_55541_G1	1147	2.796359	35.57	1001	29.29	2	6.012279303	0.17	0.782657029	18
optimal_loci_55574_G1	1029	3.043686	0	3168	43.34	4	1.420567367	0.254	0.78025056	19
optimal_loci_55594_G1	1105	1.471139	0	2001	57.37	3	66.73039796	0.622	0.778881529	12
optimal_loci_55608_G1	1306	1.471139	0	3109	30.93	1	0.2447366	0.111	0.778588428	12
optimal_loci_55650_G1	1751	1.342996	0	5130	45.17	1	49.06470612	0.407	0.77698253	4
optimal_loci_55765_G1	1674	0.942	9.74	2001	37.27	2	10.95097147	0.144	0.769580065	7
optimal_loci_55788_G1	1117	0.940438	0	1205	60.42	3	5.552634446	0.785	0.768427815	7
optimal_loci_55802_G1	3244	1.072904	8.05	1001	49.72	1	1.367976704	0.43	0.76746662	11
optimal_loci_55852_G1	1157	1.193791	0	2789	54.27	1	23.8972847	0.605	0.765352078	11
optimal_loci_55854_G1	1127	1.193791	0	4268	37.88	1	23.8972847	0.366	0.76533648	11
optimal_loci_55855_G1	1137	1.193791	2.81	6367	47.31	2	15.46044253	0.33	0.765313778	11
optimal_loci_55860_G1	1797	1.193791	4.84	3405	41.4	1	7.023600359	0.139	0.765151507	11
optimal_loci_55912_G1	1372	1.384393	0	1676	44.09	1	23.09232088	0.392	0.76276239	9
optimal_loci_55913_G1	1159	1.384393	3.19	3081	54.01	1	23.09232088	0.511	0.762749559	9
optimal_loci_55916_G1	1650	1.384393	0	5396	38.36	1	23.09232088	0.164	0.762719354	9
optimal_loci_55920_G1	1629	1.41291	0	2649	45.54	1	16.9039453	0.413	0.762374241	9
optimal_loci_56005_G1	1726	2.428938	0	2828	51.73	1	8.007073391	0.611	0.755532637	10
optimal_loci_56043_G1	1104	2.682819	0	2167	45.83	2	5.8733667	0.42	0.753580614	11
optimal_loci_56055_G1	1538	2.682819	19.77	3010	43.43	3	5.526773013	0.315	0.753025565	11
optimal_loci_56061_G1	1067	2.682819	19.21	2397	32.52	5	8.310968529	0.131	0.752826437	11
optimal_loci_56068_G1	1741	2.682819	1.61	1415	47.21	5	130.3320266	0.37	0.752560958	11
optimal_loci_56084_G1	1396	1.709796	0	16846	41.11	2	0.368844939	0.2	0.751160893	11
optimal_loci_56086_G1	1097	1.709796	0	15180	51.95	2	0.368844939	0.566	0.75114296	11
optimal_loci_56088_G1	1444	1.709796	0	7363	38.01	2	0.368844939	0.24	0.751058816	11
optimal_loci_56089_G1	1961	1.709796	5.05	5143	37.42	2	0.368844939	0.137	0.751034919	11
optimal_loci_56093_G1	1250	1.709796	5.04	2001	37.76	2	0.368844939	0.239	0.751001098	11

optimal_loci_56114_G1	1112	2.937578	0	2001	38.03	2	16.99878001	0.168	0.749048041	13
optimal_loci_56176_G1	5187	3.638735	0.66	2569	53.05	2	2.674091323	0.496	0.744665791	5
optimal_loci_56193_G1	2763	3.638735	4.6	2103	49.54	2	2.674091323	0.355	0.744513046	5
optimal_loci_56197_G1	1030	3.638735	4.76	2001	45.72	1	4.520803575	0.258	0.744178805	5
optimal_loci_56241_G1	2499	2.050618	1.6	19188	42.69	1	11.87751763	0.311	0.741533638	5
optimal_loci_56298_G1	1355	0.263265	17.49	2001	37.26	3	3.249289947	0.114	0.737504553	4
optimal_loci_56391_G1	1309	0.234681	19.79	7043	43.92	1	1.772800061	0.538	0.733818536	3
optimal_loci_56395_G1	1651	0.234681	12.3	4303	38.34	3	26.60327168	0.192	0.733012573	3
optimal_loci_56489_G1	1499	0.163024	36.02	12062	39.49	1	21.02998823	0.108	0.726558762	1
optimal_loci_56610_G1	1062	0.235226	25.8	17836	38.98	1	15.26176319	0.275	0.718888461	1
optimal_loci_56725_G1	1083	0.281964	0	1800	33.88	4	3.374048766	0.118	0.710666911	4
optimal_loci_56729_G1	1131	0.288013	21.22	8282	40.31	2	4.982776634	0.109	0.71016409	4
optimal_loci_56735_G1	1697	0.288013	7.84	2605	46.67	2	4.982776634	0.388	0.710102982	4
optimal_loci_56745_G1	1299	0.304902	0	1267	55.81	2	7.350275354	0.466	0.709546233	4
optimal_loci_56839_G1	2081	0.939652	0	5123	46.22	3	0.269991887	0.382	0.703345274	6
optimal_loci_56841_G1	1372	0.939652	0	2820	55.46	3	0.269991887	0.423	0.703320484	6
optimal_loci_56846_G1	1270	0.939652	0	5503	57.4	5	6.081095883	0.636	0.703181722	6
optimal_loci_56847_G1	1706	0.939652	0	2001	53.63	5	6.081095883	0.475	0.703095673	6
optimal_loci_56925_G1	1111	2.597109	0	4300	52.29	2	5.867393949	0.414	0.699020969	9
optimal_loci_56939_G1	1150	2.769703	4.43	2001	55.21	2	14.19833689	0.722	0.698095188	9
optimal_loci_56952_G1	1730	3.041037	0	2408	41.21	5	10.18071093	0.248	0.697242056	6
optimal_loci_56985_G1	1317	3.492072	13.82	2988	40.16	2	2.455427111	0.335	0.695353143	7
optimal_loci_56988_G1	3497	3.575022	4.46	1001	50.32	2	2.455427111	0.369	0.695193929	7
optimal_loci_57037_G1	1108	4.672555	0	14714	33.03	2	16.40735581	0.224	0.691872917	7
optimal_loci_57049_G1	1047	1.967577	16.81	1277	38.87	3	4.378017782	0.248	0.690989731	6
optimal_loci_57107_G1	2692	2.000562	10.74	10345	46.06	1	1.417662146	0.333	0.687231991	7
optimal_loci_57123_G1	1024	2.437887	5.37	2816	41.11	2	2.12969919	0.341	0.686559978	7
optimal_loci_57176_G1	1127	2.628609	4.17	14047	45.69	2	3.34074734	0.272	0.684768321	6
optimal_loci_57183_G1	1363	2.530673	0	18463	46.07	1	0.586132966	0.331	0.684237094	6
optimal_loci_57231_G1	1252	2.173337	6.55	1336	35.86	2	36.8609996	0.138	0.682009193	6
optimal_loci_57248_G1	1425	2.173337	21.33	8478	41.75	3	5.026625186	0.283	0.680818708	5
optimal_loci_57316_G1	1098	1.610734	0	1001	40.52	1	56.85964659	0.268	0.675686685	6
optimal_loci_57327_G1	1167	1.53558	0	1823	43.44	4	8.800565954	0.26	0.674040194	5

optimal_loci_57332_G1	1328	1.374017	9.79	1840	39.15	4	4.66997373	0.199	0.673389645	5
optimal_loci_57380_G1	1829	2.103329	1.59	7438	42.91	1	6.08017405	0.209	0.671024144	6
optimal_loci_57382_G1	1240	2.103329	2.74	9716	58.79	1	6.08017405	0.684	0.671005963	6
optimal_loci_57436_G1	1898	0.490461	17.23	4348	41.35	2	40.41129425	0.27	0.667368837	3
optimal_loci_57771_G1	1863	0.385137	7.25	2654	40.25	7	101.8653252	0.198	0.650111313	2
optimal_loci_57827_G1	1603	1.181745	5.12	7709	37.05	1	36.37570626	0.226	0.645407492	3
optimal_loci_57856_G1	1963	2.184472	28.32	11288	36.06	1	17.94911424	0	0.642684327	2
optimal_loci_57940_G1	1396	1.054216	0	3218	39.68	1	28.90643928	0.167	0.635681862	1
optimal_loci_58039_G1	1182	0.771803	0	15474	44.16	2	6.098778972	0.369	0.626788837	2
optimal_loci_58041_G1	1420	0.771803	9.08	13545	54.01	2	6.098778972	0.425	0.626768073	2
optimal_loci_58137_G1	1111	0.025789	0	1421	50.49	1	27.78390007	0.471	0.619769053	1
optimal_loci_58251_G1	1366	0.102661	15.89	5233	38.28	4	0.425239433	0.233	0.613867653	2
optimal_loci_58275_G1	1709	0.738232	0	2001	36.8	1	49.17211443	0.213	0.611562304	2
optimal_loci_58368_G1	1553	3.644468	15.07	4370	35.6	3	21.82553725	0.202	0.603662605	4
optimal_loci_58378_G1	1114	3.29739	0	2871	46.31	3	21.82553725	0.475	0.603548568	4
optimal_loci_58379_G1	1265	3.284549	8.54	2001	45.84	3	21.82553725	0.297	0.60338211	4
optimal_loci_58453_G1	2953	2.407803	4.98	5906	37.58	2	0.732042746	0.171	0.600186523	5
optimal_loci_58498_G1	1099	1.392645	0	2375	38.39	1	4.619369991	0.189	0.59717267	4
optimal_loci_58581_G1	1269	0.681481	26.16	5581	35.53	2	0.404540391	0	0.592344403	6
optimal_loci_58586_G1	1184	0.681481	33.36	8758	42.9	2	0.404540391	0.228	0.592311119	6
optimal_loci_58630_G1	1324	1.935422	2.11	3086	48.48	1	6.324686736	0.3	0.589804144	5
optimal_loci_58634_G1	1044	1.935422	0	6295	40.51	1	6.324686736	0.086	0.589772616	5
optimal_loci_58638_G1	1114	2.086339	0	4340	47.48	2	34.78546018	0.314	0.589581927	5
optimal_loci_58888_G1	1307	0.049323	4.74	17698	55.24	1	15.12521289	0.692	0.573768751	2
optimal_loci_58912_G1	1590	0.049323	0	1001	40.18	1	0.077017774	0.21	0.572029612	3
optimal_loci_58992_G1	2564	1.276401	11.04	5595	55.85	2	6.636684062	0.61	0.567908751	3
optimal_loci_59034_G1	2310	1.150359	0	2001	37.61	3	2.880764805	0.209	0.564135361	2
optimal_loci_59167_G1	1570	0.939513	0	4839	52.54	2	1.55573036	0.509	0.556159795	3
optimal_loci_59200_G1	1490	1.292876	6.38	3355	46.44	4	3.197208574	0.332	0.553386222	9
optimal_loci_59233_G1	1297	1.482214	8.87	4976	39.16	1	3.105819884	0.019	0.550832217	9
optimal_loci_59237_G1	1019	1.525996	0	2001	40.13	2	2.715143835	0.269	0.550703229	8
optimal_loci_59242_G1	1657	1.525996	0	4718	37.41	2	2.715143835	0.214	0.550667115	8
optimal_loci_59249_G1	1795	1.525996	0	1001	38.05	4	1.441216053	0.205	0.550521507	8

optimal_loci_59251_G1	1482	1.348277	0	2700	36.57	3	0.886348109	0	0.550438633	8
optimal_loci_59255_G1	1348	1.348277	2.74	2001	58.6	3	0.886348109	0.638	0.550303638	8
optimal_loci_59288_G1	1402	1.32119	0	1001	43.5	2	15.89512146	0.336	0.549005727	8
optimal_loci_59396_G1	1051	0.384822	3.62	3221	29.01	2	13.61818928	0.094	0.541119203	4
optimal_loci_59397_G1	1833	0.384822	0	1268	57.82	2	13.61818928	0.465	0.541098181	4
optimal_loci_59463_G1	1310	0.406852	31.53	11684	33.58	2	0.239431984	0.144	0.537732734	6
optimal_loci_59466_G1	1534	0.406852	23.53	2216	38.26	1	0.478863967	0.252	0.537530323	6
optimal_loci_59517_G1	1015	0.409826	8.97	6092	54.87	2	10.52646427	0.631	0.53333535	6
optimal_loci_59518_G1	1748	0.409826	0	7140	55.66	2	10.52646427	0.726	0.533316179	6
optimal_loci_59569_G1	1354	0.350012	0	9856	29.61	1	3.917660879	0.279	0.529621496	4
optimal_loci_59586_G1	1135	0.347562	25.37	9457	36.65	2	1.95883044	0.306	0.529308525	4
optimal_loci_59704_G1	3070	0.491023	0	2052	51.1	2	28.94230906	0.445	0.522318396	1
optimal_loci_59828_G1	1202	0.29601	0	2155	53.49	2	21.94582793	0.601	0.513457309	4
optimal_loci_59830_G1	1166	0.302693	0	4467	55.4	2	21.94582793	0.625	0.513432809	4
optimal_loci_59831_G1	2656	0.302693	0	5666	56.92	3	14.63055195	0.556	0.513403864	4
optimal_loci_59835_G1	1075	0.302693	2.6	1001	46.79	3	0.477526211	0.428	0.513253994	4
optimal_loci_59894_G1	1112	0.572388	14.3	2001	44.06	5	3.366464288	0.111	0.507375135	3
optimal_loci_59922_G1	1052	0.753055	6.75	1001	30.51	4	1.388102367	0.119	0.505227729	5
optimal_loci_59928_G1	1219	0.753055	0	3544	40.77	5	4.57970571	0.19	0.505138568	5
optimal_loci_59985_G1	1249	0.985788	0	11406	35.22	3	11.3140273	0.169	0.500987298	5
optimal_loci_59989_G1	1050	0.985788	0	17082	38.09	2	16.97104095	0.1	0.500928342	5
optimal_loci_60041_G1	1594	0.997115	8.09	17929	49.56	1	0.149828964	0.486	0.496956954	3
optimal_loci_60209_G1	1441	0.562762	2.43	2244	58.22	1	63.45891958	0.566	0.488534499	5
optimal_loci_60213_G1	1496	0.562762	0	6414	49.46	1	63.45891958	0.41	0.48848902	5
optimal_loci_60216_G1	2329	0.533052	4.42	2001	36.49	1	40.62384658	0.162	0.48814606	5
optimal_loci_60228_G1	2394	0.502394	0	6616	46.19	1	9.695191693	0.492	0.487645673	6
optimal_loci_60310_G1	1180	0.076994	22.37	6357	46.94	1	3.162919411	0.35	0.483656932	9
optimal_loci_60339_G1	2711	0.63086	26.67	3901	34.15	2	33.70008166	0.076	0.482270097	7
optimal_loci_60380_G1	1408	0.829609	26.21	3545	37.42	3	10.80570301	0.22	0.478918654	7
optimal_loci_60386_G1	1064	0.829609	0	4128	60.99	3	10.80570301	0.601	0.478823961	7
optimal_loci_60387_G1	1325	0.735036	3.7	2770	54.49	3	10.80570301	0.489	0.478809343	7
optimal_loci_60395_G1	1254	0.624604	6.14	1356	39.31	3	5.510365247	0.139	0.476989817	6
optimal_loci_60452_G1	1041	0.66594	0	8552	43.32	1	2.389457168	0.303	0.474341572	5

optimal_loci_60846_G1	1070	0.243855	0	1001	40.84	3	8.114803582	0.095	0.448465296	1
optimal_loci_61010_G1	1068	0.150746	0	5282	48.22	1	20.14093739	0.507	0.436758009	2
optimal_loci_61011_G1	1579	0.150746	7.09	6383	50.79	1	20.14093739	0.585	0.436740657	2
optimal_loci_61414_G1	1640	0.165968	23.48	4348	32.86	1	1.472908897	0.112	0.415993337	2
optimal_loci_61423_G1	1766	0.174537	22.34	3512	41.16	3	1.310246639	0.231	0.415715145	5
optimal_loci_61498_G1	1282	0.1718	8.03	7131	42.35	1	181.2765866	0.477	0.410592906	6
optimal_loci_61500_G1	1179	0.1718	0	5528	55.64	1	181.2765866	0.616	0.410575651	6
optimal_loci_61504_G1	1539	0.1718	0	1001	43.07	1	181.2765866	0.472	0.410526921	6
optimal_loci_61579_G1	2254	0.225947	0	5555	47.33	1	7.763170904	0.291	0.407631163	6
optimal_loci_61582_G1	1049	0.225947	19.54	2001	38.51	1	7.763170904	0.108	0.407520205	6
optimal_loci_61639_G1	1208	0.089137	21.85	2578	42.46	2	9.549194798	0.346	0.40319324	4
optimal_loci_61743_G1	2058	0.020553	0	6434	50.38	2	0.408172136	0.489	0.399331453	2
optimal_loci_61934_G1	1329	0.29354	2.11	15574	43.49	1	0.042964074	0.315	0.388682433	1
optimal_loci_62343_G1	1171	0.060213	15.03	16533	36.72	1	37.01180236	0	0.367727008	4
optimal_loci_62346_G1	1743	0.060213	0	2085	48.02	2	19.44962092	0.567	0.367483423	4
optimal_loci_62347_G1	1032	0.060213	0	1001	45.83	2	19.44962092	0.212	0.367456814	4
optimal_loci_62420_G1	1000	0.060213	25.7	10812	32.2	1	24.92560473	0.112	0.364359645	4
optimal_loci_62519_G1	1765	0.062732	6.12	1001	55.18	3	4.351212408	0.422	0.357206136	2
optimal_loci_62533_G1	1002	0.062732	0	2149	40.11	4	3.26780254	0.092	0.357061087	2
optimal_loci_62665_G1	1114	0.908022	34.65	2766	41.65	2	31.20642875	0.054	0.34692803	4
optimal_loci_62668_G1	1295	0.908022	0	10540	41.54	2	31.20642875	0.412	0.3468424	4
optimal_loci_62707_G1	1144	0.91196	0	3201	64.16	2	8.60997208	0.586	0.34467225	4
optimal_loci_62708_G1	1675	0.91196	0	4378	60	2	8.60997208	0.48	0.344653864	4
optimal_loci_62911_G1	1561	1.446414	0	16387	37.15	1	36.99848904	0.195	0.334381302	4
optimal_loci_62916_G1	1803	1.446414	1.61	3730	37.27	2	18.49924452	0.174	0.334245059	4
optimal_loci_62920_G1	1058	1.446414	38.19	2207	32.51	3	12.37256848	0.089	0.334105479	4
optimal_loci_62922_G1	1217	1.446414	0	17069	48.8	1	0.11921639	0.439	0.33375817	4
optimal_loci_63010_G1	1578	0.355447	5.7	16937	43.53	1	0.212678551	0.368	0.327311141	2
optimal_loci_63068_G1	2511	0.230249	18.76	3733	42.29	1	3.934653932	0.211	0.32486901	2
optimal_loci_63195_G1	1098	0.633987	18.12	17737	37.34	1	2.299679245	0.232	0.316762347	1
optimal_loci_63393_G1	1324	0.379011	22.73	1001	42.82	1	15.16130782	0.206	0.303606577	3
optimal_loci_63429_G1	1294	0.341812	0	3964	37.17	1	11.67543858	0.1	0.301012239	3
optimal_loci_63432_G1	2150	0.341812	0	7276	44.04	1	11.67543858	0.288	0.300967374	3

optimal_loci_64279_G1	1151	0.043322	0	2785	41	2	0.138593898	0.169	0.238686792	1
optimal_loci_64364_G1	1987	0.113114	0	1001	46.35	2	1.663704877	0.406	0.232390764	1
optimal_loci_64459_G1	1214	0.262699	35.09	2154	41.1	1	0.524037974	0.238	0.226087772	4
optimal_loci_64542_G1	1330	0.3038	0	1006	61.2	1	0.715489091	0.623	0.222765931	6
optimal_loci_64548_G1	2584	0.301896	0	5119	40.82	1	0.715489091	0.297	0.222657169	6
optimal_loci_64549_G1	1534	0.301896	0	7770	39.11	1	0.715489091	0.198	0.222639935	6
optimal_loci_64601_G1	1155	0.307976	19.65	3356	43.72	2	1.994071778	0.292	0.219961658	5
optimal_loci_64643_G1	1009	0.298863	2.97	2261	38.55	1	3.428961566	0.118	0.217672939	5
optimal_loci_64718_G1	1001	0.29993	12.99	5147	38.86	1	57.30804893	0.01	0.211157578	2
optimal_loci_64722_G1	1195	0.29993	0	1340	37.07	1	57.30804893	0.156	0.211047234	2
optimal_loci_65456_G1	2080	0.212068	32.74	6538	35.76	1	0.36554036	0.156	0.157810883	1
optimal_loci_66070_G1	1261	0.08838	0	3471	38.38	1	2.331633188	0.209	0.110458116	1
optimal_loci_66202_G1	1105	0.001621	21.18	7199	34.38	1	570.0691809	0.217	0.101346512	1
optimal_loci_72631_G1	1154	0.095364	23.22	1001	37.78	1	0.620692925	0.156	0.229969623	1
optimal_loci_72780_G1	1101	0.211837	14.99	2149	37.05	2	21.05567121	0.329	0.235203358	3
optimal_loci_72781_G1	1084	0.211837	0	3369	36.16	2	21.05567121	0	0.235211927	3
optimal_loci_72848_G1	1615	0.216185	7.37	2208	35.78	1	2.955888264	0.121	0.238005621	3
optimal_loci_73221_G1	1417	0.136835	2.54	6827	44.88	2	2.314418708	0.329	0.257333006	1
optimal_loci_74607_G1	1003	0.527827	0	2624	46.95	3	5.324750317	0.351	0.315660566	1
optimal_loci_75292_G1	1087	0.273015	14.08	3341	41.58	2	3.411811943	0.257	0.33953596	5
optimal_loci_75335_G1	1914	0.370377	4.75	5148	33.17	2	4.021732259	0.119	0.341028506	5
optimal_loci_75336_G1	1585	0.370377	0	3493	37.79	2	4.021732259	0.225	0.341042441	5
optimal_loci_75365_G1	1609	0.43707	12	7988	46.36	2	1.392626699	0.477	0.342012997	5
optimal_loci_75406_G1	1033	0.441903	0	2332	39.49	1	9.042942286	0.251	0.342940778	5
optimal_loci_75644_G1	1477	0.323534	0	1672	51.65	1	9.780469832	0.527	0.351884102	1
optimal_loci_76564_G1	2912	0.220784	0	5326	33.03	1	0.771893338	0.153	0.394009658	1
optimal_loci_76728_G1	1437	0.354409	0	3503	41.19	1	0.067250271	0.094	0.400231025	4
optimal_loci_76729_G1	1039	0.354409	0	1315	38.11	1	0.067250271	0.126	0.400283502	4
optimal_loci_76733_G1	1345	0.354409	15.39	5410	40.29	1	0.067250271	0.169	0.400312265	4
optimal_loci_76739_G1	1174	0.335078	30.83	19784	46.67	1	2.546029973	0.386	0.400462522	4
optimal_loci_77426_G1	1018	0.053786	17.98	13675	41.94	1	2.419882565	0.137	0.429997469	2
optimal_loci_77444_G1	1046	0.046849	21.7	8628	36.23	2	8.36328374	0	0.430375929	2
optimal_loci_77581_G1	1960	0.107655	6.63	10853	38.06	1	18.39136289	0.052	0.437082107	3

optimal_loci_77595_G1	2466	0.147621	18.9	8002	40.59	1	18.39136289	0.136	0.437374664	3
optimal_loci_77617_G1	1120	0.270816	0	1001	39.01	3	14.89693922	0.201	0.439621187	3
optimal_loci_77899_G1	1374	0.174429	37.26	14398	38.35	2	15.27714915	0.199	0.45136341	1
optimal_loci_78701_G1	1094	1.158249	39.12	6418	37.93	2	2.105190329	0.003	0.483630562	3
optimal_loci_78754_G1	1006	1.022099	15.11	2001	43.33	2	3.064378014	0.298	0.485518502	3
optimal_loci_78771_G1	1005	1.000883	0	4682	42.58	2	12.38342965	0.219	0.486292794	3
optimal_loci_79826_G1	1524	0.531361	0	10778	42.78	2	42.67109101	0.328	0.530368446	3
optimal_loci_79832_G1	1040	0.531361	0	1001	33.07	2	42.67109101	0.217	0.530510521	3
optimal_loci_79861_G1	2898	0.867296	25.81	1001	33.98	1	15.08917488	0.087	0.532378549	3
optimal_loci_80142_G1	3506	0.444441	21.02	2519	50.28	1	0.034628146	0.444	0.546395096	1
optimal_loci_80265_G1	2563	0.280857	23.14	6374	35.31	3	0.55274231	0.156	0.552279114	6
optimal_loci_80271_G1	1425	0.282972	32.63	9700	35.71	1	12.95031067	0.184	0.552574017	6
optimal_loci_80282_G1	1037	0.282972	6.75	2307	40.79	2	7.749850619	0.185	0.552935711	6
optimal_loci_80300_G1	1200	0.280402	16.5	1663	35.75	3	0.292572339	0.057	0.553188898	6
optimal_loci_80375_G1	1086	0.27258	0	8214	39.59	1	4.347792074	0.255	0.555365589	6
optimal_loci_80379_G1	1772	0.27258	16.82	5333	56.43	1	4.347792074	0.611	0.555381007	6
optimal_loci_80524_G1	1101	0.229017	38.51	9069	37.96	2	25.19927316	0.199	0.560230086	4
optimal_loci_80564_G1	1465	0.306843	39.18	2004	39.18	3	6.450586453	0.26	0.560911408	4
optimal_loci_80591_G1	1964	0.324387	0	5833	47.14	1	0.084283601	0.273	0.56123001	4
optimal_loci_80592_G1	1196	0.322676	0	3919	40.63	1	0.084283601	0.194	0.561248848	4
optimal_loci_80792_G1	1074	1.358911	3.54	13605	42.08	1	0.46401909	0.353	0.568808359	2
optimal_loci_80795_G1	1341	1.358911	0	6447	44.81	1	0.46401909	0.19	0.56899807	2
optimal_loci_80882_G1	1603	0.762472	0	5895	34.12	3	2.307557167	0.201	0.573541325	1
optimal_loci_81004_G1	1046	3.277338	6.41	6719	53.34	1	12.11621969	0.722	0.578886847	3
optimal_loci_81035_G1	1105	2.13142	0	1848	40.45	1	21.33850973	0.104	0.579971333	3
optimal_loci_81064_G1	1641	2.073291	23.77	1542	33.94	1	1.505375619	0.235	0.581187125	3
optimal_loci_81339_G1	1086	0.81191	0	8853	38.85	1	0.693298688	0.099	0.590732589	1
optimal_loci_81521_G1	2012	0.465219	4.62	3462	33.79	2	6.166519574	0.043	0.595244095	4
optimal_loci_81527_G1	1046	0.465219	0	1990	49.71	1	12.33303915	0.535	0.595359127	4
optimal_loci_81594_G1	1625	0.759473	31.32	5005	35.38	3	7.589845294	0	0.597899662	8
optimal_loci_81602_G1	1336	0.759473	0	15830	48.8	2	5.932192909	0.588	0.597975697	8
optimal_loci_81625_G1	1370	0.863975	2.63	3545	33.57	1	0.043143423	0.163	0.598976695	6
optimal_loci_81629_G1	1424	0.863975	0	1705	44.38	1	0.043143423	0.385	0.599033428	6

optimal_loci_81630_G1	2059	0.863975	3.59	3415	51.18	1	0.043143423	0.476	0.599045439	6
optimal_loci_81673_G1	1203	0.521485	12.55	11171	37.24	2	0.069341888	0.19	0.600417593	10
optimal_loci_81773_G1	1645	0.245818	28.94	1490	46.2	1	2.815875433	0.312	0.602865761	6
optimal_loci_81774_G1	1249	0.245818	0	3282	34.82	1	2.815875433	0.081	0.602878348	6
optimal_loci_81775_G1	1833	0.245818	33.01	4564	38.02	1	2.815875433	0.271	0.602887353	6
optimal_loci_81803_G1	1075	0.180336	0	1985	31.72	1	2.004374813	0.171	0.603827088	7
optimal_loci_81833_G1	1174	0.184792	6.56	13362	42.75	1	60.64609925	0.208	0.605105858	8
optimal_loci_81871_G1	1713	0.295723	11.85	5888	56.21	1	8.306698442	0.595	0.60705693	6
optimal_loci_81882_G1	1395	0.39234	2.87	1101	43.65	1	1.505133326	0.198	0.607409156	5
optimal_loci_81887_G1	1280	0.389163	0	14788	42.26	1	1.505133326	0.184	0.607505294	5
optimal_loci_81941_G1	2606	0.421443	6.22	2430	43.93	2	0.353018069	0.472	0.609111909	5
optimal_loci_81992_G1	1321	1.465365	0	3782	38.45	1	61.58131348	0.124	0.6120573	2
optimal_loci_82147_G1	1466	0.913901	19.3	1687	61.32	2	0.593551887	0.828	0.617787302	3
optimal_loci_82184_G1	1611	0.114827	0	1147	43.51	1	2.374861876	0.23	0.619344834	4
optimal_loci_82185_G1	1802	0.114827	0	3002	33.9	1	2.374861876	0.222	0.619357863	4
optimal_loci_82253_G1	1861	0.367807	14.78	4231	42.34	3	24.71939846	0.504	0.621551939	8
optimal_loci_82315_G1	1317	0.591994	18.45	4406	59.68	2	12.05657654	0.616	0.624115877	7
optimal_loci_82317_G1	1362	0.591994	0	2595	47.94	2	12.05657654	0.439	0.624128281	7
optimal_loci_82331_G1	1070	0.6583	0	4950	31.02	1	5.137654584	0.119	0.624522117	7
optimal_loci_82335_G1	1548	0.6583	0	2001	38.5	1	5.137654584	0.092	0.624539474	7
optimal_loci_82339_G1	1259	0.664743	24.38	8423	36.06	1	5.137654584	0.034	0.624630575	8
optimal_loci_82404_G1	1517	0.958667	9.1	17906	41.92	1	68.21290415	0.286	0.627105091	9
optimal_loci_82425_G1	1318	0.904861	27.16	9448	34.67	2	33.25438587	0	0.628063432	5
optimal_loci_82430_G1	1171	0.821632	0	2001	54.31	1	62.27839978	0.807	0.62823224	4
optimal_loci_82477_G1	1479	1.149908	0	4291	51.52	1	2.321872031	0.489	0.630056607	4
optimal_loci_82562_G1	1365	0.964232	0	19263	46.44	1	0.115192164	0.42	0.633642819	10
optimal_loci_82576_G1	1276	0.926744	2.59	2529	46.39	2	2.203966447	0.349	0.634008264	11
optimal_loci_82579_G1	1029	0.926744	0	4864	32.94	1	4.392706201	0.136	0.634078736	11
optimal_loci_82590_G1	1249	1.211737	18.73	6821	40.11	2	0.452598027	0.191	0.634330322	11
optimal_loci_82591_G1	1530	1.211737	3.59	5109	45.09	2	0.452598027	0.548	0.634340373	11
optimal_loci_82593_G1	1951	1.211737	0	2048	49.82	2	0.452598027	0.314	0.634358916	11
optimal_loci_82596_G1	1007	1.211737	0	1689	54.51	2	0.452598027	0.528	0.634413402	11
optimal_loci_82622_G1	1677	1.372215	7.81	2870	54.8	3	8.798611899	0.586	0.635829526	12

optimal_loci_82628_G1	1010	1.372215	5.74	5555	53.06	2	4.539368733	0.639	0.635986765	12
optimal_loci_82662_G1	2132	1.395429	3.56	2235	39.11	2	19.56689799	0.154	0.637090665	19
optimal_loci_82665_G1	1757	1.395429	0	2001	47.41	2	0.501135211	0.552	0.637291362	18
optimal_loci_82708_G1	1461	2.45223	3.15	3898	47.02	1	0.082048066	0.231	0.63917695	14
optimal_loci_82738_G1	1036	2.682853	26.25	3336	44.01	2	0.129946436	0.184	0.639647678	14
optimal_loci_82739_G1	2486	2.682853	1.77	1016	39.5	2	0.129946436	0.142	0.639703624	14
optimal_loci_82742_G1	1307	2.65809	2.91	4070	50.42	2	0.129946436	0.601	0.639772459	14
optimal_loci_82750_G1	3165	2.657429	14.28	2021	47.45	2	0.396643696	0.405	0.640134463	14
optimal_loci_82751_G1	1124	2.657429	0	7805	35.14	2	0.396643696	0.107	0.640175089	14
optimal_loci_82773_G1	1477	2.657429	0	12318	46.58	1	0.229040038	0.326	0.640373497	14
optimal_loci_82774_G1	1035	2.657429	7.15	13857	46.18	1	0.229040038	0.429	0.640384306	14
optimal_loci_82804_G1	1614	2.569516	0	1675	58.05	3	16.50467876	0.601	0.642443205	13
optimal_loci_82808_G1	1683	2.51687	6.36	2001	54.07	4	12.46982241	0.408	0.642545594	13
optimal_loci_82810_G1	2798	2.488398	11.97	2001	59.04	2	16.30058404	0.543	0.642706865	12
optimal_loci_82821_G1	1109	2.397035	0	3594	49.77	2	0.456900746	0.456	0.643123887	12
optimal_loci_82871_G1	1596	1.801366	10.9	2001	50.43	1	1.059336159	0.472	0.645059893	6
optimal_loci_82929_G1	1085	1.056971	26.91	4343	47.28	1	1.322952263	0.455	0.646873506	2
optimal_loci_83027_G1	1188	1.547525	23.74	5629	52.69	2	4.149400251	0.541	0.650802089	3
optimal_loci_83029_G1	1316	1.547525	0	3038	42.09	2	4.149400251	0.46	0.650819389	3
optimal_loci_83082_G1	1303	1.048143	0	2001	48.34	2	2.885339313	0.525	0.653858755	3
optimal_loci_83168_G1	1122	1.337105	27.54	8916	56.14	2	4.508065677	0.417	0.657978258	6
optimal_loci_83171_G1	1154	1.61711	27.56	9547	38.21	2	2.765199131	0.126	0.658100784	6
optimal_loci_83175_G1	2475	1.61711	18.83	4318	50.14	3	16.2057168	0.343	0.658128234	6
optimal_loci_83182_G1	1007	1.600375	25.22	4028	46.97	3	16.2057168	0.478	0.658299964	6
optimal_loci_83243_G1	1166	1.813988	0	2001	37.9	3	0.287424547	0.152	0.661056585	9
optimal_loci_83244_G1	1140	1.813988	31.49	2001	52.01	2	0.431136821	0.425	0.661136771	9
optimal_loci_83327_G1	1318	1.557795	35.96	1343	43.85	4	2.541765292	0.292	0.663782925	8
optimal_loci_83338_G1	1083	1.557795	16.34	3715	47.55	3	69.2761174	0.506	0.663869545	8
optimal_loci_83342_G1	1189	1.322586	17.41	1288	38.18	3	69.2761174	0.13	0.663961412	8
optimal_loci_83359_G1	1408	1.27797	0	1748	46.8	2	16.80514131	0.399	0.664693855	7
optimal_loci_83392_G1	2237	1.53744	13.95	2624	36.65	3	70.21294953	0.13	0.66583914	8
optimal_loci_83402_G1	1469	1.369757	0	1001	43.09	5	0.317954935	0.265	0.666393391	8
optimal_loci_83471_G1	1288	1.504483	0	15347	44.56	2	0.341393827	0.433	0.667548278	5

optimal_loci_83489_G1	1435	1.021454	13.87	3687	52.61	2	0.638262375	0.52	0.668309736	4
optimal_loci_83584_G1	1150	0.654857	15.3	15134	34.86	2	4.14295712	0.178	0.672186939	3
optimal_loci_83639_G1	1305	1.024099	4.44	7542	50.49	4	9.012114771	0.321	0.675452267	9
optimal_loci_83642_G1	1190	1.029107	0	10428	39.91	4	9.012114771	0.298	0.675472538	9
optimal_loci_83650_G1	1401	1.001315	0	9056	29.47	1	3.932177444	0.132	0.675880275	9
optimal_loci_83671_G1	2032	1.097556	0	7537	39.76	2	5.285228115	0.281	0.676494861	11
optimal_loci_83691_G1	1452	1.097556	0	18291	51.72	1	16.28147624	0.527	0.677185778	11
optimal_loci_83701_G1	1951	1.097556	8.97	5954	51.2	1	16.28147624	0.337	0.677268928	11
optimal_loci_83705_G1	1349	1.097556	0	2038	39.28	2	9.564685099	0.256	0.677346705	11
optimal_loci_83708_G1	2713	1.097556	0	1001	49.24	3	8.110177109	0.466	0.677465073	11
optimal_loci_83735_G1	1381	1.080667	0	1001	40.47	1	15.1238849	0.19	0.679051993	9
optimal_loci_83739_G1	1266	1.076307	28.12	12693	33.49	1	1.486389794	0.127	0.679416518	8
optimal_loci_83748_G1	1549	1.082664	6.46	4132	36.79	1	1.486389794	0.187	0.679474663	8
optimal_loci_83838_G1	3351	2.221731	2.54	1001	43.39	2	1.344032019	0.292	0.684344484	3
optimal_loci_83889_G1	3245	3.049467	1.45	3322	50.5	4	10.25521947	0.524	0.686510829	5
optimal_loci_83890_G1	1464	3.049467	9.08	6676	38.72	3	13.42341371	0.181	0.686534387	5
optimal_loci_83937_G1	2241	1.934145	13.92	2974	53.36	1	0.024284288	0.512	0.688680186	4
optimal_loci_83950_G1	1164	1.798398	2.75	16319	48.28	1	9.904671615	0.484	0.689069843	4
optimal_loci_84193_G1	1645	0.671661	0	3870	45.41	3	12.71895587	0.544	0.700926564	6
optimal_loci_84195_G1	1213	0.671661	0	6941	52.18	3	12.71895587	0.62	0.700948135	6
optimal_loci_84200_G1	1309	0.671661	13.9	4055	50.87	3	12.71895587	0.489	0.700974082	6
optimal_loci_84201_G1	1653	0.671661	0	2369	60.37	3	12.71895587	0.41	0.700983508	6
optimal_loci_84227_G1	1343	0.522907	2.08	3496	47.43	2	0.117912108	0.272	0.701830877	6
optimal_loci_84300_G1	1005	0.135331	0	2570	42.38	1	8.897749882	0.225	0.703815173	6
optimal_loci_84411_G1	1097	1.550632	21.57	3179	41.84	4	11.35247296	0.294	0.708274153	2
optimal_loci_84433_G1	3251	1.249915	36.08	4777	36.11	2	0.350700835	0.029	0.709016324	3
optimal_loci_84502_G1	1365	0.659103	0	1327	41.53	4	0.991178407	0.285	0.712550594	5
optimal_loci_84519_G1	1015	0.185577	13.99	1115	42.26	1	28.57665239	0.11	0.713101086	4
optimal_loci_84521_G1	2299	0.052863	0	15717	46.45	1	28.57665239	0.425	0.713203651	4
optimal_loci_84562_G1	1074	0.048891	23.84	1619	39.75	2	8.684408378	0.223	0.714371238	5
optimal_loci_84630_G1	1561	0.342027	6.09	2645	45.8	3	0.028469586	0.307	0.716749208	4
optimal_loci_84708_G1	1407	0.686497	0	2001	54.72	1	6.18230174	0.581	0.719552419	3
optimal_loci_84721_G1	1601	0.76537	11.12	7407	54.65	2	124.4424985	0.476	0.720051644	3

optimal_loci_84852_G1	1249	0.774525	0	2001	34.5	1	0.08957153	0	0.725275819	2
optimal_loci_84860_G1	1287	0.802195	4.04	1442	35.43	2	81.52330742	0.103	0.725731136	2
optimal_loci_84952_G1	2376	0.759116	26.77	7898	44.14	2	16.92609664	0.298	0.730546115	7
optimal_loci_84976_G1	2355	0.721081	4.63	3189	39.74	2	6.108550255	0.225	0.73133805	7
optimal_loci_84980_G1	1437	1.900563	9.81	2005	39.87	1	0.751166042	0.199	0.731634562	8
optimal_loci_84983_G1	1859	1.900563	0	5011	38.35	1	0.751166042	0.163	0.731655676	9
optimal_loci_84984_G1	3137	1.900563	0	7480	40.99	1	0.751166042	0.067	0.731673018	9
optimal_loci_85008_G1	1014	1.873361	0	2001	40.72	5	7.546109899	0.28	0.733787855	9
optimal_loci_85014_G1	1029	1.873361	0	1001	40.71	6	6.288424916	0.287	0.733854155	9
optimal_loci_85047_G1	1098	2.117557	8.47	2977	43.8	1	8.657201424	0.36	0.735048264	7
optimal_loci_85048_G1	1884	2.193398	25.21	18191	43.52	1	3.198457741	0.291	0.735179241	6
optimal_loci_85384_G1	1402	0.256766	3.42	2980	44.07	2	4.020391698	0.379	0.754724166	2
optimal_loci_85388_G1	1038	0.285582	35.07	3480	33.42	2	15.56875499	0.134	0.755017271	2
optimal_loci_85488_G1	1149	0.524632	0	2502	39.86	1	2.214837968	0.178	0.760090501	2
optimal_loci_85558_G1	1082	0.44152	0	2001	38.81	4	8.197937511	0.287	0.762446458	5
optimal_loci_85595_G1	1162	0.540193	26.25	2001	34.59	3	3.887895567	0.101	0.764806265	5
optimal_loci_85599_G1	1030	0.538448	7.18	3140	33.98	5	10.0081613	0.082	0.764975045	5
optimal_loci_85600_G1	1565	0.538448	0	5510	47.15	4	11.43836096	0.39	0.764991692	5
optimal_loci_85651_G1	1878	0.530569	9.42	2159	36.36	1	2.991803332	0.254	0.767054046	6
optimal_loci_85720_G1	1726	0.215523	7.65	6388	31.17	1	1.602431615	0.132	0.76860914	3
optimal_loci_85742_G1	2230	0.17068	0	12630	46.77	3	53.57748885	0.353	0.769536688	3
optimal_loci_85833_G1	1227	0.105989	0	2117	52.64	4	4.630873727	0.547	0.773161216	1
optimal_loci_85950_G1	1017	2.26771	2.95	2603	45.91	2	26.01360757	0.561	0.780205144	3
optimal_loci_85971_G1	1561	2.26771	0	2768	42.79	5	18.45458198	0.345	0.781305138	4
optimal_loci_85987_G1	1107	0.654578	6.78	1001	62.87	2	25.72255991	0.608	0.782081551	4
optimal_loci_86058_G1	1080	0.336656	22.41	16742	48.24	1	24.68027051	0.205	0.784572798	4
optimal_loci_86108_G1	1508	0.204868	8.75	1447	58.88	2	69.60766525	0.578	0.786158945	2
optimal_loci_86203_G1	1112	1.841541	0	2001	49.64	4	0.248704055	0.306	0.790409593	4
optimal_loci_86235_G1	1290	1.902968	10.08	6327	50.46	3	15.56845767	0.571	0.791400632	4
optimal_loci_86326_G1	1931	2.102728	2.02	2919	42.51	1	30.81380457	0.199	0.793666021	6
optimal_loci_86328_G1	1014	2.102728	8.58	1540	41.71	1	30.81380457	0.093	0.793682148	6
optimal_loci_86389_G1	1204	1.474655	2.82	2728	53.32	2	6.890812982	0.602	0.795614095	6
optimal_loci_86403_G1	1197	1.304148	0	8185	47.2	2	9.999407553	0.651	0.796280989	7

optimal_loci_86453_G1	1476	1.860015	2.03	2652	39.76	4	10.20509395	0.143	0.797358387	5
optimal_loci_86465_G1	1062	1.835867	17.61	3590	38.32	3	0.840604054	0.221	0.798211875	5
optimal_loci_86505_G1	1903	1.962831	1.47	1412	50.39	2	40.98072025	0.521	0.799624199	5
optimal_loci_86657_G1	1648	4.302462	2.37	1001	52.06	1	0.102628809	0.671	0.802424635	7
optimal_loci_86688_G1	1277	2.833247	6.19	1001	51.68	3	1.850414474	0.458	0.80360391	6
optimal_loci_86692_G1	1400	2.891595	28.21	1001	34.85	4	3.87894362	0.156	0.803693585	6
optimal_loci_86702_G1	1367	2.68791	14.19	4230	47.69	2	2.03580737	0.402	0.804446074	8
optimal_loci_86705_G1	1127	2.68791	0	7737	33.89	2	2.03580737	0.116	0.804470708	8
optimal_loci_86713_G1	1202	2.68791	27.12	1212	50.66	3	270.1361783	0.524	0.804782243	8
optimal_loci_86764_G1	1012	1.192267	5.24	6254	52.47	2	3.736518746	0.496	0.807251372	5
optimal_loci_86770_G1	1781	1.192267	9.83	1221	56.31	1	7.473037491	0.586	0.807391789	5
optimal_loci_86959_G1	1125	1.347902	0	3413	36.88	1	47.49057092	0.111	0.813622266	6
optimal_loci_86985_G1	1667	1.50466	9.84	6940	46.19	2	5.173485636	0.364	0.814318352	6
optimal_loci_86996_G1	1464	1.369816	0	13057	56.14	1	7.303676816	0.643	0.814512776	6
optimal_loci_86998_G1	1817	1.363365	0	15069	49.31	1	7.303676816	0.428	0.814526909	6
optimal_loci_87009_G1	1013	1.290087	0	19745	37.7	1	20.4725122	0.159	0.814950864	7
optimal_loci_87027_G1	1035	1.121851	36.91	9973	36.52	3	8.913720419	0.243	0.815865867	8
optimal_loci_87098_G1	2371	0.90211	17.55	2001	45.84	2	1.344209394	0.499	0.818201406	7
optimal_loci_87130_G1	1181	0.893715	0	8413	42.67	1	9.539303345	0.204	0.818613448	7
optimal_loci_87177_G1	1091	1.012629	28.14	5361	35.1	1	41.59911262	0.098	0.82021325	6
optimal_loci_87183_G1	1586	1.012629	7.31	1010	48.61	4	35.93989433	0.321	0.820305791	6
optimal_loci_87190_G1	2852	1.012629	9.26	1001	51.26	6	27.8916882	0.449	0.820453696	6
optimal_loci_87230_G1	1094	1.08565	0	2001	56.58	4	7.470672994	0.711	0.82209817	5
optimal_loci_87332_G1	1222	1.18849	0	3155	32.56	2	15.66537482	0.115	0.826566127	5
optimal_loci_87345_G1	2437	1.266821	1.4	4006	47.02	2	0.024511781	0.414	0.826812522	5
optimal_loci_87353_G1	1425	1.388246	0	15631	39.36	1	1.094216667	0.099	0.827153362	5
optimal_loci_87354_G1	1006	1.388246	0	14562	43.63	1	1.094216667	0.205	0.827163814	5
optimal_loci_87395_G1	1672	1.759951	0	1001	44.25	4	16.43946296	0.361	0.829502956	7
optimal_loci_87433_G1	1203	0.725128	0	1449	47.54	7	3.626615983	0.412	0.832144854	3
optimal_loci_87446_G1	1693	0.725128	9.16	2310	39.16	3	9.204188115	0.155	0.832434018	3
optimal_loci_87547_G1	2166	1.563942	35.04	2427	39.75	4	21.34866467	0.214	0.836616274	3
optimal_loci_87548_G1	1244	1.563942	0	2920	53.53	4	21.34866467	0.386	0.836637577	3
optimal_loci_87554_G1	1436	1.563942	5.57	2840	31.12	5	17.07893173	0.016	0.836696326	3

optimal_loci_87703_G1	1809	1.961675	7.85	1234	50.08	1	18.4295397	0.346	0.843960414	1
optimal_loci_87837_G1	1344	1.197831	0	5421	38.02	2	1.551540488	0.27	0.851966019	3
optimal_loci_87838_G1	1016	1.197831	27.17	4226	38.28	2	1.551540488	0.069	0.851976717	3
optimal_loci_87839_G1	1701	1.197831	0	2492	44.26	2	1.551540488	0.207	0.851984085	3
optimal_loci_87921_G1	1118	3.25338	29.79	2520	36.04	4	8.571376858	0	0.855955726	1
optimal_loci_88032_G1	1143	2.884469	32.11	3959	38.05	3	2.498140545	0.102	0.859916444	2
optimal_loci_88072_G1	1235	2.095163	3.48	3248	38.62	1	1.612436606	0.096	0.862289062	2
optimal_loci_88369_G1	1128	2.611449	36.26	4641	33.95	2	3.458568121	0	0.872733213	1
optimal_loci_88529_G1	1442	2.348597	0	2067	41.19	1	11.45554116	0.28	0.878707869	3
optimal_loci_88592_G1	1083	2.481125	13.3	13318	36.65	1	0.84705245	0.024	0.880533746	3
optimal_loci_88611_G1	1022	2.482981	25.24	2008	39.62	1	2.643203904	0.364	0.881139334	3
optimal_loci_88802_G1	1263	1.077159	0	1559	44.97	1	60.41854779	0.413	0.885935594	1
optimal_loci_89030_G1	1132	2.617259	20.14	4749	40.37	2	26.40137481	0.238	0.895940491	6
optimal_loci_89040_G1	1573	2.603599	7.5	2017	42.65	3	17.60091654	0.141	0.896031038	6
optimal_loci_89054_G1	2721	2.984412	0	13438	30.72	2	7.159012921	0.149	0.89638195	6
optimal_loci_89114_G1	1007	3.693577	0	2846	43.99	3	2.485318477	0.18	0.898678913	9
optimal_loci_89116_G1	1671	3.693577	15.02	1040	43.38	3	2.485318477	0.152	0.898727884	9
optimal_loci_89120_G1	1001	3.161579	0	2001	30.36	3	0.138323	0	0.898875704	9
optimal_loci_89225_G1	1026	3.791541	28.17	3720	43.17	1	11.7832491	0.257	0.90096319	8
optimal_loci_89229_G1	2716	3.791541	15.1	7053	41.56	1	11.7832491	0.251	0.900986601	8
optimal_loci_89230_G1	1339	3.791541	0	10077	48.24	1	11.7832491	0.46	0.901007842	8
optimal_loci_89294_G1	1003	2.767074	9.57	12875	47.35	2	0.333939177	0.363	0.903043083	7
optimal_loci_89320_G1	1493	2.591261	0	1001	49.63	4	0.042548743	0.37	0.903957658	7
optimal_loci_89367_G1	1912	1.81778	0	3801	40.89	1	0.517046598	0.14	0.905691366	5
optimal_loci_89386_G1	1175	1.509206	0	4450	38.8	1	3.482425682	0.315	0.9062052	6
optimal_loci_89505_G1	1016	0.161936	0	1001	37.5	3	1.809201126	0	0.909073123	6
optimal_loci_89515_G1	1263	0.142407	18.45	10558	40.61	3	0.474215007	0.33	0.909315578	5
optimal_loci_89535_G1	1452	0.14545	23.69	2313	40.28	1	0.312954528	0.177	0.90984103	4
optimal_loci_89606_G1	1150	0.370485	4.43	12168	40.17	2	1.283570485	0.28	0.911588287	5
optimal_loci_89659_G1	1893	0.33763	15.76	1001	30.53	3	18.87122558	0.095	0.914201533	2
optimal_loci_89795_G1	1323	1.274968	25.17	1001	34.16	2	0.060986176	0.2	0.918973967	2
optimal_loci_89825_G1	1319	1.894018	10.99	6994	43.21	3	3.108866102	0.433	0.920042234	3
optimal_loci_89916_G1	1377	2.698104	5.81	2611	44.51	2	20.13790954	0.384	0.92353037	9

optimal_loci_89921_G1	1058	2.716525	0	6605	42.72	2	20.13790954	0.056	0.923615248	8
optimal_loci_89923_G1	1065	2.729486	12.02	3176	56.43	2	20.13790954	0.463	0.923639285	8
optimal_loci_89937_G1	1070	2.884781	14.67	3410	53.08	1	34.91664371	0.729	0.924550685	8
optimal_loci_89953_G1	1915	3.548448	0	2915	40.83	2	5.049996849	0.342	0.925187137	8
optimal_loci_89995_G1	1018	3.548448	7.66	4840	35.85	1	5.157505072	0.093	0.926403857	8
optimal_loci_90016_G1	1581	3.548448	31.69	2753	36.11	1	6.061646288	0.135	0.926724018	8
optimal_loci_90017_G1	1430	3.548448	35.87	4968	41.6	1	6.061646288	0.346	0.926739576	8
optimal_loci_90267_G1	1232	1.349498	17.05	1001	38.23	4	6.086645335	0.156	0.936846554	1
optimal_loci_90457_G1	1441	1.952695	33.66	2721	49.34	1	0.035363994	0.485	0.940850786	2
optimal_loci_90575_G1	1244	2.441362	0	2001	53.77	2	0.244660782	0.662	0.943404764	2
optimal_loci_90733_G1	1116	1.870238	0	14293	32.88	1	42.40723381	0	0.947906429	2
optimal_loci_90804_G1	2221	3.018455	14.99	3731	37.37	2	0.377507679	0.261	0.949730135	2
optimal_loci_90930_G1	1132	6.280686	20.05	12230	48.49	2	0.053849283	0.358	0.954306248	4
optimal_loci_90949_G1	1006	5.587964	4.57	1309	38.36	3	0.669726461	0.009	0.954766643	4
optimal_loci_91003_G1	1185	5.313728	8.86	3280	38.56	4	5.816485694	0.097	0.956517426	5
optimal_loci_91018_G1	1080	6.041724	12.41	2868	48.7	2	0.08082029	0.313	0.956986195	5
optimal_loci_91074_G1	1006	3.872765	0	1964	48.4	1	18.54919225	0.611	0.958820697	3
optimal_loci_91337_G1	1025	5.880001	5.85	1001	41.07	4	10.26254782	0.118	0.967763403	2
optimal_loci_91374_G1	1014	6.506823	13.71	10010	42.8	1	0.177041819	0.429	0.969538728	4
optimal_loci_91432_G1	1349	4.081849	0	2376	52.18	3	5.924057577	0.548	0.971387629	4
optimal_loci_91447_G1	1082	3.815219	19.96	6758	39.92	1	6.631383893	0.356	0.972097363	5
optimal_loci_91493_G1	1831	3.886717	10.16	2184	38.39	1	1.942544638	0.195	0.974200695	4
optimal_loci_91512_G1	1077	4.238125	0	3200	59.14	3	7.178659308	0.726	0.975532847	3
optimal_loci_92289_G1	1793	3.996078	29.5	8560	33.24	1	3.13304653	0.221	0.989022528	4
optimal_loci_92364_G1	1017	4.101608	9.73	10471	45.52	3	2.593329365	0.153	0.986571815	4
optimal_loci_92390_G1	2735	4.882398	14.55	3470	38.68	4	13.57047167	0.236	0.984320181	4
optimal_loci_92391_G1	2056	4.908309	0	1381	44.06	4	13.57047167	0.283	0.984299228	4
optimal_loci_92455_G1	1647	7.100221	1.82	2548	52.45	4	5.663576615	0.582	0.978418716	5
optimal_loci_92543_G1	1027	7.964583	0	7079	30.96	2	0.297320817	0.071	0.974078124	8
optimal_loci_92568_G1	3365	7.289776	0	12872	48.35	2	1.508985501	0.431	0.973808124	8
optimal_loci_92573_G1	2002	7.128469	0	1001	60.93	1	2.423329369	0.709	0.973638044	8
optimal_loci_92579_G1	1131	7.232928	0	11631	39.16	1	2.423329369	0	0.973484774	8
optimal_loci_92607_G1	2094	5.415292	0	4118	34.57	5	1.300125005	0.126	0.972370401	8

optimal_loci_92613_G1	1626	5.415292	0	3137	48.21	5	1.300125005	0.253	0.972315426	8
optimal_loci_92643_G1	1583	6.507184	0	12883	37.52	1	30.42260173	0.143	0.970954473	8
optimal_loci_92714_G1	1509	5.44412	15.24	2812	47.24	3	5.091620723	0.414	0.967751565	8
optimal_loci_92768_G1	1398	7.533335	0	4166	55.36	4	18.45278064	0.544	0.965178044	5
optimal_loci_92769_G1	2097	7.533335	5.01	2001	58.22	4	18.45278064	0.581	0.965156329	5
optimal_loci_92773_G1	2043	7.533335	0	3001	61.23	3	14.98255843	0.707	0.964879298	6
optimal_loci_92791_G1	1753	8.043398	0	2001	55.16	3	2.057370917	0.522	0.964332086	6
optimal_loci_92850_G1	1631	3.440993	0	5757	55.79	1	0.406583997	0.616	0.959996279	3
optimal_loci_92958_G1	2248	10.539975	4	2001	52.13	3	2.95083908	0.635	0.953133601	7
optimal_loci_92959_G1	1203	10.539975	3.16	2001	48.79	3	4.503898924	0.456	0.95281008	7
optimal_loci_92962_G1	1816	10.539975	7.54	2230	46.14	3	4.503898924	0.48	0.952657954	7
optimal_loci_92963_G1	1114	10.539975	25.4	1001	43.08	3	4.503898924	0.343	0.952645627	7
optimal_loci_92974_G1	1460	10.539975	0	1001	36.23	3	0.041836287	0.308	0.95234016	7
optimal_loci_93007_G1	1521	7.480889	23.14	2501	42.93	3	5.976980771	0.247	0.951153701	8
optimal_loci_93017_G1	1377	7.480889	0	1504	51.56	4	4.482735578	0.49	0.95105013	8
optimal_loci_93120_G1	1709	6.39582	0	11936	33.87	2	4.520340744	0.213	0.946338004	6
optimal_loci_93187_G1	2574	8.192837	6.1	2001	43.82	4	21.17224075	0.357	0.943919488	9
optimal_loci_93189_G1	1126	8.192837	2.49	2420	38.45	4	21.17224075	0.062	0.943905266	9
optimal_loci_93248_G1	1719	8.121026	2.79	1699	38.91	4	2.36836902	0.131	0.942081444	9
optimal_loci_93279_G1	1553	7.482869	2.38	3723	49.25	1	2.895684693	0.347	0.941017783	8
optimal_loci_93280_G1	1002	7.482869	10.68	2558	54.69	1	2.895684693	0.515	0.941006098	8
optimal_loci_93296_G1	1670	6.765297	0	6154	50.77	1	16.75781258	0.562	0.940332487	10
optimal_loci_93308_G1	1320	6.765297	0	2001	41.59	3	4.161743516	0.242	0.940018556	10
optimal_loci_93314_G1	2475	6.765297	0	3160	52.52	3	4.161743516	0.422	0.939792558	10
optimal_loci_93409_G1	2228	5.743544	0	4363	47.08	1	14.34804309	0.442	0.935525356	9
optimal_loci_93413_G1	1369	5.748781	19.28	2046	46.67	1	14.34804309	0.623	0.93542663	9
optimal_loci_93433_G1	1630	4.964327	10.37	2001	39.5	2	3.759998601	0.198	0.934627081	7
optimal_loci_93463_G1	1635	5.27922	2.81	1001	38.59	1	0.596945696	0.166	0.933287141	7
optimal_loci_93469_G1	1134	5.27922	0	13866	51.85	2	0.298472848	0.287	0.933163129	7
optimal_loci_93486_G1	1164	5.25572	24.48	1001	46.13	2	2.100276392	0.386	0.932372628	11
optimal_loci_93549_G1	1866	5.21642	0	2001	59.75	3	0.10385989	0.713	0.930010632	9
optimal_loci_93575_G1	1159	5.129063	18.21	2169	36.92	1	5.813227482	0.219	0.927698546	6
optimal_loci_93576_G1	1149	5.129063	0	3444	52.74	1	5.813227482	0.716	0.927685858	6

optimal_loci_93581_G1	1240	5.129063	33.63	8768	41.04	1	5.813227482	0.123	0.927631545	6
optimal_loci_93582_G1	1238	5.129063	10.9	10455	39.09	1	5.813227482	0.2	0.927614644	6
optimal_loci_93690_G1	2365	5.789913	3	2796	54.33	3	0.479558801	0.591	0.920311695	5
optimal_loci_93741_G1	1247	5.886068	0	1087	49.87	3	5.471303881	0.336	0.917583751	6
optimal_loci_93761_G1	1354	5.886068	0	11012	36.63	6	0.349433712	0.096	0.916487864	6
optimal_loci_93764_G1	1306	5.886068	27.03	8673	34.53	5	0.419320454	0.048	0.916464403	6
optimal_loci_93765_G1	1506	5.886068	0	4716	34.66	5	0.419320454	0.138	0.916424714	6
optimal_loci_93801_G1	1592	4.919716	18.72	17301	35.42	1	64.17713743	0.117	0.914123852	5
optimal_loci_93934_G1	1324	6.630209	0	2344	43.65	2	0.35503881	0.398	0.908627834	7
optimal_loci_93980_G1	1044	6.99864	18.01	1033	41.85	4	1.204642407	0.239	0.90650656	8
optimal_loci_93986_G1	1002	6.99864	0	2427	42.31	4	1.204642407	0.126	0.906381936	8
optimal_loci_93987_G1	1201	6.99864	14.57	3506	40.63	4	1.204642407	0.26	0.906369117	8
optimal_loci_93998_G1	1385	6.81365	17.55	1840	49.24	2	1.468351871	0.262	0.905351926	8
optimal_loci_94020_G1	1356	6.81365	22.79	3152	42.62	2	8.256710826	0.329	0.90514317	8
optimal_loci_94042_G1	1169	7.066986	0	14995	50.21	2	11.35040419	0.562	0.904073109	9
optimal_loci_94067_G1	1072	3.806593	10.35	4143	41.04	3	24.6794355	0.105	0.901506038	12
optimal_loci_94089_G1	1953	1.721165	0	2238	41.16	1	1.656069974	0.351	0.899618766	11
optimal_loci_94098_G1	1302	1.784235	26.88	5128	39.7	2	45.60650498	0.212	0.899015025	11
optimal_loci_94104_G1	2096	1.784235	0	1110	31.63	2	48.9176243	0.127	0.898897803	11
optimal_loci_94134_G1	1508	3.03801	3.12	2001	48.47	1	21.90083607	0.447	0.89697995	12
optimal_loci_94135_G1	1198	3.105639	0	1001	52.42	1	21.90083607	0.425	0.896836249	12
optimal_loci_94161_G1	1113	4.897769	10.42	18176	32.34	1	1.57270471	0.075	0.895348004	11
optimal_loci_94184_G1	1759	5.094538	0	7994	58.1	1	1.57270471	0.617	0.895045005	13
optimal_loci_94189_G1	2024	5.094538	0	11059	49.65	1	1.57270471	0.575	0.895011605	13
optimal_loci_94193_G1	1450	5.094538	14.48	14642	62.62	1	1.57270471	0.726	0.894981424	13
optimal_loci_94205_G1	1560	4.800464	31.67	4948	50.51	3	0.919781937	0.315	0.894383561	12
optimal_loci_94227_G1	1202	5.417254	9.9	2236	50.83	3	4.435023881	0.456	0.893443541	10
optimal_loci_94271_G1	1882	5.126693	11.26	4697	47.55	2	2.330441357	0.212	0.890171765	13
optimal_loci_94273_G1	1291	5.126693	5.5	8408	40.89	2	2.330441357	0.3	0.890140471	13
optimal_loci_94313_G1	1342	2.949452	0	2001	53.05	1	1.837424622	0.573	0.887562698	9
optimal_loci_94314_G1	2006	2.949452	14.31	1155	45.06	1	1.837424622	0.132	0.887474112	9
optimal_loci_94317_G1	1711	2.949452	6.31	4805	41.61	1	1.837424622	0.27	0.887440461	9
optimal_loci_94324_G1	1074	2.949452	0	12416	37.24	1	1.837424622	0.168	0.887370512	9

optimal_loci_94326_G1	2729	2.949452	10.59	14356	46.86	1	1.837424622	0.279	0.887334453	9
optimal_loci_94358_G1	1196	0.395627	0	1971	43.31	2	1.063206442	0.39	0.885145697	9
optimal_loci_94402_G1	2260	0.076665	0	2823	35	2	13.68002819	0.188	0.883366861	7
optimal_loci_94557_G1	1548	3.346806	0	2001	54.32	5	5.45308408	0.741	0.874353581	10
optimal_loci_94570_G1	1362	3.306759	0	2236	37.88	1	474.455905	0.197	0.873523882	11
optimal_loci_94571_G1	1687	3.306759	17.55	3841	35.56	1	474.455905	0.099	0.873504524	11
optimal_loci_94574_G1	1731	3.306759	0	6607	39.34	1	474.455905	0.202	0.873476339	11
optimal_loci_94602_G1	1034	3.381197	26.89	5064	41.48	1	0.321127918	0.128	0.873240983	11
optimal_loci_94618_G1	1205	3.763484	0	6145	40.58	2	2.795134847	0.182	0.871776489	11
optimal_loci_94627_G1	1077	4.250963	0	13145	46.98	1	5.590269693	0.391	0.8713501	11
optimal_loci_94635_G1	1841	4.250963	3.69	2822	38.07	1	1.31734256	0.237	0.870815757	11
optimal_loci_94640_G1	1963	4.250963	9.42	2139	38.81	1	1.31734256	0.136	0.870738445	11
optimal_loci_94662_G1	1044	3.193717	15.52	4213	43.86	1	5.32091876	0.364	0.869660572	11
optimal_loci_94688_G1	2178	2.970021	0	12666	37.09	2	5.689191879	0.234	0.868717503	11
optimal_loci_94752_G1	1065	1.06929	0	5950	38.4	6	0.818748272	0.227	0.864360491	4
optimal_loci_94779_G1	1363	0.431884	0	3922	57.22	3	9.620412902	0.686	0.862392738	3
optimal_loci_94784_G1	1035	0.366221	0	1068	52.94	3	9.632769842	0.405	0.862319519	3
optimal_loci_94946_G1	1106	0.827231	4.25	2667	38.96	2	2.12019871	0.331	0.850153109	1
optimal_loci_95111_G1	1659	0.375226	11.33	14557	38.33	2	3.329760586	0.091	0.840700752	1
optimal_loci_95244_G1	1025	1.238781	0	2001	44.58	4	32.23821141	0.437	0.833712197	5
optimal_loci_95264_G1	1609	1.609796	26.6	5054	46.86	2	12.38934556	0.418	0.832934473	5
optimal_loci_95297_G1	1674	1.892877	14.34	8710	35.96	1	7.089186664	0.111	0.830809328	8
optimal_loci_95324_G1	1206	2.150173	12.02	16139	39.46	1	33.53686511	0.185	0.829634012	9
optimal_loci_95334_G1	1028	2.150173	23.54	1001	43.77	3	1.950014597	0.341	0.829124313	9
optimal_loci_95359_G1	1096	1.624693	0	11151	32.84	4	9.53021744	0.079	0.827848947	7
optimal_loci_95360_G1	1119	1.624693	30.56	9155	30.65	4	9.53021744	0.075	0.827828927	7
optimal_loci_95371_G1	1065	1.624693	0	3639	40	4	9.53021744	0.063	0.827571184	7
optimal_loci_95425_G1	1002	2.119723	0	5514	50.09	2	91.61850376	0.32	0.825054303	6
optimal_loci_95526_G1	1200	1.894349	0	12710	46	2	5.664797499	0.333	0.819021424	1
optimal_loci_95651_G1	2457	0.500424	2.16	4796	40.98	1	8.793879726	0.244	0.813041515	3
optimal_loci_95734_G1	1385	0.999496	11.12	2195	39.92	2	12.24664446	0.183	0.809482999	5
optimal_loci_95748_G1	1653	1.169318	36.6	1001	36.29	3	0.03642109	0.119	0.808473862	5
optimal_loci_95783_G1	1421	1.750163	0	1001	50.52	2	22.35103934	0.494	0.804768004	7

optimal_loci_95784_G1	1336	1.750163	5.01	7019	42.44	2	22.35103934	0.257	0.804708495	7
optimal_loci_95846_G1	1750	0.882787	1.89	1425	54.74	2	22.37561353	0.564	0.801808415	5
optimal_loci_95864_G1	1776	0.447218	0	13383	39.92	1	302.8164291	0.251	0.800969368	5
optimal_loci_95872_G1	1833	0.740351	0	2301	51.77	3	15.20134326	0.495	0.80008343	5
optimal_loci_96164_G1	1295	1.333484	0	1451	51.42	2	4.518550494	0.589	0.783770171	4
optimal_loci_96166_G1	1317	1.333484	15.64	2917	42.59	2	4.518550494	0.341	0.783750321	4
optimal_loci_96196_G1	1271	1.333484	0	1161	40.83	1	0.541361095	0.285	0.78255989	4
optimal_loci_96212_G1	1120	1.620923	14.37	1235	37.76	3	5.13751094	0.035	0.780797934	4
optimal_loci_96348_G1	2060	3.952223	0	1893	49.56	2	12.96901622	0.38	0.77367678	7
optimal_loci_96380_G1	2780	3.003905	1.65	9000	58.74	1	67.04883832	0.672	0.772029228	10
optimal_loci_96381_G1	1042	3.003905	0	2861	49.52	1	67.04883832	0.399	0.771967653	10
optimal_loci_96419_G1	1158	1.879857	0	1001	57.08	1	28.93141046	0.603	0.769713671	10
optimal_loci_96444_G1	1516	1.763894	0	2001	40.89	1	0.480275002	0.098	0.769234604	10
optimal_loci_96445_G1	2111	1.763894	0	1001	54.57	1	0.480275002	0.606	0.769148736	10
optimal_loci_96446_G1	2442	1.763894	0	6030	52.17	1	0.480275002	0.708	0.769094975	10
optimal_loci_96490_G1	1031	1.130493	29.97	1765	36.17	1	0.98496388	0.205	0.767493992	9
optimal_loci_96491_G1	1696	1.130493	36.26	3050	46.63	1	0.98496388	0.354	0.767474433	9
optimal_loci_96494_G1	1374	0.54087	6.04	6530	41.7	1	0.98496388	0.223	0.767442758	9
optimal_loci_96614_G1	1180	0.362862	0	1332	35	1	0.661749592	0.082	0.762411284	2
optimal_loci_96647_G1	1077	0.562961	0	3760	45.86	1	3.803388273	0.522	0.761355577	2
optimal_loci_96777_G1	1510	0.019763	20.66	3428	38.14	2	13.40216323	0.126	0.750735296	4
optimal_loci_96778_G1	1623	0.019763	8.69	1001	42.94	2	13.40216323	0.196	0.750710953	4
optimal_loci_96782_G1	1701	2.355961	4.23	1001	56.55	2	0.410686774	0.679	0.75018332	6
optimal_loci_96849_G1	1451	1.327294	27.43	5245	35.21	1	3.064081603	0.282	0.746070181	6
optimal_loci_96876_G1	1017	1.327294	24.98	2143	42.57	1	1.827255687	0.173	0.745675878	4
optimal_loci_96877_G1	2222	1.329844	24.08	3228	40.09	1	1.827255687	0.254	0.745652909	4
optimal_loci_96967_G1	1163	0.980747	31.3	1001	45.57	2	12.00896394	0.094	0.739959478	2
optimal_loci_96999_G1	2092	1.619304	0	1649	38.04	4	3.296160303	0.146	0.738292828	2
optimal_loci_97232_G1	1128	0.584351	0	7510	43.43	3	3.016489057	0.464	0.724532166	2
optimal_loci_97235_G1	1345	0.584351	0	10328	38.21	3	3.016489057	0.269	0.724501725	2
optimal_loci_97394_G1	1813	0.915759	0	5730	41.69	2	0.652683983	0.316	0.716995416	3
optimal_loci_97398_G1	1481	0.915759	17.22	2439	50.03	2	0.652683983	0.345	0.716962407	3
optimal_loci_97417_G1	1134	1.506023	0	3025	46.47	4	9.02533564	0.46	0.715668847	4

optimal_loci_97503_G1	1082	1.814439	0	1553	29.39	2	23.33396509	0.1	0.710754654	2
optimal_loci_97629_G1	1966	0.182846	17.29	10868	32.96	2	10.43551162	0.051	0.704531986	3
optimal_loci_97648_G1	1681	0.165505	0	1001	39.91	2	23.02037987	0.187	0.702989037	6
optimal_loci_97656_G1	1434	0.473277	0	9018	37.16	2	5.9604257	0.24	0.702676018	6
optimal_loci_97741_G1	1253	0.771775	0	1001	36.95	2	20.16275075	0.17	0.699335537	7
optimal_loci_97752_G1	2790	0.79018	16.7	3645	48.67	2	4.540887177	0.419	0.698617492	8
optimal_loci_97755_G1	2376	0.79018	14.81	2606	38.17	2	4.540887177	0.146	0.698579759	8
optimal_loci_97772_G1	1355	0.971452	0	16197	43.76	1	98.84169754	0.343	0.696984885	7
optimal_loci_97776_G1	1227	0.971452	0	13547	51.42	1	98.84169754	0.606	0.696958305	7
optimal_loci_97851_G1	2140	0.73704	8.97	4747	36.3	5	0.183769808	0.182	0.693817944	6
optimal_loci_97861_G1	2031	0.744302	0	6987	34.36	4	0.019948038	0.096	0.693542197	4
optimal_loci_97998_G1	1208	0.045538	36.75	6787	38.65	3	10.47373593	0.09	0.684389488	4
optimal_loci_98002_G1	1318	0.045538	0	5246	36.87	3	10.47373593	0.147	0.684346078	4
optimal_loci_98015_G1	1335	0.045538	27.64	11281	37.3	1	0.022642537	0.167	0.684151946	4
optimal_loci_98088_G1	1151	0.01486	0	13106	36.14	1	161.2649901	0.123	0.679880822	5
optimal_loci_98130_G1	1096	0.01486	18.52	1001	40.87	3	44.94372997	0.208	0.676588425	3
optimal_loci_98167_G1	1626	0.01486	23.25	2487	41.02	3	20.81323665	0.365	0.674384664	2
optimal_loci_98324_G1	1189	0.193778	7.4	5617	41.46	4	16.65345629	0.116	0.661406199	3
optimal_loci_98329_G1	1476	0.193778	17.28	2756	34.55	3	43.61228861	0.242	0.661173942	3
optimal_loci_98336_G1	1493	0.193778	0	7633	30.94	2	56.26362648	0.163	0.661107202	3
optimal_loci_98623_G1	1055	0.265685	0	5449	37.44	2	1.771233691	0.105	0.644668656	1
optimal_loci_98842_G1	2284	0.211144	2.06	2715	44.13	1	0.123542338	0.144	0.63196318	2
optimal_loci_98857_G1	1261	0.166764	0	11726	30.68	1	21.20492645	0.058	0.630677623	3
optimal_loci_98900_G1	1435	0.035619	3.62	3683	41.39	1	12.80667229	0.335	0.626426449	2
optimal_loci_99247_G1	1399	0.312157	0	16086	36.81	1	5.554745907	0.176	0.606465637	1
optimal_loci_99490_G1	2029	0.037212	24.79	3759	35.58	1	0.034043404	0.209	0.587408606	2
optimal_loci_99566_G1	1048	0.071635	0	11319	36.64	1	27.33974387	0.027	0.582604082	4
optimal_loci_99591_G1	1032	0.080129	0	1001	39.43	2	19.96148101	0.169	0.58133671	3
optimal_loci_99593_G1	1024	0.111	0	3097	54.49	2	19.96148101	0.504	0.58126329	3
optimal_loci_99886_G1	1323	0.125709	11.56	1260	41.26	2	0.707506865	0.302	0.56512325	3
optimal_loci_99888_G1	1087	0.125709	0	2001	41.85	2	0.707506865	0.265	0.565056038	3
optimal_loci_99889_G1	1377	0.125709	8.42	3121	47.78	2	0.707506865	0.463	0.565041896	3
optimal_loci_100036_G	1203	0.010913	19.78	1001	37.57	2	0.899231745	0.172	0.55774654	1

optimal_loci_100127_G	1170	0.732804	24.7	1453	40.85	1	4.94259971	0.195	0.552625145	1
optimal_loci_100850_G	1532	0.042448	11.29	2385	35.83	1	16.43238712	0.113	0.513636961	2
optimal_loci_100860_G	1571	0.042448	2.16	9711	56.52	1	16.43238712	0.405	0.513475928	2
optimal_loci_100985_G	1164	0.19792	22.08	3490	40.03	1	7.08339202	0.249	0.506983922	7
optimal_loci_101003_G	1231	0.220347	0	2001	43.21	2	0.589384396	0.43	0.506172076	7
optimal_loci_101090_G	1291	0.22203	0	16795	38.1	1	2.995538678	0.141	0.503049408	7
optimal_loci_101091_G	1387	0.22203	25.67	15375	40.08	1	2.995538678	0.14	0.503035165	7
optimal_loci_101092_G	1416	0.22203	12.08	12766	33.96	1	2.995538678	0.132	0.503008997	7
optimal_loci_101094_G	1099	0.21634	0	1523	32.66	1	2.995538678	0	0.502817322	7
optimal_loci_101100_G	1606	0.227319	6.41	2194	38.97	1	41.00466169	0.192	0.502220873	9
optimal_loci_101170_G	1128	0.213115	20.83	2001	46.89	2	34.80368924	0.289	0.497464935	3
optimal_loci_101177_G	2052	0.212037	1.8	14961	49.85	1	69.60737847	0.616	0.497325677	3
optimal_loci_102395_G	1108	0.178336	18.86	18229	35.1	1	8.818024758	0.247	0.42948333	2
optimal_loci_102398_G	1371	0.178336	6.71	9242	34.64	1	8.818024758	0.1	0.42939319	2
optimal_loci_102571_G	1534	0.590242	6.52	16935	37.94	2	3.259670745	0.205	0.41763652	1
optimal_loci_102780_G	1440	0.021241	0	2001	36.45	1	18.00860226	0.116	0.40498339	1
optimal_loci_106202_G	1498	0.014448	0	10926	37.11	1	11.63450677	0.181	0.140936459	3
optimal_loci_106240_G	1801	0.011793	19.16	17321	47.41	1	0.317910372	0.407	0.139892257	3
optimal_loci_106255_G	1582	0.011793	13.53	11702	37.48	1	0.317910372	0.256	0.13958332	3
optimal_loci_106433_G	1202	0.012254	17.72	9150	50.99	2	2.218181655	0.625	0.129082106	1
optimal_loci_106888_G	1052	0.00041	36.88	8205	41.15	1	7.04433304	0.305	0.103122528	1
optimal_loci_107176_G	1402	0.00041	0	17506	41.79	1	0.050969819	0.238	0.082724453	1
optimal_loci_107462_G	1181	0.00041	5.42	2917	40.98	1	1.787186992	0.152	0.066342377	2
optimal_loci_107480_G	1149	0.00041	21.15	1001	35.07	4	8.915392752	0.079	0.065367482	2
optimal_loci_107909_G	1526	0.00041	4	14283	38.99	1	0.634618813	0.251	0.03683337	1
optimal_loci_108229_G	1030	0.00041	0	3332	49.51	4	0.02441353	0.6	0.012642628	2
optimal_loci_108231_G	1047	0.00041	0	2675	37.15	5	0.019530824	0.123	0.012396499	2
optimal_loci_108411_G	1268	0.00041	20.98	7175	50.86	1	3.55594749	0.468	0.004282457	1
optimal_loci_109456_G	6844	0.00041	35.13	9236	59.32	1	1.446754759	0.623	0.051411329	1
optimal_loci_109578_G	1089	0.00041	19.93	19776	37.74	1	6.023590263	0.205	0.056806392	1
optimal_loci_109890_G	1125	0.00041	28.8	11727	38.13	1	11.7378535	0.101	0.07596841	1
optimal_loci_110490_G	1472	0.345352	20.24	11981	41.84	2	2.119402476	0.327	0.107732268	2
optimal_loci_110554_G	1248	0.031071	7.21	15157	39.66	1	0.172345895	0.044	0.111134226	2

optimal_loci_110785_G	1159	0.373729	0	2877	36.75	1	107.3769514	0.068	0.12600417	1
optimal_loci_110941_G	1724	0.287245	18.62	1001	34.39	2	11.71167563	0.242	0.132980058	1
optimal_loci_111607_G	1346	0.122762	0	1001	56.09	4	5.071803034	0.383	0.162568957	3
optimal_loci_111669_G	1532	0.070136	0	16440	52.08	1	5.57909494	0.481	0.165815004	3
optimal_loci_111678_G	1033	0.070136	0	1049	41.81	1	5.57909494	0.264	0.165935896	3
optimal_loci_111796_G	2028	0.135747	14.89	5830	46.84	1	5.250484844	0.381	0.172732334	1
optimal_loci_111975_G	1206	0.142186	2.4	18429	42.7	1	34.23265137	0.429	0.182332108	1
optimal_loci_112169_G	1682	0.24827	17.42	2388	39.83	2	2.852559127	0.286	0.190272823	1
optimal_loci_112289_G	1079	0.390346	0	1001	40.4	1	0.100859877	0.158	0.196341584	1
optimal_loci_112423_G	1269	0.242172	0	17575	32.78	1	5.094646605	0.061	0.200998091	3
optimal_loci_112438_G	1518	0.199743	15.02	8776	36.62	1	0.997195423	0.23	0.201834228	4
optimal_loci_112470_G	1063	0.194449	0	1001	34.61	2	4.805464976	0.243	0.202368258	4
optimal_loci_112558_G	1672	0.034003	2.27	3391	38.27	2	0.155232006	0.071	0.205365127	4
optimal_loci_112632_G	1402	0.097822	25.68	1056	46.07	1	13.39153571	0.244	0.208451154	2
optimal_loci_112689_G	1011	0.549276	21.76	4569	34.42	1	24.70841842	0.218	0.212803994	2
optimal_loci_112750_G	2272	1.216792	28.3	8210	38.55	2	13.49388864	0.18	0.215572295	4
optimal_loci_112780_G	1199	1.141597	12.84	7878	39.86	3	9.227681327	0.233	0.216871457	3
optimal_loci_112804_G	1051	1.141597	0	2177	37.39	4	0.931192423	0.313	0.217525092	3
optimal_loci_112882_G	1966	0.055938	15.51	5301	38.4	1	21.24317763	0.176	0.222784717	1
optimal_loci_113176_G	2376	0.050046	0	1001	35.52	1	2.488572814	0.082	0.233057718	2
optimal_loci_113238_G	1300	0.051581	30.92	1811	34.84	2	2.993222397	0.138	0.23524981	3
optimal_loci_113314_G	1477	0.056977	22.88	4052	35.61	1	1.56834174	0.268	0.238315114	3
optimal_loci_113401_G	1478	0.043871	30.04	1799	35.72	2	11.96121663	0.13	0.241120405	3
optimal_loci_113475_G	1500	0.042875	0	6403	42.4	1	15.82305722	0.553	0.243378299	2
optimal_loci_113659_G	1022	0.394851	27.3	16417	36.39	1	50.7569753	0.103	0.252662896	1
optimal_loci_113785_G	1046	0.601292	0	1221	37.47	3	14.29754402	0.188	0.259224041	2
optimal_loci_113813_G	1595	0.72677	35.92	4177	34.35	1	3.218359211	0.186	0.26026386	2
optimal_loci_114018_G	1082	0.03152	39.74	2969	29.02	1	30.76055926	0.123	0.270545397	2
optimal_loci_114050_G	1510	0.043365	0	1079	34.83	1	71.26925227	0.088	0.271778026	2
optimal_loci_114184_G	1278	0.497788	8.45	5165	49.6	2	0.013555916	0.358	0.277990426	3
optimal_loci_114185_G	1269	0.497788	11.51	4817	44.2	2	0.013555916	0.32	0.278001055	3
optimal_loci_114188_G	1060	0.497788	16.32	2150	45.84	2	0.013555916	0.365	0.278022935	3
optimal_loci_114499_G	1260	0.168963	0	16113	40	1	0.104345728	0.096	0.292574248	3

optimal_loci_114514_G	1045	0.165803	0	18649	46.88	1	2.108894506	0.691	0.293248235	3
optimal_loci_114546_G	1672	0.157898	36.24	17749	56.04	1	0.835108697	0.768	0.295393446	4
optimal_loci_114606_G	1061	0.148252	4.24	10643	39.3	1	9.186593584	0.141	0.297910013	4
optimal_loci_114664_G	1112	0.182127	6.56	16234	36.06	1	3.552323115	0.117	0.299809022	3
optimal_loci_114666_G	1034	0.181217	0	17917	31.72	1	3.552323115	0.005	0.300086388	3
optimal_loci_114793_G	1304	0.142266	26.69	10888	41.33	2	1.453796334	0.306	0.306203551	2
optimal_loci_114856_G	1357	0.034144	0	1547	38.24	1	0.154236269	0.178	0.309999521	2
optimal_loci_115045_G	1506	0.026228	20.19	1188	41.69	2	8.724651537	0.199	0.31974629	1
optimal_loci_115279_G	1411	0.064159	0	2001	37.84	5	14.94592871	0.084	0.33008825	2
optimal_loci_115303_G	1064	0.079136	28.1	11610	29.88	1	5.277330433	0.076	0.332139525	3
optimal_loci_115348_G	1693	0.096384	25.58	11585	38.33	1	4.624021369	0.131	0.334106846	2
optimal_loci_115496_G	1605	0.087519	4.67	2001	32.21	2	8.629852916	0.238	0.34306919	1
optimal_loci_115620_G	1078	0.571523	0	2048	46.01	3	19.19266424	0.279	0.349648365	1
optimal_loci_115698_G	1534	0.507342	6	9550	45.5	1	1.096707961	0.378	0.353662222	3
optimal_loci_115703_G	3148	0.423253	25.64	1001	39.89	2	202.4731514	0.233	0.354374295	3
optimal_loci_115740_G	1139	0.351334	20.02	1969	53.46	1	10.02509308	0.431	0.356724543	4
optimal_loci_115806_G	1158	0.197921	9.59	14903	40.06	1	10.52368719	0.211	0.359977027	3
optimal_loci_115875_G	2396	0.121669	11.14	8503	44.32	2	0.675884777	0.322	0.362127123	2
optimal_loci_116108_G	2450	0.53275	7.88	1532	44.32	2	16.92292422	0.286	0.371693117	2
optimal_loci_116203_G	1135	0.611213	30.84	1069	43.08	1	3.156525497	0.406	0.375481236	2
optimal_loci_116472_G	1236	0.081218	15.53	2001	36.24	3	7.146987696	0.216	0.387365137	2
optimal_loci_116502_G	1410	0.096584	12.7	2856	40.85	1	7.213491589	0.356	0.389802664	5
optimal_loci_116543_G	1163	0.137791	13.84	4787	33.87	1	18.92745917	0.206	0.391580188	4
optimal_loci_116545_G	1069	0.137791	0	3011	43.4	1	18.92745917	0.376	0.391594415	4
optimal_loci_116547_G	1181	0.137791	11.52	1001	40.47	2	9.463729583	0.178	0.391682401	4
optimal_loci_116807_G	1465	0.209709	30.17	4229	43.82	4	16.92833486	0.311	0.403809363	1
optimal_loci_116936_G	1020	0.220951	0	6199	39.5	2	0.039034682	0.191	0.409731875	3
optimal_loci_116937_G	1127	0.220951	0	4664	46.31	2	0.039034682	0.245	0.40974274	3
optimal_loci_116939_G	1233	0.220951	4.14	1001	43.3	2	0.039034682	0.263	0.409769801	3
optimal_loci_117229_G	1018	0.475788	20.83	3736	46.26	2	96.73892877	0.27	0.420471895	1
optimal_loci_117303_G	1163	0.395027	32.42	10664	35.51	1	31.07617667	0.24	0.424513437	1
optimal_loci_117457_G	1302	0.192487	0	1001	46	2	13.10311082	0.386	0.434118978	2
optimal_loci_117502_G	1344	0.212829	17.71	7019	31.25	1	0.910890761	0.216	0.435378403	2

optimal_loci_117595_G	1426	0.399315	1.96	1001	38.35	2	10.57726032	0.096	0.439257506	3
optimal_loci_117597_G	1014	0.399315	0	1001	46.15	2	10.57726032	0.434	0.439351975	3
optimal_loci_117607_G	1414	0.398113	9.05	2263	44.83	3	53.11964645	0.266	0.439786842	3
optimal_loci_117803_G	1344	0.865648	11.38	1280	38.61	2	0.099217312	0.283	0.447553052	10
optimal_loci_117811_G	1761	0.845866	27.37	9629	48.04	1	0.198434624	0.389	0.447773395	10
optimal_loci_117865_G	1902	1.0448	0	15020	48.47	2	0.401056927	0.525	0.449634934	10
optimal_loci_117866_G	2863	0.787718	13.06	12059	48.89	2	0.401056927	0.413	0.44965015	10
optimal_loci_117872_G	1085	0.787718	0	8163	45.34	2	0.401056927	0.462	0.449693318	10
optimal_loci_117875_G	1073	0.787718	0	6079	58.43	2	0.401056927	0.469	0.449709265	10
optimal_loci_117876_G	1080	0.787718	0	4966	62.4	2	0.401056927	0.688	0.449717679	10
optimal_loci_117888_G	1724	0.766953	5.92	11724	43.56	1	42.04874619	0.247	0.450092466	10
optimal_loci_117891_G	1494	0.766953	9.71	6270	45.58	1	42.04874619	0.163	0.45013571	10
optimal_loci_117894_G	2722	0.766953	0	2244	55.03	1	42.04874619	0.552	0.450156997	10
optimal_loci_117967_G	1667	0.476252	1.68	2993	38.15	2	27.43362495	0.203	0.455124451	4
optimal_loci_117981_G	1885	0.500261	8.01	4488	45.14	1	11.7140411	0.32	0.455488479	4
optimal_loci_118016_G	1807	0.452463	12.17	9520	42.28	3	8.771993168	0.313	0.456988652	4
optimal_loci_118038_G	1003	0.504162	16.55	1881	44.06	1	17.54648729	0.399	0.45823191	4
optimal_loci_118122_G	1611	0.593353	2.23	3345	55.99	2	14.76138819	0.573	0.463618285	8
optimal_loci_118123_G	1151	0.593353	0	2001	47.08	2	14.76138819	0.324	0.463632009	8
optimal_loci_118157_G	3181	0.914192	3.3	1389	55.39	1	169.8951554	0.577	0.466046172	8
optimal_loci_118161_G	1255	0.914192	0	6181	51.63	1	169.8951554	0.448	0.46608263	8
optimal_loci_118162_G	1202	0.914192	0	12858	51.83	1	169.8951554	0.355	0.466133429	8
optimal_loci_118163_G	2807	0.914192	0	14093	48.59	1	169.8951554	0.396	0.466142825	8
optimal_loci_118183_G	1036	0.915466	0	11626	61	2	8.020616816	0.769	0.466965389	8
optimal_loci_118184_G	1159	0.915466	0	12771	47.1	2	8.020616816	0.276	0.4669741	8
optimal_loci_118265_G	1247	0.340257	0	10683	44.5	3	0.436406453	0.193	0.470838665	1
optimal_loci_118636_G	1033	0.667661	0	2001	44.33	2	6.138514142	0.338	0.488922489	2
optimal_loci_118682_G	2178	0.893231	0	4685	48.85	1	0.035491946	0.355	0.490468645	2
optimal_loci_118758_G	1356	1.771824	20.8	17839	53.31	1	427.833818	0.353	0.494550289	7
optimal_loci_118761_G	1403	1.771824	0	2677	55.31	3	193.7742902	0.76	0.494786312	7
optimal_loci_118782_G	1461	1.771824	0	3028	50.3	3	4.272245543	0.356	0.495762118	7
optimal_loci_118788_G	1524	1.771824	0	3527	46.85	3	4.272245543	0.375	0.495815663	7
optimal_loci_118791_G	1883	1.771824	2.18	2023	60.75	3	11.94895211	0.618	0.495876877	7

optimal_loci_118813_G	2480	1.90189	3.43	2001	42.58	2	6.510274005	0.32	0.496860511	10
optimal_loci_118819_G	1035	1.90189	0	2635	43.28	1	4.793192902	0.2	0.497538972	10
optimal_loci_118862_G	1791	1.12585	7.59	3664	34.72	3	5.835603566	0.154	0.499807897	7
optimal_loci_118872_G	1969	0.987701	0	5736	45.86	1	6.747282326	0.328	0.500030721	7
optimal_loci_118877_G	1003	0.987701	0	2001	43.46	3	37.37659111	0.205	0.500066487	7
optimal_loci_118979_G	1162	2.490342	0	12122	41.48	2	12.1012004	0.086	0.502737588	6
optimal_loci_118981_G	1027	2.490342	0	10163	37.87	2	12.1012004	0.072	0.502753519	6
optimal_loci_119006_G	1068	2.490342	0	2643	57.2	2	19.19520665	0.46	0.504939395	4
optimal_loci_119035_G	1612	0.198807	1.8	3406	55.76	2	19.20558999	0.808	0.507270152	2
optimal_loci_119177_G	1108	1.13953	0	1001	40.25	2	0.983526318	0.085	0.515375984	1
optimal_loci_119289_G	3103	1.496568	2.58	8180	39.54	1	54.60949822	0.346	0.520303191	2
optimal_loci_119309_G	3455	2.254597	5.93	1001	56.81	1	0.07282161	0.559	0.521249926	2
optimal_loci_119456_G	1772	2.377729	38.54	4222	48.53	2	0.248809979	0.381	0.52767386	2
optimal_loci_119517_G	1103	2.097235	3.41	3627	42.88	4	6.123606603	0.31	0.530675865	4
optimal_loci_119569_G	1111	2.981068	21.06	2553	41.4	1	10.89792037	0.482	0.533155274	6
optimal_loci_119570_G	1642	2.981068	0	3860	42.08	1	10.89792037	0.221	0.533165218	6
optimal_loci_119626_G	1688	1.732973	0	9453	49.76	2	2.610195145	0.585	0.535002533	5
optimal_loci_119631_G	1527	1.732973	30.91	3458	36.21	2	2.610195145	0.09	0.535049368	5
optimal_loci_119632_G	1926	1.732973	2.28	1001	45.58	2	2.610195145	0.465	0.535065025	5
optimal_loci_119728_G	1284	0.406428	0	5205	45.87	2	4.105316792	0.463	0.540191167	2
optimal_loci_119742_G	1635	0.406428	0	2001	48.56	1	126.1205552	0.547	0.540584099	2
optimal_loci_119833_G	1659	1.336395	27.73	2803	32.85	2	53.85132024	0.125	0.545032548	3
optimal_loci_119847_G	2480	2.69177	1.29	2001	50.12	2	2.80818371	0.456	0.545346577	3
optimal_loci_119875_G	1262	3.48216	0	4206	60.3	1	2.562121581	0.599	0.547548765	4
optimal_loci_119929_G	1016	2.674687	6.45	1001	43.3	3	14.33268782	0.189	0.550160159	5
optimal_loci_119963_G	1638	1.546549	5.92	14442	37.42	2	13.16845477	0.185	0.552767436	7
optimal_loci_119971_G	1164	1.546549	0	1001	52.49	3	8.778969847	0.476	0.552909501	7
optimal_loci_119988_G	1653	1.546549	1.69	5116	57.65	1	9.374383759	0.636	0.553966879	7
optimal_loci_119989_G	1731	1.546549	3.99	3250	55.97	1	9.374383759	0.342	0.553980482	6
optimal_loci_119993_G	1282	1.546549	0	2037	61.46	1	9.374383759	0.668	0.554044124	6
optimal_loci_120002_G	2074	1.546549	7.57	17272	47.97	1	0.324309051	0.532	0.554248239	6
optimal_loci_120112_G	1167	0.083044	12.08	1749	33.59	1	54.01599179	0.145	0.561706446	4
optimal_loci_120131_G	1478	0.169587	0	7207	35.99	1	1.862177086	0.087	0.563005752	5

optimal_loci_120143_G	1270	0.191055	0	8136	57.32	2	37.68721961	0.746	0.563631337	5
optimal_loci_120151_G	1397	0.191055	0	6421	40.65	3	301.9148538	0.1	0.563868509	5
optimal_loci_120230_G	1525	0.609116	21.64	4423	37.18	1	0.524260256	0.018	0.566430344	7
optimal_loci_120279_G	1562	1.50222	0	2994	42.63	4	5.492528377	0.251	0.569328317	9
optimal_loci_120290_G	2445	1.50222	0	6845	54.35	4	5.224567913	0.537	0.569382942	9
optimal_loci_120292_G	1251	1.50222	0	4777	33.49	4	5.224567913	0.257	0.56940776	9
optimal_loci_120314_G	1237	1.83009	5.25	7970	35.65	2	4.636256852	0.128	0.570427722	8
optimal_loci_120316_G	1179	1.83009	26.63	2001	51.06	5	1.854502741	0.535	0.570579593	8
optimal_loci_120345_G	1108	2.430701	38.36	5661	34.38	1	8.273033949	0.089	0.572051046	13
optimal_loci_120376_G	2052	2.864346	12.91	2403	47.22	2	0.104410067	0.471	0.572587221	13
optimal_loci_120380_G	1243	2.864346	0	2815	37.24	3	0.239788598	0.179	0.572653404	13
optimal_loci_120436_G	1077	3.395007	0	1001	47.35	1	65.20676087	0.365	0.574878241	9
optimal_loci_120459_G	1571	3.429523	0	3439	50.92	2	0.717740042	0.571	0.575364797	9
optimal_loci_120460_G	1511	3.429523	13.37	2790	56.51	3	1.245118537	0.6	0.575549367	9
optimal_loci_120463_G	2865	3.429523	0	2001	49.66	2	1.177512028	0.493	0.575610019	9
optimal_loci_120464_G	1700	3.429523	0	2728	53.23	2	1.177512028	0.515	0.575632394	9
optimal_loci_120513_G	1013	4.510093	4.34	1093	56.86	4	17.90017579	0.592	0.577150461	6
optimal_loci_120569_G	1129	1.274088	28.34	7888	35.25	1	6.207861066	0.043	0.58136523	3
optimal_loci_120570_G	1083	1.274088	39.89	6711	40.9	1	6.207861066	0.171	0.581374535	3
optimal_loci_120574_G	1129	1.274088	0	2691	53.76	1	6.207861066	0.484	0.581404769	3
optimal_loci_120710_G	2903	1.405194	0	6811	52.7	2	1.347005744	0.539	0.588401039	8
optimal_loci_120714_G	2609	1.405194	4.18	1824	49.06	2	1.347005744	0.407	0.588441217	8
optimal_loci_120724_G	1857	1.51106	0	1001	45.66	1	7.897281976	0.358	0.589105162	10
optimal_loci_120729_G	2151	1.51106	1.44	13845	51.97	1	7.897281976	0.425	0.589251076	10
optimal_loci_120772_G	1240	1.47241	0	2347	37.25	3	0.024486732	0.111	0.590110304	10
optimal_loci_120777_G	2469	1.616359	1.4	6963	50.14	3	0.019536392	0.581	0.590324584	10
optimal_loci_120787_G	1043	1.616359	0	6899	40.84	4	0.08767579	0.115	0.590398838	10
optimal_loci_120789_G	1757	1.80373	2.11	2001	45.58	6	0.158971102	0.313	0.590514898	10
optimal_loci_120843_G	1011	1.566836	0	1918	36.99	4	2.14951692	0.031	0.592356504	8
optimal_loci_120847_G	1007	1.612141	0	2322	41.7	4	2.14951692	0.083	0.592420845	8
optimal_loci_120961_G	1651	1.455547	0	1001	46.94	1	19.90216431	0.444	0.597699726	6
optimal_loci_120993_G	1052	1.27343	5.04	2905	40.58	2	4.212882754	0.374	0.59889837	6
optimal_loci_120997_G	1973	1.27343	0	16950	32.18	2	4.212882754	0.107	0.599005225	6

optimal_loci_120998_G	3003	1.27343	4	19367	57.74	1	6.835740357	0.638	0.599023614	6
optimal_loci_121020_G	1024	1.261677	0	8288	49.7	1	13.38190785	0.461	0.599532849	7
optimal_loci_121023_G	1115	1.261677	0	5429	34.26	1	13.38190785	0.198	0.599681479	8
optimal_loci_121116_G	1020	0.930525	11.96	3281	37.74	2	39.60728573	0.055	0.603344325	5
optimal_loci_121117_G	1084	0.930525	0	4334	39.29	2	39.60728573	0.049	0.603352336	4
optimal_loci_121153_G	1108	0.983086	0	1001	46.38	3	20.16618967	0.316	0.604846993	5
optimal_loci_121239_G	1639	1.106871	3.84	12691	50.09	2	4.784908042	0.529	0.607756202	7
optimal_loci_121240_G	1854	1.106871	8.41	11150	33.33	2	4.784908042	0.087	0.607769311	7
optimal_loci_121279_G	1700	1.114771	0	7542	42.64	3	87.75710412	0.27	0.609103135	6
optimal_loci_121292_G	2273	1.14436	31.59	2910	35.45	1	0.509325275	0.162	0.610423484	7
optimal_loci_121304_G	1542	1.150198	10.83	2675	55.44	2	0.054381028	0.631	0.61146815	7
optimal_loci_121306_G	1239	1.150198	0	4919	40.27	2	0.054381028	0.055	0.611485222	7
optimal_loci_121339_G	1034	1.170287	19.54	1001	37.42	1	1.897677167	0.172	0.613044502	4
optimal_loci_121468_G	2736	2.685469	35.45	2906	41.92	1	1.534396657	0.267	0.617845462	1
optimal_loci_121718_G	1092	1.983024	0	11687	50.36	1	22.14690716	0.699	0.627155895	7
optimal_loci_121719_G	1323	1.904672	0	19930	54.42	1	22.14690716	0.815	0.627218608	7
optimal_loci_121745_G	1151	1.674269	27.98	2001	38.05	3	12.60817674	0.222	0.628057728	7
optimal_loci_121786_G	2243	1.413096	23.72	3922	36.2	1	9.124720469	0.08	0.629007361	8
optimal_loci_121792_G	1109	1.402641	0	2202	41.92	1	9.124720469	0.319	0.629114718	8
optimal_loci_121802_G	1712	1.403564	36.62	1271	47.13	1	2.826165485	0.304	0.629518004	9
optimal_loci_121804_G	2005	1.403564	7.63	5146	39.25	1	6.029548641	0.212	0.629776122	9
optimal_loci_121863_G	1227	0.971668	26.57	3659	38.87	4	20.48470312	0.332	0.632806763	13
optimal_loci_121875_G	2112	0.983523	0	4327	43.98	2	20.90984025	0.319	0.632954655	11
optimal_loci_121889_G	1287	1.179131	31.31	1319	54.54	1	2.085529633	0.508	0.633770798	11
optimal_loci_121905_G	1550	1.184294	0	3847	61.41	2	18.68311821	0.56	0.634314293	11
optimal_loci_121919_G	1170	1.277527	30	1001	52.99	1	0.779753562	0.625	0.634642351	12
optimal_loci_121921_G	1132	1.274532	0	13547	42.75	3	3.138624579	0.251	0.634803428	13
optimal_loci_121949_G	2013	1.319041	0	1001	40.23	4	61.98942337	0.343	0.635841375	14
optimal_loci_121962_G	2941	1.50039	23.22	4143	51.47	1	27.91651112	0.521	0.636458021	15
optimal_loci_121967_G	1976	1.497532	0	2093	55.66	2	13.95825556	0.576	0.636545764	15
optimal_loci_121999_G	2449	1.927578	24.17	5658	43.56	3	133.5716673	0.365	0.637193641	14
optimal_loci_122000_G	1821	1.927578	14.55	3747	38.82	2	4.139253575	0.183	0.637212957	14
optimal_loci_122036_G	1532	1.927578	9.4	1431	56.98	2	15.17385712	0.573	0.638375342	12

optimal_loci_122041_G	1465	1.927578	0	2001	39.11	2	4.365339516	0.24	0.638574063	11
optimal_loci_122051_G	1226	1.927578	0	1001	56.93	1	8.899921747	0.657	0.638894818	10
optimal_loci_122079_G	3459	0.982763	12.63	3956	41.71	1	33.87327695	0.213	0.640156015	9
optimal_loci_122090_G	1093	0.78971	21.5	3755	52.79	1	0.599409629	0.482	0.640802591	7
optimal_loci_122254_G	1035	0.398021	16.91	2001	53.42	3	11.34215609	0.644	0.647162047	6
optimal_loci_122285_G	1019	0.200816	29.44	3343	36.5	1	18.61911978	0.31	0.648480334	6
optimal_loci_122291_G	1595	0.200816	0	6905	46.33	1	18.61911978	0.492	0.648507434	6
optimal_loci_122317_G	1261	0.200816	0	11794	55.03	2	1.595629333	0.665	0.649928179	6
optimal_loci_122327_G	1364	0.126026	0	4743	44.28	5	18.50808255	0.275	0.650649268	6
optimal_loci_122329_G	1017	0.126026	9.14	2835	37.36	5	18.50808255	0.409	0.650677334	6
optimal_loci_122515_G	2043	0.890327	1.52	4482	56.82	3	3.827267163	0.497	0.656654228	5
optimal_loci_122516_G	1871	0.890327	23.3	5282	46.87	3	3.827267163	0.388	0.656678034	5
optimal_loci_122567_G	1155	0.890327	30.04	1001	38.61	2	7.750494028	0.137	0.658241764	7
optimal_loci_122582_G	1284	0.890327	23.05	7403	36.83	2	0.032033787	0.166	0.658634642	7
optimal_loci_122603_G	1607	0.711742	35.72	2001	57.24	3	62.81464372	0.582	0.659834884	7
optimal_loci_122629_G	1123	0.586331	0	5699	50.13	2	117.892046	0.228	0.661271469	5
optimal_loci_122664_G	1267	0.605907	10.5	3926	36.22	3	27.59563669	0.165	0.661939271	5
optimal_loci_122800_G	1500	0.217765	9.33	4713	53.66	2	37.53375558	0.545	0.669227347	4
optimal_loci_122801_G	1627	0.217765	35.96	2497	51.01	2	37.53375558	0.479	0.669243241	4
optimal_loci_122804_G	1499	0.217765	19.55	2001	49.36	1	75.06751116	0.279	0.669297798	4
optimal_loci_122842_G	1218	0.556262	0	2001	60.59	1	1.399096294	0.632	0.670296716	4
optimal_loci_122927_G	1045	0.942278	0	2538	39.23	2	69.37589178	0.279	0.674525043	1
optimal_loci_123075_G	2055	1.203249	20.34	1363	45.59	2	0.720300064	0.459	0.680020083	4
optimal_loci_123080_G	1544	1.203249	0	3741	55.44	1	0.551029504	0.343	0.68009312	4
optimal_loci_123095_G	1121	1.209568	0	11591	46.38	1	0.03090145	0.185	0.680546041	4
optimal_loci_123098_G	1506	1.257051	7.37	7282	55.64	1	0.03090145	0.473	0.680575895	4
optimal_loci_123251_G	1687	0.626688	6.4	1373	44.16	2	24.16054688	0.343	0.686482095	5
optimal_loci_123264_G	1325	0.578523	0	12952	58.64	1	2.95215727	0.632	0.686702408	5
optimal_loci_123265_G	1377	0.578523	0	14355	52.65	1	2.95215727	0.487	0.686713082	5
optimal_loci_123298_G	1327	0.709301	0	2950	31.8	1	13.64743462	0.182	0.687919471	5
optimal_loci_123299_G	1135	0.709301	0	1762	41.05	1	13.64743462	0.333	0.68792997	5
optimal_loci_123383_G	1170	1.267998	0	16388	55.29	1	10.1242837	0.54	0.692670736	7
optimal_loci_123391_G	1270	1.282656	4.33	3394	55.98	2	7.368163888	0.632	0.692916338	7

optimal_loci_123393_G	1182	1.211721	0	5413	48.22	2	7.368163888	0.296	0.692931698	7
optimal_loci_123394_G	1784	1.211721	0	6673	46.52	2	7.368163888	0.42	0.692941284	7
optimal_loci_123419_G	1224	0.915756	6.94	6033	45.58	3	1.262336802	0.354	0.69469132	8
optimal_loci_123429_G	1581	0.915756	15.12	3030	36.3	2	0.332598363	0.191	0.69496037	8
optimal_loci_123450_G	1570	0.894396	32.23	2675	39.23	1	4.851726451	0.16	0.695450959	8
optimal_loci_123505_G	1341	0.472787	27.37	1086	46.6	3	3.68454408	0.413	0.697694116	4
optimal_loci_123810_G	1259	0.863292	0	5288	36.06	1	44.77702782	0.165	0.709828184	4
optimal_loci_123860_G	1284	0.787444	10.2	2065	53.81	1	0.125011157	0.43	0.711746851	7
optimal_loci_123868_G	1329	0.817326	0	1241	40.4	2	7.566769946	0.254	0.712543335	7
optimal_loci_123895_G	3426	1.009745	0	3054	54.58	3	1.180327503	0.565	0.713388686	9
optimal_loci_123955_G	1225	1.221988	31.18	17888	33.87	2	4.363049483	0.062	0.71530695	8
optimal_loci_123956_G	1122	1.221988	34.4	14369	33.33	1	8.726098966	0.023	0.715334506	8
optimal_loci_123958_G	1050	1.221988	0	12774	57.23	1	8.726098966	0.586	0.715347189	8
optimal_loci_123992_G	2284	1.241493	0	9039	52.62	1	5.116274663	0.447	0.716471374	6
optimal_loci_123995_G	2348	1.183065	1.19	2794	51.19	1	5.116274663	0.445	0.716598709	6
optimal_loci_124131_G	2171	2.781551	4.51	16135	53.38	1	4.622748638	0.621	0.723006986	12
optimal_loci_124148_G	1153	2.832272	0	3738	51.17	1	4.622748638	0.608	0.723109047	12
optimal_loci_124151_G	1280	2.832272	2.34	1001	46.71	2	2.311374319	0.214	0.723162098	12
optimal_loci_124182_G	1426	3.055165	0	6071	51.96	3	1.444868996	0.439	0.72442611	13
optimal_loci_124185_G	1945	3.055165	3.86	2001	38.92	4	3.050252616	0.124	0.724453126	13
optimal_loci_124188_G	1271	3.055165	28.17	1001	48.7	5	4.705438701	0.389	0.72462309	14
optimal_loci_124189_G	1076	3.055165	4.93	2305	41.54	5	4.705438701	0.413	0.724633011	14
optimal_loci_124192_G	1935	3.055165	0	2385	57.51	1	11.32618304	0.545	0.724800798	14
optimal_loci_124208_G	1116	3.402982	13.53	3674	41.57	3	15.76403463	0.184	0.725469802	14
optimal_loci_124212_G	1214	3.402982	0	1975	45.88	3	15.76403463	0.365	0.725496118	14
optimal_loci_124234_G	1237	4.189987	0	2001	42.19	2	10.71779386	0.205	0.726530855	14
optimal_loci_124235_G	1126	4.189987	17.41	1173	52.75	2	10.71779386	0.51	0.726589695	14
optimal_loci_124257_G	1349	2.829145	0	1893	45.81	1	11.85600426	0.412	0.72773395	11
optimal_loci_124293_G	1995	1.212419	36.74	3741	48.42	2	0.181424856	0.401	0.72843029	11
optimal_loci_124354_G	1277	0.045162	29.29	3386	37.27	2	3.05893284	0.219	0.731557819	3
optimal_loci_124363_G	1205	0.061264	9.46	7361	37.75	1	5.108757822	0.245	0.73210581	3
optimal_loci_124513_G	2086	0.253998	14.33	2001	48.94	1	9.259337464	0.273	0.739916298	3
optimal_loci_124525_G	2017	0.285718	16.91	3086	51.46	2	0.552782824	0.438	0.74052618	3

optimal_loci_124583_G	1163	0.34939	30.61	2001	42.99	4	26.19732374	0.301	0.743138639	3
optimal_loci_124694_G	1596	0.314181	33.02	5872	40.72	2	10.50866178	0.17	0.748131039	5
optimal_loci_124720_G	1840	0.561059	19.35	2265	42.01	1	29.17529525	0.22	0.748694307	6
optimal_loci_124736_G	1776	1.050425	0	2509	36.99	5	4.382086912	0.193	0.749822417	8
optimal_loci_124740_G	1652	1.050425	7.51	4811	44.55	5	4.382086912	0.257	0.749860495	8
optimal_loci_124781_G	1027	1.16114	30.77	3917	33.1	2	48.57456276	0.277	0.751637821	8
optimal_loci_124791_G	1923	1.32175	0	3558	49.03	3	21.42699045	0.375	0.752501218	7
optimal_loci_124792_G	1524	1.32175	0	2001	53.28	3	21.42699045	0.507	0.752516099	6
optimal_loci_124795_G	2671	1.221744	34.71	2918	55.78	5	52.89677981	0.514	0.752768975	7
optimal_loci_124875_G	1791	0.534359	34.67	4361	46.67	3	7.185935828	0.443	0.756419829	3
optimal_loci_124897_G	1039	0.616001	13.86	6572	43.98	1	41.02160289	0.385	0.757641397	4
optimal_loci_124985_G	1464	0.952591	14.75	2246	40.98	2	15.36161189	0.179	0.760764498	4
optimal_loci_124986_G	1191	0.952591	0	1001	59.36	2	15.36161189	0.477	0.760776047	4
optimal_loci_125047_G	1052	0.75794	0	4470	48.09	1	16.92482008	0.472	0.763234481	6
optimal_loci_125071_G	1087	0.579466	15.82	2181	50.13	4	4.286517962	0.494	0.764793228	8
optimal_loci_125085_G	1010	0.515327	0	2001	55.04	2	3.211625724	0.616	0.765337849	8
optimal_loci_125104_G	1363	0.520405	9.68	9776	43.43	1	19.31673218	0.318	0.765882553	8
optimal_loci_125141_G	1377	0.969821	0	11953	42.84	2	2.068657529	0.296	0.767342662	13
optimal_loci_125160_G	1529	0.993207	6.47	17794	36.1	1	13.90923326	0.129	0.767674326	13
optimal_loci_125179_G	1588	1.308572	0	9565	39.67	1	13.90923326	0.259	0.767943338	14
optimal_loci_125184_G	1075	1.308572	7.81	8680	54.32	2	87.97966062	0.534	0.768182748	14
optimal_loci_125225_G	1235	1.164363	0	1779	39.27	2	49.70160091	0.117	0.769978066	11
optimal_loci_125230_G	2345	1.164363	8.66	4474	45.75	4	1.917911838	0.356	0.770215109	11
optimal_loci_125235_G	1301	1.173374	0	2207	52.57	1	56.2780183	0.424	0.770655728	13
optimal_loci_125236_G	1112	1.173374	10.97	3936	47.12	1	56.2780183	0.533	0.770668882	13
optimal_loci_125238_G	2075	1.173374	1.88	6740	47.66	1	56.2780183	0.392	0.770690215	13
optimal_loci_125246_G	1737	1.20312	2.94	2001	38.91	3	12.56425016	0.126	0.771085407	13
optimal_loci_125267_G	1259	1.390089	2.22	6727	50.91	4	27.48896004	0.707	0.771668706	13
optimal_loci_125311_G	1032	0.916339	0	12933	38.08	1	21.78193314	0	0.774107922	12
optimal_loci_125314_G	1300	0.908111	14.62	17385	52.69	1	0.048223629	0.46	0.774423769	12
optimal_loci_125374_G	1006	0.701684	0	1001	55.16	1	0.023734225	0.604	0.774938133	8
optimal_loci_125375_G	1858	0.701684	2.96	2413	46.87	1	0.023734225	0.443	0.774948875	8
optimal_loci_125429_G	1959	0.328045	1.43	5242	38.48	2	6.003371758	0.183	0.776469742	7

optimal_loci_125431_G	1900	0.330291	11.26	2732	36.68	2	6.003371758	0.26	0.776489287	7
optimal_loci_125456_G	1238	0.200055	14.05	10546	39.66	2	0.215097449	0.123	0.777682484	8
optimal_loci_125535_G	1076	0.12462	21.93	1001	42.93	1	4.214565228	0.2	0.780511786	5
optimal_loci_125555_G	1339	0.099255	0	4591	38.61	3	3.426650536	0.166	0.782017528	7
optimal_loci_125567_G	1041	0.099255	14.7	12420	37.94	1	10.27995161	0.125	0.782259022	7
optimal_loci_125571_G	1800	0.099255	26.06	17078	34	1	10.27995161	0.135	0.78229446	7
optimal_loci_125623_G	1247	0.149563	29.59	17908	37.28	1	0.028898055	0.039	0.784735495	6
optimal_loci_125625_G	1267	0.149563	0	13877	36.62	2	12.63932979	0.171	0.784766011	6
optimal_loci_125639_G	1038	0.140294	25.82	2486	39.88	2	12.84356224	0.167	0.78507126	6
optimal_loci_125746_G	1276	2.299265	0	7583	38.63	2	97.00878502	0.154	0.789356571	8
optimal_loci_125749_G	1179	2.299265	9.25	3883	43.93	2	97.00878502	0.211	0.789385458	8
optimal_loci_125753_G	1380	2.299265	2.46	1001	57.02	2	97.00878502	0.492	0.789451024	8
optimal_loci_125797_G	1026	3.125287	0	3733	32.06	2	10.64292978	0.115	0.790730276	8
optimal_loci_125805_G	1642	3.125287	0	2674	47.5	3	10.01591641	0.394	0.790774927	8
optimal_loci_125809_G	1311	3.193339	0	2441	40.35	4	7.84234752	0.274	0.790841999	8
optimal_loci_125811_G	1505	3.646885	0	2001	44.25	3	8.622149186	0.245	0.790912084	8
optimal_loci_125813_G	1947	3.646885	9.5	2716	40.67	2	5.041765257	0.158	0.790980032	8
optimal_loci_126156_G	1463	0.503484	28.5	1863	37.25	3	8.595827315	0.157	0.80268379	9
optimal_loci_126157_G	1199	0.503484	21.18	3416	37.61	3	8.595827315	0.333	0.802695605	9
optimal_loci_126203_G	1699	2.242129	0	4296	49.44	1	0.224603298	0.422	0.805366683	10
optimal_loci_126206_G	1032	2.242129	0	12970	51.55	1	13.12477661	0.29	0.805587103	10
optimal_loci_126208_G	1788	2.242129	19.46	10400	43.56	1	13.12477661	0.298	0.805600904	10
optimal_loci_126215_G	1090	2.242129	14.68	3429	32.38	1	13.12477661	0.238	0.80565925	10
optimal_loci_126218_G	4830	2.242129	3.23	1001	54.45	1	13.12477661	0.63	0.805714827	10
optimal_loci_126220_G	1255	2.242129	0	6634	37.52	1	13.12477661	0.151	0.805757683	10
optimal_loci_126239_G	2489	1.975652	0	5436	46.44	4	1.87207005	0.324	0.806318531	10
optimal_loci_126290_G	1010	2.433767	9.01	2001	48.91	5	36.59305702	0.592	0.807524753	9
optimal_loci_126368_G	2212	1.859813	0	2800	48.96	2	1.193987169	0.329	0.810600791	5
optimal_loci_126431_G	1079	1.226676	8.71	4734	36.05	2	9.95558252	0.1	0.812856791	5
optimal_loci_126434_G	3034	1.214984	11.31	1001	38.1	2	9.95558252	0.229	0.812870318	5
optimal_loci_126470_G	1719	0.651101	8.09	14047	37.63	1	7.409532728	0.058	0.81435707	5
optimal_loci_126484_G	3024	0.651101	5.22	4794	53.76	2	3.704766364	0.592	0.814540043	4
optimal_loci_126599_G	1064	2.767694	0	10091	37.96	1	16.8511709	0.251	0.819808828	9

optimal_loci_126605_G	1519	3.131968	22.58	4015	33.17	4	12.83142476	0.075	0.820341747	11
optimal_loci_126640_G	1494	5.044848	8.3	12469	41.36	2	1.76353648	0.148	0.821668891	16
optimal_loci_126657_G	1019	5.044848	0	17098	37.97	1	7.860521121	0.049	0.822161899	16
optimal_loci_126660_G	1506	5.044848	3.45	14229	52.52	1	7.860521121	0.455	0.822180021	16
optimal_loci_126671_G	1019	5.044848	4.51	4995	40.03	1	7.860521121	0.164	0.822377487	16
optimal_loci_126676_G	1027	5.044848	0	1001	44.69	1	31.21916018	0.229	0.822622587	16
optimal_loci_126685_G	3043	5.044848	0	12471	46.89	1	10.20607328	0.357	0.822989302	16
optimal_loci_126699_G	2382	5.044848	30.65	1219	31.02	3	7.657872333	0.06	0.823152707	16
optimal_loci_126711_G	1191	4.077711	27.2	2525	37.11	3	0.07113113	0.178	0.824058069	15
optimal_loci_126715_G	1137	4.077711	34.48	1050	35.53	3	0.07113113	0.078	0.82410024	15
optimal_loci_126731_G	1342	3.592384	0	2817	51.34	4	13.65268256	0.417	0.824511538	15
optimal_loci_126742_G	2691	3.592384	0	1490	35.63	3	12.68854499	0.073	0.824637983	15
optimal_loci_126747_G	1331	3.506942	4.51	5386	36.88	2	12.21957331	0.101	0.82473634	15
optimal_loci_126748_G	1023	3.506942	20.72	13588	54.64	2	18.06034173	0.641	0.824801837	15
optimal_loci_126749_G	1275	3.506942	0	11902	44.39	2	18.06034173	0.227	0.824812747	15
optimal_loci_126831_G	1044	1.343029	0	6283	36.68	1	4.097741754	0.121	0.82802894	11
optimal_loci_126854_G	1393	1.6791	38.19	2005	36.75	2	10.36388213	0.184	0.828705202	6
optimal_loci_126864_G	4213	2.366671	8.05	2759	49.91	3	17.39530034	0.457	0.828965481	6
optimal_loci_126877_G	1426	2.366671	0	2909	37.23	2	8.468543611	0.16	0.829571969	7
optimal_loci_126886_G	1127	2.366671	0	1013	35.66	1	3.075210519	0.157	0.830062101	7
optimal_loci_126893_G	1308	2.366671	17.74	6550	34.86	2	4.397544243	0.167	0.830267472	7
optimal_loci_126954_G	1113	1.758263	5.39	2800	34.14	2	7.971939438	0.088	0.83325493	9
optimal_loci_127005_G	1187	1.11869	3.29	1767	42.88	4	85.27050481	0.318	0.835505148	8
optimal_loci_127008_G	1421	1.116533	11.26	2858	49.26	4	85.27050481	0.422	0.835561188	8
optimal_loci_127020_G	1677	1.116533	24.75	6058	52.23	1	69.6756097	0.495	0.835694192	8
optimal_loci_127038_G	1588	0.970938	35.64	16290	49.74	1	0.015030147	0.385	0.836149312	8
optimal_loci_127044_G	1386	0.88854	13.85	1113	39.68	1	2.329149325	0.399	0.836640965	9
optimal_loci_127097_G	1126	0.838173	2.58	2001	43.25	1	3.808692665	0.346	0.838973349	8
optimal_loci_127103_G	1031	0.838173	16.49	4723	54.41	1	3.808692665	0.833	0.83905703	8
optimal_loci_127133_G	2612	0.935983	0	3646	47.47	3	23.57138316	0.406	0.840230187	6
optimal_loci_127197_G	1215	1.839918	0	1001	55.3	1	10.27406219	0.563	0.843203038	12
optimal_loci_127221_G	1154	1.839918	9.1	1001	30.76	1	10.38832075	0.158	0.843832191	12
optimal_loci_127236_G	1347	2.030549	6.68	3190	38.53	1	0.75864597	0.158	0.844316016	11

optimal_loci_127240_G	1304	2.030549	0	2002	46.93	1	0.75864597	0.352	0.844373251	11
optimal_loci_127248_G	1711	2.172199	39.86	2935	32.96	4	22.10193686	0.038	0.844758278	11
optimal_loci_127250_G	1910	2.172199	19.11	5231	43.29	5	17.95287966	0.306	0.844775746	11
optimal_loci_127252_G	1367	2.172199	0	8093	45.35	5	17.95287966	0.365	0.84479752	11
optimal_loci_127259_G	1801	2.205567	5.5	2001	52.13	2	0.95879553	0.47	0.844895633	12
optimal_loci_127268_G	2149	2.212146	2.19	2758	47.97	2	0.95879553	0.344	0.845007235	12
optimal_loci_127306_G	1515	2.560096	0	6825	33.79	1	13.47122548	0.142	0.846313548	12
optimal_loci_127340_G	1137	2.554222	22.16	2001	58.48	3	37.03752722	0.601	0.846995227	12
optimal_loci_127359_G	1095	2.973201	0	4375	53.05	2	7.078007944	0.618	0.848704697	6
optimal_loci_127455_G	1391	2.780624	0	1001	44.21	1	0.254642274	0.427	0.852420608	2
optimal_loci_127574_G	1908	2.979594	5.66	2488	47.06	1	31.01107108	0.438	0.857383132	6
optimal_loci_127581_G	1207	2.979594	2.82	17104	56.33	1	31.01107108	0.582	0.85749433	6
optimal_loci_127583_G	1827	2.979594	0	19164	56.43	1	31.01107108	0.514	0.857510003	6
optimal_loci_127626_G	1432	2.979594	39.87	1001	48.67	3	14.03301076	0.435	0.858912778	6
optimal_loci_127627_G	1006	2.979594	0	1191	47.01	5	49.27924357	0.516	0.859018058	6
optimal_loci_127644_G	1991	1.113133	0	1399	54.79	5	7.658875309	0.554	0.860421518	9
optimal_loci_127732_G	1362	0.011428	0	8425	40.08	3	2.058117192	0.184	0.863443181	7
optimal_loci_127733_G	1553	0.011428	0	6839	42.49	3	2.058117192	0.268	0.863453795	7
optimal_loci_127734_G	2532	0.011428	0	4274	33.68	3	2.058117192	0.078	0.863465861	7
optimal_loci_127788_G	1685	0.011525	6.17	8259	50.86	1	13.55318398	0.607	0.864411112	6
optimal_loci_127828_G	1038	0.011525	33.04	5520	44.02	2	9.134301835	0.384	0.865685076	10
optimal_loci_127873_G	2276	2.510335	0	1001	37.12	2	0.047166509	0.172	0.866916891	12
optimal_loci_127930_G	3282	1.991287	1.07	2954	55.81	4	3.764156101	0.616	0.868329267	8
optimal_loci_127935_G	2095	1.991287	7.35	2212	49.88	1	0.274622514	0.577	0.868478925	8
optimal_loci_127937_G	1996	1.991287	8.02	3319	49.39	1	0.274622514	0.557	0.86857035	8
optimal_loci_127954_G	1240	1.698374	0	3589	37.17	1	2.456349409	0.219	0.868795852	8
optimal_loci_127989_G	1452	1.471422	0	6831	36.98	1	2.115040627	0.095	0.869936569	10
optimal_loci_127990_G	1492	1.471422	0	8452	47.92	1	2.115040627	0.458	0.869948902	10
optimal_loci_128058_G	1157	0.984794	0	16550	30.85	1	82.26376666	0	0.872693846	7
optimal_loci_128077_G	1206	0.99956	0	1001	53.89	2	190.6464465	0.536	0.873219477	7
optimal_loci_128078_G	3047	0.99956	8.6	2491	46.4	2	190.6464465	0.439	0.873268731	7
optimal_loci_128128_G	1308	1.081884	0	7682	41.81	3	1.02978178	0.112	0.875508222	8
optimal_loci_128140_G	1281	0.998191	0	1209	47.07	1	0.135143806	0.327	0.876042723	8

optimal_loci_128196_G	1305	1.060897	21.15	10742	33.71	1	7.503547688	0.108	0.878306514	6
optimal_loci_128207_G	1320	1.058573	0	1906	36.06	4	7.944110451	0	0.879050442	6
optimal_loci_128209_G	1284	1.064397	0	2001	46.33	4	7.290190058	0.376	0.879186899	6
optimal_loci_128232_G	1137	1.164767	2.99	2001	60.07	5	40.93059429	0.363	0.880768204	6
optimal_loci_128314_G	1522	1.510218	0	1623	36.07	2	12.26290847	0.095	0.883843946	5
optimal_loci_128355_G	1288	1.909735	3.57	18938	39.36	1	56.25114998	0.18	0.884552953	5
optimal_loci_128380_G	1727	2.888969	0	2876	42.79	2	56.7248922	0.286	0.885925691	8
optimal_loci_128404_G	3429	3.627362	0.85	4217	48.46	2	2.083654179	0.317	0.886515792	10
optimal_loci_128484_G	1821	3.894286	12.9	2001	41.79	4	17.98153763	0.358	0.889051973	9
optimal_loci_128488_G	1155	3.894286	0	3244	50.47	4	17.80222952	0.376	0.88919864	9
optimal_loci_128505_G	1122	3.408946	14.44	3707	39.12	1	69.60586615	0.377	0.88966238	9
optimal_loci_128508_G	1377	3.408946	2.83	6465	34.64	1	69.60586615	0.192	0.889683363	9
optimal_loci_128517_G	1592	3.408946	13.51	8228	51.38	2	1.570919287	0.503	0.889791663	8
optimal_loci_128519_G	2104	3.408946	18.87	4765	42.91	2	1.570919287	0.406	0.889814114	8
optimal_loci_128579_G	1500	3.208603	14.8	1815	44.26	1	2.351402635	0.196	0.891977524	7
optimal_loci_128678_G	1330	4.448565	0	2054	36.84	3	2.962521286	0.239	0.89613127	1
optimal_loci_128771_G	1276	3.625382	5.8	4987	37.61	3	2.759717332	0.118	0.901366244	5
optimal_loci_128772_G	1046	3.625382	0	3194	30.78	3	2.759717332	0.083	0.901381635	5
optimal_loci_128775_G	1162	3.625382	21.34	2001	40.7	2	4.139575998	0.236	0.901446585	5
optimal_loci_128776_G	1142	3.71562	23.03	1001	45.7	2	4.139575998	0.313	0.90146966	5
optimal_loci_128823_G	1854	1.870192	0	1001	45.09	2	1.800589461	0.272	0.903729555	5
optimal_loci_128957_G	1124	0.530133	13.97	2820	38.87	1	0.718400452	0.191	0.907881878	2
optimal_loci_129054_G	1001	2.596095	0	1001	38.16	3	86.31756703	0	0.911583661	5
optimal_loci_129063_G	1059	5.228885	27.57	2178	53.63	3	23.40429408	0.667	0.912569189	4
optimal_loci_129067_G	1102	5.228885	0	2269	36.75	3	17.33205238	0	0.912672209	4
optimal_loci_129084_G	1261	5.228885	18.32	2792	34.81	3	23.98652266	0.09	0.913429139	5
optimal_loci_129164_G	1516	5.377074	13.39	4485	50.59	2	19.03122322	0.505	0.917117068	8
optimal_loci_129240_G	1336	14.329869	0	6152	54.11	5	43.52710853	0.609	0.91949208	8
optimal_loci_129241_G	1837	14.329869	2.07	4282	54.43	5	43.52710853	0.454	0.919502495	8
optimal_loci_129243_G	1335	14.329869	12.13	2370	48.61	5	43.52710853	0.572	0.919520861	8
optimal_loci_129255_G	1132	14.329869	0	1631	33.48	6	11.25024042	0.116	0.919995762	8
optimal_loci_129269_G	1394	14.329869	18.72	1001	37.8	3	31.85056347	0.17	0.920511943	8
optimal_loci_129270_G	1517	2.794552	0	2557	45.81	3	31.85056347	0.328	0.920523781	8

optimal_loci_129317_G	1089	2.794552	35.9	1993	37.09	5	0.842434685	0.092	0.922171603	7
optimal_loci_129396_G	1009	1.348583	29.73	3490	39.74	3	12.48289127	0.275	0.927253467	4
optimal_loci_129413_G	1066	1.079304	15.1	8415	36.02	2	17.15889008	0.125	0.927509804	4
optimal_loci_129463_G	1362	1.207893	31.79	10005	34.58	1	0.078486601	0.042	0.929009863	6
optimal_loci_129496_G	1461	1.207893	0	18782	34.22	1	53.26413211	0.175	0.930232328	8
optimal_loci_129571_G	1244	1.485285	0	11996	43.32	3	15.19887314	0.272	0.932684903	10
optimal_loci_129573_G	1417	1.485285	0	8591	39.44	3	15.19887314	0.267	0.932709493	10
optimal_loci_129585_G	1101	2.241472	0	6236	40.96	1	84.76962961	0.172	0.933098445	9
optimal_loci_129586_G	1211	2.241472	0	2685	38.64	2	42.3848148	0.115	0.933124624	9
optimal_loci_129622_G	1341	3.940308	4.62	6560	54.88	3	6.35298416	0.509	0.934555176	8
optimal_loci_129653_G	1116	4.296468	0	6521	37	1	0.088239714	0.12	0.935474112	8
optimal_loci_129662_G	1232	4.32355	7.71	6598	36.6	4	8.497624401	0.109	0.935578517	8
optimal_loci_129663_G	1069	4.32355	0	5320	39.85	4	8.497624401	0.211	0.93558948	8
optimal_loci_129793_G	1465	3.983841	34.06	11781	40.34	2	12.41773026	0.325	0.941449804	7
optimal_loci_129807_G	1314	3.796356	2.13	6122	39.42	3	12.46467482	0.038	0.941675039	7
optimal_loci_129812_G	2360	3.796356	0	3704	42.24	2	35.28247761	0.365	0.941818093	7
optimal_loci_129846_G	1304	2.747528	9.82	9363	57.82	1	15.29094785	0.525	0.943112857	7
optimal_loci_129849_G	1860	2.742141	0	4396	53.92	1	15.29094785	0.684	0.943146416	7
optimal_loci_129866_G	1014	2.218016	0	9063	54.53	1	15.29094785	0.78	0.94329599	7
optimal_loci_129894_G	1010	0.80332	0	4699	44.45	3	6.17892546	0.34	0.945161355	11
optimal_loci_129949_G	1127	0.237623	0	2677	32.56	3	10.32657005	0	0.947337935	7
optimal_loci_129983_G	1015	0.320021	0	1334	39.01	3	12.10420311	0.197	0.948193008	9
optimal_loci_129984_G	1901	0.320021	21.25	2001	39.76	4	9.73159355	0.149	0.948232304	9
optimal_loci_129998_G	1064	0.320021	6.48	13084	49.62	1	2.613764871	0.352	0.948475897	9
optimal_loci_130011_G	1452	2.074055	17.29	1537	48.48	1	40.25478744	0.275	0.949146796	8
optimal_loci_130014_G	1109	2.074055	12.8	5120	59.33	1	40.25478744	0.392	0.949174055	8
optimal_loci_130118_G	1150	0.292894	0	1001	31.56	5	44.23087748	0.147	0.951482026	7
optimal_loci_130128_G	1098	4.39774	0	1122	48.45	2	78.71941345	0.381	0.951997142	7
optimal_loci_130272_G	1000	3.190607	0	2294	53.7	2	114.9074331	0.553	0.959173905	7
optimal_loci_130317_G	2115	3.363991	0	1619	45.91	3	24.92407881	0.42	0.960601726	7
optimal_loci_130348_G	1459	3.50156	0	2711	43.45	1	25.43299669	0.27	0.961324458	10
optimal_loci_130353_G	1182	3.616659	0	5284	41.37	1	1.264912316	0.207	0.961491073	10
optimal_loci_130391_G	1202	3.61333	9.07	4067	44.75	1	6.832817341	0.288	0.962660625	10

optimal_loci_130404_G	1009	3.678618	20.12	5612	41.52	1	14.03136204	0.422	0.962968118	10
optimal_loci_130405_G	1554	3.678618	0	3767	36.16	1	14.03136204	0.044	0.962978009	10
optimal_loci_130447_G	1529	3.082673	0	1001	39.24	2	8.483973245	0.021	0.964512387	9
optimal_loci_130452_G	1061	3.30523	6.13	4117	34.3	2	8.483973245	0.121	0.96457488	9
optimal_loci_130457_G	1017	3.30523	0	3407	43.55	2	8.483973245	0.299	0.964621425	9
optimal_loci_130540_G	1896	2.88584	6.28	8216	35.39	2	4.729089955	0.189	0.967960602	4
optimal_loci_130666_G	1039	0.954189	0	6839	37.43	1	1.42162878	0	0.971852198	3
optimal_loci_130675_G	1091	0.980203	0	15109	37.85	1	7.121792745	0.09	0.97251682	3
optimal_loci_130688_G	1548	0.689511	0	14142	36.75	2	5.391416695	0.12	0.97338084	4
optimal_loci_130752_G	1589	3.337613	19.45	2001	40.02	2	2.749075785	0.18	0.97672074	4
optimal_loci_130777_G	1419	4.221166	19.45	2197	40.87	4	4.109283093	0.273	0.977918768	5
optimal_loci_130785_G	1565	4.216929	0	3870	38.53	1	49.05459414	0.022	0.978418372	5
optimal_loci_130824_G	1768	3.621243	0	2002	35.63	3	0.013032351	0	0.980649805	6
optimal_loci_130840_G	1289	4.252115	32.2	3870	34.98	1	0.109826069	0.032	0.981699058	6
optimal_loci_130888_G	1668	4.245	0	11512	37.47	3	46.95041566	0.064	0.983582432	5
optimal_loci_130897_G	1039	4.245	0	2286	37.92	4	40.29911578	0.074	0.983657409	5
optimal_loci_130943_G	1216	1.97504	23.93	16097	34.53	1	12.19515724	0.136	0.986838035	4
optimal_loci_130967_G	1168	2.688817	0	2122	41.6	5	10.20076422	0.188	0.987676097	3
optimal_loci_131035_G	1716	0.581406	0	1001	37.93	3	2.595131653	0.201	0.991102903	2
optimal_loci_131332_G	1052	0.681654	30.51	5120	39.73	1	2.346964998	0.133	0.995176258	2
optimal_loci_131346_G	1366	1.164085	3.51	11860	41.72	2	1.91475527	0.247	0.994325204	2
optimal_loci_131459_G	2036	1.762211	0	1001	41.4	4	3.346704666	0.132	0.987952469	1
optimal_loci_131605_G	1796	2.300563	22.61	2001	45.71	2	6.41424284	0.391	0.981183333	5
optimal_loci_131609_G	1058	2.667337	0	3377	26.55	2	6.41424284	0.116	0.981009972	5
optimal_loci_131623_G	1507	3.520287	6.5	3547	42.4	5	1.834819545	0.264	0.980642232	5
optimal_loci_131632_G	1544	4.683605	0	3617	40.34	6	1.640764931	0.234	0.980366401	5
optimal_loci_131696_G	1035	6.503542	0	5276	42.41	2	3.320696549	0.175	0.97648641	7
optimal_loci_131802_G	1543	9.046044	12.77	1609	37.58	2	2.431915449	0.156	0.972239867	10
optimal_loci_131819_G	1104	8.844509	4.98	6426	38.4	2	2.431915449	0.159	0.972050389	10
optimal_loci_131858_G	1291	8.614337	0	15970	37.95	1	53.29644046	0.141	0.971218262	12
optimal_loci_131859_G	2442	8.614337	0	13184	34.43	1	53.29644046	0.1	0.971191804	12
optimal_loci_131861_G	1775	8.614337	6.76	9270	37.74	1	53.29644046	0.223	0.971154634	12
optimal_loci_131865_G	1339	8.614337	0	5261	39.43	1	53.29644046	0.159	0.971116562	12

optimal_loci_131868_G	1154	8.614337	12.48	2242	38.38	1	53.29644046	0.375	0.971087892	12
optimal_loci_131891_G	1978	7.689007	0	2686	41.75	1	179.8552479	0.259	0.970411814	13
optimal_loci_131984_G	1266	9.537879	27.01	2001	36.25	4	16.30825007	0.194	0.968851244	14
optimal_loci_132051_G	1133	5.396735	0	2001	41.21	7	7.100519233	0.335	0.967042308	12
optimal_loci_132052_G	1654	5.396735	21.4	1641	44.61	7	7.100519233	0.298	0.967024824	12
optimal_loci_132055_G	2593	5.670676	0	2716	35.55	1	3.172548861	0.151	0.966648585	12
optimal_loci_132069_G	1130	4.384593	21.59	6596	41.32	4	3.894387945	0.147	0.965982232	7
optimal_loci_132101_G	1314	4.213742	5.02	3027	47.71	3	8.628767514	0.36	0.964476021	9
optimal_loci_132203_G	1261	4.058497	0	5952	41.47	4	6.776792005	0.236	0.960151339	5
optimal_loci_132208_G	1782	4.058497	0	1001	35.4	3	0.232544505	0.152	0.960080237	5
optimal_loci_132212_G	1290	4.058497	14.65	2001	38.52	2	0.348816757	0.298	0.960017531	5
optimal_loci_132256_G	1027	4.894376	0	1749	38.26	3	17.09145572	0.105	0.957424245	11
optimal_loci_132358_G	1241	5.449586	16.6	2661	41.01	3	0.034827694	0.199	0.955049791	11
optimal_loci_132378_G	1082	5.204372	0	4181	41.49	3	11.61513894	0.184	0.954483533	11
optimal_loci_132401_G	1167	5.204372	0	9908	38.56	6	0.012608178	0.148	0.954207113	11
optimal_loci_132417_G	1141	5.204372	23.58	1956	46.71	6	2.982767441	0.506	0.954043476	11
optimal_loci_132435_G	1377	5.178467	0	2423	40.95	4	33.42151784	0.196	0.953683333	11
optimal_loci_132449_G	1093	4.822236	0	4066	36.32	2	6.690642573	0.273	0.953430009	11
optimal_loci_132451_G	1787	4.822236	19.36	1254	39.95	2	6.690642573	0.327	0.953403305	11
optimal_loci_132475_G	1076	5.600031	0	2960	41.91	4	11.97902888	0.296	0.952545214	12
optimal_loci_132477_G	1016	5.600031	0	2593	40.05	4	11.97902888	0.309	0.95252528	12
optimal_loci_132478_G	1430	5.600031	18.46	1001	41.11	4	11.97902888	0.316	0.952510161	12
optimal_loci_132563_G	1254	3.796758	21.61	2206	51.59	3	3.357133457	0.549	0.948571083	7
optimal_loci_132570_G	1097	3.796758	8.57	5545	39.38	4	1.690185295	0.124	0.948479734	7
optimal_loci_132647_G	1791	2.647782	0	17368	55.94	1	0.113760312	0.709	0.944504103	8
optimal_loci_132651_G	1022	2.568351	0	2919	40.7	2	1.474454921	0.209	0.944167369	8
optimal_loci_132677_G	1174	4.875804	16.61	3637	39.94	2	9.458449701	0.342	0.943476942	8
optimal_loci_132684_G	1133	4.875804	0	3694	35.3	5	4.007371632	0.198	0.943248623	8
optimal_loci_132688_G	1357	4.875804	0	2071	37.73	4	0.741245399	0.195	0.943076011	8
optimal_loci_132738_G	1143	5.824278	2.45	6541	32.63	1	0.908315347	0.089	0.941370703	14
optimal_loci_132781_G	1042	4.966134	0	5054	38.57	4	7.068621726	0.226	0.938943495	13
optimal_loci_132782_G	1409	4.966134	0	6208	37.82	3	6.65251045	0.366	0.93892905	13
optimal_loci_132816_G	1279	4.649727	0	6655	37.13	1	11.46963483	0.198	0.938035888	12

optimal_loci_132819_G	2579	4.649727	0	2001	36.87	1	11.46963483	0.156	0.93799169	13
optimal_loci_132822_G	1185	4.649727	0	4836	45.99	3	7.495686068	0.288	0.937838984	13
optimal_loci_132840_G	3019	5.051751	12.39	1665	34.84	2	48.34091575	0.083	0.93702359	13
optimal_loci_132843_G	2140	4.40511	0	12864	39.62	1	40.13881237	0.163	0.936925584	13
optimal_loci_132845_G	1916	4.40511	0	15959	33.55	1	40.13881237	0.134	0.936898319	13
optimal_loci_132901_G	1297	2.597625	33.77	2577	36.08	4	2.209162043	0.148	0.935086258	13
optimal_loci_132947_G	2043	2.703185	4.36	1793	40.23	3	6.83394289	0.15	0.933404292	12
optimal_loci_132948_G	1066	2.703185	8.35	2001	39.3	3	6.83394289	0.073	0.933393466	12
optimal_loci_132949_G	1076	2.703185	15.43	5107	39.4	2	4.674219817	0.188	0.933237654	11
optimal_loci_133080_G	1730	2.384243	0	5846	33	1	11.43464048	0.158	0.930616904	6
optimal_loci_133102_G	1045	1.932006	8.8	10970	33.77	1	0.060692001	0.246	0.929247075	5
optimal_loci_133408_G	2331	3.94605	0	11438	42.81	1	20.61300748	0.348	0.908394055	6
optimal_loci_133439_G	1066	4.660472	34.9	2001	32.73	4	10.51363413	0.099	0.907407445	6
optimal_loci_133450_G	1095	4.863953	7.49	1203	40	1	6.669761224	0.386	0.906363362	7
optimal_loci_133462_G	1034	4.863953	0	16724	33.26	1	35.28135119	0	0.905856192	7
optimal_loci_133490_G	1484	4.989573	0	12973	45.82	2	1.070836912	0.382	0.904971852	7
optimal_loci_133502_G	1169	4.989573	19.85	6717	34.3	2	2.702637536	0.226	0.904578044	7
optimal_loci_133576_G	1206	5.905701	23.55	1401	34.41	2	0.058410659	0.174	0.901737635	8
optimal_loci_133658_G	1505	6.123902	0	7523	43.78	3	2.634035529	0.417	0.898925366	4
optimal_loci_133662_G	1433	6.123902	0	3678	45.35	3	2.634035529	0.287	0.898888851	4
optimal_loci_133665_G	1040	6.123902	0	1146	38.55	3	2.634035529	0.012	0.898809449	4
optimal_loci_133801_G	1296	3.446106	30.48	2726	39.89	1	1.158079822	0.163	0.893054435	3
optimal_loci_133810_G	1386	3.39408	0	6713	34.92	1	1.158079822	0.117	0.892924777	3
optimal_loci_133813_G	1370	3.325638	0	8742	53.21	1	1.158079822	0.63	0.89290566	3
optimal_loci_133945_G	1173	2.064251	27.37	3519	36.31	1	10.55535901	0.235	0.887623542	4
optimal_loci_133947_G	1042	2.064251	0	6916	42.51	1	10.55535901	0.203	0.887592526	4
optimal_loci_134004_G	1475	1.373921	29.36	10211	45.69	1	11.38830358	0.278	0.88535151	4
optimal_loci_134039_G	2042	0.919536	1.37	3661	33.93	2	5.150542023	0.111	0.884016059	4
optimal_loci_134273_G	1707	1.07218	4.63	18546	52.78	1	230.8263123	0.462	0.872563827	1
optimal_loci_134374_G	2160	3.510306	0	7204	36.52	1	0.716779285	0.169	0.866766059	3
optimal_loci_134377_G	1100	3.510306	0	3513	49.27	1	0.716779285	0.512	0.866731007	3
optimal_loci_134378_G	1211	3.510306	8.18	2152	31.46	1	0.716779285	0.223	0.866718082	3
optimal_loci_134539_G	1316	2.546136	0	9499	47.26	1	14.54958954	0.508	0.860429801	2

optimal_loci_134544_G	1144	2.546136	0	13453	39.68	2	9.699946831	0.149	0.860312545	2
optimal_loci_134810_G	2012	1.172884	17.15	4755	37.72	1	10.93901172	0.178	0.8496785	5
optimal_loci_134830_G	1165	1.514368	32.27	13719	40.08	1	9.085555896	0.163	0.848414217	6
optimal_loci_134853_G	1065	1.506985	0	2001	40.09	1	23.69184809	0.199	0.846835337	6
optimal_loci_134861_G	1662	1.506985	0	2033	46.38	2	9.842418425	0.587	0.846459117	6
optimal_loci_134885_G	1769	0.984704	0	7775	41.66	2	0.037166867	0.318	0.845093808	7
optimal_loci_134904_G	1052	0.701252	13.21	1352	43.15	1	2.128590795	0.258	0.844455518	6
optimal_loci_134993_G	2852	1.274329	0	5088	39.97	1	13.23284359	0.136	0.840449791	3
optimal_loci_135093_G	1328	1.841197	19.05	5894	41.26	1	1.142547466	0.309	0.835049962	1
optimal_loci_135280_G	1224	1.959903	9.64	15471	46.48	1	33.76928983	0.36	0.828997987	1
optimal_loci_135413_G	1507	1.634493	17.52	1783	34.7	4	45.19078194	0	0.823630674	2
optimal_loci_135476_G	1049	1.351397	8.67	23522	42.99	1	2.10902829	0.349	0.82015585	3
optimal_loci_135533_G	1267	1.008605	0	3204	38.75	1	14.56143021	0.181	0.818444986	2
optimal_loci_135655_G	2802	0.035436	23.95	2714	38.57	1	0.433546484	0.271	0.811396201	2
optimal_loci_135697_G	1249	0.617158	0	3152	56.84	1	10.04144049	0.44	0.808382764	2
optimal_loci_135845_G	1426	2.605959	0	3886	36.46	2	1.456574293	0.206	0.797465024	1
optimal_loci_136086_G	3484	0.658666	0	4381	34.98	2	25.70024146	0.057	0.785992507	4
optimal_loci_136109_G	1509	0.234225	0	1306	32.8	1	3.385430756	0.117	0.785116657	4
optimal_loci_136110_G	1009	0.234225	27.25	3701	35.18	1	3.385430756	0.099	0.785098661	4
optimal_loci_136152_G	1281	0.011706	0	19586	26.85	1	3.75573775	0.121	0.782877388	8
optimal_loci_136219_G	1932	0.012393	0	7544	36.95	1	0.777821556	0.167	0.780065774	8
optimal_loci_136225_G	1026	0.012393	30.02	3661	58.67	1	0.777821556	0.542	0.780028898	8
optimal_loci_136231_G	2154	0.012393	25.95	2015	42.47	3	1.337413504	0.181	0.779700532	8
optimal_loci_136247_G	1721	0.012393	8.37	10520	33.52	2	0.183149399	0.327	0.778116562	8
optimal_loci_136275_G	1313	1.767127	0	14020	41.58	1	3.873442664	0.172	0.777686638	7
optimal_loci_136311_G	1169	1.767127	18.48	2002	34.64	1	22.92700678	0.242	0.775656211	7
optimal_loci_136318_G	1173	1.767127	38.7	16857	47.39	1	22.92700678	0.384	0.775322678	7
optimal_loci_136716_G	1296	0.348347	22.38	5770	32.56	3	26.21881803	0.079	0.756407028	2
optimal_loci_136760_G	1816	0.510529	28.19	10024	35.57	3	1.197206617	0.084	0.75304095	3
optimal_loci_136789_G	1232	0.470878	24.51	9811	36.28	2	17.74234503	0.046	0.751466078	3
optimal_loci_136871_G	1219	0.446287	36.83	8972	46.51	2	10.74722105	0.258	0.748208234	4
optimal_loci_136884_G	1508	0.509857	19.89	1693	32.75	3	4.658827832	0.125	0.746608215	3
optimal_loci_136909_G	1437	0.457924	0	10914	37.23	2	4.327523678	0.199	0.745392963	3

optimal_loci_137076_G	1284	0.134784	0	1001	58.33	3	1.0382422	0.679	0.734263875	1
optimal_loci_137250_G	1195	0.195893	33.72	16621	45.85	1	6.761215945	0.347	0.72637246	2
optimal_loci_137288_G	2578	0.405494	39.64	18645	33.51	1	6.37894121	0.148	0.724527047	2
optimal_loci_137489_G	1459	0.343124	2.26	6423	43.66	1	0.426015487	0.382	0.716051994	1
optimal_loci_137604_G	1145	1.266448	0	2595	44.89	1	2.464144614	0.113	0.711031567	3
optimal_loci_137606_G	1261	1.266448	27.68	6844	37.82	1	2.464144614	0.125	0.710922251	3
optimal_loci_137664_G	1051	1.041735	0	6312	45	2	31.88357623	0.246	0.706373599	8
optimal_loci_137693_G	3392	0.94655	20.99	4070	45.04	5	8.629299032	0.362	0.704441035	7
optimal_loci_137708_G	1334	0.940201	0	1001	41.97	1	76.63367966	0.428	0.703219193	7
optimal_loci_137709_G	1151	0.940201	0	2409	41.7	1	76.63367966	0.282	0.703207559	7
optimal_loci_137713_G	1555	0.940201	14.86	7082	44.95	2	38.31683983	0.335	0.703159345	7
optimal_loci_137731_G	1102	0.729266	3.45	2322	46.73	1	0.030060293	0.303	0.702280513	8
optimal_loci_137801_G	1297	0.54044	12.49	2738	43.4	1	11.01857171	0.357	0.700168746	7
optimal_loci_137845_G	2934	0.011394	14.96	10520	41.17	1	0.143540892	0.367	0.697700912	3
optimal_loci_138642_G	1122	1.235952	0	2835	44.38	6	5.135781045	0.475	0.649427645	4
optimal_loci_138653_G	1038	1.164067	0	1960	43.25	2	19.45447632	0.24	0.648525973	4
optimal_loci_138689_G	1889	0.842614	5.77	11726	35.83	1	3.614165813	0.276	0.645912754	5
optimal_loci_138700_G	1054	0.842614	0	2150	43.45	2	14.17743424	0.496	0.645508405	5
optimal_loci_138738_G	1329	0.626999	35.13	1476	40.63	1	0.05550816	0.296	0.641698841	3
optimal_loci_138952_G	1460	0.905718	13.56	2732	37.26	2	5.767806748	0.241	0.630057702	3
optimal_loci_138985_G	2505	0.713022	13.41	7963	40.39	2	7.686015538	0.303	0.627165802	3
optimal_loci_138993_G	2682	0.243185	5.22	2030	42.35	2	48.53604192	0.227	0.62642528	3
optimal_loci_139322_G	1005	0.064994	0	8529	53.03	1	4.620770115	0.721	0.602548025	2
optimal_loci_139359_G	1307	0.182869	13.01	2192	36.34	2	9.918529513	0.058	0.599784406	2
optimal_loci_139485_G	1521	0.274608	0	5644	46.81	2	12.28282104	0.337	0.593487645	2
optimal_loci_139557_G	1348	0.336592	35.16	3450	40.43	3	0.7140649	0.262	0.590069877	4
optimal_loci_139634_G	1015	0.377667	6.4	10006	32.41	1	1.002314112	0.06	0.585901785	3
optimal_loci_139637_G	1109	0.377667	12.44	7666	46.25	2	3.725723076	0.482	0.585528414	3
optimal_loci_139762_G	1437	0.257628	14.2	3935	45.85	1	0.257102836	0.33	0.577357075	2
optimal_loci_139764_G	1022	0.257628	0	2001	56.65	1	0.257102836	0.753	0.577338708	2
optimal_loci_140389_G	1622	0.152955	26.14	3904	39.51	1	18.35359027	0.329	0.542590085	1
optimal_loci_141963_G	1372	0.146021	0	18255	54.44	1	2.742190676	0.415	0.453259639	2
optimal_loci_142025_G	1162	0.143765	0	15941	44.06	1	0.661259257	0.424	0.449860313	2

optimal_loci_142143_G	1122	0.137832	0	17269	33.68	2	1.308659786	0.052	0.444301643	1
optimal_loci_142744_G	1049	0.015546	36.03	9241	38.13	2	1.661991749	0.08	0.408116543	2
optimal_loci_142752_G	1298	0.015546	3.78	12044	45.91	2	1.661991749	0.268	0.407840579	2
optimal_loci_143055_G	2161	0.041782	38.87	11005	43.91	1	0.505949159	0.371	0.3911110361	1
optimal_loci_143731_G	1584	0.087083	0	7762	41.72	1	176.4965014	0.27	0.350286372	4
optimal_loci_143777_G	1157	0.093783	0	13627	36.47	1	16.19311723	0.17	0.347074805	4
optimal_loci_143779_G	1602	0.093783	1.81	4441	38.51	2	8.6936098	0.134	0.346812688	4
optimal_loci_143784_G	1393	0.07254	0	2179	41.34	2	8.6936098	0.164	0.346682564	4
optimal_loci_143849_G	1081	0.034114	0	4371	39.68	1	0.176391887	0.157	0.340923932	1
optimal_loci_144083_G	1070	0.021655	32.9	2375	42.8	1	16.36436873	0.288	0.327185793	3
optimal_loci_144125_G	1439	0.02137	12.02	14642	35.02	2	2.190054031	0.236	0.325350997	3
optimal_loci_144167_G	1317	0.011559	0	2575	45.02	2	0.541360199	0.262	0.323751709	3
optimal_loci_145661_G	1467	0.210258	0	2818	40.35	2	5.844657868	0.141	0.225068794	2
optimal_loci_145696_G	1440	0.297337	37.64	10744	38.81	2	51.55152018	0.23	0.223418205	2
optimal_loci_145798_G	2392	0.404242	0	1721	32.94	2	0.03520484	0.105	0.217816686	4
optimal_loci_145828_G	1203	0.396736	20.95	6534	34.58	1	73.39037653	0	0.215933789	4
optimal_loci_145842_G	2094	0.396736	0	18895	48.18	1	5.106747491	0.383	0.214957892	4
optimal_loci_145861_G	1937	0.412409	9.71	1290	30.4	2	12.66657073	0.113	0.213916515	6
optimal_loci_145950_G	1192	0.068969	0	7607	50.75	2	177.6722775	0.51	0.209981282	3
optimal_loci_145958_G	1437	0.068969	35.21	16292	36.04	1	16.2263167	0.16	0.209719582	3
optimal_loci_151664_G	1035	0.21345	34.2	3421	32.94	2	1.005029473	0.051	0.143217494	1
optimal_loci_151807_G	2281	0.063399	0	3976	34.23	2	5.735885921	0.066	0.147018932	1
optimal_loci_152337_G	2390	0.055303	0	2945	51.79	1	19.87891117	0.398	0.17679303	1
optimal_loci_152901_G	2942	0.065307	11.32	1001	34.39	1	15.59616825	0.049	0.202099969	1
optimal_loci_153296_G	2531	0.053223	29.79	10845	35.32	1	9.111673717	0.115	0.220098063	1
optimal_loci_153894_G	1629	0.151554	4.54	2001	45.11	2	3.746844386	0.406	0.250267563	1
optimal_loci_154285_G	1532	1.59459	0	19929	45.62	1	8.060565028	0.258	0.270047837	3
optimal_loci_154390_G	2236	2.789566	31.17	2109	33	2	99.52481283	0.059	0.273125035	3
optimal_loci_154391_G	1241	2.789566	6.29	1001	52.37	2	99.52481283	0.433	0.273175	3
optimal_loci_154770_G	2124	0.357022	5.08	6560	45.15	2	4.740515565	0.465	0.29014841	3
optimal_loci_154805_G	1740	0.418893	5.06	2069	47.7	2	9.293132204	0.305	0.291914339	3
optimal_loci_154824_G	1209	0.637938	4.3	2038	29.36	1	6.318888299	0.067	0.292734212	3
optimal_loci_155031_G	1747	0.538084	0	11918	43.44	2	1.630830534	0.264	0.302063475	1

optimal_loci_155124_G	1454	0.451306	21.25	2001	35.69	2	0.219516141	0.089	0.306422193	5
optimal_loci_155133_G	2340	0.424573	9.7	7265	39.35	2	0.235678272	0.166	0.307007965	5
optimal_loci_155162_G	1647	0.317313	0	14921	36.18	1	0.071659859	0.162	0.307620559	5
optimal_loci_155217_G	1863	0.156958	1.61	1071	45.3	3	0.049135409	0.231	0.308849382	5
optimal_loci_155222_G	2404	0.156958	9.03	2793	36.27	3	0.049135409	0.323	0.308930786	5
optimal_loci_155801_G	1349	0.739224	0	2001	45.14	1	41.54082346	0.359	0.334686217	4
optimal_loci_155807_G	1125	0.739224	20.09	5680	34.84	1	41.54082346	0.213	0.334713394	4
optimal_loci_155814_G	1227	1.038125	0	8556	32.68	2	15.51638267	0.177	0.335498511	4
optimal_loci_155853_G	1887	1.552126	8.27	7313	51.93	5	6.127509621	0.481	0.337080261	7
optimal_loci_155922_G	1155	2.297014	0	2595	41.64	1	0.282451138	0.264	0.339599225	5
optimal_loci_155924_G	1890	2.281794	6.46	1177	39.94	1	0.282451138	0.315	0.33964348	5
optimal_loci_155931_G	1217	2.273589	3.37	9350	48.23	1	0.282451138	0.38	0.339703854	5
optimal_loci_156007_G	1096	1.513409	0	11635	40.05	1	159.2008283	0.255	0.342343218	6
optimal_loci_156064_G	1328	1.381597	2.26	19141	49.92	1	0.067346206	0.275	0.344193913	4
optimal_loci_156071_G	1361	1.721654	0	1164	49.52	1	0.067346206	0.331	0.344364057	4
optimal_loci_156124_G	1267	1.847856	0	3849	48.53	1	0.032990699	0.47	0.346800287	7
optimal_loci_156176_G	1035	2.620604	2.71	12254	55.07	1	1.007896296	0.443	0.348335846	6
optimal_loci_156179_G	1139	2.620604	0	9910	59.43	1	1.007896296	0.683	0.348352393	6
optimal_loci_156188_G	1507	2.620604	0	2393	45.25	1	1.007896296	0.181	0.348405202	6
optimal_loci_156199_G	1408	1.239478	0	5485	39.41	1	5.26386293	0.168	0.348860439	6
optimal_loci_156281_G	1527	0.614596	22.53	4915	32.54	2	175.8580793	0.27	0.351221189	5
optimal_loci_156385_G	1179	3.194469	3.65	6984	43	2	6.143935836	0.126	0.355844316	3
optimal_loci_156388_G	1635	2.840069	4.77	12541	45.5	1	730.3712301	0.315	0.356022306	3
optimal_loci_156393_G	1370	2.83222	2.55	2001	53.94	1	730.3712301	0.687	0.35615451	4
optimal_loci_156503_G	1398	2.987021	13.95	2397	34.33	1	43.43608945	0.13	0.359759248	3
optimal_loci_156548_G	1697	2.337073	21.51	5315	52.2	2	22.87870804	0.401	0.361343051	3
optimal_loci_156598_G	1244	1.510861	0	17311	46.86	1	5.935958859	0.446	0.363549709	2
optimal_loci_156848_G	1478	1.679143	22.12	2001	38.97	3	0.203290027	0.308	0.371470196	3
optimal_loci_156884_G	1156	2.15672	14.45	1380	44.29	1	75.23696147	0.418	0.372141191	4
optimal_loci_156894_G	1642	2.306981	1.83	4382	50.97	3	0.63962081	0.36	0.372379679	4
optimal_loci_156994_G	1295	2.415503	0	1001	45.71	5	17.02422336	0.371	0.375788729	4
optimal_loci_157006_G	1583	2.634004	5.24	5836	43.01	2	12.30748277	0.356	0.376652273	3
optimal_loci_157055_G	1234	1.975672	0	5413	48.94	1	0.362676786	0.505	0.379500083	2

optimal_loci_157215_G	1227	2.043836	0	3223	54.36	3	15.98062835	0.596	0.384345544	3
optimal_loci_157280_G	1075	1.295428	0	11459	35.9	2	12.81653573	0.238	0.386873306	5
optimal_loci_157315_G	1275	0.83237	0	3507	43.76	1	0.340361374	0.434	0.388633724	3
optimal_loci_157316_G	1284	0.83237	0	15938	41.82	1	0.340361374	0.233	0.388725551	3
optimal_loci_157478_G	1213	0.990581	0	6384	62.07	1	5.992951922	0.714	0.395630293	3
optimal_loci_157544_G	1320	1.336437	18.11	2001	41.96	1	25.9526279	0.194	0.397513113	6
optimal_loci_157567_G	1640	1.651075	21.71	2692	49.93	3	0.965091509	0.514	0.398937934	6
optimal_loci_157594_G	1323	1.89211	0	12476	55.63	2	0.081871459	0.505	0.400003482	5
optimal_loci_157615_G	1420	1.919021	20.35	2001	48.59	3	0.054580972	0.315	0.40024104	5
optimal_loci_157634_G	1013	1.931987	9.67	9448	50.54	2	3.225659721	0.678	0.40074444	5
optimal_loci_157701_G	1055	1.0272	25.5	2191	30.42	5	68.59525017	0.233	0.405718382	2
optimal_loci_157716_G	1057	1.109799	0	5453	41.72	1	7.164009145	0.254	0.406738293	2
optimal_loci_157857_G	2626	1.689406	9.86	2001	45.43	1	16.01739839	0.198	0.412292564	2
optimal_loci_157922_G	1063	1.86511	11.76	1068	37.44	2	0.144637597	0.211	0.415492584	2
optimal_loci_157993_G	1138	2.199724	12.21	1811	48.76	2	0.109739655	0.413	0.419317129	1
optimal_loci_158063_G	1594	0.918346	5.21	2001	51.06	2	8.980367734	0.49	0.423267747	2
optimal_loci_158084_G	1597	0.45362	5.64	1368	40.95	6	4.428149977	0.16	0.42509809	3
optimal_loci_158148_G	1093	2.177851	17.2	1081	48.12	4	1.171394018	0.536	0.428407541	3
optimal_loci_158162_G	1574	2.177851	20.08	14311	50.38	2	0.271226807	0.617	0.429114836	2
optimal_loci_158474_G	1513	1.021396	0	4691	54.32	3	14.90921109	0.488	0.439738629	4
optimal_loci_158487_G	1401	1.021396	0	1296	37.4	2	48.96717145	0.087	0.440221618	4
optimal_loci_158515_G	1196	1.548322	32.02	7337	49.33	2	10.6659207	0.41	0.44130833	4
optimal_loci_158526_G	1177	1.424397	0	2001	41.71	3	4.910850869	0.2	0.442317353	4
optimal_loci_158719_G	1047	0.671147	0	2618	52.62	3	16.9413519	0.64	0.448839509	6
optimal_loci_158723_G	1945	0.662613	1.54	2617	58.92	4	7.026340292	0.558	0.449171028	7
optimal_loci_158724_G	1085	0.662613	0	1499	48.01	4	7.026340292	0.223	0.44918564	7
optimal_loci_158740_G	1134	0.876159	17.9	10651	46.29	4	9.86603085	0.347	0.450026055	7
optimal_loci_158784_G	1052	0.876159	11.69	1001	36.59	2	9.982021438	0.137	0.451438355	7
optimal_loci_158803_G	1348	0.792225	31.9	6054	43.99	2	0.073816706	0.227	0.452063655	7
optimal_loci_158825_G	1193	0.807754	0	2936	46.26	2	1.243561829	0.159	0.452811349	6
optimal_loci_159036_G	1036	0.569473	38.8	2544	44.3	2	1.996722854	0.158	0.467695451	1
optimal_loci_159103_G	1069	0.841423	15.34	1001	38.63	4	87.1609349	0.263	0.471826363	2
optimal_loci_159105_G	1711	0.86576	26.01	1001	34.07	3	0.77323855	0.11	0.472188361	2

optimal_loci_159200_G	1122	2.333163	0	1001	44.29	5	2.987708248	0.272	0.478017692	4
optimal_loci_159206_G	1042	1.927979	0	2001	41.93	2	42.12625663	0.269	0.478842994	4
optimal_loci_159220_G	1467	1.823043	39.47	8347	45.67	1	3.223119473	0.413	0.479786414	4
optimal_loci_159235_G	1325	1.827713	0	1001	38.64	1	4.321815338	0.185	0.480362095	4
optimal_loci_159308_G	1157	3.302544	0	1001	45.28	4	3.076852788	0.408	0.484554592	3
optimal_loci_159350_G	1157	3.639672	0	2001	50.38	3	4.309154299	0.436	0.486153775	3
optimal_loci_159391_G	1460	2.312772	4.32	11415	55.41	1	0.029593301	0.68	0.487701515	8
optimal_loci_159501_G	1259	2.064171	0	3064	38.84	2	0.243662702	0.102	0.490120829	8
optimal_loci_159519_G	1457	2.294056	16.82	6820	32.6	1	10.14659406	0.158	0.490597946	8
optimal_loci_159522_G	1258	2.294056	0	4543	47.37	1	10.14659406	0.301	0.490616236	8
optimal_loci_159525_G	1070	2.294056	15.61	2527	56.16	1	10.14659406	0.554	0.490632517	8
optimal_loci_159527_G	1186	2.294056	19.06	1001	39.46	1	10.14659406	0.181	0.490642933	8
optimal_loci_159603_G	1741	3.307841	4.94	6281	56.97	2	94.16707403	0.64	0.492501103	7
optimal_loci_159605_G	2972	3.307841	3.47	8789	53.29	3	62.77804936	0.478	0.492519629	7
optimal_loci_159726_G	3112	2.233782	4.37	1001	38.07	4	46.03036734	0.216	0.49659703	2
optimal_loci_159795_G	2853	2.296878	3.54	2053	45.84	4	3.464231912	0.453	0.500061696	5
optimal_loci_159805_G	1019	2.022229	31.6	10844	39.35	1	11.44202609	0.064	0.500381677	4
optimal_loci_159834_G	1671	1.906596	0	1235	43.62	5	30.38708549	0.246	0.501636199	4
optimal_loci_159841_G	1180	1.906596	22.88	1992	36.27	5	3.26761272	0.183	0.501921521	4
optimal_loci_159954_G	1359	2.534425	0	1001	55.7	2	3.517643661	0.628	0.507800079	9
optimal_loci_159965_G	1900	2.820214	0	1919	45.63	2	29.21915684	0.336	0.508652454	11
optimal_loci_159987_G	1577	3.426591	18.45	4514	39.69	2	27.06442492	0.174	0.509881431	11
optimal_loci_159988_G	1574	3.426591	11.25	2654	58.57	2	27.06442492	0.462	0.509895193	11
optimal_loci_159993_G	1501	3.426591	39.84	1520	32.11	2	27.06442492	0	0.509997496	11
optimal_loci_160000_G	1317	3.517411	24.68	1001	55.73	2	1.220388089	0.361	0.510603294	11
optimal_loci_160006_G	1702	3.517411	0	10495	54.34	1	0.042519257	0.566	0.510917195	11
optimal_loci_160010_G	1030	3.650194	19.22	3350	60.19	1	0.042519257	0.594	0.510974939	11
optimal_loci_160011_G	1436	3.650194	0	1001	55.29	1	0.042519257	0.601	0.510989292	11
optimal_loci_160026_G	1384	1.150371	0	2585	50.86	1	2.820544473	0.567	0.511709935	10
optimal_loci_160028_G	1072	1.150371	18	1060	44.4	1	2.820544473	0.29	0.511723505	10
optimal_loci_160138_G	1880	0.027159	0	2737	39.94	1	1.778263358	0.205	0.516244176	1
optimal_loci_160231_G	1111	0.190415	0	7181	49.14	3	45.2119066	0.44	0.520112111	3
optimal_loci_160235_G	1418	0.186539	3.53	1527	37.16	1	8.46682769	0.169	0.520270857	3

optimal_loci_160237_G	2393	0.186539	3.34	3899	36.1	1	8.46682769	0.178	0.520288379	3
optimal_loci_160307_G	2995	2.964264	6.58	1087	56.62	1	28.69608577	0.668	0.524157504	4
optimal_loci_160318_G	1334	3.353737	0	1001	57.42	1	1.514985022	0.734	0.5246636	5
optimal_loci_160368_G	1098	4.177704	26.78	3498	43.16	2	5.950851156	0.324	0.52600811	6
optimal_loci_160371_G	2881	4.42764	0.97	2148	53.31	4	2.975425578	0.486	0.526121109	6
optimal_loci_160411_G	1238	3.00826	4.04	7804	57.51	2	1.068586984	0.642	0.528145788	6
optimal_loci_160436_G	1783	2.752382	0	4308	53.28	5	4.881364991	0.463	0.528439842	5
optimal_loci_160492_G	2160	1.450894	4.58	18815	35.74	1	13.67604459	0.078	0.531731268	6
optimal_loci_160559_G	1233	2.345865	0	5329	44.84	1	6.457370756	0.464	0.533928146	11
optimal_loci_160563_G	1510	2.813928	0	2001	56.42	1	6.457370756	0.597	0.533950684	11
optimal_loci_160576_G	1337	3.027291	19.82	2501	33.8	3	1.990332386	0.154	0.534880629	11
optimal_loci_160592_G	1239	2.68722	0	1001	35.83	5	16.02394923	0.171	0.535496658	12
optimal_loci_160593_G	1293	2.68722	15.31	1654	42.53	4	17.35064969	0.178	0.535506837	12
optimal_loci_160604_G	2509	2.929963	0	1001	48.82	4	9.767080195	0.43	0.535965797	12
optimal_loci_160614_G	1944	2.991906	0	1001	50.72	4	6.817258411	0.409	0.536576463	12
optimal_loci_160623_G	1434	3.540848	3.7	4886	58.15	4	6.817258411	0.595	0.536669148	12
optimal_loci_160625_G	1069	3.540848	30.22	3664	40.78	4	6.817258411	0.018	0.536682023	12
optimal_loci_160644_G	1381	3.540848	25.34	1001	38.08	2	0.033915007	0.154	0.537200825	12
optimal_loci_160669_G	1210	3.754164	27.69	5654	40.99	1	3.182940752	0.182	0.539075039	9
optimal_loci_160672_G	1753	3.754164	10.55	1466	43.98	1	3.182940752	0.272	0.539101965	9
optimal_loci_160710_G	1692	2.183845	0	2273	62.47	4	34.27561849	0.618	0.543041916	6
optimal_loci_160711_G	1516	2.183845	0	3998	55.67	4	34.27561849	0.582	0.543054659	6
optimal_loci_160712_G	1594	2.183845	0	5527	51.5	4	34.27561849	0.341	0.543066825	6
optimal_loci_160713_G	1183	2.183845	16.4	4223	45.9	4	34.27561849	0.428	0.543079494	6
optimal_loci_160718_G	1972	2.183845	12.47	1488	54.76	4	59.63397575	0.65	0.543156422	6
optimal_loci_160772_G	1391	1.650504	0	1174	50.68	4	4.904679439	0.49	0.544410012	7
optimal_loci_160808_G	2128	0.91147	23.12	3542	51.87	4	7.352758847	0.649	0.547416036	4
optimal_loci_160840_G	1593	0.811049	0	3231	38.79	1	14.99049574	0.287	0.548672442	3
optimal_loci_160842_G	1033	0.811049	0	5552	47.04	1	14.99049574	0.524	0.548689587	3
optimal_loci_160936_G	1024	0.823861	0	2001	43.75	2	0.97932431	0.141	0.552482464	2
optimal_loci_160953_G	1528	0.963097	9.1	2130	54.31	1	43.40187262	0.677	0.553739778	2
optimal_loci_161049_G	1243	3.207586	0	1350	38.05	3	3.64846942	0.101	0.559042795	8
optimal_loci_161065_G	1471	3.207763	1.9	2866	54.04	2	40.19820982	0.618	0.559754839	9

optimal_loci_161067_G	3499	3.207763	1.4	2459	49.58	3	27.633754	0.412	0.559776151	9
optimal_loci_161072_G	1145	3.207763	0	3077	47.16	2	31.4350188	0.365	0.559883594	9
optimal_loci_161085_G	2418	3.525489	3.39	8080	41.77	1	5.344784515	0.208	0.560648426	9
optimal_loci_161093_G	1050	3.631991	0	6787	44.47	1	23.06979845	0.289	0.561028907	9
optimal_loci_161094_G	1938	3.631991	4.18	1001	43.8	1	23.06979845	0.312	0.561065088	9
optimal_loci_161102_G	2235	2.847941	24.38	1426	37.8	2	7.019224312	0.177	0.562048058	9
optimal_loci_161119_G	1935	2.74326	8.89	2219	53.95	2	2.89304656	0.47	0.56281874	9
optimal_loci_161183_G	1235	0.310824	6.4	1130	48.5	2	33.49926354	0.542	0.566151623	3
optimal_loci_161223_G	1112	0.43137	0	3219	40.1	1	16.74368512	0.09	0.56896139	2
optimal_loci_161340_G	1056	0.037195	17.14	9311	35.98	3	10.19776346	0.129	0.574936909	2
optimal_loci_161342_G	1621	0.037195	0	6563	42.81	2	15.29664518	0.309	0.574954409	2
optimal_loci_161510_G	1046	1.90431	7.84	6339	45.79	2	2.619220665	0.233	0.584289618	5
optimal_loci_161527_G	1010	2.224456	8.22	2749	44.85	2	1.264396105	0.364	0.585153059	5
optimal_loci_161541_G	1131	2.224456	19.1	2429	37.93	1	0.104734184	0.324	0.585280654	5
optimal_loci_161570_G	1177	2.792477	20.05	8194	49.87	1	40.27829374	0.434	0.586021257	5
optimal_loci_161613_G	1330	2.566963	9.47	3539	49.32	2	1.649782421	0.467	0.587620979	6
optimal_loci_161722_G	1035	2.047858	0	1484	45.02	3	12.51537145	0.258	0.590602804	2
optimal_loci_161875_G	1019	0.01286	10.6	2001	48.18	4	4.399801337	0.338	0.597968913	1
optimal_loci_161989_G	1034	0.997205	33.27	1762	44.39	1	18.80170859	0.255	0.601976868	2
optimal_loci_162024_G	1608	0.818656	0	2633	40.42	2	54.82025997	0.287	0.604106443	2
optimal_loci_162129_G	1078	0.457003	0	2001	41.92	3	0.262012516	0.121	0.607861055	3
optimal_loci_162150_G	1136	0.451688	27.73	1516	39.7	1	0.046150691	0.173	0.608810045	3
optimal_loci_162197_G	1191	0.866178	38.71	2001	33.5	2	1.926875242	0.089	0.609998372	6
optimal_loci_162305_G	1756	1.29254	0	2012	43.9	1	1.102782913	0.271	0.613189129	6
optimal_loci_162326_G	2248	0.530107	0	18709	49.11	1	45.50407826	0.426	0.613341544	6
optimal_loci_162350_G	1139	0.530107	18.53	14471	41.43	2	22.77836057	0.398	0.613662183	6
optimal_loci_162354_G	2053	0.525217	16.03	5364	40.18	1	0.05264289	0.199	0.613722705	5
optimal_loci_162355_G	1392	0.525217	0	3867	33.54	1	0.05264289	0.095	0.613738646	5
optimal_loci_162512_G	1590	1.084973	0	1001	40.94	1	3.602782711	0.107	0.618374509	5
optimal_loci_162531_G	2349	0.448169	1.66	4371	49.72	1	0.032388318	0.568	0.619005799	7
optimal_loci_162532_G	1849	0.448169	0	2057	57.49	1	0.032388318	0.688	0.619026586	7
optimal_loci_162534_G	1087	0.549911	0	2001	38.82	1	0.032388318	0.04	0.619087329	7
optimal_loci_162551_G	1257	0.661831	2.31	1001	40.33	1	362.2877937	0.205	0.620129239	7

optimal_loci_162628_G	1313	1.133579	18.66	1488	49.96	2	0.291461491	0.386	0.622517675	7
optimal_loci_162630_G	1047	1.133579	0	2155	41.92	2	0.291461491	0.182	0.622592594	7
optimal_loci_162689_G	1228	2.48251	35.59	3252	34.28	1	0.301715917	0.107	0.624333828	6
optimal_loci_162728_G	1247	0.376962	23.82	10295	36.32	1	15.15218947	0.263	0.626800921	4
optimal_loci_162732_G	1820	0.376962	5.44	4067	34.28	2	7.883141785	0.05	0.626842694	4
optimal_loci_162738_G	1019	0.376962	16.68	2089	40.13	2	7.883141785	0.238	0.62699197	4
optimal_loci_162852_G	1026	0.204277	15.01	19158	38.59	1	0.249383602	0	0.631011324	2
optimal_loci_162954_G	1089	0.829554	3.95	2544	49.49	2	9.781407343	0.31	0.634230543	2
optimal_loci_163451_G	1164	0.015973	33.08	2054	35.91	2	1.988662431	0.005	0.650932098	1
optimal_loci_163651_G	2250	0.599673	24.18	9012	38.13	3	1.843289657	0.158	0.658054895	3
optimal_loci_163696_G	1165	0.386578	0	2001	51.07	2	4.210173808	0.424	0.660710858	3
optimal_loci_163706_G	1334	0.386578	19.94	4098	35.15	2	4.210173808	0.02	0.660786848	3
optimal_loci_163976_G	1206	0.335795	11.86	3614	36.65	2	19.8464633	0.161	0.671000169	2
optimal_loci_163992_G	1426	0.330819	4.77	3220	56.8	4	13.29300851	0.52	0.6717933	2
optimal_loci_164095_G	1542	0.378785	27.17	3970	58.88	4	27.73507414	0.542	0.67690249	3
optimal_loci_164114_G	1309	0.333556	0	13872	43.77	2	0.976795369	0.314	0.677396878	3
optimal_loci_164120_G	2062	0.333556	0	2001	42.24	1	1.953590737	0.171	0.677479007	3
optimal_loci_164326_G	1164	0.17222	3.44	2695	49.74	3	3.835306388	0.505	0.68464286	6
optimal_loci_164332_G	1186	0.217975	16.44	2001	36.76	3	2.474502374	0.043	0.685142907	7
optimal_loci_164340_G	1029	0.422263	0	7342	40.91	2	0.054798356	0.167	0.685728051	7
optimal_loci_164350_G	1437	0.453152	0	8907	50.59	1	0.527503277	0.455	0.686147054	7
optimal_loci_164362_G	1216	0.453152	6.99	8354	52.79	1	0.527503277	0.572	0.686308726	7
optimal_loci_164397_G	1413	0.690691	0	2022	35.52	1	9.59346209	0.18	0.687619056	7
optimal_loci_164416_G	1046	0.964242	4.49	2113	38.71	2	0.787101057	0.263	0.68835649	7
optimal_loci_164520_G	1296	1.029211	12.73	14469	46.21	2	1.495529476	0.43	0.691634325	2
optimal_loci_164764_G	1058	0.712241	0	1001	38.56	2	0.198094272	0.052	0.699113011	3
optimal_loci_164808_G	1096	0.473764	0	1420	52.28	4	2.526621845	0.682	0.701953537	4
optimal_loci_164809_G	1482	0.473764	0	2549	50.74	4	2.526621845	0.42	0.701961877	4
optimal_loci_164837_G	1000	0.108697	0	2001	38.7	3	4.066967065	0	0.704594741	4
optimal_loci_164911_G	1298	0.124915	0	7535	50.3	1	4.005041913	0.464	0.707506219	5
optimal_loci_164987_G	1043	0.267355	0	3830	49.56	1	5.127011227	0.494	0.710027067	4
optimal_loci_164988_G	1194	0.267355	3.27	2454	48.49	1	5.127011227	0.555	0.710036116	4
optimal_loci_165002_G	1201	0.287991	0	3370	57.28	1	0.028122461	0.569	0.710439622	4

optimal_loci_165139_G	1122	0.410016	21.84	1254	46.7	1	0.572139301	0.434	0.715928584	3
optimal_loci_165190_G	1286	0.411852	3.97	5703	43.85	2	15.37339161	0.278	0.71744357	4
optimal_loci_165218_G	1725	0.406267	8.75	12381	42.14	1	9.583350479	0.288	0.719355178	4
optimal_loci_165234_G	1513	0.406267	2.18	2248	36.81	2	1.647941891	0.169	0.719884631	3
optimal_loci_165424_G	1175	0.056108	0	10535	39.57	1	8.710616417	0.242	0.728201562	2
optimal_loci_165433_G	1543	0.056108	12.57	11733	40.44	1	1.87260785	0.226	0.728350719	2
optimal_loci_166843_G	1658	0.141179	1.75	2676	39.92	1	0.360840151	0.216	0.778473408	1
optimal_loci_166977_G	2323	0.136665	5.77	3620	45.75	2	34.72362747	0.386	0.783942602	3
optimal_loci_166984_G	1493	0.146228	0	1137	32.21	3	9.369055455	0.075	0.784562945	3
optimal_loci_166986_G	1124	0.146228	0	2496	39.94	3	9.369055455	0.082	0.784580179	3
optimal_loci_167152_G	3110	0.135131	0.9	2154	40.25	2	0.844806515	0.188	0.792385222	1
optimal_loci_167587_G	1037	0.150391	0	4246	52.84	1	0.315433617	0.683	0.811799457	2
optimal_loci_167588_G	2080	0.150391	7.55	2068	39.08	1	0.315433617	0.12	0.811807841	2
optimal_loci_167667_G	1907	0.145303	5.14	8756	43.47	1	66.60938009	0.456	0.81623384	2
optimal_loci_167691_G	1090	0.145303	12.84	15880	52.29	1	78.78707302	0.441	0.816676246	2
optimal_loci_167826_G	1619	0.060404	25.2	6872	37.12	2	5.713214945	0.051	0.82352164	2
optimal_loci_167845_G	2163	0.025018	6.52	1001	33.88	2	2.056008849	0.153	0.824195331	2
optimal_loci_168190_G	1429	0.135928	15.75	12671	33.17	1	6.515082485	0.083	0.837436593	2
optimal_loci_168236_G	1375	0.469301	0	10464	43.49	1	2.870748422	0.368	0.840111038	3
optimal_loci_168286_G	3473	0.509046	15.2	1710	44.22	2	9.240645857	0.262	0.841281489	2
optimal_loci_168380_G	1021	0.773638	9.11	1594	39.66	1	41.18401497	0.21	0.845170522	2
optimal_loci_168431_G	1639	0.777011	13.97	2862	37.58	1	0.038119272	0.222	0.848347355	2
optimal_loci_168586_G	1071	0.768576	0	2099	37.72	1	0.882320723	0.121	0.854348418	1
optimal_loci_168819_G	1282	0.096599	17.32	18487	36.19	1	5.483459851	0.249	0.864056714	2
optimal_loci_168857_G	1131	0.041765	12.29	3362	40.14	2	0.311260143	0.285	0.865097368	2
optimal_loci_169233_G	1436	0.691439	3.41	8324	39.2	1	14.94355901	0.15	0.87789875	2
optimal_loci_169239_G	1665	0.690182	0	2042	36.63	1	14.94355901	0.204	0.877943464	2
optimal_loci_169812_G	1082	0.21463	0	7628	46.76	1	0.072716696	0.57	0.897174036	2
optimal_loci_169839_G	1026	0.24238	0	2001	32.45	1	5.757380565	0.121	0.89793895	2
optimal_loci_170176_G	1364	0.742024	0	4065	37.6	1	3.469902773	0.103	0.906726016	2
optimal_loci_170193_G	1112	0.772878	8.27	1718	50.44	3	6.174509951	0.426	0.907372007	3
optimal_loci_170300_G	2806	1.099277	2.39	2354	41.41	1	25.14178974	0.265	0.910834908	3
optimal_loci_170338_G	1528	1.291649	5.82	4136	42.53	1	47.46623562	0.306	0.913278465	3

optimal_loci_170410_G	1245	0.60126	10.2	15605	42.81	2	9.753958205	0.238	0.914847827	3
optimal_loci_170476_G	1688	0.372666	0	13084	40.52	1	4.269720418	0.223	0.917940427	3
optimal_loci_170547_G	1242	0.794721	0	1458	40.74	1	51.35023773	0.286	0.92112034	3
optimal_loci_170572_G	1120	1.10307	34.29	5851	36.25	2	0.015367738	0.1	0.922188858	2
optimal_loci_170646_G	1221	2.669682	0	12392	48.15	2	14.68999676	0.342	0.926281268	4
optimal_loci_170655_G	1309	2.675913	9.32	6899	52.55	2	14.68999676	0.412	0.926321195	4
optimal_loci_170668_G	2144	2.679722	7.93	5619	50.32	1	1.957520789	0.389	0.926441211	4
optimal_loci_170759_G	1501	2.408529	7.53	3822	41.63	2	51.84654518	0.133	0.929970366	4
optimal_loci_170952_G	1009	2.161414	3.77	1001	45.19	5	11.17513711	0.557	0.939009165	2
optimal_loci_171036_G	1360	0.808171	15.22	5007	43.01	2	198.0757641	0.217	0.942093181	2
optimal_loci_171119_G	1143	3.387746	21.87	2001	39.02	2	1.761221722	0.111	0.946285693	4
optimal_loci_171120_G	1890	3.387746	0	3327	39.62	2	1.761221722	0.124	0.94631106	4
optimal_loci_171141_G	1380	3.614118	0	3285	41.44	2	10.17076553	0.291	0.947370661	5
optimal_loci_171183_G	1062	4.810016	2.92	12249	46.04	3	70.31953957	0.406	0.948593013	5
optimal_loci_171244_G	2573	5.766052	12.09	1001	39.21	3	48.28404688	0.144	0.950080896	5
optimal_loci_171326_G	1937	4.456232	11.98	6542	38.61	1	30.23497514	0.187	0.952804996	4
optimal_loci_171355_G	1136	4.222203	9.51	1232	52.2	1	71.55095467	0.434	0.953418928	4
optimal_loci_171379_G	1801	2.762931	10.88	1001	52.91	2	7.886630372	0.477	0.954601338	3
optimal_loci_171577_G	1945	3.880572	1.69	1250	43.03	2	1.03906273	0.487	0.961106946	4
optimal_loci_171599_G	1468	4.512519	9.81	2493	34.4	2	12.00679257	0.062	0.962213913	4
optimal_loci_171615_G	1596	5.331916	0	3510	54.26	4	18.18279084	0.386	0.962537063	4
optimal_loci_171635_G	1271	5.544922	0	2704	32.65	1	13.03118814	0.124	0.963119777	4
optimal_loci_171803_G	1118	8.447715	8.68	7558	34.43	3	11.95295441	0.207	0.970393896	3
optimal_loci_171814_G	1081	9.801385	29.32	7823	40.14	1	7.946838901	0.166	0.971305426	3
optimal_loci_171855_G	1080	9.138135	13.24	6099	41.2	3	9.537407006	0.238	0.973858902	6
optimal_loci_171923_G	1349	4.945275	0	5089	59.82	1	132.686346	0.628	0.975191475	4
optimal_loci_171964_G	1527	3.321432	39.88	2001	33.52	3	8.958205043	0.089	0.977176457	6
optimal_loci_171965_G	1329	3.321432	0	3862	51.69	3	3.613063865	0.392	0.977190204	6
optimal_loci_171996_G	1013	3.700822	27.84	1001	37.8	1	0.155921951	0.227	0.980199419	6
optimal_loci_171997_G	1422	3.624098	11.46	4861	39.87	2	0.094544326	0.33	0.980256003	6
optimal_loci_172015_G	1182	11.223488	31.73	1862	35.44	3	10.94684869	0.035	0.981877702	5
optimal_loci_172034_G	1189	10.168608	0	8651	34.06	3	2.036237267	0	0.98345892	5
optimal_loci_172074_G	1170	9.773439	19.91	2064	35.29	3	7.898757532	0.213	0.985003927	4

optimal_loci_172112_G	1386	9.32077	28.64	15084	39.75	2	8.802834527	0.131	0.987261089	2
optimal_loci_172219_G	1000	3.067724	0	4936	47.1	1	24.08918624	0.516	0.99166625	1
optimal_loci_172493_G	1381	0.936547	0	12465	38.66	1	6.771211744	0.077	0.992873998	2
optimal_loci_172513_G	1224	0.843439	0	1001	38.88	9	14.0691662	0.037	0.990852903	4
optimal_loci_172554_G	1433	4.613844	26.52	3461	36.35	2	0.798344746	0.053	0.987955425	3
optimal_loci_172571_G	1165	5.09895	27.64	3157	33.9	3	26.98090145	0.071	0.987030371	4
optimal_loci_172640_G	1186	7.302241	36.76	3756	34.73	5	15.18607302	0.018	0.983019189	3
optimal_loci_172656_G	1065	9.779606	4.98	4629	35.68	4	3.322894587	0.09	0.981743021	5
optimal_loci_172761_G	1012	8.009054	0	2158	52.96	7	10.1759304	0.544	0.977934252	4
optimal_loci_172777_G	1983	6.635119	10.74	3643	58.44	4	3.211410773	0.526	0.977278495	5
optimal_loci_172794_G	1121	6.711555	0	1664	43.62	4	3.723336365	0.28	0.977105601	5
optimal_loci_172865_G	1867	4.240066	39.53	2256	51.68	3	5.618866336	0.682	0.972977322	5
optimal_loci_172937_G	1204	4.180058	0	15773	28.57	2	16.39890078	0.211	0.969066295	5
optimal_loci_172938_G	1938	4.347428	35.86	1001	43.08	1	11.47441612	0.393	0.968620098	5
optimal_loci_172953_G	1631	3.68488	25.87	2558	39.23	4	0.991771548	0.299	0.967527322	4
optimal_loci_172954_G	1452	3.68488	0	1001	36.22	4	0.991771548	0.085	0.967512102	4
optimal_loci_173048_G	1595	5.026511	0	5166	54.54	2	0.025738296	0.613	0.961069863	4
optimal_loci_173102_G	1115	6.99211	0	9440	41.25	2	0.219278982	0.427	0.95950132	5
optimal_loci_173125_G	1283	8.0016	20.97	4379	38.81	4	6.232105487	0.217	0.957975982	6
optimal_loci_173131_G	1053	8.0016	0	1227	41.88	4	8.201090107	0.395	0.957900587	6
optimal_loci_173187_G	1025	9.288736	4.59	11451	44.48	4	2.009885071	0.362	0.954714008	8
optimal_loci_173208_G	1195	8.702383	8.54	2001	40.66	4	3.481360161	0.33	0.953494829	7
optimal_loci_173220_G	1705	7.78034	0	6845	57	1	30.06807843	0.565	0.951994624	5
optimal_loci_173223_G	1403	7.78034	10.55	3353	63.15	3	10.36760993	0.702	0.951865044	5
optimal_loci_173224_G	1659	7.642499	3.19	5004	44.9	4	8.0924746	0.245	0.951846403	5
optimal_loci_173336_G	1001	4.716414	35.06	2001	28.47	3	10.86697229	0.123	0.946836628	6
optimal_loci_173344_G	2561	4.555051	0	1001	35.92	1	8.633121241	0.113	0.946296334	6
optimal_loci_173358_G	1169	4.26967	8.98	3317	48.75	3	1.266826834	0.407	0.945525611	6
optimal_loci_173359_G	1153	4.26967	10.58	2001	45.44	3	1.266826834	0.237	0.945512747	6
optimal_loci_173389_G	1631	4.169173	0	2001	48.31	5	16.05679597	0.448	0.94233566	8
optimal_loci_173396_G	1078	4.169173	0	4978	42.94	5	22.81032319	0.486	0.942154223	8
optimal_loci_173455_G	1500	9.542767	0	1194	56.33	2	38.30289916	0.433	0.938356491	6
optimal_loci_173460_G	1096	9.281892	0	3911	38.95	5	5.187400961	0.256	0.93803738	6

optimal_loci_173533_G	2227	8.328142	0	3485	51.81	1	20.63512061	0.49	0.935393187	5
optimal_loci_173534_G	1354	8.328142	0	2001	56.79	1	20.63512061	0.691	0.93537868	5
optimal_loci_173599_G	1330	8.902126	0	17267	42.25	1	0.098716948	0.3	0.932130332	4
optimal_loci_173630_G	1838	4.365135	0	2862	33.13	5	7.093432544	0.216	0.929130371	4
optimal_loci_173679_G	1007	5.643601	35.35	18538	48.36	2	29.04903289	0.504	0.925474457	3
optimal_loci_173693_G	1544	4.394413	31.67	8938	52.91	3	15.35790833	0.598	0.924837752	4
optimal_loci_173764_G	1239	1.667895	11.95	15249	34.38	1	9.762941606	0.068	0.920240811	3
optimal_loci_173819_G	1269	0.785834	27.58	6160	39.95	3	0.01231343	0.204	0.916790743	2
optimal_loci_173990_G	1026	2.205733	11.79	1010	42.98	6	4.231808535	0.468	0.905952366	4
optimal_loci_174019_G	1526	2.543313	0	3679	57.86	3	8.249718743	0.54	0.903966276	7
optimal_loci_174020_G	2444	2.543313	9.29	5239	47.62	3	8.249718743	0.481	0.903942053	7
optimal_loci_174030_G	1127	2.85226	0	12742	34.25	1	6.858289605	0.125	0.903343773	7
optimal_loci_174085_G	1398	3.180409	9.16	3891	39.41	2	15.76079263	0.217	0.900205924	6
optimal_loci_174086_G	2325	3.100295	23.05	1459	52.98	3	21.18592479	0.521	0.900182151	6
optimal_loci_174088_G	1610	3.100295	4.72	1991	47.14	3	21.18592479	0.278	0.9000813	6
optimal_loci_174335_G	1802	3.249346	14.1	2507	58.37	1	12.32519884	0.563	0.884762893	10
optimal_loci_174338_G	2896	3.249346	0	12730	54.86	2	9.021054725	0.613	0.884652268	10
optimal_loci_174363_G	1579	3.354855	0	2665	44.83	1	4.337847196	0.369	0.883881046	10
optimal_loci_174367_G	1537	3.354855	0	2930	44.37	2	7.460225928	0.253	0.883793255	10
optimal_loci_174368_G	1008	3.354855	10.52	4571	52.97	2	7.460225928	0.363	0.883782385	10
optimal_loci_174369_G	1230	3.354855	26.5	5641	43.9	2	7.460225928	0.257	0.883769756	10
optimal_loci_174374_G	1667	3.530538	0	8187	51.22	2	7.460225928	0.585	0.8837135	10
optimal_loci_174389_G	2947	3.530538	0	1614	57.38	3	4.719294392	0.601	0.883446061	10
optimal_loci_174393_G	1784	3.530538	38.51	1122	29.65	4	1.165581067	0.043	0.883112825	10
optimal_loci_174450_G	1374	2.154936	11.57	2666	35.44	3	28.07562488	0.079	0.879877185	12
optimal_loci_174499_G	1230	1.257761	32.76	2544	49.34	2	7.500636276	0.36	0.877595249	3
optimal_loci_174513_G	1090	1.046931	0	12556	45.59	2	31.39283305	0.481	0.876225836	3
optimal_loci_174619_G	1086	1.59009	0	2417	44.38	3	24.82963616	0.328	0.869982864	6
optimal_loci_174632_G	1528	1.564432	10.8	2001	42.6	4	2.550924287	0.218	0.868982502	12
optimal_loci_174637_G	1794	1.564432	27.48	1384	39.85	4	2.550924287	0.161	0.868950714	12
optimal_loci_174676_G	1026	1.505423	0	2001	33.23	2	19.136425	0.033	0.866620274	17
optimal_loci_174680_G	1262	1.529207	0	3096	54.35	3	12.75761667	0.564	0.866528504	17
optimal_loci_174689_G	1726	1.587219	2.14	3236	52.08	5	13.90560453	0.578	0.865695347	17

optimal_loci_174696_G	1128	1.583348	6.29	1001	55.85	2	3.435104614	0.539	0.865082111	16
optimal_loci_174697_G	1185	1.583348	0	2528	52.15	2	3.435104614	0.494	0.865066628	16
optimal_loci_174698_G	1540	1.579285	16.43	1001	42.14	2	3.435104614	0.146	0.8650461	16
optimal_loci_174706_G	1191	1.570061	0	6063	56.08	2	3.435104614	0.549	0.864937849	16
optimal_loci_174709_G	1608	1.570061	18.84	8617	57.15	2	3.435104614	0.552	0.864908807	16
optimal_loci_174710_G	1348	1.570061	0	10360	41.02	2	3.435104614	0.209	0.864894311	16
optimal_loci_174735_G	3035	1.896131	22.08	1303	34	2	1.567391595	0.257	0.86288608	15
optimal_loci_174736_G	2105	1.896131	29.93	3454	37.9	2	695.3427454	0.329	0.862612522	15
optimal_loci_174747_G	1234	1.900519	0	8111	47.32	4	349.1356463	0.453	0.862235689	15
optimal_loci_174758_G	1000	1.902684	0	1586	54.5	2	8.425775413	0.611	0.862074624	15
optimal_loci_174762_G	1215	1.963324	5.93	2448	45.02	1	1.83839782	0.372	0.8618265	15
optimal_loci_174826_G	1725	1.074627	0	4693	47.65	2	2.436101851	0.439	0.858112903	8
optimal_loci_174916_G	1583	0.725959	4.86	1001	50.91	3	13.55872976	0.471	0.854932776	5
optimal_loci_174917_G	2538	0.595785	0	1001	48.34	3	13.55872976	0.334	0.85481957	5
optimal_loci_174953_G	1039	0.095117	9.82	2849	43.4	1	63.21839708	0.267	0.852549971	7
optimal_loci_174960_G	1157	0.095117	0	18922	41.05	1	63.21839708	0.293	0.852391701	7
optimal_loci_175022_G	1213	1.347953	0	5150	53.42	4	4.303597179	0.387	0.84891783	5
optimal_loci_175039_G	1157	1.336406	14.52	2001	38.37	5	32.1127383	0.279	0.84793738	5
optimal_loci_175041_G	1412	1.336406	15.65	5849	38.59	5	32.1127383	0.394	0.847897273	5
optimal_loci_175177_G	1425	0.680801	6.46	2001	46.59	2	142.5083478	0.331	0.840383744	1
optimal_loci_175265_G	1179	0.76231	36.13	2001	41.05	2	0.006219986	0.24	0.835353861	3
optimal_loci_175269_G	1092	0.76231	0	3166	37.45	2	0.006219986	0.111	0.835317634	3
optimal_loci_175271_G	1165	0.76231	0	1001	63.94	2	0.006219986	0.759	0.835296471	3
optimal_loci_175491_G	1053	1.13738	0	10137	42.26	1	0.353034289	0.147	0.822013881	5
optimal_loci_175514_G	1145	1.1237	0	1001	38.07	3	0.045623407	0.195	0.820393675	6
optimal_loci_175543_G	1518	1.011455	2.96	8573	43.93	2	13.60633797	0.253	0.818606109	6
optimal_loci_175546_G	1586	1.005172	1.89	6497	48.29	2	2.457125117	0.329	0.818446725	6
optimal_loci_175582_G	1256	1.183873	19.19	1001	46.33	2	7.571264774	0.526	0.817166989	7
optimal_loci_175599_G	1086	1.244657	0	11784	39.5	1	176.1773509	0	0.816389765	6
optimal_loci_175636_G	1298	0.956283	13.64	1131	43.52	4	24.89053453	0.294	0.813007918	3
optimal_loci_175817_G	1205	0.551024	0	2001	33.77	3	30.38418682	0.178	0.80537741	3
optimal_loci_175820_G	1277	0.555395	11.75	5138	36.57	3	30.38418682	0.303	0.80534219	3
optimal_loci_175846_G	1723	0.795453	29.77	4787	38.07	1	28.46033469	0.244	0.803469589	3

optimal_loci_175995_G	1129	0.612412	0	1423	35.34	3	3.707452088	0.235	0.796574829	3
optimal_loci_176011_G	2269	0.388766	0	1224	44.2	3	5.015633461	0.392	0.795525455	3
optimal_loci_176023_G	1272	0.389206	0	2482	30.18	4	20.52662264	0	0.794919629	3
optimal_loci_176218_G	1860	0.27253	35.22	18233	40.32	1	1.139169813	0.124	0.784762033	2
optimal_loci_176247_G	2467	0.225186	0	2001	31.25	1	17.38817192	0.166	0.783988192	2
optimal_loci_176374_G	1465	0.421733	0	5147	42.45	2	17.33234536	0.438	0.778728778	3
optimal_loci_176403_G	1302	0.638094	2.46	11980	59.83	1	6.663940964	0.66	0.777358152	3
optimal_loci_176454_G	1473	0.663957	0	3225	41.81	4	7.511682107	0.336	0.775136207	4
optimal_loci_176562_G	1109	1.058175	0	6107	36.51	3	1.238357651	0.156	0.770517586	4
optimal_loci_176592_G	1218	0.729989	0	2049	40.31	1	0.156849718	0.175	0.769590782	3
optimal_loci_176656_G	1167	0.690767	29.99	3987	44.47	4	21.86422654	0.212	0.766521339	3
optimal_loci_176815_G	1130	0.012134	0	18449	42.83	1	17.31552686	0.178	0.758630518	2
optimal_loci_176826_G	1361	0.012631	31.52	1512	33.65	3	10.75716443	0.099	0.758258631	2
optimal_loci_177360_G	1258	0.107686	4.05	1756	42.84	1	22.11659613	0.204	0.728525797	6
optimal_loci_177364_G	2471	0.107686	18.7	6248	48.88	1	22.11659613	0.389	0.728470029	6
optimal_loci_177462_G	1171	0.111411	2.48	6732	38.85	1	7.098794566	0.119	0.725121251	6
optimal_loci_177464_G	1276	0.111411	0	11115	41.14	1	7.098794566	0.255	0.72507738	6
optimal_loci_177465_G	2482	0.111411	6.73	12424	60.95	1	7.098794566	0.715	0.725052796	6
optimal_loci_177471_G	1035	0.115991	0	3780	30.91	3	15.88263972	0.053	0.724427038	7
optimal_loci_177554_G	1125	0.115496	6.13	11543	41.51	1	13.35447792	0.045	0.720153304	7
optimal_loci_177564_G	1477	0.107595	20.92	14624	36.15	1	22.63768656	0.202	0.719479365	6
optimal_loci_177641_G	1345	0.072773	11.6	1871	39.62	1	7.379036728	0.275	0.716006305	6
optimal_loci_177647_G	1013	0.072773	0	8251	42.94	1	7.379036728	0.223	0.715882297	6
optimal_loci_177648_G	1145	0.072773	14.41	9307	40.34	1	7.379036728	0.325	0.715870684	6
optimal_loci_177649_G	1283	0.072773	0	10485	40.29	1	7.379036728	0.143	0.71585782	6
optimal_loci_178120_G	1112	0.29798	32.1	13207	31.29	1	0.733778415	0.126	0.691499492	6
optimal_loci_178129_G	1208	0.280192	5.71	12859	46.27	2	42.18723981	0.239	0.690809521	6
optimal_loci_178170_G	1882	0.226911	15.3	4710	44.42	1	24.83013804	0.411	0.688810147	7
optimal_loci_178172_G	1005	0.217121	18.21	6924	38.9	1	24.83013804	0.085	0.688797077	7
optimal_loci_178199_G	1486	0.215407	0	3026	44.07	2	16.19483704	0.392	0.688387654	7
optimal_loci_178230_G	1131	0.209494	35.63	2993	34.74	1	1.141237502	0.235	0.687644858	7
optimal_loci_178298_G	1053	0.175451	0	1362	41.88	2	2.082857241	0.257	0.684745396	6
optimal_loci_178311_G	1036	0.195858	0	25590	50.28	1	4.858256996	0.575	0.682647654	3

optimal_loci_178388_G	1373	0.250388	23.16	2655	40.71	2	5.124616433	0.106	0.678675934	2
optimal_loci_178513_G	1121	0.326429	18.02	12880	43.8	1	0.380599041	0.593	0.671931896	1
optimal_loci_178978_G	1250	1.327903	9.92	4654	53.36	1	0.531750712	0.761	0.650268231	1
optimal_loci_179377_G	1056	0.012112	0	1001	40.24	2	32.7910287	0.17	0.629290841	2
optimal_loci_179383_G	1248	0.012112	0	11977	37.17	2	32.7910287	0.052	0.629030567	2
optimal_loci_179499_G	1591	0.020752	7.17	1810	38.96	1	26.48594165	0.261	0.623821153	1
optimal_loci_179635_G	1415	0.021961	0	1001	42.61	1	47.02240083	0.064	0.614327067	2
optimal_loci_179731_G	1228	0.022316	31.51	2625	29.8	2	0.947874871	0.166	0.609543822	3
optimal_loci_179775_G	1020	0.023427	0	3443	36.27	1	28.00873719	0	0.60669173	2
optimal_loci_179884_G	2028	0.022752	4.24	8015	34.02	3	0.013307576	0.209	0.599767889	1
optimal_loci_179978_G	1309	0.013432	0	2001	40.18	1	18.44632713	0.279	0.593821359	3
optimal_loci_179997_G	1021	0.023001	3.13	2749	38.58	1	2.718160805	0.142	0.591467107	5
optimal_loci_179998_G	1260	0.021238	10.16	13897	46.9	1	27.30605067	0.404	0.591277058	6
optimal_loci_180080_G	1192	0.010634	0	1755	44.29	1	0.040195564	0.33	0.587182141	5
optimal_loci_180081_G	1230	0.010634	0	3076	59.02	1	0.040195564	0.666	0.587168856	5
optimal_loci_180086_G	2780	0.012352	8.13	2081	56.33	2	26.12993987	0.627	0.586531769	4
optimal_loci_180179_G	3100	0.485886	0	18345	58.45	1	19.45980698	0.615	0.581158739	2
optimal_loci_180190_G	1639	0.485886	2.99	2001	38.49	1	19.45980698	0.141	0.580998974	2
optimal_loci_180774_G	1544	0.139227	8.55	2679	38.4	2	2.463830844	0.092	0.542831808	1
optimal_loci_180888_G	1091	0.121812	0	3249	42.89	1	214.418926	0.15	0.534940616	1
optimal_loci_181036_G	1870	0.156667	38.29	4395	35.77	1	29.66248883	0.118	0.527326696	2
optimal_loci_181114_G	1726	0.121119	0	2382	45.3	1	0.79586752	0.366	0.522642659	3
optimal_loci_181147_G	2292	0.115107	0	2001	52.83	1	0.326483438	0.486	0.519466598	2
optimal_loci_181259_G	1451	0.032512	0	3961	56.71	2	1.082034062	0.58	0.512834653	1
optimal_loci_181590_G	1189	0.163615	13.54	6926	43.98	1	195.7226469	0.22	0.493042962	2
optimal_loci_181591_G	1178	0.176009	0	5640	41.08	1	195.7226469	0.178	0.493030391	2
optimal_loci_181751_G	1006	0.234684	0	2689	45.82	2	8.262507091	0.52	0.48182696	2
optimal_loci_181810_G	2534	0.178362	7.42	2122	49.92	1	34.17474517	0.446	0.477969384	4
optimal_loci_181825_G	1752	0.121903	0	1449	34.18	2	0.176909489	0.09	0.47681913	3
optimal_loci_181873_G	1118	0.040227	0	2001	49.1	1	20.11741708	0.518	0.47307522	4
optimal_loci_181916_G	1521	0.028369	5.52	6459	60.02	2	66.30038607	0.723	0.470308074	3
optimal_loci_181950_G	1473	0.027454	30.55	3476	35.91	2	0.457529484	0.153	0.467414457	2
optimal_loci_182110_G	2762	0.025639	0	15773	35.11	1	6.110706755	0.078	0.46041697	1

optimal_loci_182673_G	1011	0.163782	10.88	19813	48.66	1	4.313974662	0.491	0.425933421	2
optimal_loci_182684_G	2022	0.163782	2.82	2189	44.75	1	40.55541666	0.255	0.425625973	2
optimal_loci_182869_G	1579	0.339379	1.96	1001	36.73	1	1.332147884	0.132	0.41213868	4
optimal_loci_182884_G	2591	0.33961	0	3900	46.46	1	5.867454045	0.32	0.411082414	4
optimal_loci_182885_G	1270	0.33961	0	2532	42.99	1	5.867454045	0.08	0.411069042	4
optimal_loci_182924_G	1457	0.184202	36.86	2760	38.84	1	21.52004084	0.184	0.408427879	6
optimal_loci_182953_G	1436	0.158024	2.09	1001	42.89	1	29.1648112	0.391	0.405562424	3
optimal_loci_182959_G	1015	0.15405	0	9218	38.02	1	3.610682471	0.268	0.40431477	3
optimal_loci_183137_G	1813	0.167639	39.82	3829	36.56	2	13.78164832	0.046	0.391397273	2
optimal_loci_183198_G	1144	0.193846	37.41	2188	34.7	3	0.612665122	0	0.387135445	2
optimal_loci_183636_G	1687	0.910168	23.18	15262	39.83	1	10.16141817	0.162	0.354773812	1
optimal_loci_184065_G	2590	0.45162	22.05	1001	36.91	2	19.74693642	0.182	0.316029511	2
optimal_loci_184092_G	1472	0.532986	14.06	12588	35.66	1	0.377215939	0.205	0.313923969	2
optimal_loci_184485_G	1619	0.067131	14.89	10643	52.31	2	60.06002071	0.547	0.28957218	5
optimal_loci_184486_G	3398	0.067131	7.92	7212	40.96	3	50.26225106	0.277	0.289538641	5
optimal_loci_184489_G	1253	0.067131	0	2970	35.43	3	50.26225106	0	0.289497175	5
optimal_loci_184523_G	1713	0.062831	3.91	2001	34.73	4	28.90161842	0.104	0.286084272	5
optimal_loci_184530_G	2003	0.062831	9.49	12485	43.13	1	2.596425841	0.326	0.285323558	5
optimal_loci_184746_G	2593	2.312398	1.81	1141	46.23	4	8.226437838	0.392	0.267700332	1
optimal_loci_184929_G	1192	0.216022	0	6395	54.53	3	2.807590431	0.539	0.253233607	3
optimal_loci_184936_G	1263	0.190403	6.02	2429	46.87	3	7.938515853	0.433	0.252830098	3
optimal_loci_184969_G	1191	0.252401	12.26	1245	37.53	1	1.059832639	0.092	0.249933245	3
optimal_loci_185181_G	1466	0.088905	0	2207	58.66	2	22.63873569	0.66	0.23368958	3
optimal_loci_185183_G	1999	0.088905	0	5573	36.16	2	22.63873569	0.136	0.233651466	3
optimal_loci_185230_G	1689	0.128571	0	2001	34.51	2	8.262524263	0.03	0.230009218	3
optimal_loci_185386_G	1277	0.127124	0	6369	51.05	2	33.98612781	0.535	0.219438025	2
optimal_loci_185454_G	1085	0.140354	5.25	2245	38.15	1	13.12114406	0.207	0.215334761	3
optimal_loci_185506_G	1488	0.158068	6.59	9501	47.78	1	11.09802151	0.398	0.213510821	4
optimal_loci_185582_G	1347	0.550341	0	3369	47.29	2	17.65426497	0.295	0.209920938	3
optimal_loci_185589_G	1230	0.550341	0	4888	33.49	1	22.51014442	0.22	0.209757077	3
optimal_loci_186110_G	2323	0.137029	8.27	2001	41.15	3	3.894832413	0.185	0.180278807	1
optimal_loci_186270_G	1137	0.013666	0	2131	54	1	0.048871315	0.527	0.168377292	2
optimal_loci_186304_G	1695	0.01084	11.09	2204	43.3	2	13.53415751	0.242	0.166767947	2

optimal_loci_186646_G	1739	0.628406	0	1001	55.72	3	8.57254153	0.53	0.148492229	1
optimal_loci_186743_G	1228	0.217116	6.03	8237	32.24	2	0.291898589	0.276	0.140624223	1
optimal_loci_186956_G	1069	0.094783	10.85	1869	38.82	1	0.290291838	0.095	0.130004242	1
optimal_loci_187078_G	2361	0.012266	0	3870	57.72	3	4.056981883	0.631	0.123064154	1
optimal_loci_187450_G	1666	0.361464	1.74	2411	34.75	2	20.38733942	0.119	0.097157263	4
optimal_loci_187451_G	1093	0.361464	0	5161	34.94	2	20.38733942	0.161	0.097135982	4
optimal_loci_187455_G	1139	0.361464	0	2792	32.39	2	20.38733942	0.09	0.097104262	4
optimal_loci_187512_G	1351	0.316739	23.09	12541	44.18	2	180.2383542	0.244	0.092940489	4
optimal_loci_187687_G	1521	0.132719	25.64	2905	34.31	3	1.805149137	0.081	0.082750342	1
optimal_loci_191534_G	1629	0.05168	0	13009	38.18	3	0.209746659	0.246	0.13825083	1
optimal_loci_192637_G	2054	0.043001	2.09	7257	57.83	1	2.23689201	0.635	0.205763975	2
optimal_loci_192638_G	1092	0.043001	18.13	6053	36.81	1	2.23689201	0.209	0.205783906	2
optimal_loci_194905_G	1074	0.283729	0	3356	35.1	1	1.049104226	0.216	0.331454088	1
optimal_loci_195101_G	1153	0.41929	0	8409	41.8	2	0.204460297	0.231	0.342195427	6
optimal_loci_195112_G	3326	0.419187	8.45	14061	36.83	1	0.085293027	0.172	0.342435524	7
optimal_loci_195115_G	1300	0.415341	0	7967	36.61	1	0.085293027	0	0.342510243	7
optimal_loci_195117_G	1555	0.415341	0	5412	34.14	1	0.085293027	0.068	0.342531408	7
optimal_loci_195118_G	1121	0.415341	0	3834	33.89	1	0.085293027	0.131	0.342549922	7
optimal_loci_195119_G	1212	0.415341	15.35	2490	46.03	1	0.085293027	0.543	0.342561452	7
optimal_loci_195211_G	2197	0.193354	16.02	5405	48.74	5	20.62068273	0.475	0.34685707	6
optimal_loci_195885_G	1162	0.678756	0	15359	38.55	1	1.951820052	0.104	0.381040621	1
optimal_loci_196090_G	1451	0.912543	10.13	1040	42.1	2	1.111344212	0.286	0.38851556	3
optimal_loci_196093_G	1508	0.925224	29.31	9958	34.35	2	47.22927012	0	0.388635728	3
optimal_loci_196158_G	1000	1.163345	0	2125	52	3	3.241055057	0.442	0.391167345	4
optimal_loci_196240_G	2281	0.865371	6.18	8724	34.5	1	2.600510719	0.083	0.395686606	2
optimal_loci_196357_G	1192	0.141548	0	8830	49.91	1	0.808433092	0.345	0.401517032	2
optimal_loci_196360_G	1459	0.141548	5.35	2643	41.19	1	0.808433092	0.271	0.401571507	2
optimal_loci_196784_G	2011	0.773668	0	3760	34.51	2	0.024684805	0.099	0.42167305	6
optimal_loci_196799_G	1151	0.846075	0	4421	32.66	4	0.003821069	0.041	0.422390488	6
optimal_loci_196800_G	1627	0.846075	7.44	5140	34.72	4	0.003821069	0.073	0.422401383	6
optimal_loci_196803_G	1564	0.846075	8.44	2351	45.33	4	0.003821069	0.303	0.422427627	6
optimal_loci_196864_G	1412	0.910911	0	2212	41.71	1	40.429997	0.26	0.423739473	6
optimal_loci_196884_G	1054	0.960007	0	5505	38.33	1	5.262836943	0	0.425236185	6

optimal_loci_197223_G	1277	0.105199	32.26	2276	45.96	2	0.013284428	0.47	0.447183884	1
optimal_loci_197372_G	1081	0.165991	0	3057	43.2	1	97.18032461	0.428	0.455317037	3
optimal_loci_197377_G	1060	0.165991	7.26	2569	55.09	1	97.18032461	0.679	0.455422132	3
optimal_loci_197410_G	1356	0.15413	25.52	7267	33.7	2	239.3939186	0.098	0.457121757	3
optimal_loci_197574_G	1576	0.117958	0	2526	46.38	2	4.66170485	0.349	0.468154135	2
optimal_loci_197620_G	1453	0.114295	0	11525	42.67	1	20.7257088	0.327	0.471790176	3
optimal_loci_197700_G	1188	0.121064	0	2455	39.05	1	6.777956424	0.249	0.475065907	2
optimal_loci_198016_G	1076	0.112729	0	12749	35.87	2	19.43142885	0.164	0.492757161	2
optimal_loci_198027_G	1045	0.112729	0	3439	49.09	2	19.43142885	0.348	0.492843116	2
optimal_loci_198224_G	1210	0.411467	0	12013	41.65	1	27.77410267	0.195	0.501751523	3
optimal_loci_198225_G	1280	0.427413	7.34	2757	41.71	1	27.77410267	0.445	0.501836052	3
optimal_loci_198287_G	1039	0.23925	0	18284	44.46	1	31.29691316	0.361	0.505580087	3
optimal_loci_198387_G	1190	0.278298	0	6502	44.2	2	96.9243239	0.428	0.510821028	3
optimal_loci_198422_G	4126	0.271655	13.09	2315	50.77	2	10.38257277	0.431	0.512183337	4
optimal_loci_198424_G	1368	0.271818	7.09	7681	38.23	2	10.38257277	0.217	0.512232715	4
optimal_loci_198523_G	1043	0.298684	23.97	9645	42.28	1	1.876257861	0.164	0.516514851	5
optimal_loci_198567_G	1198	0.287714	0	9763	39.48	1	1.043855559	0.169	0.519399684	5
optimal_loci_198569_G	1507	0.287714	0	2180	51.16	1	1.043855559	0.325	0.519466619	5
optimal_loci_198591_G	1201	0.25106	0	4381	47.37	2	4.558938751	0.307	0.521377759	4
optimal_loci_198620_G	1058	0.424518	0	6536	47.25	2	0.168402765	0.431	0.523084459	6
optimal_loci_198700_G	1015	0.397251	0	11745	46.3	2	37.70460123	0.337	0.526434394	3
optimal_loci_198727_G	2061	0.379954	4.22	1621	34.54	4	3.105411679	0.104	0.527237447	3
optimal_loci_199079_G	1197	0.160896	0	1109	41.01	2	0.023434942	0.337	0.545949664	5
optimal_loci_199109_G	1154	0.874876	0	11539	46.53	2	2.352594614	0.285	0.548850195	5
optimal_loci_199110_G	1145	0.874876	3.23	10247	41.65	2	2.352594614	0.271	0.548862167	5
optimal_loci_199111_G	1950	0.874876	0	3659	52.46	3	2.845185658	0.404	0.548915381	5
optimal_loci_199118_G	1279	0.748865	0	2001	44.01	4	22.55093329	0.409	0.549292854	5
optimal_loci_199355_G	1216	1.585813	0	2472	43.17	1	10.80624466	0.479	0.560952123	4
optimal_loci_199360_G	1140	1.789354	0	4829	40.61	1	10.80624466	0.469	0.561043489	4
optimal_loci_199394_G	1361	1.744959	32.77	2698	50.99	1	16.5446122	0.478	0.561765693	4
optimal_loci_199396_G	2004	1.744959	0	2281	35.72	1	16.5446122	0	0.561827051	4
optimal_loci_199571_G	1172	0.150114	0	3062	45.05	2	7.973077424	0.164	0.570239226	2
optimal_loci_199583_G	3559	0.150114	0	6368	57.12	3	8.275172285	0.571	0.570371918	2

optimal_loci_199812_G	1400	0.426897	0	2439	40.64	2	5.08642522	0.24	0.583255329	2
optimal_loci_199880_G	1794	0.468627	0	1001	39.4	5	0.861589625	0.16	0.58632282	3
optimal_loci_199951_G	2460	0.532196	13.33	1657	40.08	1	8.132114844	0.211	0.588564198	2
optimal_loci_200139_G	1064	0.32318	20.49	1001	44.07	2	11.52571955	0.268	0.599533221	1
optimal_loci_200220_G	1460	0.343178	26.64	3580	45.27	1	2.989926986	0.415	0.605335066	2
optimal_loci_200253_G	3103	1.328926	22.66	2001	45.85	4	1.257887191	0.407	0.607476889	3
optimal_loci_200324_G	1386	1.126214	20.71	1001	46.82	4	7.510233022	0.401	0.612013725	3
optimal_loci_200335_G	1658	0.992052	27.93	4345	34.68	1	8.404693585	0.212	0.613362526	3
optimal_loci_200379_G	1653	0.147097	7.86	4233	47	1	21.34578674	0.505	0.616763256	2
optimal_loci_200497_G	1820	0.212214	9.12	2337	40.43	4	73.83760965	0.216	0.622782275	6
optimal_loci_200519_G	1283	0.236935	2.18	9952	48.4	1	88.18239482	0.372	0.623051984	6
optimal_loci_200531_G	1245	0.236935	0	6527	51.64	1	1.411477062	0.443	0.623744144	6
optimal_loci_200536_G	2072	0.238238	0	2001	55.83	1	1.411477062	0.608	0.623778182	6
optimal_loci_200537_G	1034	0.255878	37.81	1001	44.29	1	1.411477062	0.211	0.62384358	6
optimal_loci_200594_G	1031	0.407304	0	3737	35.79	3	0.079008988	0.219	0.62615297	7
optimal_loci_200728_G	1333	1.384854	13.5	1203	50.78	3	1.114789105	0.465	0.629964446	5
optimal_loci_200751_G	1257	1.507592	0	14006	35.24	2	0.015673868	0.049	0.630912502	4
optimal_loci_200759_G	2254	2.2351	0	9437	50.04	2	9.816223777	0.404	0.631742701	4
optimal_loci_200789_G	2931	1.177049	7.2	8825	41.89	2	3.599991705	0.378	0.633664505	5
optimal_loci_200835_G	1156	0.782404	0	5423	34.86	1	0.675021889	0.451	0.636390669	6
optimal_loci_200876_G	1161	1.404143	14.73	3682	42.46	3	3.481118403	0.307	0.638619947	5
optimal_loci_200929_G	1159	1.399572	12.68	2369	34.42	1	194.5931614	0.163	0.639911328	5
optimal_loci_200931_G	1907	1.399572	7.34	3854	35.86	1	194.5931614	0.273	0.639924992	5
optimal_loci_200944_G	1265	1.399572	0	6831	31.62	4	18.29918728	0.032	0.640601491	6
optimal_loci_201017_G	1917	0.58821	0	1982	36.98	2	1.370424275	0.054	0.644787495	4
optimal_loci_201044_G	1109	0.408574	36.25	2050	45.98	1	5.881357467	0.405	0.647335169	3
optimal_loci_201054_G	3004	0.345651	0	2181	32.62	1	9.360415398	0	0.648371242	4
optimal_loci_201123_G	1637	1.345463	29.75	17796	38.91	1	0.52531928	0.072	0.652691796	5
optimal_loci_201152_G	2106	1.293048	12.63	1955	59.35	1	9.376919617	0.584	0.654866516	4
optimal_loci_201194_G	1234	1.722705	0	10300	39.7	2	5.403762572	0.172	0.656745201	4
optimal_loci_201200_G	1478	1.722705	19.22	5107	35.92	1	8.718667709	0.143	0.656906271	4
optimal_loci_201386_G	1333	0.793124	7.43	6746	38.03	3	11.59078826	0.077	0.668791245	1
optimal_loci_201486_G	1495	1.137193	5.89	2291	45.55	4	1.421744451	0.245	0.675342477	1

optimal_loci_201553_G	1238	2.26057	0	2001	42.56	4	33.66411624	0.266	0.680404983	2
optimal_loci_201597_G	1213	1.369462	8.66	10276	55.39	3	15.7313361	0.523	0.683667141	4
optimal_loci_201690_G	1024	1.575339	13.87	3498	45.5	2	1.056963397	0.266	0.687097768	8
optimal_loci_201693_G	1294	1.456188	14.76	1334	52.24	2	1.056963397	0.291	0.687115196	8
optimal_loci_201729_G	1042	1.90295	0	2173	42.41	4	6.058433688	0.347	0.688793048	9
optimal_loci_201747_G	1315	2.242058	12.02	9077	47.98	1	6.271919391	0.581	0.689762886	9
optimal_loci_201748_G	1004	2.242058	0	8040	58.36	1	6.271919391	0.547	0.68977529	9
optimal_loci_201750_G	1196	2.242058	0	5754	50.16	1	6.271919391	0.389	0.689794559	9
optimal_loci_201784_G	2216	2.030037	0	3288	51.44	1	4.269727315	0.31	0.690898496	11
optimal_loci_201813_G	1006	2.272942	0	2001	45.32	2	4.482019124	0.379	0.692432062	9
optimal_loci_201819_G	1807	2.272942	0	1211	56.28	2	0.331176867	0.655	0.692630686	9
optimal_loci_201858_G	1646	2.739638	22.36	8389	34.69	2	4.64728989	0.147	0.694649276	5
optimal_loci_201863_G	1559	2.739638	25.66	5213	43.81	2	4.64728989	0.182	0.694679302	5
optimal_loci_201983_G	1361	1.149965	0	2001	57.75	1	3.686430848	0.552	0.702117646	6
optimal_loci_201994_G	1031	1.149965	25.22	2668	51.89	1	0.198013616	0.622	0.702432103	6
optimal_loci_201995_G	1118	1.149965	12.25	3839	42.75	1	0.198013616	0.233	0.702442879	6
optimal_loci_202012_G	1083	1.107999	36.2	6043	38.59	2	0.513261649	0.179	0.703278359	6
optimal_loci_202017_G	1879	1.107999	1.54	1801	54.76	4	2.172817992	0.567	0.703474544	6
optimal_loci_202022_G	1052	1.107999	0	1001	41.25	3	2.897090656	0.324	0.703567769	6
optimal_loci_202126_G	1154	0.939762	2.6	4416	31.62	1	4.041338556	0.17	0.708842748	11
optimal_loci_202127_G	1059	0.939762	0	3149	31.06	1	4.041338556	0.039	0.708855281	11
optimal_loci_202131_G	1362	0.985131	0	5764	37.15	1	4.041338556	0.173	0.708962483	11
optimal_loci_202140_G	3448	0.985131	6.93	14127	47.38	1	4.041338556	0.395	0.709039439	11
optimal_loci_202145_G	1577	0.985131	1.78	19350	31.95	1	0.146004044	0.112	0.709107055	11
optimal_loci_202158_G	1483	1.645007	23.2	12623	43.49	1	7.050557084	0.255	0.710386417	14
optimal_loci_202159_G	1420	1.645007	16.48	10838	39.22	1	7.050557084	0.326	0.710403423	14
optimal_loci_202164_G	2522	1.645007	6.19	3441	45.2	1	7.050557084	0.275	0.710559414	14
optimal_loci_202179_G	1523	2.334804	0	11818	39.13	1	10.29492625	0.249	0.711240016	16
optimal_loci_202180_G	2229	2.334804	13.01	9215	45.04	1	10.29492625	0.286	0.711257472	16
optimal_loci_202223_G	1591	2.503775	15.15	1608	37.52	2	37.20611384	0.261	0.713361254	17
optimal_loci_202236_G	1194	2.748502	31.57	1001	40.11	1	13.27927324	0.199	0.714061751	12
optimal_loci_202240_G	1152	2.748502	0	2001	46.26	3	10.58048318	0.406	0.714384776	12
optimal_loci_202250_G	1413	2.748502	0	1061	41.61	1	0.013158696	0.396	0.714775361	12

optimal_loci_202266_G	1636	3.144546	1.83	2001	55.07	5	16.2415291	0.56	0.715542351	9
optimal_loci_202267_G	1426	2.265017	11.08	3893	39.13	3	26.21447674	0.043	0.715687014	9
optimal_loci_202272_G	1235	2.38015	25.67	2940	39.51	3	5.704571352	0.114	0.716161963	7
optimal_loci_202457_G	1618	1.230933	17.37	6465	41.53	1	43.4842053	0.327	0.725965506	5
optimal_loci_202513_G	1425	3.91051	0	2564	49.54	4	25.16663021	0.392	0.729498366	10
optimal_loci_202514_G	1436	3.91051	3.13	4098	55.71	4	25.16663021	0.643	0.729512482	10
optimal_loci_202526_G	1222	3.91051	0	1001	48.85	3	17.32364188	0.468	0.729600508	10
optimal_loci_202528_G	1170	4.282038	32.65	3515	42.73	1	11.89297008	0.382	0.72966056	10
optimal_loci_202558_G	1917	4.314463	14.76	4484	52.58	4	11.11200819	0.487	0.73130431	10
optimal_loci_202593_G	1033	4.803676	6.78	3284	41.91	1	6.576916432	0.458	0.731638901	10
optimal_loci_202600_G	2093	4.798447	35.4	3187	44.67	2	3.676402883	0.343	0.73197882	10
optimal_loci_202616_G	1914	4.229378	1.62	2036	47.49	4	22.38224408	0.38	0.732684378	13
optimal_loci_202629_G	1345	4.256245	0	2001	42.52	2	3.66137274	0.157	0.733390332	13
optimal_loci_202653_G	2442	4.302276	17.53	3603	37.26	4	6.898027199	0.048	0.734782998	9
optimal_loci_202715_G	2455	2.010984	0	9609	47.16	2	8.874777299	0.416	0.737047372	6
optimal_loci_202718_G	1030	2.010984	27.67	13696	40.38	2	8.874777299	0.193	0.737107985	6
optimal_loci_202720_G	1177	1.95719	5.86	11635	46.81	2	8.874777299	0.45	0.737125598	6
optimal_loci_202819_G	1049	0.339244	3.62	2001	37.36	2	6.472732413	0.103	0.742472628	5
optimal_loci_202830_G	1321	0.338254	0	2145	47.53	2	0.161892458	0.252	0.742702483	5
optimal_loci_202854_G	1027	0.224173	0	18017	44.49	1	4.417031987	0.288	0.743820287	5
optimal_loci_202859_G	1087	0.224173	18.86	9279	48.94	1	4.417031987	0.349	0.743900142	5
optimal_loci_202888_G	1055	0.974037	31.85	2001	26.72	3	24.67443468	0.121	0.745784798	7
optimal_loci_202979_G	1313	1.130566	0	15468	50.03	1	46.17921307	0.502	0.750115843	5
optimal_loci_202987_G	1714	1.118046	0	1712	56.53	3	102.2507939	0.472	0.750343646	5
optimal_loci_203009_G	2084	1.350932	1.39	17100	51.58	2	0.153828795	0.528	0.752101666	6
optimal_loci_203012_G	1902	1.350932	0	1001	50.26	2	23.32836401	0.349	0.752305985	6
optimal_loci_203075_G	3826	0.763609	4.08	1001	52.87	4	6.314651272	0.382	0.756129985	6
optimal_loci_203081_G	2702	0.845474	4.89	4663	50.25	3	0.637291665	0.401	0.756261113	7
optimal_loci_203147_G	1900	0.966271	2.16	3655	44.84	1	0.51136178	0.224	0.760602952	12
optimal_loci_203149_G	1354	0.966271	0	6262	44.16	1	0.51136178	0.329	0.760626941	12
optimal_loci_203160_G	3490	0.987765	35.04	3012	47.24	2	5.142421817	0.326	0.760859152	11
optimal_loci_203172_G	1064	0.987765	11.28	3028	54.32	3	16.80217533	0.419	0.760979163	10
optimal_loci_203173_G	1879	0.987765	0	1001	54.12	3	16.80217533	0.507	0.760990316	10

optimal_loci_203174_G	1149	0.987765	17.75	1604	47.6	2	25.203263	0.42	0.761067842	11
optimal_loci_203182_G	1045	0.886879	0	1673	36.26	3	0.485867958	0.226	0.761801282	11
optimal_loci_203198_G	1060	0.724375	9.06	2516	45.84	4	8.882766102	0.389	0.763349709	11
optimal_loci_203199_G	1415	0.724375	12.23	2138	39.92	3	11.84368814	0.205	0.763369319	11
optimal_loci_203200_G	1990	0.724375	0	1001	57.13	3	11.84368814	0.489	0.763430098	11
optimal_loci_203239_G	1925	0.123734	15.84	2001	47.74	2	0.962696125	0.34	0.765669498	14
optimal_loci_203328_G	1417	0.142642	0	1467	54.19	2	0.141233349	0.628	0.769846281	9
optimal_loci_203330_G	1069	0.142642	16.65	7523	39	1	0.282466697	0.2	0.769980068	9
optimal_loci_203331_G	2760	0.142642	12.32	8625	37.17	1	0.282466697	0.239	0.769990209	9
optimal_loci_203332_G	1418	0.142642	0	11456	41.81	1	0.282466697	0.42	0.770016259	9
optimal_loci_203333_G	1023	0.142642	11.34	12962	37.82	1	0.282466697	0.244	0.770030118	9
optimal_loci_203335_G	1315	0.142642	0	15030	36.12	1	0.282466697	0	0.770049147	9
optimal_loci_203337_G	1512	0.142642	9.19	17065	36.11	1	0.282466697	0.037	0.770067873	9
optimal_loci_203339_G	1549	0.142642	3.1	18952	40.6	1	0.282466697	0.11	0.770085237	9
optimal_loci_203476_G	1471	1.775677	0	3594	39.42	2	4.623712889	0.182	0.777072787	8
optimal_loci_203488_G	1505	1.791077	10.63	2001	43.58	3	4.874015548	0.428	0.777872177	8
optimal_loci_203517_G	1211	1.90707	11.73	8193	57.88	1	2.166501508	0.631	0.779636831	8
optimal_loci_203521_G	2561	1.90707	0	12377	47.63	1	2.166501508	0.384	0.779675332	8
optimal_loci_203542_G	1293	1.957392	5.18	1226	36.96	3	27.71720621	0.09	0.781236302	10
optimal_loci_203545_G	3043	1.957392	0	2001	45.87	2	6.443581111	0.33	0.781372104	10
optimal_loci_203547_G	1230	1.957392	7.4	6201	53.49	1	3.969136079	0.413	0.781410752	10
optimal_loci_203550_G	1935	1.957392	0	9570	46.09	1	3.969136079	0.51	0.781441753	10
optimal_loci_203661_G	1929	1.698317	37.79	2665	45.72	1	3.251593275	0.401	0.785508464	11
optimal_loci_203668_G	1156	1.698317	6.83	8770	41.17	1	3.251593275	0.226	0.785564641	11
optimal_loci_203676_G	1833	1.698317	39.77	14593	47.19	1	0.526063791	0.304	0.786257372	8
optimal_loci_203686_G	3968	1.246423	7.43	11635	51.48	1	10.0579225	0.521	0.786669066	8
optimal_loci_203702_G	1792	0.704049	13.84	6308	38.5	2	17.25868013	0.182	0.787884209	8
optimal_loci_203704_G	3948	0.704049	1.7	2001	54.88	1	13.96843145	0.622	0.78801898	8
optimal_loci_203706_G	1189	0.706073	0	8565	37.17	2	6.984215723	0.241	0.788079382	8
optimal_loci_203772_G	1483	0.41744	8.83	3103	48.81	1	1.185166525	0.53	0.790740755	10
optimal_loci_203803_G	1770	0.47785	4.01	2368	40.28	2	22.11803098	0.444	0.793566032	9
optimal_loci_203810_G	2790	0.47785	0	7541	45.19	2	21.6906323	0.405	0.793861921	9
optimal_loci_203813_G	1172	0.47785	15.44	3382	40.1	1	1.414699578	0.094	0.794016347	9

optimal_loci_203827_G	2695	0.47785	20.37	4365	33.46	2	0.085751625	0.041	0.794601774	9
optimal_loci_203850_G	1949	0.47785	38.38	15089	46.63	1	37.57153767	0.336	0.795603966	8
optimal_loci_203853_G	1494	0.47785	0	11916	40.69	1	37.57153767	0.063	0.79563735	8
optimal_loci_203859_G	1343	0.47785	11.17	2561	33.87	1	37.57153767	0.037	0.795724824	8
optimal_loci_203867_G	1612	0.298052	0	7420	55.52	1	37.57153767	0.595	0.795838357	9
optimal_loci_203938_G	1165	0.451625	0	1001	53.56	1	9.157393558	0.386	0.800377108	5
optimal_loci_203953_G	1018	0.489219	7.47	2909	42.23	2	0.327162262	0.348	0.801074062	6
optimal_loci_204027_G	1517	0.924317	13.45	3691	34.8	1	0.87011381	0.092	0.804911644	8
optimal_loci_204028_G	2332	0.924317	20.63	1001	37.34	1	0.87011381	0.116	0.804928898	8
optimal_loci_204029_G	1575	0.972153	6.1	2001	38.98	1	0.87011381	0.038	0.804996587	7
optimal_loci_204053_G	1398	0.972153	0	8680	54.22	1	3.782119797	0.53	0.805641983	7
optimal_loci_204061_G	2621	0.972153	0	2259	47.53	1	3.782119797	0.416	0.805689815	6
optimal_loci_204093_G	1162	0.823062	0	11476	36.83	1	0.038517625	0.229	0.807207277	6
optimal_loci_204231_G	2163	1.329988	18.77	1358	40.96	5	8.009643437	0.264	0.814458803	7
optimal_loci_204244_G	1563	1.810688	5.82	2001	39.47	2	7.9592497	0.329	0.81511733	7
optimal_loci_204246_G	1906	1.810688	1.47	2202	52.57	2	7.9592497	0.488	0.815188066	7
optimal_loci_204260_G	3164	1.810688	0	6886	39.22	1	4.509288676	0.189	0.81600608	9
optimal_loci_204267_G	1160	1.810688	2.41	2031	53.96	4	1.594730189	0.422	0.816769758	9
optimal_loci_204292_G	1137	2.008872	13.9	3420	50.48	4	1.690378979	0.395	0.818987984	9
optimal_loci_204293_G	2119	2.008872	0	1688	49.36	4	1.690378979	0.424	0.819000315	9
optimal_loci_204304_G	2057	1.698251	5.79	3158	42.1	4	0.786788352	0.17	0.819906153	7
optimal_loci_204305_G	1385	1.698251	0	2925	39.63	4	0.786788352	0.325	0.819928486	7
optimal_loci_204363_G	1119	0.770134	0	1513	37.8	2	4.46019173	0.184	0.824365123	11
optimal_loci_204380_G	1110	0.848398	12.7	3271	52.34	1	11.15737429	0.358	0.824629126	9
optimal_loci_204400_G	1623	0.930211	1.91	2864	40.11	3	9.137081974	0.34	0.825181491	10
optimal_loci_204431_G	1560	0.948966	32.63	18669	35.76	1	1.306222297	0.198	0.82661597	11
optimal_loci_204442_G	1462	0.881452	2.94	2872	40.15	3	0.602020334	0.187	0.827457763	11
optimal_loci_204448_G	1079	0.858476	32.9	2001	40.12	4	2.779952182	0.31	0.827809166	11
optimal_loci_204453_G	1297	0.858476	2.54	4170	43.09	1	47.81292201	0.272	0.82817624	11
optimal_loci_204455_G	1031	0.858476	0	2001	58.97	2	31.14351895	0.607	0.828198647	11
optimal_loci_204461_G	1335	1.05233	3.45	1948	51.53	1	14.4741159	0.452	0.828465503	13
optimal_loci_204480_G	1864	1.090718	23.93	4114	57.99	2	6.129614113	0.62	0.829690427	11
optimal_loci_204491_G	1839	1.126698	25.12	2613	38.66	3	4.875293924	0.307	0.829956759	11

optimal_loci_204550_G	1143	1.200724	34.27	16398	36.92	1	3.835220607	0.09	0.832815568	7
optimal_loci_204555_G	1845	1.20243	0	11558	44.39	1	3.835220607	0.37	0.832853646	7
optimal_loci_204578_G	1948	0.924314	25.82	3303	35.42	2	6.727541419	0.208	0.834454211	6
optimal_loci_204612_G	4044	1.425558	1.93	2112	56.2	2	5.554639585	0.553	0.836613435	5
optimal_loci_204637_G	3213	1.323857	0	2874	52.38	1	0.598434408	0.515	0.838279297	6
optimal_loci_204726_G	4938	1.459479	31.75	11370	49.89	4	31.36805452	0.473	0.841661264	6
optimal_loci_204727_G	1220	1.459479	0	10093	42.04	4	31.36805452	0.252	0.841707228	6
optimal_loci_204729_G	1374	1.459479	0	7643	48.1	3	2.660155201	0.272	0.841728355	6
optimal_loci_204767_G	1363	1.277011	2.2	8197	42.62	3	5.960639714	0.152	0.843790315	6
optimal_loci_204800_G	1388	1.188513	0	8416	50.93	1	122.4374275	0.438	0.845757191	8
optimal_loci_204854_G	2373	2.472563	1.47	6179	51.62	2	5.03695566	0.645	0.84834228	6
optimal_loci_204855_G	1122	2.472563	0	1515	36.27	1	7.658571816	0.181	0.848472929	5
optimal_loci_204904_G	1295	2.090612	3.17	1035	40.54	2	1.876760159	0.293	0.850345245	7
optimal_loci_204917_G	1466	2.078275	26.81	2001	39.69	1	0.056133324	0.226	0.851118134	7
optimal_loci_204969_G	1205	2.463743	0	4458	38.25	1	10.80876262	0.085	0.853746656	10
optimal_loci_204991_G	1806	1.107412	6.64	14876	33.88	1	26.07699669	0.215	0.855717921	9
optimal_loci_205028_G	1116	1.107412	32.89	2001	35.66	4	11.91484622	0.194	0.856618348	8
optimal_loci_205043_G	1050	1.257825	5.9	2352	33.8	1	4.665454171	0.118	0.857538219	8
optimal_loci_205044_G	1039	1.257825	0	1193	45.9	1	4.665454171	0.256	0.857548986	8
optimal_loci_205047_G	1883	1.257825	15.14	4120	42.85	2	2.482012998	0.282	0.857624487	8
optimal_loci_205050_G	1825	1.257825	14.19	1759	54.3	2	2.482012998	0.382	0.857735674	8
optimal_loci_205132_G	1126	0.901441	0	4648	37.03	1	223.7403057	0.054	0.863420213	5
optimal_loci_205133_G	1323	0.901441	7.94	2391	39.98	1	223.7403057	0.123	0.863439169	5
optimal_loci_205136_G	1292	0.901441	0	2116	48.29	1	223.7403057	0.363	0.863537887	5
optimal_loci_205142_G	1827	0.901441	0	1393	44.71	2	0.046265242	0.33	0.864117057	5
optimal_loci_205145_G	1631	0.887633	0	3731	38.74	1	0.092530484	0.205	0.864193249	5
optimal_loci_205239_G	1565	2.736545	17.64	12512	42.74	1	5.36045474	0.308	0.870342512	4
optimal_loci_205268_G	1081	4.007577	0	3066	42.92	2	7.397621315	0.308	0.871827888	4
optimal_loci_205276_G	1254	4.007577	37.64	9786	35.24	1	52.94366576	0.04	0.872297204	4
optimal_loci_205293_G	1037	4.365962	7.23	2001	55.15	4	33.83836196	0.754	0.873086399	5
optimal_loci_205343_G	1212	6.171158	0	7281	45.29	5	0.864069217	0.287	0.877302447	4
optimal_loci_205423_G	1326	6.703742	11.39	3268	40.19	2	17.35396886	0.25	0.879980733	5
optimal_loci_205453_G	2246	5.927539	3.25	2001	53.02	2	12.95569707	0.493	0.88187946	8

optimal_loci_205474_G	1895	6.400222	16.09	2503	50.39	3	35.14553124	0.408	0.882859861	9
optimal_loci_205496_G	1571	6.655608	0	7589	57.54	3	5.48386164	0.73	0.884225087	13
optimal_loci_205563_G	1282	7.049948	15.68	2534	36.42	2	0.116424673	0.064	0.886232414	14
optimal_loci_205574_G	1247	6.762664	28.47	2193	33.68	2	7.407838359	0.086	0.886431829	14
optimal_loci_205576_G	1110	6.736451	15.05	2001	51.26	2	7.407838359	0.488	0.886500034	14
optimal_loci_205578_G	1437	6.736451	0	2345	40.77	2	7.407838359	0.333	0.886517499	13
optimal_loci_205579_G	2511	6.763297	0	1001	43.92	4	10.35620596	0.295	0.88665113	15
optimal_loci_205629_G	1166	5.449158	3	2132	40.65	4	60.22253411	0.15	0.888280976	16
optimal_loci_205637_G	1080	5.695731	4.35	1001	52.68	2	120.4450682	0.397	0.888396175	16
optimal_loci_205642_G	1170	5.445189	2.48	3348	40.51	3	18.37968788	0.124	0.888653543	17
optimal_loci_205643_G	1706	5.445189	1.88	1567	58.32	3	18.37968788	0.465	0.888665	17
optimal_loci_205657_G	1016	5.493787	0	6374	56.39	2	0.898820066	0.509	0.889129651	16
optimal_loci_205661_G	2362	5.493787	19.05	1598	47.03	2	0.898820066	0.432	0.889161214	16
optimal_loci_205683_G	1170	4.739728	0	1001	50.08	5	1.67187047	0.377	0.891178507	14
optimal_loci_205684_G	1515	4.739728	7.72	2223	41.12	4	2.089838088	0.24	0.891189752	14
optimal_loci_205692_G	1618	3.861749	0	6068	45.85	1	7.462795998	0.305	0.892211608	16
optimal_loci_205693_G	1975	3.861749	17.11	7719	43.44	1	7.462795998	0.407	0.8922268	16
optimal_loci_205706_G	1948	3.604223	2.93	3806	39.16	1	2.645777844	0.207	0.893191521	15
optimal_loci_205744_G	1907	3.558513	0	1001	61.24	2	1.249140088	0.7	0.895173267	14
optimal_loci_205745_G	1360	3.558513	0	2001	44.55	2	1.249140088	0.344	0.895225985	14
optimal_loci_205761_G	1007	3.462435	4.97	2001	43.89	4	14.03620547	0.344	0.895944601	12
optimal_loci_205766_G	1006	3.525275	6.46	1576	38.56	4	14.03620547	0	0.895995469	12
optimal_loci_205775_G	3729	3.525275	9.81	8997	58.86	4	13.66318173	0.584	0.896280683	12
optimal_loci_205795_G	1874	3.462648	0	3207	52.13	3	231.1515294	0.447	0.897391273	13
optimal_loci_205826_G	1330	4.054678	27.74	1001	30.67	4	64.52104508	0.159	0.899107212	12
optimal_loci_205827_G	1939	4.054678	16.04	2001	45.84	2	42.6972966	0.416	0.899186956	12
optimal_loci_205831_G	1537	4.054678	0	1394	53.8	2	42.6972966	0.465	0.899284745	12
optimal_loci_205867_G	2237	4.285543	10.68	9773	41.17	2	7.824223977	0.254	0.901082977	8
optimal_loci_205869_G	1731	4.285543	0	7263	60.25	2	7.824223977	0.614	0.90111073	8
optimal_loci_205873_G	1744	4.293883	0	2734	37.09	2	7.824223977	0.123	0.901152286	8
optimal_loci_205987_G	2932	3.411791	0	1847	57.7	3	9.664670144	0.53	0.904551626	6
optimal_loci_205998_G	1653	6.134124	0	6011	43.19	2	4.917973405	0.261	0.906126951	6
optimal_loci_206017_G	1221	6.287112	31.12	1013	36.11	4	2.690070125	0.096	0.908121681	10

optimal_loci_206062_G	2087	5.513891	1.72	2529	48.49	3	5.364206168	0.349	0.910045041	12
optimal_loci_206072_G	1128	5.184591	0	2164	51.5	3	30.7568263	0.399	0.910618192	12
optimal_loci_206075_G	2036	4.620298	0	2001	46.95	4	23.07092851	0.247	0.910699841	12
optimal_loci_206111_G	2233	6.94875	0	1001	36.67	3	10.76691185	0.139	0.912335705	11
optimal_loci_206112_G	1081	6.94875	0	2099	46.8	3	10.76691185	0.261	0.912399676	11
optimal_loci_206113_G	1788	6.94875	10.07	4743	37.13	3	10.76691185	0.098	0.912424006	11
optimal_loci_206117_G	1113	6.94875	11.68	3611	42.58	4	13.75201614	0.284	0.912490527	11
optimal_loci_206130_G	1761	7.537268	0	1782	49.68	1	3.884076875	0.598	0.913121614	11
optimal_loci_206146_G	1161	6.78703	4.31	4018	45.04	2	8.383856579	0.425	0.91422556	14
optimal_loci_206150_G	1192	6.342049	3.02	2562	53.43	2	8.383856579	0.61	0.914379527	14
optimal_loci_206222_G	1830	4.103012	24.04	3114	47.15	3	2.314429755	0.457	0.917617898	8
optimal_loci_206231_G	1904	4.014605	0	1531	46.95	1	6.085419372	0.286	0.918259493	8
optimal_loci_206243_G	1480	4.014605	25.41	10486	50.33	1	6.085419372	0.487	0.918341896	8
optimal_loci_206245_G	1915	4.014605	35.3	12629	38.17	1	6.085419372	0.126	0.918361616	8
optimal_loci_206277_G	1112	3.952644	20.32	8195	38.84	2	20.52669003	0.365	0.919815089	6
optimal_loci_206337_G	1337	2.625117	5.68	1001	58.71	1	5.194680637	0.767	0.922653893	9
optimal_loci_206366_G	1667	3.453412	5.22	2871	43.79	5	22.2235948	0.287	0.92495249	5
optimal_loci_206371_G	1122	3.453412	5.07	2063	55.25	5	14.60265071	0.475	0.92502928	5
optimal_loci_206376_G	1290	3.453412	0	3260	47.51	3	21.28393624	0.325	0.925131209	5
optimal_loci_206383_G	1444	3.474885	11.29	2278	36.63	1	0.64912643	0.277	0.925317917	5
optimal_loci_206477_G	1779	4.468436	0	3605	47.55	6	8.70728771	0.489	0.930192197	9
optimal_loci_206488_G	1541	5.265215	0	4671	52.17	2	23.8962544	0.49	0.931388273	9
optimal_loci_206511_G	1531	5.265215	19.79	5684	41.34	2	11.83338132	0.356	0.932108858	9
optimal_loci_206512_G	1337	5.265215	0	4203	38.51	1	5.921318351	0.222	0.932124271	9
optimal_loci_206522_G	1447	5.166015	0	2412	41.18	3	31.61388228	0.302	0.933084622	12
optimal_loci_206564_G	1062	4.816518	25.99	1457	44.35	5	9.296374676	0.38	0.934346151	17
optimal_loci_206567_G	1133	4.816518	6	2680	52.16	5	17.85295235	0.466	0.934530604	17
optimal_loci_206570_G	2134	4.816518	0	3314	48.59	5	17.85295235	0.367	0.934630914	17
optimal_loci_206572_G	1297	4.816518	0	3416	51.34	4	21.27488003	0.336	0.934656606	17
optimal_loci_206608_G	1712	5.452764	2.16	6194	43.04	1	14.62278127	0.254	0.93717718	17
optimal_loci_206616_G	1862	5.624144	5.75	2001	46.24	1	1.147670134	0.274	0.937400971	19
optimal_loci_206621_G	2930	5.624144	11.98	5688	43.34	1	1.147670134	0.288	0.937524351	19
optimal_loci_206636_G	2033	6.995374	18.1	14141	45.49	4	0.019756421	0.324	0.938227341	18

optimal_loci_206640_G	1297	7.132876	7.09	7439	46.26	3	0.026341895	0.264	0.938295785	18
optimal_loci_206641_G	2530	7.132876	37.35	4797	38.77	3	0.026341895	0.082	0.938308751	18
optimal_loci_206653_G	1167	7.368363	0	2134	45.67	4	13.64476912	0.25	0.938606829	18
optimal_loci_206654_G	2374	7.323095	21.27	2001	34.83	3	18.1666836	0.06	0.938702308	18
optimal_loci_206673_G	2091	6.510909	5.83	2148	33.33	4	0.158454659	0.128	0.939478049	16
optimal_loci_206682_G	1055	6.510909	0	1001	32.98	1	6.529605762	0.083	0.940007979	16
optimal_loci_206705_G	1413	8.713109	0	16692	36.58	2	14.60505443	0.188	0.941076627	16
optimal_loci_206713_G	1072	8.586637	0	2232	56.43	3	12.20210996	0.353	0.941667234	17
optimal_loci_206718_G	1837	8.349983	4.08	2001	54.76	2	3.929952964	0.518	0.941843507	16
optimal_loci_206719_G	1747	8.349983	0	3871	54.49	2	3.929952964	0.525	0.941860714	16
optimal_loci_206771_G	1602	8.088671	0	4990	57.17	4	1.177050277	0.735	0.943481745	13
optimal_loci_206774_G	1410	8.016082	3.55	3949	36.87	2	2.354100555	0.387	0.943629141	13
optimal_loci_206852_G	1436	6.950288	0	4253	36.83	2	12.36513864	0.239	0.946274052	13
optimal_loci_206867_G	1236	5.064047	14.64	17847	44.41	1	5.106629622	0.22	0.947297205	10
optimal_loci_206875_G	1595	5.372976	13.29	5455	45.14	2	28.11815731	0.359	0.947407932	10
optimal_loci_206876_G	1256	5.372976	10.59	3701	50	3	19.27733664	0.425	0.947427192	10
optimal_loci_206891_G	1193	5.523011	4.95	8878	61.44	5	7.658588491	0.524	0.947982988	10
optimal_loci_206931_G	1130	5.47426	18.14	2034	37.87	4	14.75137598	0.115	0.949223372	10
optimal_loci_206934_G	1571	5.538371	8.85	4263	40.29	4	14.75137598	0.235	0.949316495	12
optimal_loci_206994_G	1130	3.5065	0	1001	57.61	1	5.252675917	0.531	0.950766029	13
optimal_loci_207048_G	1010	5.92464	0	2014	50.39	2	7.500590404	0.679	0.95321147	13
optimal_loci_207049_G	1127	5.982208	0	3057	47.29	1	15.00118081	0.395	0.953221068	13
optimal_loci_207052_G	1310	7.420276	0	2532	53.2	2	17.52092248	0.702	0.953906639	12
optimal_loci_207053_G	1438	7.420276	1.95	1001	49.09	2	17.52092248	0.287	0.953919549	12
optimal_loci_207074_G	1316	7.659254	25.68	6110	46.35	3	9.351224941	0.445	0.955354756	11
optimal_loci_207078_G	3935	7.332317	3.51	2001	53.11	3	60.0210457	0.412	0.955612355	10
optimal_loci_207084_G	1160	7.296204	9.83	3527	39.65	2	84.20122369	0.221	0.955735697	11
optimal_loci_207085_G	2020	7.296204	0	4720	48.36	2	84.20122369	0.361	0.955746675	11
optimal_loci_207123_G	1153	5.899516	0	1001	43.45	6	45.19522634	0.252	0.957639126	16
optimal_loci_207127_G	1115	5.899516	3.23	4428	58.47	7	44.12583174	0.573	0.957679375	16
optimal_loci_207201_G	4298	5.318964	30.57	1001	44.27	4	43.60356957	0.355	0.960277844	10
optimal_loci_207208_G	1218	4.665826	0	7698	35.38	3	1.79996244	0.073	0.960512217	9
optimal_loci_207234_G	1933	5.28357	38.59	2359	39.83	2	18.64613657	0.187	0.961798923	12

optimal_loci_207244_G	1016	5.28357	0	4291	45.66	4	12.20192703	0.363	0.961987894	12
optimal_loci_207249_G	1219	5.28357	22.31	1001	43.72	4	12.20192703	0.311	0.9620163	12
optimal_loci_207251_G	1350	5.28357	20.81	1001	49.33	3	7.911238049	0.542	0.962104767	12
optimal_loci_207280_G	1421	3.923801	14.14	2001	33.99	6	3.387717199	0.107	0.964955967	15
optimal_loci_207281_G	1668	3.923801	3.78	2001	43.4	7	2.188285493	0.271	0.965133684	14
optimal_loci_207289_G	1777	3.959995	10.75	3335	35	6	9.441252323	0.138	0.965334314	14
optimal_loci_207293_G	1692	4.418718	0	1001	52.36	7	8.89220457	0.517	0.965446163	14
optimal_loci_207324_G	1397	4.045853	0	4250	52.18	2	15.1841454	0.429	0.966884186	10
optimal_loci_207333_G	2066	3.894344	5.32	2001	43.07	2	35.1955547	0.305	0.967489571	10
optimal_loci_207335_G	1765	3.894344	2.78	4788	45.66	2	35.1955547	0.464	0.967515217	10
optimal_loci_207338_G	1611	3.546894	1.74	12652	42.08	2	35.1955547	0.175	0.967587581	11
optimal_loci_207364_G	1642	4.585713	25.03	3369	46.77	7	6.03702924	0.293	0.969132686	13
optimal_loci_207365_G	2368	5.918711	2.87	3183	56.75	6	7.04320078	0.693	0.969153253	13
optimal_loci_207414_G	1311	4.773658	12.74	2360	50.87	1	38.19217464	0.279	0.972170363	9
optimal_loci_207448_G	1587	5.236097	0	2512	34.71	2	0.619326454	0.117	0.972724522	8
optimal_loci_207455_G	1268	5.236097	21.21	12398	52.91	2	0.619326454	0.443	0.972859164	8
optimal_loci_207499_G	1238	4.557163	3.8	4462	49.83	5	10.88352323	0.288	0.974222384	7
optimal_loci_207501_G	1093	4.557163	12.63	2910	47.48	5	10.88352323	0.505	0.974238	7
optimal_loci_207532_G	1628	4.874136	20.76	5249	41.76	1	6.630113628	0.248	0.975643365	9
optimal_loci_207595_G	2167	2.485756	0	3384	50.39	4	4.229528534	0.345	0.978333954	6
optimal_loci_207613_G	1602	2.520048	0	1001	62.92	2	5.678992584	0.618	0.979341133	4
optimal_loci_207615_G	1049	4.633571	0	2012	41.65	3	72.76778525	0.277	0.979672798	4
optimal_loci_207772_G	1414	14.808028	0	1772	43.21	5	20.37849283	0.271	0.988382085	2
optimal_loci_207807_G	2374	62.423938	22.37	5993	35.97	1	18.46352135	0.142	0.990539321	2
optimal_loci_208014_G	2421	1.246241	21.93	16310	33.66	2	2.725665049	0.189	0.993128488	4
optimal_loci_208070_G	1222	1.246241	2.62	16298	38.95	1	14.14031958	0.157	0.986285464	4
optimal_loci_208071_G	1921	1.246241	10.15	17614	41.48	1	14.14031958	0.217	0.986244839	4
optimal_loci_208074_G	1107	1.246241	0	18069	43.08	1	0.077914133	0.246	0.986203528	4
optimal_loci_208210_G	1421	0.504941	0	1552	47.85	4	6.249223552	0.657	0.969082379	1
optimal_loci_208312_G	1100	3.725884	0	6757	42.54	3	2.825117102	0.348	0.958351472	2
optimal_loci_208314_G	1013	3.725884	0	19049	38.3	1	0.011877076	0.351	0.958105403	2
optimal_loci_208398_G	1037	2.129966	0	5054	42.91	1	16.5882398	0.131	0.945235766	1
optimal_loci_208514_G	2104	2.343371	9.41	15029	34.88	1	1.484414573	0.121	0.922287661	5

optimal_loci_208518_G	1786	2.343371	22.68	1283	40.2	1	1.484414573	0.252	0.921856573	5
optimal_loci_208578_G	1683	3.040093	29.28	10651	34.46	1	0.874183818	0.089	0.913403609	5
optimal_loci_208582_G	1623	3.044395	0	1855	47.87	1	0.874183818	0.203	0.913066331	5
optimal_loci_208583_G	1082	3.044395	0	3511	50.73	1	0.874183818	0.626	0.913043851	5
optimal_loci_208855_G	2878	3.393745	5.39	16017	48.78	1	0.374992495	0.426	0.867993448	2
optimal_loci_208867_G	2042	3.393745	0	3659	34.32	1	3.068347935	0.183	0.866644194	2
optimal_loci_208978_G	1497	3.13603	2.34	12549	36.47	3	27.72616774	0.156	0.855356794	1
optimal_loci_209238_G	1038	0.040301	20.71	3590	39.59	1	0.339869373	0.39	0.815636613	3
optimal_loci_209241_G	1279	0.279427	0	2001	37.13	1	0.339869373	0	0.815406875	3
optimal_loci_209266_G	1478	0.396573	35.05	2001	42.21	2	13.94913604	0.146	0.808353206	3
optimal_loci_209699_G	1108	0.396698	31.86	2001	40.43	2	3.777450835	0.112	0.735856835	3
optimal_loci_209704_G	1599	0.396698	13.57	17754	43.9	2	3.777450835	0.23	0.735529335	3
optimal_loci_209732_G	1175	0.396698	0	17201	48.08	2	0.999594445	0.323	0.734046976	3
optimal_loci_209926_G	1017	0.40779	0	14767	38.24	1	3.029378108	0.227	0.721462218	4
optimal_loci_209963_G	1489	0.404914	24.18	5345	37.27	6	0.481164768	0.027	0.717987923	5
optimal_loci_209973_G	1103	0.404914	0	2555	38.25	3	0.151233854	0.112	0.717193407	5
optimal_loci_209993_G	1848	0.407242	5.9	11336	35.49	1	0.287539009	0.273	0.715674093	5
optimal_loci_210085_G	1840	0.398554	0	15873	36.41	1	0.753066471	0.105	0.71099125	6
optimal_loci_210189_G	1077	0.410267	0	8929	35.74	1	2.021437371	0.245	0.703826673	3
optimal_loci_210220_G	1250	0.397906	34.72	2763	37.68	4	3.954756317	0.329	0.702342702	3
optimal_loci_210421_G	1139	0.412384	19.4	1164	37.48	3	0.019226093	0.182	0.687698609	1
optimal_loci_210577_G	1274	0.392655	19.86	11050	31.55	1	0.083644958	0.134	0.671771935	1
optimal_loci_210852_G	1108	0.408346	0	18012	37.81	1	21.87342803	0.268	0.637542097	1
optimal_loci_211377_G	1680	0.189008	22.2	13233	35.47	1	14.28249772	0.254	0.553805645	1
optimal_loci_211704_G	1620	1.161246	25.31	2001	35.55	3	8.721140317	0.1	0.509782903	1
optimal_loci_211853_G	1108	0.339481	3.7	6363	37.18	1	0.677061103	0.197	0.490269315	1
optimal_loci_212402_G	1158	0.033994	5.87	2122	37.56	1	52.81214516	0	0.41499621	1
optimal_loci_212590_G	1719	0.337883	19.02	13790	34.32	1	0.104340552	0.152	0.393286935	2
optimal_loci_212593_G	1137	0.337883	12.05	9668	37.29	1	0.104340552	0.073	0.393203831	2
optimal_loci_212844_G	1138	0.091092	0	7059	43.58	3	48.05068035	0.237	0.366308488	2
optimal_loci_212845_G	1145	0.091092	0	8281	52.31	3	48.05068035	0.73	0.36628371	2
optimal_loci_213435_G	1181	0.896227	31.24	2001	40.89	1	2.359933929	0.199	0.302259778	1
optimal_loci_213788_G	1202	0.010948	8.4	17969	46.83	1	2.940756569	0.435	0.262009758	2

optimal_loci_213849_G	1370	0.023637	0	1001	47.88	1	3.922831122	0.354	0.255020867	2
optimal_loci_214039_G	1044	0.464584	23.56	1001	42.24	2	18.67324611	0.228	0.22847252	2
optimal_loci_214065_G	1945	0.342918	37.79	15291	38.97	1	47.14990045	0.124	0.225985827	2
optimal_loci_214256_G	1005	0.582877	6.57	12701	42.98	2	6.691961392	0.136	0.200640282	1
optimal_loci_217402_G	1240	0.165641	24.03	1001	41.53	1	6.534667875	0.196	0.115480812	2
optimal_loci_217438_G	1001	0.230197	0	11240	35.46	1	23.31437264	0.21	0.117156122	2
optimal_loci_217622_G	1421	0.243024	8.8	1516	46.16	1	4.613967965	0.363	0.128117289	2
optimal_loci_217658_G	2037	0.245255	23.66	5043	38.14	2	19.49993507	0.05	0.130040203	4
optimal_loci_217718_G	1077	0.499971	0	4432	52.64	1	10.46210256	0.581	0.133640021	4
optimal_loci_217719_G	1349	0.499971	0	5542	54.18	1	10.46210256	0.41	0.133649335	4
optimal_loci_217732_G	1638	0.57077	30.46	3771	34.18	1	1.194959827	0.134	0.134534626	4
optimal_loci_217787_G	1798	0.563638	22.58	15629	35.76	1	19.04097008	0.052	0.138076974	2
optimal_loci_217939_G	1031	0.341231	7.57	7564	40.05	1	0.035114173	0.112	0.144558603	1
optimal_loci_219497_G	2380	0.06231	14.33	2007	36.47	1	11.26349084	0.206	0.222203698	1
optimal_loci_219916_G	1090	0.163653	0	3922	38.07	2	0.111810599	0.115	0.245166483	1
optimal_loci_220195_G	1212	0.247533	0	2582	47.52	3	9.315895334	0.262	0.260031435	1
optimal_loci_220274_G	1641	0.025395	10.12	1172	38.39	3	38.09412791	0.143	0.265953044	1
optimal_loci_220411_G	1303	0.585211	21.26	3982	44.51	2	1.142359979	0.405	0.27488328	2
optimal_loci_220414_G	2008	0.585211	3.78	1349	46.86	3	0.852538802	0.517	0.274951147	2
optimal_loci_220737_G	1193	1.039195	0	1269	41.24	1	8.919995903	0.216	0.288438411	2
optimal_loci_220783_G	1083	0.612956	5.63	5757	42.47	2	2.62129855	0.263	0.290869404	2
optimal_loci_220850_G	1117	0.060649	0	10713	51.02	1	0.732662645	0.262	0.295309638	3
optimal_loci_220931_G	1120	0.564696	22.77	2379	38.48	3	3.483902892	0.348	0.298761379	3
optimal_loci_220933_G	1080	0.564696	25.93	1855	38.42	2	5.225854339	0.133	0.298808377	3
optimal_loci_221034_G	1743	1.863065	1.66	5876	43.02	2	1.00222894	0.22	0.306831479	2
optimal_loci_221040_G	1135	1.266289	8.11	9398	41.93	3	12.6863103	0.228	0.307237817	2
optimal_loci_221139_G	1014	0.17171	32.25	1001	32.44	2	16.3959169	0.126	0.316175318	2
optimal_loci_221239_G	1226	0.55195	0	2001	32.78	2	1.53724278	0.221	0.319551045	2
optimal_loci_221602_G	1623	0.189132	37.89	2461	42.02	3	7.268081753	0.533	0.340129843	1
optimal_loci_221720_G	1398	0.623812	0	3300	49.07	3	3.362565074	0.481	0.3466154	4
optimal_loci_221721_G	2626	0.623812	7.39	4731	54.11	3	3.362565074	0.579	0.346627407	4
optimal_loci_221773_G	1167	0.40367	31.45	13073	58.86	2	3.788454293	0.556	0.349207551	4
optimal_loci_221776_G	1146	0.40367	37.96	9183	40.4	3	3.291305855	0.105	0.349240369	4

optimal_loci_222089_G	1326	1.559128	0	1001	48.03	1	38.1923557	0.4	0.365717328	1
optimal_loci_222396_G	2317	0.793049	7.68	2204	52.09	4	1.708898911	0.533	0.380232843	5
optimal_loci_222397_G	1018	0.793049	3.05	1001	59.03	4	1.708898911	0.411	0.380253837	5
optimal_loci_222415_G	1230	0.199064	0	3860	44.06	1	4.142484042	0.215	0.380736172	5
optimal_loci_222471_G	1217	0.199069	0	9875	44.53	1	0.170784409	0.566	0.38348235	6
optimal_loci_222483_G	1009	0.199069	0	18028	38.85	1	0.170784409	0	0.383741206	6
optimal_loci_222501_G	1060	2.22655	0	1001	38.86	2	3.213980605	0.332	0.3854722	4
optimal_loci_222591_G	1170	2.437794	3.59	2015	40	1	0.052121769	0.132	0.38925037	3
optimal_loci_222629_G	2413	3.015037	0	2041	48.52	2	24.8860771	0.295	0.390725872	2
optimal_loci_222830_G	1560	2.447469	2.88	3852	44.1	1	0.478935295	0.284	0.401760755	4
optimal_loci_222843_G	1107	2.539517	32.79	5933	38.39	2	8.977031659	0.326	0.402112391	4
optimal_loci_222870_G	1062	2.331461	0	7076	30.13	3	1.793372641	0.068	0.403624965	4
optimal_loci_222883_G	1297	2.241648	0	11208	35.85	1	0.042099993	0.192	0.403892321	4
optimal_loci_223677_G	1011	1.026516	0	10047	36.39	2	7.992431294	0.064	0.438366424	6
optimal_loci_223692_G	1237	0.998958	0	2001	50.92	5	31.82278556	0.363	0.438902546	6
optimal_loci_223707_G	1971	0.932079	14.16	15802	34.44	1	0.278095495	0.055	0.439470647	6
optimal_loci_223716_G	2041	0.932079	4.95	1001	40.96	3	15.13791224	0.206	0.439834853	6
optimal_loci_223728_G	1040	1.144191	0	1864	48.26	1	1.530100277	0.244	0.440222864	6
optimal_loci_223784_G	1103	1.626206	24.2	5403	38.89	2	0.042870839	0.07	0.442099006	6
optimal_loci_223945_G	1270	1.394901	19.06	2001	36.37	2	15.5846507	0.142	0.447682598	2
optimal_loci_223994_G	1731	0.871632	25.36	9152	38.82	1	0.065226309	0.271	0.45015902	3
optimal_loci_224042_G	1023	1.320048	0	1311	42.03	2	21.38644426	0.096	0.4519764	2
optimal_loci_224166_G	1031	0.927513	13.77	5485	36.17	2	1.677001344	0.106	0.456878746	5
optimal_loci_224169_G	1350	0.932465	2.59	3457	45.55	2	1.677001344	0.38	0.456893087	5
optimal_loci_224176_G	1021	1.15421	31.54	9269	38.88	1	3.354002688	0.168	0.457027763	5
optimal_loci_224181_G	1560	1.168496	33.01	14904	34.48	1	3.354002688	0.139	0.457075047	6
optimal_loci_224216_G	1173	4.473598	5.37	17515	34.27	1	60.73644691	0.15	0.459647069	11
optimal_loci_224238_G	1238	4.732286	0	3344	44.91	4	9.377925119	0.278	0.461264019	10
optimal_loci_224253_G	1211	4.21703	3.14	3741	39.8	3	13.01876193	0.087	0.4621369	10
optimal_loci_224259_G	1309	4.21703	29.72	2869	37.05	2	19.5281429	0.3	0.46226201	10
optimal_loci_224263_G	1191	3.965408	34.68	2640	34.84	2	19.5281429	0.124	0.462360211	10
optimal_loci_224264_G	1331	3.965408	0	4209	36.58	2	19.5281429	0.14	0.462373377	10
optimal_loci_224270_G	1193	3.847372	0	3081	38.8	3	0.400305143	0.145	0.462595723	10

optimal_loci_224334_G	1974	3.637827	5.83	2983	40.47	1	1.114692374	0.221	0.464331424	9
optimal_loci_224336_G	1358	3.637827	24.96	1519	56.03	2	1.089249405	0.62	0.464397965	9
optimal_loci_224379_G	1274	3.272518	29.83	4231	40.18	2	0.81635061	0.189	0.465568225	8
optimal_loci_224473_G	1115	0.72318	14.44	2001	49.41	3	13.68049469	0.585	0.470407706	1
optimal_loci_224611_G	1630	0.777106	19.57	1015	47.36	2	1.184706545	0.342	0.47610154	2
optimal_loci_224681_G	1419	1.31141	35.73	2645	40.87	2	2.960152555	0.19	0.479196401	4
optimal_loci_224717_G	1045	1.318395	6.03	3015	37.79	1	6.926553831	0.135	0.480837349	3
optimal_loci_224749_G	1154	1.308149	0	2001	36.65	3	26.80211644	0.21	0.481545815	4
optimal_loci_224816_G	2238	2.379335	15.91	14801	44.81	1	38.75062279	0.529	0.485548791	9
optimal_loci_224846_G	1539	3.039266	0	1001	47.3	3	25.95383146	0.369	0.487205271	8
optimal_loci_224850_G	1237	3.039266	4.37	1132	34.03	3	25.95383146	0.182	0.487280086	8
optimal_loci_224853_G	1022	3.039266	0	4354	41.58	3	25.95383146	0.1	0.487360422	8
optimal_loci_224876_G	1426	2.223714	0	2001	36.53	1	0.408994506	0.159	0.487668022	8
optimal_loci_224881_G	1304	2.381483	29.75	19213	46.7	1	0.408994506	0.245	0.487889462	8
optimal_loci_224895_G	1214	2.54482	6.59	1828	37.8	2	0.549581439	0.389	0.489276153	8
optimal_loci_224918_G	1495	3.091131	0	6439	38.92	2	1.281886243	0.053	0.489490696	8
optimal_loci_225058_G	1511	2.102993	0	2382	55.32	1	0.313186665	0.559	0.4947938	5
optimal_loci_225066_G	1127	2.102993	0	3254	57.94	2	0.156593333	0.869	0.494950906	5
optimal_loci_225100_G	1849	2.758545	0	3078	38.34	4	0.84799914	0.149	0.495628921	6
optimal_loci_225104_G	3860	2.758545	0	2113	32.22	5	0.678399312	0.128	0.495721265	6
optimal_loci_225125_G	1518	2.631829	2.9	19014	54.01	1	0.86977578	0.491	0.497163362	6
optimal_loci_225224_G	1499	2.77795	3.87	2001	42.09	1	16.78556829	0.255	0.499542683	6
optimal_loci_225290_G	1149	0.463586	0	4431	48.38	2	43.10249518	0.556	0.502508161	5
optimal_loci_225308_G	1685	0.418	3.56	7183	41.06	1	21.66047869	0.243	0.503449555	6
optimal_loci_225345_G	1276	0.065843	0	12319	30.32	2	9.341599656	0.117	0.505734669	5
optimal_loci_225348_G	1465	0.065843	36.18	9059	35.35	2	9.341599656	0.099	0.505760438	5
optimal_loci_225369_G	2319	0.065843	0	1419	42.6	2	55.80844435	0.329	0.506742932	6
optimal_loci_225454_G	1232	0.065843	0	5716	50.32	4	5.02915573	0.426	0.510180064	5
optimal_loci_225457_G	1050	0.065843	0	1048	41.04	2	9.961242481	0.234	0.510319775	5
optimal_loci_225516_G	1208	0.065843	25.66	3870	36.83	1	33.20247008	0.074	0.513341801	4
optimal_loci_225529_G	2022	0.065843	12.56	15612	43.71	1	33.20247008	0.351	0.513525859	4
optimal_loci_225804_G	2290	2.884721	9	9128	56.06	1	2.10365983	0.655	0.525286712	5
optimal_loci_225889_G	1088	1.643552	3.12	11368	51.28	1	40.86840993	0.408	0.528162515	5

optimal_loci_225892_G	1725	1.643552	20.81	1001	48.17	2	20.43420496	0.514	0.52824416	5
optimal_loci_225895_G	1001	1.643552	0	1684	54.54	2	20.43420496	0.738	0.52833334	5
optimal_loci_225909_G	1591	1.469469	3.02	2837	40.85	2	10.87661727	0.223	0.52900382	5
optimal_loci_226024_G	1427	0.481531	9.53	1001	37.28	2	48.07012207	0.08	0.535170608	2
optimal_loci_226052_G	1191	0.487305	35.18	1001	31.65	2	1.135094886	0.203	0.537731621	2
optimal_loci_226144_G	1062	1.629687	0	3288	55.27	4	5.381872599	0.736	0.544886868	2
optimal_loci_226145_G	1207	1.625596	0	2001	43.91	4	5.381872599	0.24	0.544896451	2
optimal_loci_226257_G	1237	1.509473	21.42	2001	27.32	3	5.459149182	0	0.550115594	2
optimal_loci_226319_G	1033	0.892405	24.2	16742	44.53	1	15.96118505	0.319	0.553147362	2
optimal_loci_226475_G	1071	1.836965	0	17786	58.54	1	0.597565137	0.714	0.560291777	3
optimal_loci_226509_G	1005	1.733428	0	2901	41.29	3	67.36271486	0.123	0.562903857	8
optimal_loci_226520_G	1304	1.806919	11.04	3909	42.02	1	199.9246891	0.383	0.563119189	11
optimal_loci_226563_G	2238	2.719079	13.76	1924	38.78	1	1.792421626	0.172	0.565343778	10
optimal_loci_226569_G	1487	3.101578	1.88	18923	37.72	1	15.70056926	0.063	0.565826038	10
optimal_loci_226575_G	1155	3.101578	12.81	11081	37.57	1	15.70056926	0.269	0.565894627	10
optimal_loci_226579_G	1271	3.101578	0	3167	40.83	1	15.70056926	0.102	0.56596006	10
optimal_loci_226602_G	2620	3.529489	7.67	17665	41.94	1	4.269577181	0.097	0.567028705	11
optimal_loci_226609_G	1041	3.651855	0	8622	56.19	1	4.269577181	0.731	0.567117834	10
optimal_loci_226613_G	1948	2.572234	19.1	3156	36.24	1	4.269577181	0.075	0.567258569	11
optimal_loci_226614_G	1883	4.490662	29.26	5736	37.01	1	4.269577181	0.155	0.567280218	11
optimal_loci_226704_G	1062	3.392396	0	2634	51.31	1	5.95051182	0.349	0.570550184	6
optimal_loci_226716_G	1158	3.048752	0	4279	35.23	3	1.858679538	0.192	0.571435651	5
optimal_loci_226783_G	2643	1.765624	13.55	1001	37.3	1	19.78335344	0.168	0.57481001	3
optimal_loci_226813_G	2208	0.694809	10.6	9171	35.41	2	1.050887824	0.035	0.576319965	3
optimal_loci_226942_G	1163	0.822236	0	3119	40.24	1	8.044248866	0.232	0.58031116	2
optimal_loci_227153_G	1012	2.226716	27.47	6339	37.15	2	12.24805498	0.018	0.593030742	2
optimal_loci_227223_G	1496	2.740766	29.55	1337	33.02	2	77.11792106	0	0.596334523	3
optimal_loci_227301_G	1111	2.158002	18.9	4028	38.34	4	0.011280381	0.136	0.598498328	3
optimal_loci_227419_G	1054	0.398056	4.36	19973	36.05	1	9.514291578	0.115	0.60245741	3
optimal_loci_227473_G	1053	0.181115	8.64	6357	39.6	2	1.074489447	0.321	0.604824077	2
optimal_loci_227576_G	1043	0.602245	0	12351	36.33	2	4.699313171	0.131	0.609169256	4
optimal_loci_227588_G	1290	0.712866	33.41	15762	35.96	1	8.752694782	0.155	0.609586276	4
optimal_loci_227594_G	1051	0.712866	0	7580	45.09	1	8.752694782	0.146	0.609804662	4

optimal_loci_227627_G	1134	0.882624	0	5799	48.67	3	6.994373578	0.571	0.612316905	6
optimal_loci_227691_G	1137	0.776751	28.76	1001	34.3	2	0.05494062	0.179	0.616161717	4
optimal_loci_227700_G	1996	0.779498	2	18483	37.47	1	0.109881241	0.079	0.616360384	4
optimal_loci_227752_G	1010	0.593751	0	15726	31.68	1	432.8125754	0.225	0.619211107	3
optimal_loci_227900_G	1080	0.527461	8.15	15819	33.79	1	0.404449755	0.133	0.624903732	2
optimal_loci_227958_G	1025	0.554315	0	14939	49.26	1	12.61842458	0.511	0.626726474	3
optimal_loci_228034_G	1138	0.760966	20.04	5461	40.15	1	52.43145173	0.221	0.629484265	3
optimal_loci_228076_G	1065	0.728978	31.83	2001	33.8	2	34.28643058	0.127	0.631378355	2
optimal_loci_228254_G	1195	0.039055	4.6	3600	42.59	1	2.650962291	0.227	0.638439623	2
optimal_loci_228255_G	1070	0.039055	0	2486	41.21	1	2.650962291	0.302	0.63845002	2
optimal_loci_228499_G	1513	2.950468	9.25	1158	38.99	3	1.423393575	0	0.652523291	3
optimal_loci_228586_G	1080	2.582728	0	2568	47.96	2	45.65914798	0.342	0.654988385	4
optimal_loci_228587_G	1547	2.582728	12.73	1001	40.33	2	45.65914798	0.092	0.655002264	4
optimal_loci_228690_G	1186	1.24223	10.54	7738	38.95	1	75.33181312	0.085	0.65913254	6
optimal_loci_228716_G	1299	0.84199	37.88	4409	31.48	1	9.854864108	0.078	0.659811612	5
optimal_loci_228729_G	1167	1.07079	28.36	1108	35.64	2	1.278854241	0.06	0.66065019	5
optimal_loci_228739_G	1378	1.07079	0	1001	37.73	3	3.749661167	0.045	0.66115034	5
optimal_loci_228793_G	1082	1.645138	6.38	13827	37.98	1	16.74057427	0.197	0.663742206	9
optimal_loci_228883_G	1367	2.027838	3.73	2551	42.86	2	4.217154942	0.366	0.666799525	16
optimal_loci_228889_G	1000	2.020849	0	2568	45.4	3	2.914541775	0.337	0.666901057	16
optimal_loci_228893_G	1952	2.023413	0	6644	46.46	3	2.914541775	0.233	0.666935259	17
optimal_loci_228897_G	1137	2.023413	0	7306	36.49	2	3.345449079	0.087	0.666969847	17
optimal_loci_228913_G	2437	2.023413	2.5	7470	38.28	2	1.790991969	0.158	0.66736687	17
optimal_loci_228961_G	1121	2.425929	0	19475	33.8	1	39.40919279	0	0.669332344	20
optimal_loci_228962_G	1062	2.425929	16.85	18268	43.69	1	39.40919279	0.104	0.669342967	20
optimal_loci_228981_G	1505	2.425929	26.38	18161	33.08	1	2.702967553	0.178	0.669788314	20
optimal_loci_228992_G	2761	2.185987	0	8704	45.63	1	155.1021409	0.048	0.670180295	22
optimal_loci_228993_G	1031	2.185987	0	3719	37.92	1	155.1021409	0.122	0.670236641	22
optimal_loci_229002_G	1409	2.160047	0	5086	40.95	2	81.01536318	0.244	0.670327969	22
optimal_loci_229012_G	1068	2.160047	15.26	2552	35.11	1	6.928585514	0.113	0.670488977	22
optimal_loci_229013_G	2205	2.160047	20	4479	48.16	1	6.928585514	0.489	0.670505146	22
optimal_loci_229019_G	1381	2.10108	25.49	14388	33.59	1	6.928585514	0.088	0.670588293	22
optimal_loci_229023_G	3047	2.150331	2.26	4170	43.09	3	58.35385212	0.364	0.670916745	22

optimal_loci_229038_G	1358	1.762754	27.76	1246	30.26	3	58.35385212	0.184	0.671144948	20
optimal_loci_229111_G	1375	1.273318	0	7884	45.96	2	1.545623946	0.573	0.672540039	18
optimal_loci_229113_G	1406	1.273318	36.13	5798	46.15	2	1.545623946	0.352	0.672557283	18
optimal_loci_229145_G	1039	1.051195	17.23	11420	39.17	1	9.691507796	0.363	0.673448775	18
optimal_loci_229150_G	1224	1.051195	0	14311	40.44	1	9.691507796	0.117	0.673473033	18
optimal_loci_229168_G	1359	0.994723	21.19	13296	41.35	1	115.6975645	0.265	0.674048686	15
optimal_loci_229179_G	1234	0.905689	24.96	2766	35.08	3	38.73036295	0	0.67424789	15
optimal_loci_229242_G	1059	0.652724	10.95	2308	46.74	2	10.49882704	0.202	0.676221737	9
optimal_loci_229285_G	1523	1.245046	9	8189	39.92	2	1.145179604	0.301	0.678713213	4
optimal_loci_229296_G	1727	1.218557	16.85	1524	34.45	2	67.72734738	0.143	0.679065537	5
optimal_loci_229339_G	1121	1.259452	26.85	2759	37.46	1	17.860981	0.157	0.681418635	7
optimal_loci_229363_G	1258	1.047668	0	7715	38.71	2	10.78928119	0.161	0.683117357	8
optimal_loci_229369_G	1906	0.943044	0	2021	40.13	4	11.50941021	0.15	0.683602385	7
optimal_loci_229373_G	1363	0.929689	0	6311	35.95	4	11.50941021	0.077	0.683638383	7
optimal_loci_229391_G	1916	0.710116	7.15	3624	42.17	1	2.081962305	0.246	0.68380357	9
optimal_loci_229440_G	1047	1.095806	26.74	1845	41.16	2	1.442502956	0.264	0.686026456	13
optimal_loci_229450_G	1096	1.023215	0	2154	55.56	1	0.373698774	0.585	0.686681941	14
optimal_loci_229482_G	1331	1.370142	2.1	8970	45.37	1	3.008291468	0.195	0.687902077	11
optimal_loci_229483_G	1172	1.370142	34.39	7687	39.41	1	3.008291468	0	0.687914177	11
optimal_loci_229491_G	1013	1.370142	21.72	8237	44.42	1	3.008291468	0.542	0.688068774	10
optimal_loci_229512_G	1200	1.734029	8	7779	39.41	2	11.85831026	0.285	0.688676716	10
optimal_loci_229515_G	1017	1.734029	0	7631	63.02	2	11.85831026	0.62	0.688695679	10
optimal_loci_229553_G	1094	1.559027	24.5	1487	40.67	1	0.508118326	0.342	0.689620711	10
optimal_loci_229557_G	2505	1.559027	0	4266	40.43	1	0.508118326	0.133	0.68969785	10
optimal_loci_229575_G	1503	1.674622	0	2363	49.5	2	58.58343226	0.459	0.69029917	9
optimal_loci_229771_G	1099	0.812511	5.28	6402	38.85	1	2.859923358	0.27	0.695972916	3
optimal_loci_229777_G	1062	0.860129	10.36	1001	50	1	2.859923358	0.474	0.69629468	3
optimal_loci_229827_G	1194	0.681072	0	1377	56.44	2	125.6788602	0.555	0.698153276	3
optimal_loci_230092_G	1162	0.421472	21.51	1751	40.96	3	0.513350889	0.266	0.709563903	1
optimal_loci_230330_G	1039	0.68653	18.38	1123	34.45	1	18.29491493	0.017	0.717171387	3
optimal_loci_230335_G	1107	0.68653	0	19766	38.75	1	18.29491493	0.138	0.717327821	3
optimal_loci_230344_G	1070	0.720396	36.26	6342	36.44	3	12.03301577	0.12	0.717672308	4
optimal_loci_230421_G	3109	1.023387	13.28	2928	33.19	2	3.140970811	0.146	0.721565503	3

optimal_loci_230461_G	1407	0.113708	0	5489	38.09	1	15.97610304	0.261	0.725261231	2
optimal_loci_230703_G	1991	0.246444	0	6518	39.52	3	7.777846902	0.125	0.735616857	4
optimal_loci_230743_G	1988	0.418145	30.68	2841	35.81	1	13.21566398	0.231	0.737432885	5
optimal_loci_230771_G	1028	0.907603	0	2171	38.22	3	48.3803729	0.053	0.738963131	8
optimal_loci_230776_G	1208	0.907603	4.06	9120	50.49	3	48.3803729	0.649	0.73902144	8
optimal_loci_230824_G	1082	0.91202	0	19879	47.5	1	2.605877465	0.376	0.740984992	9
optimal_loci_230850_G	1501	0.918692	15.79	8828	40.9	1	12.93132919	0.249	0.741970548	9
optimal_loci_230857_G	1250	0.89118	0	13337	40.16	2	6.511591859	0.316	0.742209509	9
optimal_loci_230858_G	1533	0.874726	0	2001	35.81	2	0.124279328	0.097	0.742302255	9
optimal_loci_230874_G	1220	0.860197	0	6757	52.21	2	3.275931427	0.496	0.743255011	7
optimal_loci_230893_G	3074	0.860197	4.42	13040	30.25	1	0.281511493	0.079	0.743778966	7
optimal_loci_230971_G	1158	0.692081	11.31	17053	33.93	1	36.16922851	0	0.745566011	6
optimal_loci_231101_G	1033	1.012658	0	1197	41.14	3	11.55387866	0.167	0.751697943	1
optimal_loci_231274_G	1467	0.677667	26.58	5013	34.83	1	140.8965533	0.056	0.757577698	3
optimal_loci_231344_G	1327	0.35688	9.04	4951	41.59	1	0.167258405	0.277	0.759732482	3
optimal_loci_231404_G	1016	0.617115	19.09	2886	41.92	2	31.32155154	0.317	0.761103205	10
optimal_loci_231458_G	1685	0.988191	0	2001	34.59	1	0.416289397	0.216	0.763955924	9
optimal_loci_231460_G	1315	0.988191	0	4772	39.31	1	0.416289397	0	0.763979176	9
optimal_loci_231461_G	1605	1.234587	11.96	6205	34.14	1	0.416289397	0.208	0.7639912	9
optimal_loci_231467_G	1130	1.234587	4.6	15421	40.88	2	0.208144699	0.328	0.764068532	9
optimal_loci_231468_G	1074	1.234587	0	16584	37.43	3	0.138763132	0.299	0.764078291	9
optimal_loci_231479_G	3673	1.11069	20.56	3250	42.25	1	1.616759449	0.279	0.764741664	9
optimal_loci_231493_G	1106	1.086453	0	19607	41.41	1	1.616759449	0.062	0.764974944	9
optimal_loci_231516_G	1052	1.110087	18.63	6305	29.56	1	1.602142575	0.123	0.765481009	8
optimal_loci_231810_G	2544	0.488714	0	2001	47.2	1	14.74467041	0.268	0.774640874	8
optimal_loci_231814_G	2241	0.486225	0	6134	48.81	1	14.74467041	0.439	0.774675555	8
optimal_loci_231838_G	1145	0.429327	0	14971	44.89	1	9.111969425	0.164	0.775505582	8
optimal_loci_231867_G	3470	0.41475	0.92	3153	51.52	2	9.445461191	0.502	0.7766334	10
optimal_loci_231899_G	1170	0.325857	0	2001	44.27	2	6.37510008	0.538	0.778318226	10
optimal_loci_231904_G	1016	0.311866	27.46	4294	43.3	2	6.37510008	0.144	0.778405317	10
optimal_loci_231905_G	1327	0.311866	9.57	5343	37.75	3	14.96918666	0.17	0.778414119	10
optimal_loci_231906_G	1410	0.311866	0	6857	37.73	3	14.96918666	0.173	0.778426823	10
optimal_loci_231928_G	1018	0.243574	0	15847	34.18	2	0.47555532	0.231	0.779756556	7

optimal_loci_231942_G	1365	0.228922	28.57	6483	33.77	2	0.47555532	0.104	0.780011434	7
optimal_loci_232108_G	2124	0.896254	0	4086	56.21	2	3.21734985	0.653	0.788560195	3
optimal_loci_232110_G	1118	0.896254	6.53	2492	45.61	2	3.21734985	0.149	0.788582011	3
optimal_loci_232111_G	1338	0.896254	2.69	1009	46.93	2	3.21734985	0.404	0.788592609	3
optimal_loci_232205_G	1064	0.945317	21.33	5155	32.51	2	8.287255535	0.075	0.794315284	5
optimal_loci_232213_G	1156	1.001518	0	3333	47.66	2	8.287255535	0.37	0.794397004	5
optimal_loci_232219_G	1273	1.038575	30.01	5317	55.69	2	18.63705674	0.528	0.794620374	5
optimal_loci_232222_G	1552	1.038575	6.19	2832	42.07	2	18.63705674	0.191	0.794638885	5
optimal_loci_232228_G	3903	1.038575	0	2038	47.19	2	10.3498012	0.428	0.794798248	5
optimal_loci_232295_G	1269	1.64904	4.26	15992	41.6	1	24.30086711	0.411	0.79927057	6
optimal_loci_232305_G	1104	1.673739	0	5383	49.81	1	24.30086711	0.457	0.79952278	6
optimal_loci_232309_G	1533	1.689151	13.18	16993	60.66	1	24.30086711	0.634	0.7996202	6
optimal_loci_232310_G	1940	1.686067	0	3881	53.04	3	24.51393127	0.44	0.799757201	6
optimal_loci_232311_G	1194	1.687071	2.93	2544	45.05	3	24.51393127	0.342	0.79977468	6
optimal_loci_232349_G	1294	1.697732	21.1	3983	48.68	1	7.65210147	0.364	0.801631757	6
optimal_loci_232479_G	1313	0.653235	19.57	4155	41.05	1	103.771479	0.195	0.806491737	9
optimal_loci_232484_G	3417	0.712642	0	1001	57.71	1	103.771479	0.601	0.806567534	9
optimal_loci_232487_G	1653	0.712642	4.96	5993	30.67	1	103.771479	0.056	0.806609422	9
optimal_loci_232496_G	2020	0.033676	2.52	5654	43.51	3	43.40600436	0.253	0.807331918	9
optimal_loci_232497_G	2215	0.033676	0	3055	57.38	3	43.40600436	0.562	0.80735209	9
optimal_loci_232501_G	2618	1.798423	7.14	2947	45.53	3	43.40600436	0.432	0.807527539	9
optimal_loci_232524_G	1089	1.849275	9.83	2262	60.23	1	9.782199535	0.737	0.808986024	10
optimal_loci_232533_G	1307	1.849275	36.34	11888	40.78	1	38.86005017	0.262	0.809312319	10
optimal_loci_232553_G	1254	1.679326	0	1960	32.45	2	0.644938728	0.162	0.810330995	16
optimal_loci_232648_G	1652	1.886485	0	5009	38.19	1	13.28750756	0.043	0.812643548	13
optimal_loci_232692_G	1356	1.460138	16.22	5173	59.29	1	7.828503886	0.687	0.814081575	11
optimal_loci_232698_G	1266	1.460138	0	1001	53.94	2	3.914251943	0.484	0.814117338	11
optimal_loci_232704_G	1574	1.460138	39.58	5469	46.63	2	3.914251943	0.264	0.814199352	12
optimal_loci_232705_G	1210	1.460138	20.66	7113	46.94	2	3.914251943	0.375	0.814213147	12
optimal_loci_232707_G	1083	1.460138	0	6531	51.33	2	3.914251943	0.45	0.814226766	12
optimal_loci_232717_G	1000	1.460138	0	6779	56.5	2	5.103640951	0.561	0.814366376	12
optimal_loci_232729_G	1183	1.196185	4.48	2080	37.27	5	22.1823947	0.184	0.815734003	13
optimal_loci_232742_G	1044	1.448353	4.6	16143	40.42	1	0.112829814	0.062	0.816068353	13

optimal_loci_232755_G	2316	1.310768	34.24	1001	46.67	1	6.512280237	0.36	0.816513491	13
optimal_loci_232797_G	1129	2.07316	0	10022	41.89	1	0.602826613	0.326	0.81833958	14
optimal_loci_232831_G	1003	1.988382	0	8851	58.22	3	12.63394502	0.65	0.8196178	11
optimal_loci_232833_G	1671	1.988382	0	5508	37.34	3	12.63394502	0.224	0.819640246	11
optimal_loci_232874_G	1260	2.247733	8.25	2711	49.68	3	6.717555758	0.557	0.821258807	10
optimal_loci_232881_G	1205	2.247733	25.06	3918	46.55	4	24.92175329	0.362	0.821415225	10
optimal_loci_232885_G	1423	2.247733	0	4089	50.8	5	21.56526941	0.483	0.821447338	10
optimal_loci_232894_G	1050	2.247733	12.95	2431	47.8	1	35.29572647	0.294	0.822051948	10
optimal_loci_232941_G	1452	2.787325	7.99	2815	48.2	2	1.547534017	0.577	0.823151026	9
optimal_loci_233008_G	1007	1.717089	0	3171	42.2	2	29.8939863	0.276	0.824344949	8
optimal_loci_233009_G	1504	1.717089	17.82	1500	33.51	2	29.8939863	0.187	0.824354801	8
optimal_loci_233102_G	1937	0.864426	35.93	15901	40.68	1	101.7037193	0.31	0.827439961	12
optimal_loci_233119_G	1320	1.055431	4.92	1001	42.34	1	1.287526593	0.418	0.82882348	14
optimal_loci_233121_G	3784	1.008978	0	3016	53.46	1	1.287526593	0.534	0.828889132	14
optimal_loci_233124_G	1210	1.005312	9.5	8590	40.16	1	1.287526593	0.164	0.828935904	14
optimal_loci_233131_G	1345	1.005312	10.26	14809	36.8	1	11.68945318	0.162	0.829130694	14
optimal_loci_233136_G	1180	1.005312	14.41	11411	41.27	2	6.222539747	0.228	0.829160591	14
optimal_loci_233177_G	1406	0.981014	36.27	5883	36.41	3	7.529719901	0.135	0.830296171	21
optimal_loci_233178_G	1930	0.981014	17.62	4523	43.41	3	7.529719901	0.228	0.830324088	21
optimal_loci_233180_G	1240	0.981014	4.44	2592	35.88	3	7.529719901	0.115	0.830346081	21
optimal_loci_233209_G	1392	0.897982	0	7363	38.36	2	9.5145538	0.01	0.83137001	21
optimal_loci_233217_G	1600	0.831696	0	2719	49.18	1	0.262948665	0.471	0.831722879	22
optimal_loci_233219_G	1305	0.831696	0	1001	47.73	1	0.262948665	0.357	0.831779544	22
optimal_loci_233220_G	2035	0.831696	0	2391	47.22	1	0.262948665	0.439	0.831791208	22
optimal_loci_233222_G	1077	0.831696	5.48	5793	39.27	1	0.262948665	0.231	0.831819754	22
optimal_loci_233278_G	1311	0.471979	10.22	7659	36.23	1	11.65064391	0.148	0.833398449	20
optimal_loci_233283_G	1398	0.471979	36.98	3013	32.18	1	11.65064391	0.154	0.833436704	20
optimal_loci_233284_G	1423	0.486864	9.77	1001	48.98	1	11.65064391	0.516	0.833492614	20
optimal_loci_233286_G	1734	0.483016	10.84	3174	36.96	2	19.92061403	0.115	0.833510848	20
optimal_loci_233287_G	1245	0.483016	0	4941	40.48	2	19.92061403	0.209	0.833525675	20
optimal_loci_233300_G	1061	0.478229	13.38	14394	38.92	1	28.19058416	0.138	0.833810879	20
optimal_loci_233306_G	2339	0.478229	16.59	19485	37.58	1	28.19058416	0.119	0.833853598	20
optimal_loci_233355_G	2687	0.411751	7.44	4009	40.04	2	2.607652332	0.145	0.835614245	17

optimal_loci_233357_G	1247	0.396617	0	3411	52.68	1	0.212135613	0.411	0.835732542	17
optimal_loci_233379_G	2391	0.36625	10.08	3280	53.24	2	6.431751019	0.505	0.836403307	13
optimal_loci_233381_G	1626	0.36625	0	2721	39.6	2	6.431751019	0.214	0.836444549	13
optimal_loci_233395_G	1312	0.36625	14.41	12715	37.57	2	1.798330521	0.086	0.836593617	13
optimal_loci_233460_G	1341	0.37417	39.15	1001	41.01	2	4.001725411	0.288	0.838600408	8
optimal_loci_233530_G	1704	1.344638	1.7	2001	55.63	2	6.911478239	0.498	0.841599333	5
optimal_loci_233536_G	1076	1.344638	0	1001	51.3	2	6.911478239	0.436	0.841642127	5
optimal_loci_233584_G	1343	2.227047	26.21	4916	50.7	3	11.8787113	0.386	0.844954501	8
optimal_loci_233593_G	2198	2.214344	19.15	1386	43.08	5	5.575389923	0.191	0.84537966	8
optimal_loci_233629_G	1526	2.358001	0	4365	53.73	1	9.209169364	0.533	0.846121682	6
optimal_loci_233633_G	1430	2.358001	0	1001	56.08	1	9.209169364	0.556	0.846150715	6
optimal_loci_233639_G	1328	2.525553	0	2001	36.67	3	17.03228385	0.195	0.846523731	6
optimal_loci_233659_G	1671	2.078198	9.16	1001	48.83	1	5.367075729	0.516	0.847824389	6
optimal_loci_233740_G	1081	1.802393	0	2001	37.28	4	4.298133362	0.165	0.852171499	4
optimal_loci_233741_G	1607	1.802393	20.6	1001	51.58	4	2.172738473	0.472	0.852250224	4
optimal_loci_233766_G	1281	3.174946	10.93	1218	39.42	6	1.379977511	0.199	0.854040693	4
optimal_loci_233813_G	2306	3.145526	11.06	12792	45.7	1	0.161054632	0.311	0.856368333	7
optimal_loci_233864_G	1085	2.742415	0	2134	40.36	3	1.684737873	0	0.858338723	4
optimal_loci_233867_G	1860	2.759589	4.09	2001	48.7	5	1.010842724	0.391	0.858463196	4
optimal_loci_233896_G	1919	2.793442	1.56	4272	41.47	4	1.606439695	0.11	0.86009223	5
optimal_loci_233982_G	1145	1.236147	0	7214	40.52	3	0.241477259	0.018	0.863626212	9
optimal_loci_234041_G	1805	2.521089	6.98	4019	36.45	3	0.543590947	0.12	0.865886429	12
optimal_loci_234042_G	1091	2.521089	0	3406	50.87	3	0.543590947	0.636	0.865904873	12
optimal_loci_234047_G	1095	2.521089	0	3108	51.14	4	0.40769321	0.637	0.86597759	12
optimal_loci_234050_G	1168	2.521089	0	4447	53.85	5	0.326154568	0.434	0.866011809	12
optimal_loci_234051_G	1290	2.521089	15.5	3099	40.93	4	0.40769321	0.085	0.866022096	12
optimal_loci_234055_G	1126	2.521089	15.54	1422	41.91	6	0.271795473	0.192	0.866095073	12
optimal_loci_234070_G	1955	2.618862	0	4718	48.84	4	4.077873869	0.418	0.866565611	13
optimal_loci_234175_G	1750	2.915371	36	5676	37.14	1	1.143284298	0.082	0.869448412	20
optimal_loci_234187_G	1952	2.809952	6.97	9238	50.71	1	0.156630814	0.422	0.869773969	21
optimal_loci_234188_G	1918	2.809952	2.87	7243	48.33	1	0.156630814	0.577	0.869790994	21
optimal_loci_234196_G	1385	2.809952	7.8	1254	34.44	1	0.156630814	0.164	0.869845721	22
optimal_loci_234240_G	1242	2.315237	0	10488	48.95	2	16.45440651	0.485	0.870761128	16

optimal_loci_234254_G	2197	2.315237	10.15	1586	42.83	2	16.02072062	0.174	0.870950883	15
optimal_loci_234257_G	1903	2.315237	0	2001	36.88	2	16.02072062	0.335	0.871035281	15
optimal_loci_234265_G	1215	2.315237	0	5893	44.27	1	0.698189479	0.3	0.871297183	17
optimal_loci_234266_G	3404	2.315237	20.18	2276	34.45	1	0.698189479	0.087	0.871309165	17
optimal_loci_234269_G	1067	2.315237	34.49	1319	43.95	1	0.698189479	0.347	0.871381597	17
optimal_loci_234322_G	1538	2.315237	0	2177	34	2	0.190380394	0.093	0.873361041	17
optimal_loci_234323_G	2499	2.315237	0	3789	39.89	2	0.190380394	0.108	0.873374567	17
optimal_loci_234327_G	1026	2.315237	0	8214	35.28	2	0.190380394	0.074	0.873411698	17
optimal_loci_234340_G	1122	1.152369	6.95	2422	52.04	2	8.95580787	0.443	0.873805491	16
optimal_loci_234358_G	2230	1.15166	10.45	2464	45.2	3	2.018706625	0.327	0.874010812	14
optimal_loci_234379_G	1147	0.86336	6.89	2680	50.91	5	15.73350992	0.482	0.87540033	11
optimal_loci_234382_G	1039	0.86336	33.01	2691	47.64	5	15.73350992	0.514	0.875416064	11
optimal_loci_234483_G	2057	6.017833	0	2498	48.27	3	0.258847374	0.451	0.879107496	8
optimal_loci_234495_G	2537	6.017833	15.06	2001	42.84	1	0.460081012	0.165	0.87968486	6
optimal_loci_234535_G	1339	3.141935	0	2149	36.22	3	0.036674632	0.071	0.880962995	9
optimal_loci_234536_G	1080	3.315269	0	1196	54.81	2	3.146257007	0.473	0.881588298	9
optimal_loci_234555_G	1444	3.874232	7.27	3620	43.28	2	9.9227671	0.261	0.882251687	9
optimal_loci_234568_G	1522	3.892196	5.52	8689	45.46	3	18.49741958	0.229	0.882735122	9
optimal_loci_234611_G	1110	3.575748	0	15273	32.34	2	7.009157887	0	0.884708558	7
optimal_loci_234615_G	3144	3.575748	10.11	9542	41.44	3	6.807010869	0.3	0.88473958	7
optimal_loci_234616_G	1297	1.829649	0	2280	44.94	4	8.848617147	0.198	0.884816014	7
optimal_loci_234749_G	1021	1.425687	29.58	9910	38	1	3.071564224	0.083	0.889894565	6
optimal_loci_234817_G	1194	3.324183	4.02	3681	55.19	4	6.092819488	0.603	0.892747595	10
optimal_loci_234819_G	2006	3.324183	1.94	1296	42.27	5	4.874255591	0.305	0.892760794	10
optimal_loci_234828_G	1076	3.324183	15.15	3983	43.68	3	6.023422377	0.29	0.892895731	10
optimal_loci_234857_G	1541	2.893711	10.19	2001	49.31	4	35.50989733	0.3	0.893875656	10
optimal_loci_234858_G	1419	2.893711	5.99	2624	36.78	4	35.50989733	0.01	0.893891482	10
optimal_loci_234881_G	1532	3.689452	12.14	4414	42.42	2	2.304003097	0.18	0.895216893	10
optimal_loci_234892_G	1156	4.466723	0	2298	39.1	8	6.11217481	0.167	0.89580686	10
optimal_loci_234906_G	2395	4.466723	9.14	6913	53.06	2	35.82548005	0.544	0.896490732	10
optimal_loci_234908_G	1120	4.466723	17.68	10005	53.66	2	35.82548005	0.577	0.896516678	10
optimal_loci_234981_G	1031	2.622481	2.91	5610	42.87	3	0.087587551	0.184	0.899110205	5
optimal_loci_235141_G	1206	2.756633	16.92	14229	30.51	2	49.19475712	0.185	0.904550268	4

optimal_loci_235172_G	1069	4.137844	0	1001	38.16	1	5.89244858	0.09	0.906078215	6
optimal_loci_235216_G	3596	5.621854	2.31	6791	48.05	2	29.60531011	0.497	0.908673051	9
optimal_loci_235220_G	1565	5.621854	0	12215	61.27	2	29.60531011	0.781	0.908718565	9
optimal_loci_235232_G	1494	5.835868	17.6	7157	50.06	2	43.98984169	0.315	0.909544439	8
optimal_loci_235233_G	1313	5.835868	10.89	5811	42.19	2	43.98984169	0.165	0.909557252	8
optimal_loci_235251_G	1150	3.083865	12.7	7879	54.6	4	10.12834419	0.464	0.910338787	7
optimal_loci_235293_G	1343	3.428667	0	3717	52.79	3	24.7504777	0.422	0.911626002	7
optimal_loci_235294_G	1174	3.428667	0	2150	37.22	2	37.12571655	0.122	0.911640569	7
optimal_loci_235393_G	1466	3.230614	6.62	7445	58.59	3	3.839368533	0.651	0.916463159	8
optimal_loci_235394_G	1572	3.230614	0	9055	37.34	3	3.839368533	0.192	0.916476668	8
optimal_loci_235397_G	1344	3.230614	0	12114	46.94	2	0.11815611	0.353	0.916502337	8
optimal_loci_235409_G	1273	3.227189	0	13728	56.24	2	3.693697385	0.659	0.916573745	8
optimal_loci_235416_G	2339	3.227189	0	3583	40.53	4	2.766565678	0.505	0.916649927	8
optimal_loci_235467_G	1434	3.475659	18.9	1344	30.54	2	18.58522069	0.154	0.918219225	10
optimal_loci_235522_G	1030	3.451978	5.24	5037	47.28	2	21.98076889	0.319	0.920431773	11
optimal_loci_235525_G	1044	3.451978	0	7528	44.82	3	14.65384593	0.296	0.920452675	11
optimal_loci_235544_G	1018	4.712294	32.61	1292	38.7	2	39.02081559	0.127	0.92156387	6
optimal_loci_235546_G	1685	4.718129	1.72	2875	56.26	2	39.02081559	0.495	0.921577153	6
optimal_loci_235589_G	1302	5.175714	2.76	6533	46.08	2	2.667798716	0.179	0.924500433	5
optimal_loci_235792_G	1645	4.244915	14.35	1001	43.16	1	14.37370625	0.445	0.934377508	5
optimal_loci_235800_G	1556	4.835822	15.23	15532	39.65	1	14.37370625	0.37	0.934499439	5
optimal_loci_235815_G	1273	4.337274	0	1001	45.95	6	8.338401395	0.183	0.935326303	5
optimal_loci_235821_G	1205	4.337274	0	4529	57.26	5	10.00608167	0.614	0.935366924	5
optimal_loci_235855_G	1106	4.629696	0	8683	37.07	2	14.54115726	0	0.935881582	5
optimal_loci_235932_G	3137	8.032571	0	4432	50.33	3	33.30088751	0.517	0.940652138	11
optimal_loci_235933_G	2251	8.03694	2	2001	52.15	4	25.66610937	0.413	0.940679972	11
optimal_loci_235934_G	1367	8.127006	0	1001	54.57	5	19.56698701	0.609	0.940968775	12
optimal_loci_235935_G	1756	8.208402	32.46	3260	33.37	4	5.106768777	0.174	0.941028562	12
optimal_loci_235941_G	1198	8.208402	2.42	1730	55.75	3	5.88843338	0.731	0.941080251	12
optimal_loci_235948_G	3027	9.377189	0	4460	57.28	2	7.50084563	0.541	0.941155888	12
optimal_loci_235977_G	1895	9.534027	9.76	2777	40.89	2	43.25789239	0.287	0.942332164	14
optimal_loci_236016_G	1055	11.269247	27.2	1835	42.36	3	9.012274496	0.211	0.943793897	14
optimal_loci_236036_G	1098	9.793157	0	3450	44.89	5	32.72634858	0.26	0.94455458	16

optimal_loci_236038_G	1154	9.793157	0	2001	61.09	5	32.72634858	0.59	0.944566269	16
optimal_loci_236039_G	1307	9.793157	0	1001	44.37	3	50.70468857	0.483	0.944615088	16
optimal_loci_236049_G	1691	6.825543	12.66	6993	40.56	3	49.1918572	0.211	0.945127011	15
optimal_loci_236051_G	1731	6.775047	0	1308	42.05	6	9.816936084	0.407	0.945491678	11
optimal_loci_236070_G	1086	6.234291	38.4	2237	51.47	3	0.370955017	0.386	0.946005899	11
optimal_loci_236098_G	1894	6.838091	18.8	5866	47.72	4	41.78507046	0.502	0.948174562	9
optimal_loci_236100_G	1751	6.838091	0	2478	52.02	5	35.14605379	0.488	0.948204191	9
optimal_loci_236118_G	2082	5.779896	2.98	1001	54.13	2	4.273612617	0.575	0.949034487	6
optimal_loci_236220_G	1096	5.154946	0	2001	58.02	2	0.027827405	0.695	0.953784444	3
optimal_loci_236255_G	1167	6.483136	0	3332	38.38	2	1.758656551	0.082	0.955877268	5
optimal_loci_236258_G	1472	6.516435	0	4047	60.59	2	1.758656551	0.597	0.95596514	5
optimal_loci_236349_G	1459	8.504187	0	19669	46.26	1	51.24283922	0.287	0.958957277	9
optimal_loci_236364_G	1129	8.328181	0	4723	52.87	2	2.236316736	0.652	0.959231161	12
optimal_loci_236378_G	2372	8.9058	1.64	2001	36.38	3	10.0368677	0.205	0.960718117	11
optimal_loci_236380_G	1562	8.9058	3.27	2465	53.58	3	11.48054888	0.58	0.960851946	12
optimal_loci_236381_G	1298	8.9058	0	4060	55.39	3	11.48054888	0.45	0.96086533	12
optimal_loci_236382_G	1626	8.9058	0	4614	56.39	4	9.997335015	0.498	0.960890713	12
optimal_loci_236404_G	1295	7.627151	0	1475	47.1	6	23.60960396	0.355	0.961228529	12
optimal_loci_236448_G	2732	6.824329	1.13	8667	53.66	3	1.946068277	0.487	0.963197761	15
optimal_loci_236451_G	1505	6.824329	0	6161	52.89	3	1.946068277	0.43	0.963229085	15
optimal_loci_236455_G	1037	6.824329	0	2841	52.36	4	1.459551208	0.418	0.96326087	15
optimal_loci_236472_G	3474	6.374364	2.62	12938	56.73	3	3.876670344	0.501	0.963857039	14
optimal_loci_236486_G	1091	6.197435	17.23	1001	32.53	3	23.2954489	0.056	0.964935492	13
optimal_loci_236506_G	1228	5.832465	0	1001	35.34	3	9.923443437	0.286	0.966134568	11
optimal_loci_236509_G	1131	5.832465	27.59	6642	41.37	4	11.34235243	0.304	0.966181902	11
optimal_loci_236517_G	1100	5.794235	0	1001	39.72	2	14.54559463	0.378	0.966315781	11
optimal_loci_236523_G	1441	6.216131	5.9	2001	56.69	2	0.474660884	0.271	0.966673467	11
optimal_loci_236586_G	1084	6.114044	0	1598	51.01	4	0.129348208	0.466	0.969385082	7
optimal_loci_236597_G	1061	6.043179	0	3935	60.6	6	0.007265265	0.733	0.969627207	7
optimal_loci_236662_G	1295	6.280983	0	1001	49.57	3	33.14505773	0.51	0.973160022	8
optimal_loci_236675_G	1868	5.501157	9.85	3402	55.08	3	9.005356596	0.618	0.973923903	6
optimal_loci_236680_G	1041	5.160877	0	1001	39.86	3	9.005356596	0.355	0.973993238	6
optimal_loci_236682_G	1048	5.160877	16.22	2308	42.55	2	0.366060029	0.268	0.974041042	6

optimal_loci_236698_G	1526	4.983118	10.29	2354	36.1	6	29.93221135	0.055	0.974913428	8
optimal_loci_236715_G	1295	4.983118	5.95	3120	38.45	3	14.07626181	0.071	0.975417521	8
optimal_loci_236774_G	1364	2.756259	8.65	1822	46.26	2	1.968824735	0.391	0.978639456	7
optimal_loci_236777_G	2203	2.756259	2.02	2766	52.7	2	1.968824735	0.307	0.978658185	7
optimal_loci_236817_G	1811	11.690497	6.24	1766	43.4	5	28.96934848	0.271	0.980826353	5
optimal_loci_236820_G	1684	11.690497	0	2028	37.41	5	28.96934848	0.198	0.980859632	5
optimal_loci_236832_G	3692	11.690497	0	1355	43.82	3	1.848282677	0.302	0.981455616	7
optimal_loci_236900_G	2222	0.712458	34.02	2567	47.56	2	20.90668025	0.407	0.985196127	5
optimal_loci_236917_G	1079	0.684125	10.29	2089	35.68	2	20.90668025	0.195	0.985333195	5
optimal_loci_236953_G	1840	0.388682	10.49	4167	46.57	2	0.945815294	0.391	0.98710903	6
optimal_loci_236965_G	1714	0.349876	28.76	1629	38.09	4	11.01467271	0.222	0.987619207	6
optimal_loci_237011_G	1286	0.286774	39.04	8774	34.75	3	13.03805185	0	0.989719147	4
optimal_loci_237012_G	1884	0.286774	34.55	6745	32.59	3	13.03805185	0.121	0.989731155	4
optimal_loci_237323_G	1091	1.867798	0	5864	48.76	1	0.265629199	0.481	0.986821392	3
optimal_loci_237329_G	1252	1.76457	4.71	1001	27.47	1	0.265629199	0.213	0.986732326	3
optimal_loci_237332_G	2332	1.753805	0	5484	38.89	1	0.265629199	0.208	0.986550714	3
optimal_loci_237414_G	1271	1.56487	0	1510	37.68	2	0.676662174	0.179	0.971200824	2
optimal_loci_237488_G	1432	0.86848	28.7	2044	41.96	2	7.602518905	0.133	0.963541337	2
optimal_loci_237627_G	1633	1.447731	11.08	4151	38.33	3	6.309054669	0.219	0.951704359	3
optimal_loci_237682_G	1056	2.272642	0	2001	39.96	2	0.307841229	0.13	0.946657839	9
optimal_loci_237697_G	1480	2.503832	0	2001	42.43	3	6.20772626	0.189	0.945589963	9
optimal_loci_237727_G	1226	2.58698	0	1001	42.25	2	18.42423693	0.299	0.941947784	11
optimal_loci_237728_G	1987	2.581097	7.25	2477	44.18	3	16.14521133	0.419	0.941906813	11
optimal_loci_237729_G	1439	2.581097	7.86	4646	51.42	3	16.14521133	0.616	0.941877125	12
optimal_loci_237734_G	1393	2.581097	36.83	5991	45.51	3	16.14521133	0.368	0.941802308	12
optimal_loci_237735_G	1361	2.581097	0	4546	46.21	3	16.14521133	0.244	0.941775842	12
optimal_loci_237768_G	1330	2.720456	0	11057	33.53	1	1.185631488	0	0.938133388	13
optimal_loci_237793_G	1368	2.653943	0	6562	41.95	1	22.29840546	0.258	0.936315568	11
optimal_loci_237799_G	1582	2.653943	10.56	1001	36.59	1	22.29840546	0.071	0.936128645	11
optimal_loci_237867_G	1154	3.921311	0	3891	37.17	1	38.37641797	0.115	0.932952253	13
optimal_loci_237871_G	1593	3.069063	9.92	1001	48.02	1	38.37641797	0.429	0.932720073	11
optimal_loci_237912_G	1148	4.99331	37.89	2017	47.64	3	1.029288094	0.446	0.929095586	9
optimal_loci_237950_G	2468	1.995311	1.18	2530	44.08	1	10.78613988	0.309	0.926086245	6

optimal_loci_237959_G	1017	1.995311	4.03	9780	51.03	2	5.338302969	0.619	0.925505238	6
optimal_loci_237975_G	1564	2.029543	13.62	2621	33.63	2	20.20641309	0.126	0.922022289	6
optimal_loci_238023_G	1055	0.182944	0	10018	40.66	1	0.29222959	0.204	0.916246337	5
optimal_loci_238024_G	1477	0.182944	0	1192	48.88	1	0.29222959	0.656	0.915992601	5
optimal_loci_238071_G	1836	7.151505	12.25	2484	40.68	2	15.19423851	0.231	0.9114787	8
optimal_loci_238100_G	1482	8.198409	0	1001	52.76	2	3.90964965	0.468	0.910243443	8
optimal_loci_238128_G	1055	7.352549	10.52	3499	39.33	3	38.0251897	0.329	0.90559641	8
optimal_loci_238164_G	1042	7.352549	12.28	10828	38.86	1	50.96586211	0.117	0.903633187	8
optimal_loci_238171_G	2169	7.352549	14.52	1487	40.94	1	50.96586211	0.295	0.903462106	8
optimal_loci_238186_G	1061	6.872562	0	3015	52.4	3	3.555449872	0.562	0.90246511	8
optimal_loci_238232_G	8267	7.796719	15.19	18180	31.3	1	56.96225817	0.162	0.899308223	8
optimal_loci_238241_G	1356	7.796719	0	4826	38.42	4	30.0717534	0.038	0.898654267	8
optimal_loci_238349_G	1111	5.363033	0	6428	45	1	7.540472236	0.357	0.890663571	5
optimal_loci_238350_G	1163	5.363033	0	5181	52.79	1	7.540472236	0.598	0.890640733	5
optimal_loci_238375_G	1107	4.161429	0	1001	57.54	2	15.5194822	0.801	0.884510476	3
optimal_loci_238472_G	1299	1.032715	3.16	1001	42.18	2	3.461394478	0.361	0.873234505	2
optimal_loci_238496_G	1246	1.808467	14.77	2887	38.2	1	2.342062349	0.107	0.871564542	2
optimal_loci_238665_G	1307	1.56546	0	1158	37.41	2	3.664403858	0.305	0.84684467	1
optimal_loci_238754_G	1195	4.737437	12.38	2748	37.65	1	12.03486097	0.02	0.836530073	5
optimal_loci_238755_G	1099	4.953374	0	1437	40.12	1	12.03486097	0.373	0.836506062	5
optimal_loci_238758_G	1904	4.953374	17.96	2490	38.39	1	12.03486097	0.3	0.836356062	5
optimal_loci_238819_G	1056	4.586489	32.01	1714	49.9	1	8.347436938	0.321	0.830521245	6
optimal_loci_238821_G	1674	4.586489	26.7	8230	46.77	1	8.347436938	0.434	0.830205092	6
optimal_loci_238863_G	1584	5.015371	33.96	3101	38.44	1	8.622610041	0.164	0.82418315	3
optimal_loci_238948_G	3408	1.723582	28.29	2375	32.86	1	13.16741202	0.131	0.813862234	4
optimal_loci_238965_G	1317	1.723582	0	13823	40.24	1	13.16741202	0.134	0.813519744	4
optimal_loci_239023_G	1354	0.830904	18.83	5715	39.51	2	1.182472579	0.14	0.80689989	6
optimal_loci_239030_G	1474	0.851701	0	2181	40.29	3	2.279848906	0.129	0.806687253	6
optimal_loci_239044_G	1039	1.064792	5.2	2608	44.56	1	18.68971353	0.319	0.804184963	4
optimal_loci_239096_G	1479	1.452708	0	16142	58.14	1	210.3457443	0.606	0.798729799	4
optimal_loci_239188_G	1027	0.214013	0	2137	40.89	1	22.10912462	0.258	0.786183242	2
optimal_loci_239193_G	1335	0.214013	0	5089	36.25	1	22.10912462	0.287	0.786123535	2
optimal_loci_239347_G	1341	0.966047	36.99	15862	34.37	1	1.192940787	0.186	0.771854762	1

optimal_loci_239613_G	2785	1.311004	21.9	2495	35.47	2	16.21180011	0.153	0.744217363	3
optimal_loci_239618_G	1074	1.311004	0	1168	35.75	1	27.32460569	0.216	0.743899377	3
optimal_loci_239625_G	1265	1.311004	0	7449	40.79	2	13.66230285	0.111	0.743780842	3
optimal_loci_239863_G	1744	0.696661	3.61	5139	42.94	1	27.76303224	0.365	0.725287619	3
optimal_loci_239881_G	1350	0.642382	0	19248	39.48	1	4.819363941	0.18	0.724265147	3
optimal_loci_239968_G	2125	0.951654	24.52	1001	44.42	3	10.66907216	0.28	0.716686264	5
optimal_loci_240012_G	1247	0.865346	19.41	15739	34.48	1	0.028576965	0.145	0.712851667	3
optimal_loci_240014_G	1704	0.865346	37.32	17583	35.03	1	0.028576965	0.252	0.712809524	3
optimal_loci_240136_G	1072	0.333696	0	2183	43.09	2	0.213663782	0.091	0.703487271	1
optimal_loci_240290_G	1571	0.581251	8.34	12073	36.09	1	22.62691296	0.073	0.684206319	9
optimal_loci_240293_G	1095	0.581251	0	8189	36.71	1	22.62691296	0.297	0.684135183	9
optimal_loci_240298_G	1070	0.544182	12.9	1001	38.41	1	22.62691296	0.246	0.683926777	9
optimal_loci_240299_G	1114	0.544182	0	16408	40.12	2	37.42998125	0	0.683643791	9
optimal_loci_240342_G	1051	0.425238	12.56	10922	48.62	2	40.72428502	0.448	0.679612454	9
optimal_loci_240394_G	1023	0.275766	9.48	4512	40.17	1	17.32849652	0.21	0.675959835	9
optimal_loci_240396_G	1940	0.275766	7.99	1810	41.23	2	8.664248258	0.326	0.675910348	9
optimal_loci_240399_G	1478	0.275766	28.69	1001	35.31	2	8.664248258	0.192	0.67552663	9
optimal_loci_240402_G	1245	0.275766	30.12	3131	36.94	2	8.664248258	0.028	0.675491886	9
optimal_loci_240602_G	1335	0.269813	12.96	5607	45.61	2	1.811099366	0.277	0.662339231	2
optimal_loci_240632_G	1707	0.631504	3.57	2439	46.92	2	10.90183562	0.373	0.658911136	2
optimal_loci_240729_G	1497	0.465549	12.36	1417	35.87	2	0.273189636	0.257	0.645458553	2
optimal_loci_240735_G	1182	0.465549	12.77	6942	36.71	2	0.273189636	0.144	0.645363132	2
optimal_loci_240876_G	1288	0.271511	26.55	1791	31.36	1	12.63473843	0.263	0.629126941	3
optimal_loci_241003_G	1512	0.240366	8.07	9440	34.19	1	1.349989385	0.102	0.620447326	4
optimal_loci_241008_G	1057	0.240366	27.44	13417	37.93	1	1.349989385	0.246	0.620382821	4
optimal_loci_241104_G	1671	0.570313	0	3136	36.5	4	5.084757628	0.158	0.612975311	4
optimal_loci_241171_G	1001	0.482155	0	2001	45.35	2	1.195896152	0.449	0.605913535	4
optimal_loci_241230_G	1214	0.366645	15.57	1001	37.97	1	9.259766043	0.189	0.600769945	3
optimal_loci_241284_G	1970	0.013371	5.18	2001	36.59	1	4.265386025	0.18	0.597026172	3
optimal_loci_242236_G	1067	0.633814	23.9	16083	37.58	1	18.37321293	0.074	0.492696355	1
optimal_loci_242556_G	2612	0.042361	0	2628	39.2	4	0.035363185	0.122	0.458798626	1
optimal_loci_242675_G	1105	0.254837	9.5	1215	51.13	2	0.406100779	0.438	0.447445165	2
optimal_loci_242736_G	1085	0.471442	0	2564	36.31	1	1.466478705	0.176	0.441348187	2

optimal_loci_243300_G	1658	0.259696	12.73	16089	43.96	1	0.119669684	0.284	0.368976245	4
optimal_loci_243301_G	1700	0.259696	18.53	11133	30.7	1	0.119669684	0.073	0.368885476	4
optimal_loci_243311_G	1419	0.259696	15.08	11646	37.27	1	0.119669684	0.247	0.368427875	4
optimal_loci_243330_G	1176	0.262935	12.41	2993	43.28	1	0.433766583	0.36	0.365722033	5
optimal_loci_243398_G	2619	0.393519	30.58	1001	32.98	2	2.956948361	0.14	0.357150623	2
optimal_loci_244009_G	1981	0.307829	14.54	4785	38.06	3	0.815890807	0.197	0.292860769	1
optimal_loci_244110_G	1945	0.195305	27.4	14442	37.99	1	7.201711661	0.147	0.282684267	2
optimal_loci_244203_G	1262	0.293409	13.15	2001	41.91	1	0.032357511	0.403	0.273903223	2
optimal_loci_244324_G	1173	0.181465	0	13488	39.3	1	0.261277516	0.137	0.261894066	1
optimal_loci_244428_G	1555	0.071478	0	5392	40.19	1	36.5873831	0.196	0.248207033	4
optimal_loci_244439_G	1458	0.071604	0	13880	42.24	1	36.5873831	0.196	0.247797656	4
optimal_loci_244502_G	2505	0.276457	0	2001	62.07	1	1090.895878	0.775	0.241236484	4
optimal_loci_244521_G	2889	0.350988	7.44	6236	41.12	1	94.60190765	0.295	0.239015586	4
optimal_loci_248922_G	1073	0.176505	0	2001	38.95	1	12.31339092	0.126	0.117301614	1
optimal_loci_249178_G	1248	0.104462	17.07	2266	38.22	1	0.094938333	0.209	0.135284358	1
optimal_loci_250162_G	1594	0.056531	0	3492	42.91	1	0.843850412	0.254	0.194250429	2
optimal_loci_250167_G	1656	0.056531	1.75	8155	51.69	1	0.843850412	0.619	0.19437843	2
optimal_loci_250331_G	1399	0.332307	0	1001	46.03	1	9.248119705	0.345	0.203075328	1
optimal_loci_251259_G	1390	0.291191	0	14625	46.97	2	2.826669347	0.461	0.255582644	2
optimal_loci_251281_G	1401	0.211503	20.06	9326	38.54	1	0.090746257	0.117	0.257012936	2
optimal_loci_251383_G	1008	0.414332	0	1780	37.79	1	13.73609138	0.048	0.26163451	1
optimal_loci_251605_G	1321	0.011814	4.84	8987	32.7	1	0.071918559	0.069	0.273369422	3
optimal_loci_251640_G	1513	0.102824	3.44	2001	51.09	2	46.03009779	0.362	0.275842748	3
optimal_loci_251643_G	1385	0.102824	39.78	1855	39.56	2	46.03009779	0.314	0.27592798	3
optimal_loci_251856_G	1020	0.01893	0	15309	41.66	2	12.14830752	0.302	0.288956704	1
optimal_loci_252525_G	1329	0.053973	0	1481	41.3	1	3.258974981	0.159	0.322079951	2
optimal_loci_252544_G	1459	0.167915	15.35	7073	44.48	1	25.68150488	0.416	0.322874265	3
optimal_loci_252609_G	1715	0.44717	0	13904	38.07	1	33.70648043	0.175	0.326724148	4
optimal_loci_252636_G	1290	0.499771	0	2327	34.18	1	0.987923138	0.194	0.32776712	3
optimal_loci_252700_G	1121	0.649517	0	3727	46.65	2	21.48091522	0.435	0.330334482	4
optimal_loci_252745_G	1017	0.510956	10.42	1623	52.5	1	4.997590966	0.645	0.332793981	2
optimal_loci_253330_G	1185	0.263832	39.41	6607	33.83	1	3.559629209	0.03	0.362041151	4
optimal_loci_253362_G	1834	0.223269	0	10103	47.05	1	5.748642192	0.408	0.36282021	4

optimal_loci_253408_G	1852	0.228629	0	14805	34.5	1	9.167418616	0.152	0.365621389	4
optimal_loci_253410_G	1633	0.228629	10.78	18856	45.62	1	9.167418616	0.413	0.365656842	4
optimal_loci_253521_G	1109	0.061873	0	13598	40.93	1	35.36578175	0.12	0.370798646	6
optimal_loci_253522_G	1366	0.061873	0	2863	40.19	1	35.36578175	0.184	0.370890345	6
optimal_loci_253556_G	1308	0.135543	0	2631	46.86	2	4.712705811	0.339	0.372451325	6
optimal_loci_253600_G	2069	0.194147	3.82	13048	36.92	1	2.183733993	0.068	0.373996386	7
optimal_loci_253626_G	1377	0.260906	19.39	10287	44.8	1	7.485189881	0.325	0.375032444	8
optimal_loci_253634_G	2373	0.260906	8.85	1001	51.41	2	21.16734203	0.422	0.375104995	8
optimal_loci_253669_G	1111	0.422093	7.92	3014	55.26	2	1.109797779	0.651	0.377608996	7
optimal_loci_253701_G	1570	0.428551	22.04	18737	34.77	1	7.464667464	0.008	0.378456571	6
optimal_loci_253717_G	1400	0.431506	0	1922	38.92	1	7.423529894	0.207	0.379941368	4
optimal_loci_253720_G	1471	0.431506	9.99	16717	33.58	1	7.423529894	0.103	0.380070848	4
optimal_loci_253932_G	1203	0.41254	34.16	1001	45.71	1	2.273566413	0.219	0.391467109	3
optimal_loci_253933_G	1594	0.41254	0	2001	30.74	1	2.273566413	0.093	0.391561897	3
optimal_loci_253939_G	1751	0.416753	0	18344	37.63	1	2.273566413	0.003	0.391704925	3
optimal_loci_254110_G	1738	1.664432	25.49	17383	37.74	1	12.12222427	0.113	0.396769312	1
optimal_loci_254232_G	1153	1.221316	0	13032	38.07	1	2.312574739	0.326	0.402534309	4
optimal_loci_254305_G	1185	1.268555	0	16869	51.98	1	185.5291197	0.429	0.405419739	4
optimal_loci_254308_G	1037	1.252857	0	2890	33.75	1	185.5291197	0.118	0.40562934	6
optimal_loci_254318_G	1344	1.252857	24.48	12847	38.09	1	185.5291197	0.257	0.40571648	6
optimal_loci_254375_G	1390	0.786588	24.03	12656	44.74	2	2.487167865	0.318	0.409943268	8
optimal_loci_254377_G	1142	0.775669	0	14801	42.99	2	2.487167865	0.335	0.409962041	8
optimal_loci_254413_G	1032	0.45098	19.09	5857	38.85	1	0.218237523	0.112	0.411563217	6
optimal_loci_254416_G	1217	0.45098	26.05	2651	41.74	1	0.218237523	0.201	0.411589655	6
optimal_loci_254418_G	1316	0.45098	2.2	2001	44.75	1	0.218237523	0.267	0.411663431	6
optimal_loci_254422_G	1358	0.45098	0	6663	53.09	1	0.218237523	0.525	0.411704231	6
optimal_loci_254673_G	1013	0.592459	19.25	1592	41.95	1	15.14804298	0.098	0.427345256	4
optimal_loci_254676_G	1779	0.592459	30.69	5658	34.23	1	15.14804298	0.233	0.427460165	4
optimal_loci_254692_G	1092	0.534116	0	3247	43.22	2	26.29676889	0.261	0.428067876	4
optimal_loci_254694_G	1064	0.534116	0	4992	39.47	2	26.29676889	0.101	0.428087104	4
optimal_loci_254925_G	1145	1.945442	0	2394	37.72	1	2.02168132	0.03	0.438691554	1
optimal_loci_255412_G	1322	1.210496	0	9306	53.63	1	21.43449471	0.602	0.460703913	2
optimal_loci_255452_G	1445	1.269899	2.28	7779	40.69	2	1.050345179	0.284	0.461955384	4

optimal_loci_255556_G	1254	0.874345	0	6233	38.99	1	21.1750647	0.263	0.465586232	3
optimal_loci_255563_G	1763	0.874345	22.75	9365	48.38	2	16.22487922	0.414	0.465613642	3
optimal_loci_255654_G	1067	0.030672	38.99	2558	66.35	2	15.9209879	0.635	0.470676288	3
optimal_loci_255675_G	1630	0.030672	3.25	8408	59.63	3	14.96959866	0.634	0.471667862	3
optimal_loci_255679_G	1138	0.030672	0	19419	34.97	1	21.9745335	0.224	0.471764226	3
optimal_loci_255770_G	1280	1.374214	31.95	1359	41.32	3	0.451301915	0.251	0.479213522	5
optimal_loci_255775_G	1083	1.374214	23.82	3711	33.33	2	0.258278883	0.233	0.479284357	5
optimal_loci_255779_G	1430	1.147514	10.84	9625	41.74	1	2.111712888	0.355	0.479612901	6
optimal_loci_255824_G	1016	0.856567	0	3173	61.71	3	5.126806066	0.471	0.481583622	7
optimal_loci_255827_G	1139	0.856567	0	4990	50.04	3	5.126806066	0.354	0.481599524	7
optimal_loci_255888_G	1027	0.772546	2.73	2579	35.05	1	5.432103828	0	0.483808954	5
optimal_loci_255924_G	1095	0.820266	13.87	9310	53.51	1	10.32213959	0.635	0.485409343	4
optimal_loci_256135_G	1030	0.294235	6.7	16790	32.71	1	2.992741361	0.068	0.493836499	1
optimal_loci_256401_G	1087	0.723175	0	1923	38.08	2	0.02196994	0.202	0.504079272	2
optimal_loci_256427_G	1042	1.291442	7.2	4715	39.92	1	54.24198674	0.033	0.506244384	2
optimal_loci_256564_G	2090	2.166557	14.4	13923	40.57	1	4.463879735	0.284	0.511923308	10
optimal_loci_256591_G	1321	3.464695	0	2090	41.86	3	3.003830273	0.279	0.51354155	11
optimal_loci_256599_G	1201	3.003233	0	1001	57.03	2	149.5423779	0.753	0.513910334	11
optimal_loci_256611_G	1195	3.003233	38.83	2001	42.84	2	21.74874489	0.423	0.514148526	11
optimal_loci_256616_G	1219	3.546912	8.12	9338	43.06	2	1.240698793	0.396	0.51440571	11
optimal_loci_256631_G	1070	3.546912	10.09	2001	57.66	1	9.385623896	0.476	0.515079478	11
optimal_loci_256641_G	1101	3.546912	0	2702	53.58	2	4.692811948	0.698	0.515235511	11
optimal_loci_256643_G	1026	3.839311	12.77	1393	50.38	3	15.85998052	0.511	0.515456112	11
optimal_loci_256644_G	1921	3.839311	0	2507	33.68	3	15.85998052	0.049	0.515467236	11
optimal_loci_256646_G	1250	3.839311	12.72	1001	29.04	3	15.85998052	0.147	0.515571642	11
optimal_loci_256671_G	1174	1.524971	0	2074	42.33	2	8.231807791	0.166	0.517042332	10
optimal_loci_257043_G	3297	1.954656	0	4444	46.83	3	1.185633609	0.357	0.533708117	5
optimal_loci_257063_G	1762	4.164617	22.02	10420	46.19	1	0.943299162	0.279	0.534620498	5
optimal_loci_257067_G	3259	4.164617	11.78	4201	55.78	1	0.943299162	0.535	0.534661823	5
optimal_loci_257069_G	1186	4.164617	0	2356	41.73	1	0.943299162	0.267	0.534696112	5
optimal_loci_257098_G	1919	2.707125	0	13078	51.38	1	0.776100801	0.447	0.535568288	5
optimal_loci_257181_G	1162	0.51691	18.59	2001	52.06	2	2.177765896	0.699	0.540163318	2
optimal_loci_257190_G	1568	0.532815	0	11340	51.02	1	15.63992217	0.617	0.540549597	3

optimal_loci_257263_G	1139	0.848381	17.91	1001	42.4	2	47.34418506	0.264	0.544804032	3
optimal_loci_257267_G	1557	0.867852	6.49	1001	53.24	1	176.4343507	0.634	0.545835259	2
optimal_loci_257371_G	1488	21.212109	0	2213	43.68	3	25.94823509	0.401	0.550479403	3
optimal_loci_257500_G	1285	0.513894	8.33	4100	48.94	2	8.39126897	0.392	0.554466345	4
optimal_loci_257502_G	1248	0.513894	0	2297	45.75	2	8.39126897	0.345	0.554482448	4
optimal_loci_257541_G	2500	0.513894	4.08	2001	43.2	1	14.1375841	0.263	0.555538461	3
optimal_loci_259947_G	1631	0.459307	21.03	2001	34.88	1	21.27594365	0.064	0.674723796	1
optimal_loci_260062_G	1160	0.438312	12.07	9156	44.05	3	0.616455974	0.414	0.680422736	3
optimal_loci_260134_G	1111	0.938652	39.69	1001	42.3	1	61.18717599	0.299	0.68330302	3
optimal_loci_260141_G	1080	0.774389	0	2507	35	5	8.305668568	0.082	0.684227295	4
optimal_loci_260207_G	1858	0.9862	6.94	1273	44.99	5	24.93180294	0.306	0.688143647	12
optimal_loci_260238_G	1331	1.119254	15.7	7021	36.06	1	1.710791349	0.18	0.690934717	13
optimal_loci_260241_G	1116	1.119254	2.6	4774	59.85	1	1.710791349	0.603	0.690956263	13
optimal_loci_260260_G	2318	1.283521	1.21	5429	48.27	2	0.833453712	0.414	0.69154831	13
optimal_loci_260261_G	3203	1.283521	2.15	2001	52.66	3	1.386190364	0.515	0.691574914	13
optimal_loci_260269_G	1224	1.283521	0	1001	39.86	3	1.302246127	0.108	0.691756606	13
optimal_loci_260274_G	1415	1.283521	0	1001	45.08	4	23.79072504	0.521	0.692023198	13
optimal_loci_260276_G	1648	1.283521	1.88	4698	47.08	4	23.79072504	0.395	0.692108403	13
optimal_loci_260278_G	1124	1.283521	0	6759	45.9	4	23.79072504	0.387	0.692126441	13
optimal_loci_260288_G	1044	1.283521	0	7704	34.38	2	16.68429527	0.221	0.692297062	13
optimal_loci_260289_G	1674	1.176545	0	8813	47.78	2	16.68429527	0.377	0.692306767	13
optimal_loci_260319_G	1793	1.956403	0	12018	51.47	1	13.73393641	0.548	0.693076646	12
optimal_loci_260336_G	1263	1.956403	9.9	1766	39.27	2	5.633547591	0.191	0.693911917	12
optimal_loci_260418_G	1304	1.317766	26.3	5079	43.4	4	10.79162991	0.258	0.699327672	7
optimal_loci_260477_G	1318	1.968136	26.56	5011	37.63	2	21.09425035	0.426	0.702787636	9
optimal_loci_260479_G	1160	1.968136	3.02	1468	48.18	2	21.09425035	0.525	0.702888665	9
optimal_loci_260484_G	2705	2.065234	1.52	19495	44.21	1	1.218343917	0.379	0.703455174	9
optimal_loci_260489_G	1250	2.065234	13.2	15143	49.6	1	1.218343917	0.442	0.703505994	9
optimal_loci_260495_G	1082	2.069264	9.89	2526	51.2	1	1.218343917	0.558	0.703617884	9
optimal_loci_260499_G	2675	2.341785	6.8	2001	57.45	1	1.218343917	0.503	0.703683372	10
optimal_loci_260564_G	2429	2.766827	0	1402	41.21	4	12.66464838	0.384	0.706223096	9
optimal_loci_260570_G	1847	2.922754	3.57	13874	37.79	3	8.394445862	0.135	0.706552428	9
optimal_loci_260602_G	1398	1.389535	7.94	1001	47.35	5	32.84207413	0.463	0.70806495	4

optimal_loci_260765_G	1221	1.42487	10.97	2001	31.85	3	6.156118367	0.084	0.715094002	4
optimal_loci_260782_G	1145	1.405874	19.21	3750	43.14	2	5.928576719	0.248	0.715927864	4
optimal_loci_260799_G	2732	0.470454	6.77	1530	41.87	2	6.40730521	0.238	0.717955865	5
optimal_loci_260802_G	1255	0.470454	10.36	7375	47.01	2	6.40730521	0.353	0.718007018	5
optimal_loci_260880_G	1238	0.589502	0	1001	39.57	1	48.83970593	0.188	0.720804774	6
optimal_loci_260963_G	2144	0.514488	33.3	8894	38.05	1	4.963980972	0.194	0.724144947	8
optimal_loci_260978_G	1242	0.71122	0	10317	35.1	2	9.384461973	0.081	0.724526666	9
optimal_loci_260985_G	1426	0.71122	0	14403	47.26	1	5.500718281	0.491	0.724834459	9
optimal_loci_260988_G	1228	0.733963	0	2104	38.84	1	5.896354053	0.143	0.725323814	8
optimal_loci_261014_G	1104	0.474898	9.87	2001	33.87	2	12.82032801	0.069	0.727509239	8
optimal_loci_261023_G	1153	0.455439	8.15	4995	53.42	3	9.815964812	0.421	0.728232769	8
optimal_loci_261029_G	1007	0.449549	0	2034	49.75	4	18.07092446	0.389	0.728313529	8
optimal_loci_261037_G	1502	0.349736	1.93	2598	53.12	4	23.13951047	0.649	0.728663619	7
optimal_loci_261272_G	2183	1.4394	0	5139	48.28	1	5.946381381	0.429	0.741218811	1
optimal_loci_261498_G	2562	0.012998	0	2001	59.99	2	15.79648235	0.642	0.752272035	1
optimal_loci_261708_G	1046	1.940837	3.25	5118	38.62	1	17.08608298	0.168	0.762499168	9
optimal_loci_261732_G	1008	1.940837	15.38	3912	50.89	2	37.27638099	0.479	0.763607962	9
optimal_loci_261781_G	2164	1.661377	2.82	2809	49.35	3	3.008722972	0.427	0.765894765	9
optimal_loci_261784_G	1909	1.661377	0	2001	55	5	9.459740153	0.475	0.766014417	9
optimal_loci_261785_G	2029	1.661377	0	3996	46.77	5	9.459740153	0.402	0.766031876	9
optimal_loci_261786_G	1441	1.661377	0	4855	60.86	4	11.00552326	0.829	0.766050648	9
optimal_loci_261787_G	1343	1.661377	0	3203	39.31	4	11.00552326	0.233	0.766065964	9
optimal_loci_261793_G	1983	1.277627	9.93	5473	37.51	2	19.13626592	0.128	0.76623157	9
optimal_loci_261799_G	1166	1.33692	7.2	7801	42.36	1	3.019754098	0.399	0.766448339	9
optimal_loci_261928_G	1268	1.087301	12.62	5300	38.64	3	15.52355135	0.143	0.773429599	2
optimal_loci_261982_G	2124	0.84203	0	1001	52.77	3	25.34599191	0.551	0.776599263	2
optimal_loci_262113_G	2139	0.608678	13.09	1001	54.88	1	10.01601331	0.464	0.784790791	2
optimal_loci_262148_G	1973	0.577243	2.33	17207	47.84	2	9.703880981	0.335	0.786525543	3
optimal_loci_262218_G	2074	0.318453	6.12	2291	40.59	4	0.016978501	0.297	0.790355158	4
optimal_loci_262250_G	1199	0.12187	12.43	2441	36.53	3	22.50317014	0.2	0.79153518	3
optimal_loci_262299_G	1140	0.188103	0	4181	47.45	2	19.84677049	0.33	0.793660122	4
optimal_loci_262354_G	1153	2.058939	7.63	4067	37.81	3	12.38163997	0.285	0.797126755	9
optimal_loci_262370_G	1753	1.593231	16.03	2312	39.3	2	3.615953405	0.218	0.798114348	8

optimal_loci_262375_G	1366	1.593231	0	1342	34.26	2	7.012867173	0.214	0.798332096	8
optimal_loci_262398_G	1235	2.31158	0	2001	47.28	3	75.17734328	0.326	0.799247313	8
optimal_loci_262401_G	1130	2.31158	0	5338	59.82	3	75.17734328	0.783	0.799276517	8
optimal_loci_262405_G	1381	2.31158	15.93	4182	38.45	4	57.42214069	0.09	0.799338697	8
optimal_loci_262406_G	1026	2.31158	0	2607	41.81	4	57.42214069	0.231	0.799355588	8
optimal_loci_262409_G	2640	2.31158	0	2617	43.37	2	20.80192154	0.273	0.799453781	8
optimal_loci_262547_G	1515	1.630735	0	2984	44.68	2	18.67842085	0.289	0.804568315	3
optimal_loci_262575_G	1688	1.568143	17.54	2282	37.38	2	2.176419134	0.194	0.806053812	4
optimal_loci_262627_G	1094	1.225179	5.03	1164	38.11	1	9.767994694	0.223	0.808668126	5
optimal_loci_262649_G	1809	0.689645	0	5275	43.78	3	1.822804351	0.413	0.809993854	4
optimal_loci_262690_G	1205	0.763447	0	1001	31.28	1	1.444760995	0.168	0.811460606	6
optimal_loci_262733_G	1627	0.567219	39.7	1023	44.92	2	255.330569	0.329	0.814458827	8
optimal_loci_262734_G	1319	0.567219	10.16	8961	41.62	4	147.8145977	0.093	0.814528297	8
optimal_loci_262740_G	1131	0.506258	3.36	3447	31.38	5	35.36261336	0	0.814758849	9
optimal_loci_262771_G	1256	0.51299	0	2001	58.12	1	1.51964352	0.657	0.815981457	10
optimal_loci_262781_G	1507	0.738321	0	11111	41.6	1	1.51964352	0.327	0.816144605	10
optimal_loci_262782_G	1018	0.738321	0	13622	49.31	2	1.818350263	0.554	0.81616658	10
optimal_loci_262784_G	2004	0.738321	16.07	10123	45.85	1	2.117057006	0.333	0.816236295	10
optimal_loci_262866_G	1104	2.238463	0	3082	35.86	1	0.067075558	0.022	0.818980046	10
optimal_loci_262896_G	1008	2.466471	12.6	3042	43.94	3	10.68388336	0.248	0.820025005	13
optimal_loci_262900_G	2209	2.490084	0	1001	48.43	3	10.91276996	0.402	0.820192379	14
optimal_loci_262911_G	1084	2.243606	0	2001	37.73	3	7.06899142	0	0.820745979	12
optimal_loci_262950_G	1308	2.581895	0	7775	41.36	3	26.24655052	0.324	0.822520577	14
optimal_loci_262979_G	1777	2.539151	0	7711	55.48	2	4.538937262	0.632	0.824030168	14
optimal_loci_262980_G	1005	2.50632	15.12	6458	36.91	2	4.538937262	0.123	0.82404789	14
optimal_loci_262987_G	2232	2.485342	0	2343	55.73	1	3.452236418	0.831	0.824155132	15
optimal_loci_262990_G	2262	2.485342	35.23	7337	50.39	1	3.452236418	0.379	0.824198837	15
optimal_loci_262994_G	1643	2.50299	2.07	2429	49.66	1	1.463914811	0.534	0.824504015	17
optimal_loci_262997_G	1001	2.497022	9.99	8401	41.85	3	8.203615912	0.357	0.824627447	16
optimal_loci_263003_G	2293	2.321769	8.33	3072	43.43	3	8.203615912	0.256	0.824690354	16
optimal_loci_263018_G	1030	2.101367	0	1001	38.83	2	53.4440575	0.064	0.825335977	15
optimal_loci_263024_G	1015	2.101367	0	6105	37.24	1	91.85519633	0.162	0.825380645	15
optimal_loci_263130_G	1786	2.363758	25.03	6093	53.41	1	0.895922464	0.466	0.828420506	16

optimal_loci_263135_G	1657	2.363758	7.6	2447	48.82	1	0.895922464	0.429	0.828524335	14
optimal_loci_263137_G	1353	2.238603	24.69	8425	38.28	1	10.73075602	0.08	0.828712416	12
optimal_loci_263138_G	1363	2.238603	10.34	6942	44.38	1	10.73075602	0.231	0.828725307	12
optimal_loci_263139_G	1153	2.238603	0	5114	43.88	1	10.73075602	0.253	0.828743143	12
optimal_loci_263206_G	1449	3.158777	20.63	1882	32.09	1	12.1836852	0.089	0.831465295	7
optimal_loci_263252_G	1013	3.305048	0	4724	51.03	1	0.038874073	0.532	0.832559438	8
optimal_loci_263359_G	1101	1.538044	0	6343	50.86	1	1.83716604	0.584	0.836681391	4
optimal_loci_263398_G	1346	0.470182	4.23	6585	38.78	1	12.98071052	0.172	0.839735246	4
optimal_loci_263401_G	1369	0.470182	0	3212	55.51	1	12.98071052	0.558	0.839764564	4
optimal_loci_263438_G	2048	0.914274	0	3806	54.15	2	36.84985619	0.544	0.842375972	7
optimal_loci_263486_G	1296	0.026111	12.96	1001	41.74	3	1.739733131	0.264	0.844345232	7
optimal_loci_263489_G	1081	0.026111	0	2690	41.16	3	15.71784109	0.241	0.844463606	7
optimal_loci_263490_G	1594	0.026111	0	1063	36.88	3	15.71784109	0.125	0.844473356	7
optimal_loci_263516_G	1030	1.82438	0	10976	35.43	2	44.08593165	0.274	0.845859172	7
optimal_loci_263579_G	2200	3.514043	0	1001	35.9	3	6.844627732	0.147	0.84813725	9
optimal_loci_263584_G	1778	3.514043	15.75	2369	39.93	3	6.844627732	0.202	0.848182933	9
optimal_loci_263619_G	2041	3.100373	9.31	3860	48.6	4	4.88493513	0.318	0.851056453	6
optimal_loci_263621_G	1532	3.100373	0	2001	53.32	4	4.88493513	0.436	0.851077176	6
optimal_loci_263644_G	1047	3.369276	0	1001	52.05	2	15.58318426	0.398	0.852059544	6
optimal_loci_263669_G	1074	3.077861	18.25	3947	39.19	3	0.176114253	0.069	0.854084867	4
optimal_loci_263795_G	1578	3.123691	4.12	1001	56.78	2	3.961501092	0.535	0.858476107	8
optimal_loci_263796_G	1043	3.123691	0	2001	44.39	2	3.961501092	0.528	0.858490555	8
optimal_loci_263801_G	2058	2.994572	15.84	11155	42.22	1	7.923002184	0.391	0.858646842	8
optimal_loci_263804_G	1091	2.994572	0	14891	50.22	1	7.923002184	0.588	0.858679538	8
optimal_loci_263827_G	1737	3.463803	0	14236	61.48	1	4.610980475	0.744	0.859732452	8
optimal_loci_263831_G	4158	3.463803	2.72	3850	51.44	1	4.610980475	0.348	0.859802158	8
optimal_loci_263832_G	1246	3.463803	0	2503	44.38	1	4.610980475	0.518	0.859839432	8
optimal_loci_263846_G	1440	2.903163	0	18956	46.59	1	4.610980475	0.526	0.860049181	9
optimal_loci_263955_G	1198	2.57635	17.86	12161	33.97	4	16.54294354	0.055	0.864419724	2
optimal_loci_264061_G	1293	6.371429	0	2546	40.68	4	5.746734164	0.24	0.8691057	8
optimal_loci_264075_G	1809	7.245828	1.71	1711	52.73	2	6.236610899	0.371	0.869964513	10
optimal_loci_264079_G	1926	7.245828	0	5699	52.64	2	6.236610899	0.443	0.869999414	10
optimal_loci_264087_G	1144	7.94452	0	1443	39.59	3	10.24997567	0.298	0.870396763	10

optimal_loci_264096_G	2901	7.94452	0	8670	58.18	3	6.56367335	0.608	0.87099904	10
optimal_loci_264103_G	1614	7.94452	0	3394	57.24	2	5.687151283	0.539	0.871056477	10
optimal_loci_264147_G	1359	5.849795	24.36	9509	47.53	2	0.74573517	0.277	0.872508709	12
optimal_loci_264164_G	1125	6.151357	10.31	2001	60.71	2	60.3311558	0.543	0.873075769	12
optimal_loci_264190_G	1449	5.830491	0	3714	47.06	3	2.792067067	0.49	0.873732481	11
optimal_loci_264208_G	1226	5.819307	21.13	1001	41.02	3	0.89074764	0.312	0.874289241	11
optimal_loci_264245_G	2112	2.981373	14.54	1001	54.21	1	1.906623409	0.554	0.876618069	11
optimal_loci_264246_G	1595	2.981373	0	2001	42.82	1	1.906623409	0.182	0.876684555	11
optimal_loci_264298_G	2072	2.266942	0	2001	48.4	4	5.586342105	0.426	0.87919981	7
optimal_loci_264299_G	1157	2.266942	2.42	2330	56.69	4	7.503797887	0.524	0.879352096	7
optimal_loci_264301_G	1162	2.266942	2.75	1001	48.88	4	166.0459588	0.359	0.879376452	7
optimal_loci_264302_G	2122	2.266942	0	5324	51.36	3	221.3946118	0.468	0.879490757	7
optimal_loci_264305_G	1168	2.266942	0	2106	53.33	2	328.6700537	0.516	0.879527268	7
optimal_loci_264359_G	1247	1.179196	15.8	6855	39.05	1	21.6760173	0.093	0.883949165	5
optimal_loci_264423_G	1634	2.158553	0	2001	51.95	4	0.801956317	0.502	0.88648174	6
optimal_loci_264447_G	1647	2.654628	10.99	3507	48.14	2	13.44540222	0.408	0.887699875	6
optimal_loci_264449_G	1066	2.654628	13.7	6285	53.93	2	13.44540222	0.599	0.887724187	6
optimal_loci_264454_G	1686	2.327533	0	2946	50.47	1	2.626717171	0.558	0.887933972	6
optimal_loci_264497_G	1851	2.2635	4.81	6256	43.38	2	16.40960843	0.272	0.890467903	6
optimal_loci_264575_G	1423	1.052086	4.36	2001	37.59	1	2.635697938	0.26	0.894391737	6
optimal_loci_264584_G	1075	0.835847	3.81	6805	51.44	3	0.113572803	0.559	0.894871238	6
optimal_loci_264594_G	1791	0.841196	8.38	2001	51.31	4	29.98241156	0.557	0.895195546	7
optimal_loci_264597_G	1140	0.841196	16.67	6268	34.47	3	39.86297595	0.098	0.895232889	7
optimal_loci_264619_G	1144	3.078728	23.69	13922	32.43	1	17.96697781	0.055	0.897472853	11
optimal_loci_264641_G	1560	3.163901	25.58	1929	35.12	2	118.1692065	0.072	0.899140393	12
optimal_loci_264643_G	1932	3.650724	3.05	1120	40.57	2	118.1692065	0.202	0.899266512	11
optimal_loci_264654_G	1084	3.953259	0	1001	42.25	3	2.28781883	0.212	0.899811422	13
optimal_loci_264693_G	1523	4.001453	0	1001	39.65	3	159.0485327	0.307	0.901076843	13
optimal_loci_264694_G	1035	4.001453	2.8	1001	58.45	3	159.0485327	0.542	0.901169129	13
optimal_loci_264700_G	1097	4.001453	0	11456	41.84	3	2.313359257	0.393	0.901260627	13
optimal_loci_264737_G	1067	4.305873	35.61	4642	40.39	2	9.46289201	0.497	0.903111153	12
optimal_loci_264752_G	1675	4.522855	14.27	8550	50.8	3	26.58315531	0.56	0.903467816	12
optimal_loci_264766_G	1475	4.662529	1.9	4216	53.22	4	3.969860104	0.378	0.904025626	10

optimal_loci_264767_G	1741	4.669733	2.13	5724	51.92	4	3.969860104	0.388	0.904038823	10
optimal_loci_264770_G	1038	4.677509	16.96	6136	41.23	4	3.969860104	0.039	0.904063844	10
optimal_loci_264775_G	1920	4.666921	3.28	1036	47.23	4	3.969860104	0.324	0.904100759	10
optimal_loci_264842_G	1349	3.637391	0	2071	42.55	2	111.0105346	0.198	0.909007381	8
optimal_loci_264909_G	2466	3.835009	7.79	8564	37.18	1	0.648009224	0.119	0.912219368	10
optimal_loci_264911_G	1068	3.835009	3.18	6779	54.96	1	0.648009224	0.566	0.912247225	10
optimal_loci_264921_G	1189	3.835009	9.34	4953	41.37	1	0.648009224	0.193	0.912365599	10
optimal_loci_264922_G	2096	3.835009	2.81	6175	44.22	1	0.648009224	0.514	0.912376293	10
optimal_loci_264925_G	2534	3.835009	0	9914	44.83	1	0.648009224	0.212	0.912409015	10
optimal_loci_264943_G	1152	3.835009	20.92	3060	50.86	2	0.205345835	0.539	0.913243087	10
optimal_loci_264944_G	2446	3.835009	1.19	1146	49.3	2	0.205345835	0.36	0.913254718	10
optimal_loci_264962_G	1596	3.468197	29.14	6351	37.59	1	1.986233282	0.245	0.914112016	9
optimal_loci_264994_G	1152	2.700604	0	1186	51.99	2	3.030385497	0.431	0.915785437	15
optimal_loci_265072_G	1465	3.251914	5.26	17377	58.02	1	2.888951314	0.526	0.919698559	13
optimal_loci_265074_G	2343	3.251377	6.15	4371	46.64	1	2.888951314	0.405	0.919804699	13
optimal_loci_265081_G	1243	5.647435	0	9936	46.17	3	13.54661381	0.389	0.919967811	13
optimal_loci_265082_G	1547	5.647435	17	11578	43.89	3	13.54661381	0.304	0.919982181	13
optimal_loci_265088_G	3896	5.647435	2.72	4515	52.82	3	13.54661381	0.528	0.920025449	13
optimal_loci_265089_G	1761	5.647435	8.92	2640	44.86	2	18.87544505	0.359	0.920060543	13
optimal_loci_265104_G	1592	4.751124	3.52	2743	37.75	2	16.74602623	0.12	0.920726112	12
optimal_loci_265119_G	1174	4.054249	0	2001	59.28	5	54.48324687	0.498	0.921670086	17
optimal_loci_265120_G	1137	4.054249	24.8	1001	30.95	6	53.81427361	0.093	0.921771184	17
optimal_loci_265141_G	1040	3.514376	0	2001	50.57	2	11.1792192	0.473	0.922827354	17
optimal_loci_265142_G	1205	3.514376	0	3174	44.48	2	11.1792192	0.1	0.92283762	17
optimal_loci_265149_G	1655	3.27518	0	3306	49.66	2	5.619619577	0.334	0.923080372	17
optimal_loci_265207_G	1238	2.590308	9.13	2965	41.92	1	66.64812137	0.154	0.925555772	12
optimal_loci_265208_G	1058	2.590308	0	4345	40.26	1	66.64812137	0.132	0.925567849	12
optimal_loci_265209_G	1652	2.590308	33.78	14925	38.19	2	40.42752748	0.307	0.925660441	12
optimal_loci_265213_G	2056	2.590308	1.36	13449	51.75	2	40.42752748	0.558	0.925691133	12
optimal_loci_265222_G	2277	2.45454	7.6	3305	47.73	2	9.865621571	0.268	0.925874085	12
optimal_loci_265262_G	2265	0.967631	15.94	1001	41.1	3	18.88980502	0.323	0.928446821	9
optimal_loci_265274_G	1327	1.151059	0	2274	39.03	1	50.74281391	0.071	0.929014336	9
optimal_loci_265321_G	1137	2.689425	38.96	2880	31.66	3	13.31798612	0.164	0.931171537	6

optimal_loci_265326_G	1483	2.714183	0	2646	37.69	3	13.31798612	0.184	0.931241943	6
optimal_loci_265384_G	1973	2.294104	1.88	2509	42.16	4	0.989240097	0.244	0.933478862	5
optimal_loci_265388_G	3366	2.294104	1.31	2001	47.89	4	0.989240097	0.454	0.933518726	5
optimal_loci_265429_G	1256	2.372136	29.62	2011	37.89	1	4.122679499	0.279	0.935633183	4
optimal_loci_265520_G	1108	0.416778	23.83	12825	32.03	1	5.034416614	0.13	0.940009799	8
optimal_loci_265541_G	1076	0.820905	0	2001	40.33	3	21.38089218	0.126	0.94181473	7
optimal_loci_265542_G	2235	0.820905	0	3354	40.22	3	21.38089218	0.16	0.941826571	7
optimal_loci_265547_G	2381	0.922292	0	8306	40.1	4	16.03566913	0.193	0.941869909	7
optimal_loci_265549_G	1270	0.922292	0	11367	36.77	3	21.38089218	0.115	0.941896698	7
optimal_loci_265551_G	3547	0.922292	30.79	9252	43.67	3	21.38089218	0.328	0.941910578	7
optimal_loci_265589_G	1243	1.249147	24.22	1001	34.91	2	0.344541071	0.026	0.94347764	9
optimal_loci_265628_G	1790	6.434471	0	4879	46.08	5	14.07635451	0.397	0.946603792	8
optimal_loci_265630_G	1375	6.434471	15.2	2925	50.9	4	13.05511082	0.5	0.946626362	8
optimal_loci_265643_G	1234	6.627606	3.4	1746	49.35	3	8.266798619	0.4	0.947981951	7
optimal_loci_265658_G	1263	6.627606	0	2281	36.57	3	8.266798619	0.117	0.948062019	7
optimal_loci_265679_G	2484	6.523378	16.18	3717	38.44	2	57.81222199	0.21	0.949041866	7
optimal_loci_265698_G	2454	5.890966	8.27	11498	47.14	2	7.830246015	0.39	0.949654225	9
optimal_loci_265700_G	1589	5.890966	16.61	11500	51.29	3	23.48310845	0.408	0.949683333	9
optimal_loci_265765_G	1121	5.367164	0	3934	41.57	2	2.019315249	0.411	0.953726285	6
optimal_loci_265771_G	1007	3.97901	32.77	6558	38.23	2	2.019315249	0.172	0.953940096	6
optimal_loci_265834_G	1300	3.236379	2.15	9560	41.61	4	48.30727254	0.265	0.955811285	5
optimal_loci_265861_G	2192	3.629085	11.5	19921	44.34	1	6.326089554	0.324	0.957443319	7
optimal_loci_265902_G	1055	3.760717	25.02	4010	42.74	2	12.52405007	0.311	0.959771981	6
optimal_loci_265963_G	1226	4.352868	0	4400	46	3	1.914628548	0.341	0.961554963	11
optimal_loci_265967_G	1062	4.352868	9.13	18342	38.88	2	0.234740896	0.349	0.961676978	11
optimal_loci_265989_G	1494	4.911706	4.95	6333	43.9	1	4.693740998	0.304	0.962161327	12
optimal_loci_266046_G	1215	5.326514	12.1	1989	34.56	5	74.2002709	0.075	0.964596688	17
optimal_loci_266047_G	1800	5.326514	0	3695	38.66	6	61.84795667	0.116	0.964612389	17
optimal_loci_266057_G	1170	5.326514	0	2729	41.7	5	18.40182427	0.302	0.964834688	17
optimal_loci_266066_G	1349	4.796694	2.15	14924	45.21	2	28.98807271	0.319	0.965265101	17
optimal_loci_266070_G	1193	4.796694	0	7957	37.88	2	20.20635757	0.185	0.965370304	17
optimal_loci_266088_G	1679	4.95969	7.27	13229	47.88	1	86.06076932	0.297	0.965867141	17
optimal_loci_266104_G	1006	5.247984	21.47	7765	44.53	1	86.06076932	0.287	0.966086745	15

optimal_loci_266113_G	1487	5.247984	13.18	7332	37.05	2	71.5752131	0.234	0.966322251	15
optimal_loci_266128_G	1185	5.51557	30.04	1326	43.79	3	47.71680873	0.338	0.966573019	14
optimal_loci_266130_G	1400	5.51557	0	7704	57.85	3	9.257498067	0.716	0.966751123	14
optimal_loci_266135_G	2443	5.131372	5.94	3072	34.83	1	0.136418184	0.071	0.967351614	18
optimal_loci_266136_G	1106	5.131372	0	1717	31.64	1	0.136418184	0.079	0.967375174	18
optimal_loci_266142_G	1791	5.131372	0	11070	33.94	2	0.068209092	0.042	0.967554827	18
optimal_loci_266169_G	1287	5.011301	0	1784	39.93	3	5.26633022	0.277	0.968966461	18
optimal_loci_266215_G	1419	3.376544	10.29	14097	44.32	1	11.17313565	0.314	0.971173449	10
optimal_loci_266226_G	1071	3.376544	2.8	3030	46.49	1	11.17313565	0.266	0.971273348	10
optimal_loci_266233_G	1398	3.376544	0	6203	51.64	1	20.55354298	0.66	0.971633766	10
optimal_loci_266241_G	1278	3.62747	0	11978	40.53	1	20.55354298	0.251	0.971684306	10
optimal_loci_266330_G	1650	4.625347	0	1001	54.78	2	26.84529503	0.561	0.973543278	6
optimal_loci_266332_G	2105	4.625347	0	1785	54.63	2	26.84529503	0.652	0.97360755	7
optimal_loci_266442_G	1950	4.626778	1.88	17431	49.28	1	37.3776486	0.419	0.977970155	7
optimal_loci_266454_G	1242	4.712182	0	1381	27.45	3	17.98974153	0	0.978215226	6
optimal_loci_266456_G	1234	4.827894	0	2449	50	3	20.21043614	0.691	0.978703452	6
optimal_loci_266475_G	1091	4.7418	17.14	10867	41.7	1	32.53922849	0.08	0.979442262	7
optimal_loci_266481_G	1875	4.7418	18.61	1672	39.68	1	40.94407602	0.155	0.979646306	7
optimal_loci_266506_G	1218	3.406342	24.63	10215	48.35	4	56.40949982	0.561	0.980610698	7
optimal_loci_266553_G	1958	3.610737	14.2	11421	41.98	1	17.79476093	0.281	0.983513736	5
optimal_loci_266608_G	1442	2.759269	0	5027	39.66	2	4.615603076	0.316	0.98602416	3
optimal_loci_266674_G	1065	4.681642	0	1001	34.64	2	14.62954822	0.131	0.98924819	2
optimal_loci_266867_G	1853	0.362238	0	6643	32.54	2	0.008166354	0.131	0.998372347	2
optimal_loci_266908_G	1072	0.88141	0	2617	44.12	2	23.01877478	0.341	0.991880531	5
optimal_loci_266996_G	1857	1.662198	10.99	17075	42	1	7.21081894	0.282	0.985957408	5
optimal_loci_267002_G	1184	1.662198	0	8285	37.5	1	7.21081894	0.195	0.98577802	5
optimal_loci_267028_G	1050	1.919515	21.71	1001	32.28	3	101.2828489	0.19	0.982789776	6
optimal_loci_267081_G	1500	3.974415	9.87	16870	48	1	38.8062349	0.512	0.977322408	5
optimal_loci_267113_G	1954	3.622448	2	11530	42.42	1	17.98687008	0.263	0.972831429	3
optimal_loci_267153_G	1338	2.385767	29.37	1433	34.6	3	40.86000265	0.141	0.962546796	1
optimal_loci_267263_G	2950	1.543136	20.78	6478	41.62	1	20.23797573	0.26	0.950683306	1
optimal_loci_267433_G	1094	3.604062	0	8907	39.12	2	8.159173327	0.475	0.932986898	2
optimal_loci_267464_G	1198	3.457393	0	2156	38.23	2	0.212118514	0.318	0.928738102	4

optimal_loci_267530_G	1010	4.84612	15.45	7907	28.81	1	2.439006962	0.086	0.920900816	6
optimal_loci_267534_G	1163	4.84612	12.9	4797	38	1	2.439006962	0.094	0.920837347	6
optimal_loci_267571_G	1190	5.03074	0	15042	41	1	11.76088677	0.263	0.915765694	9
optimal_loci_267584_G	1236	5.156983	2.59	2001	51.77	2	35.21073747	0.581	0.913142531	9
optimal_loci_267599_G	2098	5.408323	0	2300	40.46	3	16.45848332	0.113	0.911120551	10
optimal_loci_267618_G	2478	5.525243	3.75	18204	37.89	1	32.63216243	0.186	0.909920408	8
optimal_loci_267634_G	1210	5.912941	29.75	3122	40.74	2	1.944132251	0.223	0.908621061	8
optimal_loci_267652_G	1281	6.539787	0	2208	36.22	2	5.379617523	0.188	0.90613202	8
optimal_loci_267661_G	1301	6.184767	39.44	3656	49.19	2	5.379617523	0.424	0.905620122	8
optimal_loci_267690_G	1801	5.414962	11.44	2455	50.63	3	6.299829196	0.397	0.902192163	6
optimal_loci_268075_G	1623	4.293766	8.87	7617	50.46	1	0.683590267	0.292	0.856563918	5
optimal_loci_268082_G	1156	4.293766	36.42	2665	38.14	1	0.683590267	0.213	0.856462857	5
optimal_loci_268143_G	1662	4.645985	11.01	4159	37.54	1	0.186657782	0.075	0.851110612	7
optimal_loci_268153_G	1050	4.55827	2.67	7304	38.47	1	0.186657782	0.05	0.850814449	7
optimal_loci_268200_G	1098	2.928632	12.84	2097	34.15	1	15.14485043	0.054	0.846654898	8
optimal_loci_268260_G	1294	1.897084	0	1838	43.19	4	3.454476312	0.14	0.841936673	6
optimal_loci_268269_G	1447	1.816463	8.29	4237	37.04	3	2.498539321	0.148	0.841347286	6
optimal_loci_268316_G	1013	4.502034	29.42	1771	37.61	1	19.67124	0.269	0.837042408	6
optimal_loci_268403_G	1465	5.722672	0	15389	35.76	1	1.702619888	0.274	0.828557327	3
optimal_loci_268404_G	1213	5.722672	0	13205	37.34	1	1.702619888	0.088	0.828512755	3
optimal_loci_268578_G	1429	0.58899	36.74	1001	28.97	4	1.262781928	0.081	0.811002653	1
optimal_loci_268682_G	1528	1.417943	0	6393	34.94	3	8.351383263	0.141	0.797694857	4
optimal_loci_268745_G	1386	1.364657	25.11	5842	37.95	2	27.77809233	0.146	0.790239612	4
optimal_loci_268748_G	1374	1.364657	0	2159	42.13	2	27.77809233	0.408	0.789894796	4
optimal_loci_268771_G	1188	1.525119	2.36	6754	34.17	1	14.97747539	0.167	0.788050327	7
optimal_loci_268875_G	1050	2.077889	0	6800	38.95	1	6.13861359	0.188	0.779537959	5
optimal_loci_268882_G	1617	3.117191	2.64	1001	47.68	3	15.66847865	0.328	0.778210592	5
optimal_loci_268883_G	1068	3.117191	0	2001	46.34	3	15.66847865	0.469	0.778185592	5
optimal_loci_268912_G	1168	4.113992	0	13484	46.31	1	46.94435784	0.45	0.775402653	4
optimal_loci_269090_G	1179	2.075402	3.56	1455	49.61	1	19.88319445	0.493	0.759114837	3
optimal_loci_269092_G	2081	1.408087	1.73	3675	54.15	1	19.88319445	0.655	0.759051122	3
optimal_loci_269118_G	1466	2.040464	1.91	1003	56.68	3	7.493550616	0.495	0.756651163	3
optimal_loci_269226_G	1696	3.855414	37.21	5100	42.09	1	2.358096668	0.268	0.742761714	3

optimal_loci_269307_G	2321	7.088075	2.41	7840	47.13	2	32.7709333	0.385	0.736448857	7
optimal_loci_269335_G	1318	8.487712	32.09	9287	44.91	1	60.25245486	0.417	0.734658061	9
optimal_loci_269371_G	2160	8.871985	0	3353	58.05	1	1.194316046	0.588	0.730285653	10
optimal_loci_269387_G	1471	6.85243	9.11	1001	50.64	2	0.695240429	0.541	0.72870849	10
optimal_loci_269389_G	1322	6.85243	0	2962	49.77	2	0.695240429	0.401	0.72867151	10
optimal_loci_269395_G	1701	6.785015	0	17126	45.79	1	1.373872349	0.293	0.728374714	10
optimal_loci_269424_G	1532	6.03504	0	3262	51.63	3	0.948099943	0.473	0.725844429	9
optimal_loci_269428_G	1028	5.449533	27.63	2377	44.16	3	0.948099943	0.152	0.725602755	9
optimal_loci_269452_G	1040	5.299934	0	1118	40.86	2	27.70044183	0.244	0.722146449	8
optimal_loci_269454_G	1012	5.299934	0	11527	38.04	1	3.052783993	0	0.721769592	8
optimal_loci_269644_G	1158	0.990087	0	14968	34.28	2	8.356432235	0.064	0.694845735	1
optimal_loci_269821_G	1371	3.344237	16.92	6994	47.26	2	0.45345545	0.384	0.666419122	6
optimal_loci_269931_G	1195	3.604313	39.83	2523	39.33	3	8.189210842	0.269	0.658385122	6
optimal_loci_269942_G	1113	3.540368	0	1638	40.43	3	3.657898351	0.314	0.657630449	6
optimal_loci_269959_G	1243	3.476328	11.42	15390	37.48	1	4.92527703	0.216	0.656418959	6
optimal_loci_269960_G	1025	3.476328	0	12524	25.17	1	4.92527703	0.119	0.656360469	6
optimal_loci_269962_G	1209	3.476328	13.07	10067	37.63	1	4.92527703	0.287	0.656310327	6
optimal_loci_270093_G	1918	2.638491	30.76	1393	35.71	2	6.421003684	0.123	0.639411429	2
optimal_loci_270127_G	1231	1.701088	0	10450	60.68	1	21.23779007	0.708	0.633002429	6
optimal_loci_270161_G	1235	1.697198	0	4296	40.08	2	12.0156428	0.097	0.628422837	5
optimal_loci_270183_G	1187	1.697198	0	2748	37.32	3	8.939836293	0.228	0.625398898	5
optimal_loci_270191_G	1327	1.702848	0	2001	45.29	4	48.01830865	0.541	0.623830388	5
optimal_loci_270193_G	1472	1.702848	12.3	3696	47.07	4	48.01830865	0.217	0.62377451	5
optimal_loci_270318_G	1277	0.0978	2.43	2562	34.84	2	1.903183613	0.131	0.609825306	2
optimal_loci_270319_G	1528	0.0978	5.24	1001	39.79	2	1.903183613	0.117	0.609793449	2
optimal_loci_270453_G	2605	1.326868	2	3239	56.77	2	1.01938037	0.553	0.595284857	2
optimal_loci_270455_G	1047	1.326868	0	2001	53.77	1	51.09027802	0.409	0.594767061	2
optimal_loci_270540_G	2552	1.775215	1.21	6652	58.5	3	9.785157012	0.797	0.581045102	6
optimal_loci_270586_G	1232	1.620883	0	2630	42.77	3	6.154228265	0.282	0.578049102	6
optimal_loci_270588_G	1816	1.620883	38.6	2357	34.03	4	11.78365912	0.219	0.577903653	6
optimal_loci_270614_G	1036	1.00276	0	14037	43.43	1	8.533128255	0.188	0.575231918	6
optimal_loci_270617_G	1951	1.00276	35.11	8599	51.2	1	8.533128255	0.489	0.575120939	6
optimal_loci_270648_G	1143	0.861921	0	4280	54.76	2	19.58274306	0.489	0.572324082	6

optimal_loci_270806_G	1357	1.566932	39.94	5768	39.42	3	35.3917928	0.191	0.554286122	2
optimal_loci_270813_G	1185	1.566932	7.43	1999	52.99	5	8.260391208	0.565	0.553793245	2
optimal_loci_270964_G	1694	1.228814	0	17023	48.22	1	12.2216317	0.29	0.534730714	2
optimal_loci_270967_G	1765	1.287103	0	2676	39.26	3	5.334833815	0.233	0.534066551	2
optimal_loci_271142_G	1338	0.256029	0	2933	55.15	1	1.441806411	0.588	0.510322714	2
optimal_loci_271143_G	1007	0.256029	0	4341	36.64	1	1.441806411	0.112	0.510300735	2
optimal_loci_271427_G	1337	0.190844	2.09	2527	47.79	1	6.228121554	0.566	0.467302327	3
optimal_loci_271429_G	1515	0.190844	0	4329	49.5	1	6.228121554	0.387	0.467261918	3
optimal_loci_271470_G	1413	0.190054	0	1341	46.14	1	2.62846104	0.36	0.462183694	5
optimal_loci_271544_G	1047	0.194034	28.65	8169	35.33	2	12.89989852	0.079	0.45439251	3
optimal_loci_271566_G	2730	0.194034	15.24	9722	36.92	2	12.89989852	0.239	0.45373251	3
optimal_loci_271925_G	1172	0.274684	0	2594	38.48	3	175.5295341	0.223	0.393387286	4
optimal_loci_271933_G	1697	0.274684	7.84	1001	35.88	3	175.5295341	0.1	0.393139592	4
optimal_loci_271941_G	1521	0.246256	6.51	5222	39.05	2	0.122464927	0.127	0.391393633	4
optimal_loci_271952_G	1063	0.185326	0	4572	52.21	5	3.161612512	0.455	0.389508796	4
optimal_loci_272676_G	1453	0.044049	14.04	2383	37.5	1	4.338804611	0.205	0.302145673	2
optimal_loci_272772_G	1237	0.027479	16.09	11338	42.19	2	1.28621299	0.294	0.292089959	2
optimal_loci_274354_G	1065	0.843707	27.79	3171	37.65	1	49.51442783	0	0.076372	1
optimal_loci_277835_G	1112	0.012239	3.78	1001	48.38	2	9.987865596	0.502	0.168025857	4
optimal_loci_277848_G	1002	0.054227	5.49	3548	34.33	1	0.192675565	0.125	0.168971218	4
optimal_loci_277850_G	1068	0.054227	4.4	1001	56.92	1	0.192675565	0.534	0.168991163	4
optimal_loci_277874_G	1680	0.177696	8.21	7886	46.6	2	8.242179455	0.454	0.171704016	4
optimal_loci_278057_G	1955	0.394799	13.76	5337	43.73	3	12.01587433	0.469	0.17964927	2
optimal_loci_278096_G	2749	0.084588	4.07	1001	42.08	4	1.784685364	0.258	0.182800361	2
optimal_loci_278641_G	1323	0.068743	13.23	1813	39.75	1	4.20098825	0.119	0.216692302	1
optimal_loci_278767_G	1024	0.034465	4.59	15296	41.4	2	106.6647028	0.355	0.22231555	2
optimal_loci_278782_G	1298	0.034465	12.25	2973	40.67	3	0.704362835	0.098	0.222930509	2
optimal_loci_280543_G	1000	0.213371	22.2	1001	37.2	1	20.57704449	0.162	0.313708954	3
optimal_loci_280584_G	1182	0.366369	0	2501	36.97	1	10.56120766	0.17	0.314917222	4
optimal_loci_280614_G	1273	0.422272	4.32	15026	41.94	1	141.9498356	0.335	0.316098021	4
optimal_loci_280655_G	1751	0.435001	0	4301	41.46	1	45.63221637	0.128	0.318568828	3
optimal_loci_280754_G	1208	0.443978	3.39	8493	42.3	1	58.04663111	0.28	0.323220894	1
optimal_loci_281185_G	1964	0.210124	18.79	1001	37.52	4	2.024380477	0.187	0.34489953	2

optimal_loci_281269_G	1493	0.300364	2.55	7575	42.73	1	60.2177995	0.299	0.348133904	2
optimal_loci_281441_G	1774	0.962341	0	3313	45.09	1	9.285652493	0.409	0.356790697	3
optimal_loci_281471_G	1125	0.922737	33.78	5797	43.55	1	67.75519299	0.354	0.358903359	3
optimal_loci_281475_G	1011	0.922737	0	2999	41.04	1	67.75519299	0.211	0.358926769	3
optimal_loci_282320_G	1065	1.304454	15.21	2539	36.33	1	3.08188714	0.111	0.396808259	6
optimal_loci_282323_G	1195	1.304454	0	5272	56.06	1	3.08188714	0.667	0.39683023	6
optimal_loci_282339_G	1268	1.381369	10.8	6188	41	2	13.7694667	0.367	0.398335892	6
optimal_loci_282341_G	1306	1.381369	0	1001	39.12	2	13.7694667	0.135	0.398377285	6
optimal_loci_282386_G	1636	1.893277	11.86	13168	52.26	2	7.374282878	0.678	0.399992792	6
optimal_loci_282388_G	1144	1.769503	0	1080	36.97	1	14.74856576	0.057	0.40018699	6
optimal_loci_282498_G	1446	1.213477	2.01	3256	52.97	2	6.667225053	0.582	0.404922742	3
optimal_loci_282499_G	1360	1.213477	0	1796	42.94	2	6.667225053	0.423	0.40493517	3
optimal_loci_282509_G	1101	1.215015	0	15543	43.96	1	12.15460606	0.173	0.405616981	3
optimal_loci_282619_G	1098	0.759206	21.68	1001	38.52	1	2.155247639	0.133	0.410039904	5
optimal_loci_282620_G	1133	0.664858	0	1001	38.21	1	5.190053046	0.212	0.410408178	5
optimal_loci_282653_G	1160	0.43392	8.97	1373	39.65	2	11.6857759	0.224	0.412438417	5
optimal_loci_282656_G	1285	0.43392	0	1001	55.48	2	11.6857759	0.515	0.412457284	5
optimal_loci_282661_G	1310	0.43392	0	19722	36.1	1	12.44017959	0.192	0.412659392	5
optimal_loci_282821_G	1352	0.09638	2.66	5151	54.58	1	73.11300839	0.434	0.419897778	2
optimal_loci_282853_G	1273	0.06929	24.51	1001	30.08	1	32.8057845	0.165	0.42048255	2
optimal_loci_282945_G	1159	0.227602	0	1001	30.37	2	1.292563237	0.114	0.425015519	4
optimal_loci_282950_G	1283	0.239708	8.26	3860	42.08	2	1.292563237	0.252	0.425053672	4
optimal_loci_282994_G	2919	0.320222	39.05	3306	39.7	2	20.52271421	0.231	0.427753679	5
optimal_loci_282995_G	1734	0.378191	10.21	1001	45.21	2	20.52271421	0.403	0.427842815	5
optimal_loci_283035_G	1527	0.397016	3.27	6445	55.73	1	0.686391753	0.574	0.429373953	3
optimal_loci_283161_G	1614	0.316771	0	2146	42.37	1	4.070216057	0.319	0.433478001	1
optimal_loci_283454_G	1230	0.751069	0	16323	42.68	1	11.97488986	0.328	0.445110417	2
optimal_loci_283492_G	2139	0.157776	33.38	13295	32.91	1	28.37262396	0	0.447839839	2
optimal_loci_283613_G	1124	0.004514	25.18	5043	43.95	2	12.26532046	0.308	0.456444804	1
optimal_loci_283802_G	1281	0.004514	0	3807	42.62	1	0.411582228	0.2	0.461585295	3
optimal_loci_283897_G	1205	0.390912	7.8	7728	42.82	2	0.059701066	0.237	0.465147886	3
optimal_loci_283898_G	1084	0.390912	0	6379	50.27	2	0.059701066	0.365	0.465159703	3
optimal_loci_284058_G	1185	0.170168	0	2068	35.69	4	12.60574952	0	0.470715577	1

optimal_loci_284165_G	1001	0.031215	5.29	2545	40.05	2	0.0189369	0.183	0.475768491	2
optimal_loci_284217_G	1195	0.031618	0	10514	47.36	1	98.45957653	0.289	0.477520942	5
optimal_loci_284284_G	1219	0.042462	18.7	17038	34.12	1	15.8654464	0.193	0.480524139	4
optimal_loci_284287_G	1060	0.042462	0	14628	54.71	1	15.8654464	0.541	0.480544792	4
optimal_loci_284292_G	1302	0.043549	0	1001	38.86	1	15.8654464	0.099	0.480735951	4
optimal_loci_284403_G	1006	0.049064	0	2001	38.66	2	46.9359797	0.084	0.485631486	1
optimal_loci_284615_G	1087	0.034447	0	5295	43.14	1	5.682016343	0.333	0.492655576	6
optimal_loci_284623_G	1576	0.034276	0	2718	33.69	2	18.23962495	0.031	0.492810319	6
optimal_loci_284638_G	1066	0.032596	0	6875	44.27	1	0.358756146	0.359	0.493268059	6
optimal_loci_284639_G	1291	0.032596	0	5501	40.66	1	0.358756146	0.169	0.493277295	6
optimal_loci_284667_G	1792	0.020566	0	8352	34.26	1	110.3450396	0.219	0.495356138	6
optimal_loci_284668_G	1831	0.020566	0	10516	43.03	1	110.3450396	0.21	0.495373534	6
optimal_loci_284976_G	2201	0.407066	0	2001	44.84	1	1.344258109	0.229	0.509847636	1
optimal_loci_285246_G	1669	0.068223	15.28	1656	37.02	1	12.20886168	0.104	0.519548621	1
optimal_loci_285395_G	1059	0.896434	12.09	3681	33.23	1	0.102252241	0	0.528973114	4
optimal_loci_285452_G	1116	0.755051	38.17	2949	35.93	3	0.33728496	0.11	0.530979187	4
optimal_loci_285467_G	1001	0.579108	0	17623	49.35	4	20.15685173	0.217	0.532116262	5
optimal_loci_285474_G	1136	0.564695	33.36	10738	39.7	1	10.8099515	0.149	0.532535029	5
optimal_loci_285555_G	1669	1.118899	0	2001	45.65	1	7.90917327	0.412	0.535996376	6
optimal_loci_285621_G	1172	1.367322	13.65	2028	53.92	1	4.803638731	0.67	0.53798002	5
optimal_loci_285630_G	1253	1.317271	3.51	7615	36.31	2	3.563789243	0	0.538495175	6
optimal_loci_285639_G	3271	1.394503	2.26	18791	46.77	1	7.127578486	0.416	0.538783646	6
optimal_loci_285689_G	1106	0.991013	6.69	18624	54.33	1	31.55014255	0.522	0.541880152	6
optimal_loci_285693_G	1545	0.862974	37.28	2192	35.72	2	4.448647906	0.119	0.542120349	5
optimal_loci_285772_G	1666	0.041794	14.17	9602	44.17	4	3.021940318	0.269	0.545485927	7
optimal_loci_285800_G	1019	0.063301	0	3030	57.99	2	174.4947999	0.52	0.546483236	5
optimal_loci_285825_G	1799	0.522924	35.77	2001	38.63	2	1.379668468	0.117	0.548148722	6
optimal_loci_285863_G	1218	0.55711	15.19	2582	41.54	2	19.90196699	0.292	0.549451753	8
optimal_loci_285865_G	2136	0.55711	0	4811	37.59	2	19.90196699	0.147	0.549469672	8
optimal_loci_285907_G	1152	0.773467	0	3074	47.13	2	151.3101745	0.466	0.550657779	6
optimal_loci_285965_G	1241	0.396476	19.82	2990	40.69	2	0.525620286	0.291	0.552641857	5
optimal_loci_285972_G	1320	0.396476	0	5520	47.12	3	0.354326552	0.291	0.552728791	5
optimal_loci_286229_G	1046	0.124091	0	5692	54.3	1	1.040834222	0.687	0.565866644	1

optimal_loci_286381_G	1006	0.142666	0	2349	48.21	2	4.489570617	0.353	0.574857087	3
optimal_loci_286489_G	1752	0.023571	0	13746	31.33	2	0.238244552	0.188	0.578060938	5
optimal_loci_286490_G	2850	0.023571	0	10699	32.14	2	0.238244552	0.091	0.578076606	5
optimal_loci_286525_G	1535	0.023571	30.23	2690	36.35	1	32.14433632	0.287	0.579397452	6
optimal_loci_286536_G	1229	0.023571	0	17844	45.48	1	1.76234819	0.304	0.579861173	6
optimal_loci_286582_G	1087	0.567314	13.25	2027	45.81	1	5.942335878	0.154	0.582131239	5
optimal_loci_286631_G	1136	0.577352	0	1001	57.74	3	3.319121686	0.552	0.582936609	6
optimal_loci_286771_G	1961	0.566926	16.93	2593	39.52	1	4.483924173	0.187	0.585960177	6
optimal_loci_286781_G	1111	0.559487	0	3642	55.98	1	2.472357099	0.654	0.586548044	5
optimal_loci_286790_G	1049	0.55713	33.46	6673	35.17	2	6.422887686	0.12	0.587470252	4
optimal_loci_286794_G	1383	0.55713	11.93	2225	32.97	1	12.84577537	0.14	0.5875889	4
optimal_loci_286886_G	1366	0.007045	2.12	1001	47.51	2	0.020236907	0.255	0.593230397	3
optimal_loci_286900_G	1178	0.007045	33.36	6301	29.71	1	7.187695509	0.041	0.594761599	3
optimal_loci_286901_G	3222	0.007045	37.12	3046	29.01	1	7.187695509	0.131	0.594771334	3
optimal_loci_287165_G	1302	0.106063	0	1773	37.94	1	14.84998821	0.191	0.60863088	1
optimal_loci_287666_G	1195	0.074725	5.19	15569	33.72	1	9.070756663	0.143	0.630029558	3
optimal_loci_287671_G	1175	0.074725	32.09	12215	44.42	1	9.070756663	0.111	0.630056682	3
optimal_loci_287717_G	1463	0.075836	31.1	2300	44.97	2	12.38904672	0.53	0.631496464	3
optimal_loci_287841_G	1101	0.197687	0	2488	41.32	2	4.408607828	0.327	0.635928439	3
optimal_loci_287878_G	1383	0.25768	0	5033	39.84	1	30.18087186	0.137	0.637782166	7
optimal_loci_287880_G	1305	0.25768	2.91	7916	42.98	1	30.18087186	0.303	0.637805342	7
optimal_loci_287953_G	1123	0.388035	28.14	3017	29.38	2	8.677094776	0.166	0.64084252	6
optimal_loci_287965_G	1007	0.388035	16.39	2139	47.56	2	2.918438086	0.371	0.641283185	6
optimal_loci_287972_G	1020	0.391697	32.45	3222	41.47	3	0.047995127	0.259	0.641604713	6
optimal_loci_287987_G	1069	0.378397	29.47	4816	36.38	4	0.035996346	0.096	0.64176509	6
optimal_loci_288074_G	1619	0.334234	3.83	2608	45.21	4	5.893194419	0.259	0.646161187	2
optimal_loci_288077_G	1061	0.311806	27.8	2279	36.56	3	7.857592558	0.217	0.64638369	2
optimal_loci_288388_G	1040	0.659341	36.25	12598	46.34	1	1.014473783	0.354	0.658316323	3
optimal_loci_288391_G	1247	0.659341	22.21	14283	40.89	1	1.014473783	0.275	0.658329868	3
optimal_loci_288425_G	1113	0.865829	3.41	9159	39.17	3	49.21351536	0.302	0.659644195	3
optimal_loci_288522_G	1212	1.383259	6.19	5826	39.43	3	0.855749646	0.066	0.664008385	1
optimal_loci_289201_G	1443	0.356801	0	1437	44	4	9.920112359	0.31	0.70141494	3
optimal_loci_289203_G	1242	0.356801	0	2812	39.77	4	9.920112359	0.258	0.701430278	3

optimal_loci_289301_G	1952	0.725929	21.93	2001	44.05	1	5.499233704	0.288	0.705025692	3
optimal_loci_289802_G	1317	0.608453	33.26	5498	39.25	2	16.35108464	0.231	0.727684353	5
optimal_loci_289879_G	1322	0.967038	0	3591	35.4	1	22.20324097	0.133	0.730757779	6
optimal_loci_289908_G	1309	1.112916	0	8613	47.13	2	0.235153526	0.396	0.731181023	6
optimal_loci_289913_G	2046	1.112916	1.86	3107	43.64	1	0.470307052	0.272	0.731219361	6
optimal_loci_289919_G	1805	0.484372	22.22	5405	39.55	1	0.470307052	0.148	0.731361386	6
optimal_loci_289955_G	1204	0.52756	33.64	5065	32.55	1	0.017815614	0.219	0.732112292	5
optimal_loci_290360_G	1355	0.195889	0	10995	43.02	2	5.768065735	0.42	0.750176325	3
optimal_loci_290371_G	1514	0.343589	0	1001	43.85	1	0.308259294	0.316	0.750255389	3
optimal_loci_290466_G	1482	0.778839	0	1001	54.72	4	9.024824696	0.649	0.754003824	6
optimal_loci_290491_G	1351	0.806529	24.2	11044	39.08	2	18.21142326	0.044	0.754401232	4
optimal_loci_290498_G	1041	0.820782	0	9453	49.66	1	6.653205347	0.437	0.754800343	4
optimal_loci_290508_G	1225	0.932607	11.92	14724	33.95	1	0.047888079	0.165	0.755415648	5
optimal_loci_290611_G	2232	1.252005	6.41	3250	50.44	2	15.84337594	0.525	0.759292643	8
optimal_loci_290640_G	1109	1.110292	19.12	10168	55.81	1	2.386058817	0.573	0.760083414	7
optimal_loci_290654_G	1830	1.124898	0	1261	43.82	2	3.898681594	0.434	0.760293746	7
optimal_loci_290661_G	2116	1.171806	5.91	12066	34.12	1	22.04087152	0.009	0.760612227	8
optimal_loci_290662_G	1705	1.186038	3.64	10233	52.9	2	31.05019761	0.645	0.760630266	8
optimal_loci_290664_G	1456	1.186038	32.83	8164	40.38	2	31.05019761	0.245	0.7606489	8
optimal_loci_290689_G	1182	1.836717	6.01	4810	46.1	2	0.075034726	0.312	0.761767767	9
optimal_loci_290732_G	1151	1.606537	0	2001	45.35	4	9.892609434	0.303	0.764330548	6
optimal_loci_290742_G	2124	1.619961	6.21	3866	42.65	2	5.499619784	0.292	0.764864031	3
optimal_loci_290841_G	1328	0.06116	5.87	2001	53.61	1	2.039268407	0.627	0.76925225	1
optimal_loci_290967_G	1004	0.444539	0	1001	47.41	4	23.47764534	0.54	0.774246946	1
optimal_loci_291057_G	1197	0.842287	0	8187	35	2	36.7182114	0.177	0.778580009	2
optimal_loci_291068_G	2380	0.842287	18.91	4243	39.15	2	36.7182114	0.145	0.778797962	2
optimal_loci_291264_G	1029	0.775121	20.99	18944	49.95	1	8.239997994	0.241	0.785634511	7
optimal_loci_291274_G	1299	0.767337	39.49	3109	36.25	2	5.741206236	0.106	0.785759638	7
optimal_loci_291315_G	1060	0.735601	0	18491	31.5	2	7.461859755	0.105	0.788182589	7
optimal_loci_291317_G	2499	0.735601	0	34809	38.09	1	14.92371951	0.115	0.788313769	7
optimal_loci_291359_G	1409	0.780001	0	6765	42.86	1	28.01250383	0.148	0.789446221	7
optimal_loci_291360_G	1399	0.780001	14.72	4720	52.25	1	28.01250383	0.46	0.789462741	7
optimal_loci_291367_G	1052	0.780001	26.05	3237	36.12	1	28.01250383	0.088	0.789549482	7

optimal_loci_291571_G	1986	1.431105	37.11	17396	30.56	1	11.98324892	0.053	0.796991616	2
optimal_loci_291669_G	1822	2.033721	1.65	4056	30.24	1	4.318034301	0.192	0.800768252	9
optimal_loci_291724_G	1938	2.696913	18.68	3640	41.58	1	3.906570893	0.276	0.802446303	9
optimal_loci_291727_G	1369	2.696913	4.31	8236	42.8	1	3.906570893	0.179	0.80248325	9
optimal_loci_291731_G	1514	2.974586	0	13529	47.22	1	3.906570893	0.274	0.8025258	10
optimal_loci_291733_G	1243	2.974586	0	15567	53.09	1	3.906570893	0.445	0.802542184	10
optimal_loci_291738_G	1027	3.111136	0	1812	48.78	2	5.10821811	0.501	0.802814802	10
optimal_loci_291758_G	1033	3.542679	0	2204	50.33	1	4.043800199	0.453	0.803431481	10
optimal_loci_291764_G	1802	3.542679	6.6	6086	58.49	1	4.043800199	0.611	0.803462688	10
optimal_loci_291818_G	2560	3.521852	1.48	2700	52.57	1	0.028900943	0.431	0.80542273	9
optimal_loci_291853_G	1567	3.521852	24.12	1419	40.01	1	7.763933339	0.233	0.806516571	7
optimal_loci_291970_G	1073	0.2801	0	11094	38.39	2	0.603514087	0.111	0.814272829	8
optimal_loci_291989_G	1068	0.2801	20.88	1659	38.01	3	48.7848361	0.194	0.814573125	8
optimal_loci_292046_G	1006	0.234705	0	1001	34.99	2	6.866701362	0	0.815905965	9
optimal_loci_292060_G	1960	0.236671	0	4732	48.46	2	3.470798133	0.448	0.816378055	9
optimal_loci_292062_G	1173	0.230649	13.98	3481	48.33	2	3.470798133	0.371	0.816498889	9
optimal_loci_292063_G	1213	0.232358	2.8	2152	41.38	2	3.470798133	0.339	0.816509251	9
optimal_loci_292069_G	1018	1.181734	8.84	2407	49.9	2	15.89586569	0.43	0.816854606	9
optimal_loci_292070_G	1360	1.181734	34.63	1001	41.98	2	15.89586569	0.165	0.81686316	9
optimal_loci_292158_G	1290	1.858621	27.83	1002	40.38	2	0.009583778	0.091	0.819804891	9
optimal_loci_292222_G	1004	1.025133	0	4257	45.51	1	1.851795395	0.342	0.822409579	3
optimal_loci_292223_G	1996	1.025133	11.22	2228	41.38	1	1.851795395	0.255	0.822417916	3
optimal_loci_292356_G	1231	0.780392	4.22	2001	46.06	3	8.943541479	0.304	0.83009773	2
optimal_loci_292438_G	1105	1.34785	0	14242	57.91	1	8.931481352	0.793	0.833203714	3
optimal_loci_292506_G	1026	0.35259	0	2519	36.25	2	0.054629179	0.225	0.837146388	3
optimal_loci_292585_G	1980	0.630302	0	4594	36.31	5	9.23245275	0.23	0.840778113	6
optimal_loci_292650_G	1066	0.760218	38.37	19002	38.08	1	0.823793759	0.337	0.84275765	6
optimal_loci_292665_G	1154	0.760218	17.5	3015	55.63	1	3.574698403	0.654	0.842982983	6
optimal_loci_292667_G	1578	0.762258	8.56	7015	58.49	1	3.574698403	0.648	0.843015139	6
optimal_loci_292684_G	1028	0.788346	0	1152	49.51	2	128.7617555	0.52	0.843854554	6
optimal_loci_292717_G	1377	0.791472	0	3541	43.13	1	0.774277851	0.266	0.846251748	6
optimal_loci_292759_G	1417	1.439505	0	2001	33.73	2	1.486953662	0.106	0.848231944	2
optimal_loci_292873_G	2890	2.939861	21.94	1320	35.46	1	10.23319704	0.211	0.854236674	8

optimal_loci_292888_G	1626	3.099502	5.47	4965	45.14	2	5.525162686	0.461	0.85477978	8
optimal_loci_292896_G	1194	3.246784	0	3390	43.71	3	4.940283259	0.509	0.854882318	8
optimal_loci_292933_G	1303	2.249947	39.22	6487	34.68	1	6.716400311	0	0.855946712	8
optimal_loci_292938_G	1610	2.256804	0	1529	39.19	1	6.716400311	0.268	0.856034634	8
optimal_loci_292951_G	1075	2.17716	24.64	2747	33.3	1	20.59103545	0.135	0.856365712	8
optimal_loci_292956_G	1076	1.677454	7.81	2001	41.63	4	35.84786485	0.129	0.85675385	8
optimal_loci_292957_G	1181	1.677454	12.79	2967	38.18	4	35.84786485	0.155	0.856764888	8
optimal_loci_293205_G	1899	3.570491	0	15970	54.81	2	14.99376424	0.761	0.865914262	3
optimal_loci_293228_G	1375	3.325221	0	8524	42.03	1	60.28918545	0.188	0.866963591	3
optimal_loci_293246_G	2239	3.18144	0	2111	40.28	2	0.033029928	0.142	0.867424096	3
optimal_loci_293392_G	1409	1.511465	22.36	2029	37.4	5	1.499082618	0.126	0.87261467	7
optimal_loci_293436_G	1734	1.266051	26.18	9104	41.52	1	41.42102399	0.198	0.873740016	7
optimal_loci_293444_G	1560	1.225719	0	1001	60.76	1	41.42102399	0.661	0.873806555	7
optimal_loci_293477_G	1233	1.194188	6	2001	44.12	3	4.311060452	0.304	0.874906666	7
optimal_loci_293480_G	2764	1.160733	12.41	3230	34.94	1	67.49439944	0.072	0.875379118	7
optimal_loci_293496_G	1220	1.230542	0	1365	39.67	5	57.50537364	0.308	0.876275288	7
optimal_loci_293498_G	1557	1.230542	0	2148	36.54	6	49.34538723	0.068	0.876308087	7
optimal_loci_293611_G	2586	0.581931	32.68	2001	35.42	2	1.118677443	0.187	0.882190046	7
optimal_loci_293613_G	1075	0.581931	0	14812	39.06	3	1.106707451	0.112	0.882293034	7
optimal_loci_293619_G	1617	0.581931	0	1136	43.22	4	10.63590035	0.291	0.882418016	7
optimal_loci_293663_G	2004	0.445122	12.08	3659	48.8	1	17.61558533	0.417	0.884167613	9
optimal_loci_293703_G	1138	0.421908	0	3215	43.32	2	1.019665829	0.308	0.885326184	11
optimal_loci_293709_G	1034	0.421908	0	6891	51.06	2	1.019665829	0.237	0.885355736	11
optimal_loci_293717_G	1964	0.421908	0	2001	53.71	3	22.04649826	0.526	0.885402161	11
optimal_loci_293827_G	1508	0.37465	0	15873	39.52	1	2.262439347	0.308	0.88801394	8
optimal_loci_293828_G	1122	0.37465	0	14529	35.02	1	2.262439347	0.114	0.888027847	8
optimal_loci_293837_G	1322	0.367499	0	3275	43.49	3	0.803565129	0.374	0.8882879	7
optimal_loci_293843_G	1130	0.367499	31.77	2805	39.73	3	0.060258218	0.22	0.888370839	7
optimal_loci_293940_G	1016	1.039875	3.25	1428	50.59	3	29.63421377	0.571	0.893456359	7
optimal_loci_293943_G	1381	1.039875	2.39	4491	56.91	3	29.63421377	0.707	0.893480982	7
optimal_loci_293947_G	1422	1.039875	0	7059	47.74	4	22.22566033	0.392	0.893525052	7
optimal_loci_293950_G	1086	1.039875	0	4828	54.41	4	22.22566033	0.475	0.893545688	7
optimal_loci_293951_G	1249	1.039875	0	3293	37.22	4	22.22566033	0.157	0.893556718	7

optimal_loci_293955_G	2194	1.039875	3.65	1001	54.46	3	5.284577029	0.548	0.893633868	7
optimal_loci_293957_G	1778	1.039875	10.35	2001	36.83	3	0.702463935	0.081	0.893791657	7
optimal_loci_294090_G	2579	1.770642	0	1001	33.96	3	60.52538931	0.081	0.899518922	5
optimal_loci_294091_G	1044	1.791261	27.01	2001	63.21	2	77.38052296	0.61	0.899659042	5
optimal_loci_294101_G	2121	1.882722	12.92	2001	45.78	5	0.492542587	0.331	0.900189116	5
optimal_loci_294122_G	1209	2.123974	0	3055	53.43	2	2.947714525	0.456	0.901357157	10
optimal_loci_294149_G	1330	3.039612	31.05	1473	41.05	3	0.773728794	0.1	0.902587926	10
optimal_loci_294168_G	1306	3.467687	0	2080	36.06	3	0.422355545	0.214	0.90436566	7
optimal_loci_294172_G	1415	3.467687	6.78	1001	49.46	3	0.422355545	0.318	0.904458028	7
optimal_loci_294176_G	1014	3.467687	0	2611	31.75	2	0.024948144	0.081	0.904514534	7
optimal_loci_294226_G	1987	3.865686	0	6357	45.09	3	0.068891888	0.351	0.905340476	7
optimal_loci_294227_G	4180	3.871392	8.23	2998	49.06	3	0.068891888	0.431	0.905357165	7
optimal_loci_294297_G	1045	4.1893	30.72	1001	64.3	2	11.80999285	0.715	0.910194739	7
optimal_loci_294298_G	1334	4.1893	0	2894	60.34	3	7.873328565	0.631	0.910259782	7
optimal_loci_294304_G	1021	4.1893	0	7881	57.1	3	7.873328565	0.722	0.910299873	7
optimal_loci_294377_G	1069	5.771985	0	2001	27.4	3	48.68006806	0.115	0.912768148	8
optimal_loci_294384_G	1776	6.242806	14.64	7556	40.42	4	36.51005105	0.268	0.912812804	8
optimal_loci_294389_G	2199	6.242806	6.41	8347	39.24	4	36.51005105	0.129	0.912874978	8
optimal_loci_294390_G	2436	6.242806	5.17	5725	44.37	3	0.055425512	0.379	0.912894151	8
optimal_loci_294447_G	1036	5.289242	28.19	6067	37.83	2	37.29427462	0.191	0.915583	9
optimal_loci_294489_G	3010	6.112561	4.98	2001	54.95	3	13.5564375	0.519	0.917652846	7
optimal_loci_294497_G	1357	5.488267	0	5696	53.86	1	7.14355909	0.463	0.918268239	8
optimal_loci_294519_G	1164	5.488267	25.26	2847	56.61	5	1.924515025	0.456	0.919006789	10
optimal_loci_294521_G	1332	5.488267	29.43	2712	59.53	5	1.924515025	0.576	0.919018236	10
optimal_loci_294554_G	3415	2.59415	2.02	1001	54.52	3	14.42653471	0.647	0.92023267	9
optimal_loci_294580_G	1200	2.392434	24.33	2385	37.41	3	1.200171734	0.097	0.921254546	9
optimal_loci_294598_G	1007	3.165397	39.72	2674	30.48	3	4.923799946	0.124	0.921947234	9
optimal_loci_294605_G	1578	3.565981	0	12537	44.55	1	6.914488156	0.3	0.922585819	11
optimal_loci_294620_G	1235	3.489276	0	2001	50.6	1	6.914488156	0.307	0.922779365	11
optimal_loci_294684_G	1227	4.556196	0	2182	40.5	4	0.31793415	0.17	0.925803754	9
optimal_loci_294697_G	1364	4.408619	36.44	2001	46.7	2	3.320108682	0.314	0.926258857	8
optimal_loci_294706_G	1127	4.343861	24.31	5915	60.15	4	9.278650197	0.705	0.926347889	8
optimal_loci_294707_G	1043	4.343861	11.31	7427	56.47	4	9.278650197	0.454	0.926360044	8

optimal_loci_294750_G	1017	5.226071	0	2726	57.22	4	6.035895463	0.783	0.928479314	9
optimal_loci_294799_G	1091	5.476795	11.09	5719	38.4	1	8.267024677	0.104	0.929357654	10
optimal_loci_294861_G	1583	4.449325	0	1001	50.09	2	2.499680946	0.459	0.930826907	6
optimal_loci_294872_G	3153	4.44163	1.46	1841	50.39	2	0.384531635	0.433	0.931084967	6
optimal_loci_294905_G	1736	3.89775	1.79	1630	37.44	4	0.382070083	0.153	0.931716896	6
optimal_loci_294928_G	1153	3.895356	3.12	13078	55.59	1	1.829251261	0.609	0.932703392	5
optimal_loci_295103_G	1015	1.597301	21.58	2001	57.43	5	2.662998723	0.713	0.937445969	3
optimal_loci_295106_G	1113	1.597301	0	4074	42.4	5	2.662998723	0.148	0.937462634	3
optimal_loci_295163_G	1199	1.117321	8.67	2153	39.19	4	13.80460322	0.198	0.939698044	3
optimal_loci_295303_G	1684	4.954896	7.84	1001	42.39	4	2.610055095	0.318	0.944736134	5
optimal_loci_295307_G	1284	4.954896	0	3398	48.13	5	2.088044076	0.433	0.944819024	5
optimal_loci_295308_G	1292	4.954896	7.59	2001	33.04	6	1.862779733	0.045	0.94483019	5
optimal_loci_295327_G	1673	5.491067	0	1001	44.88	6	36.94047036	0.275	0.945927577	6
optimal_loci_295369_G	1040	7.074688	0	1754	48.46	3	39.37108398	0.51	0.94739626	6
optimal_loci_295426_G	1228	4.61963	0	2676	44.29	3	11.83441078	0.179	0.949703272	3
optimal_loci_295514_G	1581	8.439349	22.58	1001	40.86	3	5.43326026	0.392	0.953886931	11
optimal_loci_295531_G	1536	6.169669	13.74	1891	51.95	3	4.36037612	0.609	0.954537976	11
optimal_loci_295553_G	1096	5.641429	0	15285	54.83	1	2.495669796	0.495	0.954853394	11
optimal_loci_295565_G	2145	5.785598	28.53	2985	39.95	2	5.173842788	0.077	0.955068614	11
optimal_loci_295573_G	2791	5.785598	8.31	3719	47.43	3	3.449228525	0.486	0.9551605	11
optimal_loci_295581_G	2065	5.785598	10.12	1116	48.71	2	4.114889806	0.412	0.955323337	11
optimal_loci_295586_G	1050	5.785598	34.1	7657	43.52	2	4.114889806	0.337	0.95537592	11
optimal_loci_295587_G	1624	5.785598	13.85	8811	42.73	2	4.114889806	0.265	0.955385197	11
optimal_loci_295605_G	1103	5.785598	0	9806	38.89	3	0.731242432	0.15	0.955497309	11
optimal_loci_295651_G	2662	6.900009	6.5	11687	39.4	1	3.764142907	0.282	0.95689217	14
optimal_loci_295655_G	1435	6.635994	0	11188	38.04	1	3.764142907	0.258	0.957116675	14
optimal_loci_295702_G	1168	5.179007	11.73	1103	39.81	5	0.307488911	0.376	0.959539176	6
optimal_loci_295705_G	1632	5.027718	0	1001	40.01	4	0.384361138	0.267	0.959676819	8
optimal_loci_295706_G	1887	4.798528	25.81	2704	37.83	5	1.574808586	0.264	0.959743358	8
optimal_loci_295746_G	1982	4.841382	23.61	10269	38.54	2	4.007854195	0.124	0.961421987	7
optimal_loci_295802_G	1541	7.097126	11.94	3549	32.83	1	0.083402662	0.144	0.963634815	9
optimal_loci_295803_G	1434	7.097126	23.29	2082	36.68	1	0.083402662	0.241	0.963647469	9
optimal_loci_295839_G	1055	9.053264	10.62	1167	39.62	3	19.72127118	0.167	0.964759092	7

optimal_loci_295852_G	1559	10.280511	15.52	2047	36.36	8	9.657668062	0.158	0.966186937	8
optimal_loci_295856_G	2764	10.280511	0	2001	53.47	7	11.68378243	0.607	0.966387743	8
optimal_loci_295866_G	1566	10.280511	0	2076	36.9	4	9.121556802	0.207	0.966559978	8
optimal_loci_295919_G	1177	9.681066	7.48	1424	42.31	5	0.950473418	0.3	0.969463508	11
optimal_loci_295930_G	1092	9.459949	9.16	4786	58.79	5	0.443736148	0.649	0.969678857	11
optimal_loci_295976_G	1366	7.171294	2.93	2001	44.58	6	52.16671728	0.29	0.971349576	8
optimal_loci_295977_G	1061	7.171294	9.14	4281	43.16	6	52.24372949	0.24	0.971367904	8
optimal_loci_295994_G	1219	6.906294	5	1952	54.38	2	5.13340149	0.681	0.972345574	8
optimal_loci_295997_G	1136	6.230438	7.57	5461	50.79	2	5.13340149	0.689	0.972379925	8
optimal_loci_295998_G	1300	6.230438	0	4128	50.38	2	5.13340149	0.241	0.972389322	8
optimal_loci_296004_G	1071	6.230438	37.35	2759	42.11	2	5.13340149	0.237	0.972487711	8
optimal_loci_296074_G	1014	3.821779	6.61	1001	34.12	5	8.959838196	0.102	0.977475695	3
optimal_loci_296080_G	1513	6.430839	13.09	3486	37.73	2	9.741649793	0.229	0.977630397	3
optimal_loci_296141_G	2113	4.5384	18.5	1195	34.97	4	3.001843464	0.161	0.980135675	8
optimal_loci_296201_G	1377	5.866411	8.28	3563	45.38	3	0.128591159	0.223	0.982118468	8
optimal_loci_296212_G	2318	7.070056	24.72	3056	40.37	3	4.358285351	0.255	0.982474008	8
optimal_loci_296214_G	1267	7.070056	21.78	6362	43.48	3	4.358285351	0.222	0.982500585	8
optimal_loci_296234_G	1839	7.070056	3.05	2001	35.34	2	6.072147921	0.16	0.983157547	9
optimal_loci_296257_G	1373	8.37364	5.9	10185	31.31	4	13.26235774	0.056	0.984166794	10
optimal_loci_296259_G	1045	8.37364	0	8519	53.77	4	13.26235774	0.629	0.984182824	9
optimal_loci_296288_G	2124	8.721914	9.18	1094	52.77	3	5.843749771	0.393	0.985027094	10
optimal_loci_296360_G	1243	7.333232	19.87	1001	33.22	3	22.35441365	0.206	0.986976364	8
optimal_loci_296401_G	1337	6.461192	7.33	6057	42.18	5	6.458609445	0.342	0.988112651	7
optimal_loci_296432_G	1856	3.86221	4.36	2201	40.78	3	37.11491159	0.154	0.989040592	5
optimal_loci_296433_G	1597	4.124494	30.62	2034	33.62	3	37.11491159	0.13	0.989066678	4
optimal_loci_296573_G	1056	3.135289	14.2	1467	43.08	1	103.2735874	0.339	0.995333946	2
optimal_loci_296657_G	1036	5.081912	35.33	9084	58.3	2	1.78055276	0.745	0.999084777	2
optimal_loci_296698_G	1263	1.248527	0	17237	31.43	1	3.780127648	0.044	0.995330222	1
optimal_loci_296850_G	2240	2.294539	28.17	1751	37.72	1	0.553373189	0.193	0.98665536	2
optimal_loci_297010_G	1135	3.814919	2.56	1279	56.21	1	1.701140576	0.558	0.979909834	4
optimal_loci_297045_G	1604	5.350414	10.41	3458	42.01	2	16.13531952	0.194	0.978058684	3
optimal_loci_297046_G	1310	5.350414	0	2001	30.91	2	16.13531952	0.072	0.978038504	3
optimal_loci_297221_G	1012	2.899245	0	5138	35.07	2	5.275177508	0.072	0.96861356	2

optimal_loci_297224_G	1032	2.899245	12.5	3715	41.76	2	5.275177508	0.235	0.968543947	2
optimal_loci_297529_G	1371	3.502249	21.37	1001	51.71	1	4.951604973	0.494	0.954082978	3
optimal_loci_297578_G	2276	4.029707	0	1349	43.4	1	6.700193481	0.197	0.951786427	3
optimal_loci_297653_G	3077	3.033472	0.91	1690	53.85	1	31.13736694	0.519	0.949322161	3
optimal_loci_297768_G	2308	2.754498	0	2001	38.69	3	7.920523329	0.096	0.940402825	3
optimal_loci_297811_G	1177	2.388084	0	19983	47.4	1	9.980498693	0.334	0.937274224	3
optimal_loci_297874_G	1514	2.84742	35.87	2163	39.56	1	0.343576271	0.155	0.933865776	3
optimal_loci_298133_G	1745	1.264766	0	4328	38.62	1	0.724675639	0.113	0.921559709	1
optimal_loci_298665_G	1656	4.254791	0	3504	35.99	1	316.4915148	0.178	0.892282064	4
optimal_loci_298702_G	1180	3.362305	18.05	6070	35.33	3	0.010310607	0.153	0.888880859	7
optimal_loci_298732_G	1162	3.611802	12.31	4045	43.8	3	2.472965959	0.391	0.886641219	8
optimal_loci_298733_G	1022	3.611802	0	2375	36.59	3	2.472965959	0.132	0.886618089	8
optimal_loci_298791_G	1415	3.427498	0	2899	54.91	3	7.001509253	0.408	0.883243518	7
optimal_loci_298800_G	1120	3.427498	0	11150	41.33	2	7.412435501	0.412	0.883003947	7
optimal_loci_298809_G	2197	3.427498	2.05	1243	48.97	2	2.153059929	0.461	0.882848199	7
optimal_loci_298834_G	2103	4.086664	14.55	5012	40.32	1	9.147143003	0.282	0.880654765	9
optimal_loci_298913_G	1089	3.322718	19.74	2001	34.8	3	18.55909886	0.219	0.875886801	4
optimal_loci_298920_G	4316	3.308378	3.54	2191	34.36	3	18.55909886	0.267	0.875769792	4
optimal_loci_298931_G	1271	2.628248	17.62	2933	50.82	1	2.215729991	0.271	0.875309363	4
optimal_loci_299140_G	1827	2.037028	11.33	1001	40.28	2	1.077952064	0.274	0.865281247	1
optimal_loci_299564_G	1543	6.065648	16.2	1452	34.34	5	16.30054185	0.014	0.844320042	7
optimal_loci_299596_G	1257	7.422203	29.04	16936	46.14	1	0.04486811	0.365	0.842914307	7
optimal_loci_299630_G	1110	8.213799	0	2075	42.97	3	3.12206818	0.138	0.841279972	7
optimal_loci_299655_G	1075	9.016994	0	4469	49.95	2	19.19551296	0.321	0.839948089	7
optimal_loci_299681_G	1259	9.147114	31.93	13928	41.69	1	38.39102592	0.296	0.839606939	7
optimal_loci_299695_G	1556	9.246771	23.33	19842	43.31	1	5.357514118	0.277	0.839227244	7
optimal_loci_299710_G	1215	9.515288	0	3016	33.66	2	13.67828828	0	0.837949238	7
optimal_loci_299825_G	1501	2.435346	0	10169	34.84	1	2.305088402	0.185	0.828541233	5
optimal_loci_299840_G	1203	2.435346	15.88	18236	43.72	1	4.8919305	0.285	0.827586247	5
optimal_loci_299895_G	1532	1.933594	0	2229	40.01	2	1.425716602	0.138	0.822711981	6
optimal_loci_299898_G	2289	1.933594	0	5329	52.38	2	1.425716602	0.434	0.82265856	6
optimal_loci_299907_G	3702	1.933594	15.37	13907	44.78	2	1.425716602	0.371	0.82252018	6
optimal_loci_299952_G	3112	2.386754	1	1001	51.06	2	81.12879049	0.383	0.817694266	8

optimal_loci_299986_G	2460	2.701299	9.15	3092	36.3	2	23.45904926	0.151	0.813959723	10
optimal_loci_299991_G	1353	1.473518	14.12	10764	46.04	3	8.132973163	0.328	0.813296842	11
optimal_loci_299992_G	2984	1.466996	1.04	7548	47.78	3	8.132973163	0.341	0.813252299	11
optimal_loci_299997_G	1192	1.437492	0	3221	59.22	2	8.509757475	0.582	0.813192368	12
optimal_loci_300036_G	1121	1.567047	28.01	2617	48.17	4	0.012198886	0.342	0.809414945	11
optimal_loci_300038_G	1810	1.567047	0	3319	35.91	4	0.012198886	0.211	0.809381634	11
optimal_loci_300039_G	1009	1.567047	3.17	2001	42.22	4	0.012198886	0.216	0.80936338	11
optimal_loci_300068_G	1271	2.197697	19.91	4549	35.01	1	0.744422485	0	0.807375873	11
optimal_loci_300077_G	1126	2.15789	0	4653	57.1	2	0.372211243	0.706	0.807034266	11
optimal_loci_300082_G	2242	2.15789	26.36	4551	45.45	2	0.031021048	0.324	0.80686151	10
optimal_loci_300092_G	1143	3.907731	0	4036	52.84	1	4.860200121	0.58	0.80625482	8
optimal_loci_300258_G	1341	2.132783	0	3010	44.74	4	11.59814366	0.292	0.794572839	4
optimal_loci_300312_G	1059	3.908817	33.71	3385	34.65	1	0.852808878	0.268	0.789875028	9
optimal_loci_300325_G	1024	3.908817	35.16	1987	29.98	1	0.3935799	0.107	0.788046994	9
optimal_loci_300327_G	1036	3.866042	0	16762	50.57	1	0.3935799	0.3	0.787645803	9
optimal_loci_300332_G	1637	3.601117	28.65	5970	57.17	3	10.84953682	0.714	0.78726849	8
optimal_loci_300333_G	1103	3.601117	0	4526	38.62	3	10.84953682	0.229	0.78724849	8
optimal_loci_300335_G	1134	3.601117	0	2523	59.7	3	10.84953682	0.487	0.787220748	8
optimal_loci_300336_G	1489	3.601117	0	1001	54.93	3	10.84953682	0.477	0.787199668	8
optimal_loci_300342_G	1019	3.601117	0	6671	53.97	1	1.96461718	0.474	0.786674294	8
optimal_loci_300405_G	1285	3.467444	0	1573	38.36	2	14.21188615	0.15	0.779606994	1
optimal_loci_300478_G	1541	2.452276	0	1001	43.21	3	3.395550644	0.249	0.771720152	3
optimal_loci_300497_G	1008	2.518131	0	2190	47.91	1	10.72413877	0.255	0.769363657	4
optimal_loci_300544_G	1005	1.129265	10.65	2001	33.53	2	2.313854252	0	0.764802784	4
optimal_loci_300564_G	1269	1.129265	33.02	7934	27.81	2	2.313854252	0	0.764326053	3
optimal_loci_300708_G	2163	1.326242	8	2001	46.92	2	28.78650743	0.376	0.755794349	2
optimal_loci_300741_G	1058	1.054092	9.74	4137	43.19	2	17.7091547	0.228	0.754426163	2
optimal_loci_300888_G	1521	3.234353	0	2001	49.17	3	30.04627457	0.498	0.742086745	1
optimal_loci_301076_G	1605	1.510241	0	17019	42.42	1	0.391906751	0.208	0.723656247	9
optimal_loci_301132_G	1302	2.280779	29.19	2651	38.86	1	2.516137819	0.164	0.719693172	9
optimal_loci_301172_G	1292	2.835187	0	1960	42.1	2	11.10367777	0.258	0.71862705	9
optimal_loci_301175_G	1451	2.835187	0	7198	52.3	2	11.10367777	0.627	0.718467853	10
optimal_loci_301176_G	1056	2.835187	0	6058	51.89	2	11.10367777	0.508	0.718452064	10

optimal_loci_301180_G	1198	2.835187	0	3690	43.73	2	11.10367777	0.26	0.718419266	10
optimal_loci_301186_G	1121	2.835187	0	2619	36.3	1	10.34039409	0.148	0.718246607	10
optimal_loci_301187_G	1055	2.835187	0	4032	34.4	1	10.34039409	0.111	0.71822795	10
optimal_loci_301189_G	1313	2.835187	0	1001	38.53	1	12.03613415	0.178	0.717545873	12
optimal_loci_301264_G	1328	3.033768	0	2227	34.78	2	8.033189196	0.089	0.71160018	10
optimal_loci_301273_G	1749	3.286309	0	1001	46.14	3	1.368374122	0.468	0.711001579	5
optimal_loci_301275_G	1458	3.286309	0	1422	54.52	3	1.368374122	0.504	0.710973546	5
optimal_loci_301283_G	1623	3.358807	10.91	5134	44.79	1	0.131299031	0.324	0.710486288	4
optimal_loci_301417_G	2001	5.793916	0	1184	46.47	2	17.44441319	0.339	0.699111801	7
optimal_loci_301438_G	1638	5.793916	0	3584	51.46	2	2.074196295	0.615	0.697823421	7
optimal_loci_301440_G	1286	5.793916	0	5747	49.45	2	2.074196295	0.282	0.697798338	7
optimal_loci_301442_G	1035	5.793916	0	8099	52.27	2	2.074196295	0.407	0.697769238	7
optimal_loci_301465_G	1233	0.993297	3.65	1894	36.09	2	0.79082646	0.123	0.695703296	7
optimal_loci_301466_G	1804	0.993297	0	3185	55.82	2	0.79082646	0.53	0.695677507	7
optimal_loci_301467_G	1422	0.993297	0	5100	55.2	2	0.79082646	0.423	0.695656274	7
optimal_loci_301696_G	2016	1.355245	18.7	2548	34.77	2	3.013567254	0.227	0.679582465	13
optimal_loci_301715_G	1071	0.929136	6.44	2001	48.73	2	2.335091639	0.367	0.677793532	13
optimal_loci_301721_G	1608	0.929136	2.11	2404	41.23	3	1.564302377	0.269	0.677614681	13
optimal_loci_301732_G	1431	0.854002	11.67	14321	61.56	1	14.09338886	0.654	0.676926787	13
optimal_loci_301733_G	1499	0.854002	0	12446	52.83	1	14.09338886	0.392	0.676900817	13
optimal_loci_301766_G	1022	0.854002	35.13	5132	42.85	1	3.067375447	0.182	0.675211233	13
optimal_loci_301769_G	1116	0.854002	35.22	2855	45.51	1	3.067375447	0.21	0.675179695	13
optimal_loci_301770_G	1246	0.854002	11.32	1553	43.49	1	3.067375447	0.24	0.675161662	13
optimal_loci_301773_G	2254	0.729029	0	7186	42.67	1	3.067375447	0.335	0.674961745	14
optimal_loci_301774_G	2194	0.729029	0	9762	45.03	1	3.067375447	0.402	0.674926898	14
optimal_loci_301784_G	1384	0.721942	0	7689	37.71	2	24.72493049	0.237	0.674256994	14
optimal_loci_301789_G	1917	0.721942	0	2942	59.72	2	24.72493049	0.56	0.674191247	14
optimal_loci_301793_G	1002	0.721942	0	1929	51.89	2	24.72493049	0.522	0.674063269	14
optimal_loci_301834_G	1126	0.576579	2.66	3621	59.5	1	24.8823702	0.61	0.668139501	10
optimal_loci_301840_G	2022	0.293834	22.21	2378	42.08	2	5.915466388	0.243	0.666951191	5
optimal_loci_301849_G	1631	0.406899	26.43	6774	42.3	2	23.17255207	0.243	0.665686994	5
optimal_loci_301852_G	1372	0.406899	10.2	2603	54.44	2	23.17255207	0.688	0.665629224	5
optimal_loci_301874_G	1138	0.543845	0	4647	54.83	1	5.867904192	0.362	0.662495249	5

optimal_loci_302109_G	1293	1.007802	10.83	1001	42.07	5	22.26795037	0.359	0.63143867	5
optimal_loci_302113_G	3090	1.007802	2.07	1203	41.81	4	28.48683914	0.315	0.631218837	5
optimal_loci_302132_G	1096	0.91504	21.35	3156	46.16	1	3.405570733	0.442	0.630063823	5
optimal_loci_302142_G	1038	1.06339	0	15337	47.49	2	11.42144829	0.304	0.628776551	5
optimal_loci_302154_G	1019	0.829055	0	2440	41.8	4	0.549014408	0.239	0.626608186	6
optimal_loci_302185_G	1801	0.348393	30.93	4585	37.36	1	1.261025933	0.19	0.621492853	2
optimal_loci_302339_G	1040	0.513328	0	2001	36.63	3	2.462141555	0	0.60659964	1
optimal_loci_302770_G	2919	0.306174	8.29	2318	48.13	1	100.3878471	0.292	0.567701302	1
optimal_loci_303042_G	1228	0.324949	0	18802	40.3	1	24.3577628	0.074	0.552408421	1
optimal_loci_303342_G	1619	0.175959	0	2462	40.45	1	0.839052661	0.157	0.533096039	2
optimal_loci_303348_G	1390	0.200079	0	2888	44.24	2	0.41952633	0.389	0.532814695	2
optimal_loci_303519_G	1572	0.039369	0	4686	41.98	1	7.627878268	0.141	0.520230983	3
optimal_loci_303562_G	2559	0.097458	4.69	12639	45.68	1	9.198432988	0.251	0.516485817	3
optimal_loci_303563_G	2354	0.097458	2.93	10228	35.51	1	9.198432988	0.234	0.516452424	3
optimal_loci_306860_G	1192	0.010729	20.47	2001	31.87	2	3.687360285	0.177	0.201935194	1
optimal_loci_307149_G	1144	0.011275	3.58	2211	46.24	1	21.04638119	0.347	0.17720856	2
optimal_loci_307208_G	1008	0.012079	0	1233	38.59	3	1.71895366	0.018	0.171122964	2
optimal_loci_307528_G	1511	0.010354	2.18	17662	41.82	1	0.125552643	0.227	0.143835789	2
optimal_loci_307610_G	1045	0.010682	26.6	1506	33.68	3	0.612227236	0.04	0.137802687	3
optimal_loci_307617_G	1138	0.011279	12.92	13963	40.68	1	13.16414637	0.138	0.136569155	2
optimal_loci_307893_G	1371	0.011408	14.51	19700	45	1	46.01070873	0.367	0.112016704	3
optimal_loci_307907_G	1456	0.011405	6.59	18802	33.99	1	4.431326596	0.104	0.109746288	3
optimal_loci_307919_G	1351	0.011405	14.51	6390	41.96	1	4.431326596	0.194	0.109574377	3
optimal_loci_308690_G	1339	0.104158	36.3	2051	38.76	1	6.292958617	0.188	0.038620693	1
optimal_loci_309257_G	1025	0.107333	0	2456	46.63	3	0.073732594	0.508	0.003736149	4
optimal_loci_309261_G	1068	0.098812	0	8955	40.44	3	0.073732594	0.352	0.003813472	4
optimal_loci_309307_G	1825	0.098812	2.47	13125	42.02	1	0.267430176	0.238	0.006303029	4
optimal_loci_309318_G	1131	0.098812	0	8376	43.58	1	0.267430176	0.233	0.006603466	4
optimal_loci_309558_G	2067	0.108949	21.09	2001	58.82	1	35.66343016	0.646	0.022503	1
optimal_loci_309774_G	1236	0.117134	0	15314	42.23	1	265.6740502	0.193	0.0364413	1
optimal_loci_309862_G	1709	0.146942	0	3690	52.01	2	1.398407625	0.587	0.044853175	1
optimal_loci_311097_G	1317	0.118511	22.32	2001	48.51	1	26.6767565	0.621	0.134056042	1
optimal_loci_311466_G	1448	0.083526	20.3	9486	37.91	2	0.106839862	0.069	0.162821202	2

optimal_loci_311494_G	1356	0.095641	0	3214	41.51	1	4.590601551	0.237	0.164602258	2
optimal_loci_311588_G	1955	0.159756	19.64	19760	48.23	1	35.95623478	0.292	0.175363774	2
optimal_loci_311592_G	1327	0.135634	0	12581	40.54	1	35.95623478	0.174	0.175456658	2
optimal_loci_311776_G	1073	0.281064	0	3909	43.33	1	15.6809296	0.21	0.189110595	4
optimal_loci_311834_G	1124	1.037133	0	13715	32.11	1	58.02112333	0.207	0.193231583	4
optimal_loci_311848_G	1075	1.133452	9.77	4838	39.72	1	0.476865557	0	0.194062344	4
optimal_loci_311858_G	1293	1.230924	29.39	15793	44.85	1	0.476865557	0.294	0.194329932	4
optimal_loci_313001_G	1266	0.935704	16.03	19342	31.91	1	24.08542724	0.339	0.277459716	3
optimal_loci_313012_G	1196	0.916873	0	9711	55.93	1	32.96221716	0.719	0.278257092	3
optimal_loci_313089_G	1636	1.074633	8.92	1627	36.06	1	7.804341639	0.057	0.282516984	6
optimal_loci_313135_G	1183	0.35532	0	9172	48.77	2	4.222384557	0.235	0.285466311	4
optimal_loci_313141_G	1328	0.242094	0	2727	49.77	3	3.38069006	0.419	0.285633234	4
optimal_loci_313155_G	1620	0.259872	12.65	2652	36.6	1	2.950784079	0.072	0.28637468	4
optimal_loci_313339_G	2384	0.447483	10.11	8891	34.94	1	1.823138441	0.201	0.298634303	1
optimal_loci_313453_G	2861	0.758351	38.55	2797	40.19	1	4.489935294	0.181	0.305165182	4
optimal_loci_313485_G	1038	0.652791	19.46	2578	50.38	2	4.973999062	0.278	0.306966666	5
optimal_loci_313519_G	1119	0.586322	4.11	2712	52.45	3	9.226473325	0.473	0.309001854	9
optimal_loci_313526_G	1285	0.49731	0	18525	50.5	1	74.84877919	0.433	0.310026176	9
optimal_loci_313549_G	1335	0.478572	0	3443	40.59	2	4.868496395	0.193	0.311706091	12
optimal_loci_313588_G	2985	0.456806	7.67	12018	47.93	1	2.641031546	0.307	0.313156953	12
optimal_loci_313593_G	1551	0.467523	0	1287	56.15	1	2.641031546	0.554	0.313301687	12
optimal_loci_313600_G	1728	0.467523	7.29	9571	47.85	2	0.793929829	0.516	0.31380806	12
optimal_loci_313602_G	1008	0.463976	9.62	5650	43.45	2	0.793929829	0.286	0.313863277	12
optimal_loci_313639_G	1137	0.507019	20.05	4197	54.52	2	0.588159881	0.414	0.316295904	13
optimal_loci_313660_G	1944	0.466246	0	1001	47.99	1	1.210970298	0.419	0.317208852	13
optimal_loci_313661_G	1748	0.45738	0	2001	34.09	1	1.210970298	0.017	0.317282701	13
optimal_loci_313664_G	1386	0.460026	0	19604	53.39	1	27.3816787	0.527	0.31753368	13
optimal_loci_313675_G	1509	0.454932	0	10492	46.45	2	8.334571903	0.627	0.318286036	12
optimal_loci_313735_G	1486	0.284711	15.41	1341	36	3	1.165283222	0.126	0.321060516	9
optimal_loci_313743_G	1132	0.278775	8.3	17518	31	2	0.271030307	0.16	0.321252983	9
optimal_loci_313744_G	1208	0.278775	0	18709	36.92	2	0.271030307	0.094	0.321267153	9
optimal_loci_313790_G	2532	0.158284	33.49	8026	40.91	1	0.29257768	0.211	0.325898988	4
optimal_loci_313902_G	1397	0.196334	0	1619	39.58	1	65.58173399	0.227	0.332114402	3

optimal_loci_313911_G	1164	0.197564	0	13268	36.68	2	13.08867147	0.303	0.332695528	3
optimal_loci_313985_G	1779	0.334771	11.64	7856	37.38	3	3.20851047	0.144	0.335907303	3
optimal_loci_314268_G	1033	1.539808	0	1001	42.01	1	0.330286015	0.323	0.352694706	6
optimal_loci_314275_G	1221	1.539808	0	14399	40.37	1	0.330286015	0.043	0.352998237	6
optimal_loci_314277_G	2141	1.539808	0	16421	35.91	1	0.330286015	0.101	0.353022293	6
optimal_loci_314278_G	1724	1.539808	9.57	19656	43.73	1	0.330286015	0.274	0.353060782	6
optimal_loci_314282_G	1265	1.539808	3	17710	37.86	1	0.152012393	0.124	0.353149895	6
optimal_loci_314296_G	1267	1.325461	11.52	4682	38.98	1	1000.629864	0.311	0.353908568	6
optimal_loci_314815_G	1335	1.147842	0	1104	54.38	3	0.399739849	0.596	0.385245818	3
optimal_loci_314844_G	1030	2.006968	0	3056	35.24	1	4.96829224	0.082	0.38651222	3
optimal_loci_314893_G	1131	0.389888	0	3648	54.46	1	11.53412892	0.645	0.388375322	3
optimal_loci_315232_G	1801	0.218022	0	2139	53.58	2	3.180223053	0.653	0.412099584	4
optimal_loci_315238_G	1094	0.165724	16.64	3487	54.47	2	2.831568458	0.637	0.412906633	6
optimal_loci_315280_G	1012	0.113712	0	1001	42.78	1	1.191938996	0.281	0.415543565	6
optimal_loci_315281_G	2713	0.113712	23.15	2143	36.08	1	1.191938996	0.112	0.415557152	6
optimal_loci_315318_G	1379	0.063375	0	11580	43.94	1	16.60213248	0.368	0.418239842	5
optimal_loci_315319_G	1970	0.063375	24.37	13352	44.61	1	16.60213248	0.352	0.418260925	5
optimal_loci_315523_G	1131	0.57418	28.29	2998	34.48	2	27.1679872	0.243	0.433638749	4
optimal_loci_315535_G	1041	0.585806	0	2001	58.98	5	24.25241075	0.66	0.435561802	4
optimal_loci_315575_G	1322	0.805867	15.43	4285	42.36	2	2.061064597	0.164	0.439014242	4
optimal_loci_315578_G	1016	0.805867	26.57	2001	40.94	2	2.061064597	0.274	0.439045057	4
optimal_loci_315713_G	1799	0.288484	4.89	1001	52.25	1	126.1826236	0.496	0.446690894	2
optimal_loci_315720_G	1232	0.288484	0	4224	45.94	2	12.79728343	0.35	0.447498299	2
optimal_loci_315868_G	1120	0.367956	0	6279	55.89	2	0.156249566	0.503	0.456672975	6
optimal_loci_315871_G	1058	0.367956	0	3655	51.51	2	0.156249566	0.4	0.456704932	6
optimal_loci_315880_G	1324	0.367956	0	5239	61.63	2	1.626842358	0.783	0.45684317	6
optimal_loci_315881_G	2169	0.367956	0	6596	50.89	2	1.626842358	0.546	0.456859315	6
optimal_loci_315885_G	2148	2.611025	0	1174	55.95	1	3.253684716	0.524	0.457086	6
optimal_loci_315952_G	1406	8.502763	0	2001	48.43	3	2.487738197	0.557	0.461200647	6
optimal_loci_316080_G	1054	0.322567	0	2001	58.63	1	0.226766099	0.629	0.470630205	3
optimal_loci_316091_G	1511	0.309772	8.01	2627	39.24	1	15.37181035	0.31	0.471474029	3
optimal_loci_316095_G	1175	0.309188	0	2952	49.7	1	15.37181035	0.419	0.471585926	3
optimal_loci_319409_G	1273	0.062171	15.79	1726	33.54	4	30.23738463	0.089	0.687578531	4

optimal_loci_319475_G	1105	0.301355	7.51	4484	36.56	1	0.19305246	0.002	0.691335704	4
optimal_loci_319479_G	1002	0.301355	0	2502	36.62	1	0.19305246	0	0.6915281	4
optimal_loci_319482_G	1198	0.301355	0	5430	36.39	1	0.19305246	0.111	0.691562936	4
optimal_loci_319724_G	1681	0.640679	0	1001	53.77	1	8.061666666	0.451	0.705587149	1
optimal_loci_319854_G	1097	2.507533	0	2582	47.94	1	28.64285549	0.358	0.715254385	7
optimal_loci_319855_G	1105	2.507533	0	3712	54.66	1	28.64285549	0.605	0.715267829	7
optimal_loci_319856_G	1420	2.507533	0	4850	55.63	1	28.64285549	0.457	0.715281368	7
optimal_loci_319886_G	1234	2.440566	0	10258	57.77	1	14.52145358	0.655	0.718178155	9
optimal_loci_319894_G	1083	2.440566	16.62	5964	56.32	1	0.217517623	0.742	0.718545255	9
optimal_loci_319895_G	1315	2.440566	20.08	4616	44.1	1	0.217517623	0.229	0.718558533	9
optimal_loci_319912_G	1206	2.440566	31.84	3041	39.63	1	8.937809562	0.253	0.719189997	9
optimal_loci_319986_G	1058	2.973522	0	16962	40.07	1	1.119427218	0.165	0.723379611	9
optimal_loci_319990_G	1062	2.973522	0	19105	41.14	1	1.119427218	0.385	0.723405107	9
optimal_loci_320035_G	1204	2.528445	0	1001	52.65	2	6.2750917	0.382	0.725756795	7
optimal_loci_320058_G	1478	2.009509	0	7630	36.19	1	8.607570388	0.054	0.726961984	8
optimal_loci_320090_G	1249	2.009509	0	1960	44.35	4	1.031870132	0.333	0.728167078	8
optimal_loci_320130_G	1054	1.57159	0	6119	43.35	1	7.629229229	0.268	0.73029082	7
optimal_loci_320153_G	1851	1.586047	15.72	18622	33.76	1	9.806341926	0.083	0.73119901	7
optimal_loci_320180_G	1345	1.594624	10.63	1001	43.42	4	6.399937621	0.315	0.732738354	6
optimal_loci_320242_G	2604	0.646803	21.01	7693	52.53	3	9.654484515	0.407	0.735971736	5
optimal_loci_320295_G	2123	0.72059	0	10485	42.91	2	0.040248273	0.257	0.739389221	2
optimal_loci_320417_G	1186	0.141879	0	7654	45.27	2	1.002328878	0.52	0.74573583	8
optimal_loci_320522_G	1667	0.220066	11.94	6626	44.75	2	8.958299025	0.283	0.750877429	15
optimal_loci_320524_G	2395	0.220066	0	8820	38.37	2	8.958299025	0.239	0.750903532	15
optimal_loci_320525_G	1092	0.220066	2.56	12260	52.83	2	8.958299025	0.457	0.75094446	15
optimal_loci_320529_G	2337	0.220066	7.02	16968	54.77	1	1.289057535	0.632	0.7511498	15
optimal_loci_320538_G	1292	0.219967	0	3863	55.57	2	0.644528768	0.386	0.751456377	15
optimal_loci_320539_G	2434	0.219967	0	5856	46.5	2	0.644528768	0.349	0.751480089	15
optimal_loci_320540_G	1300	0.219967	0	9042	60.23	2	0.644528768	0.691	0.751517994	15
optimal_loci_320545_G	1200	0.202832	31.58	4922	42.16	3	1.305417311	0.24	0.751751484	14
optimal_loci_320548_G	1057	0.202832	16.27	2766	45.03	3	1.305417311	0.365	0.751778837	14
optimal_loci_320572_G	1007	0.166624	0	2001	32.37	2	43.76548883	0.105	0.753450994	16
optimal_loci_320575_G	1184	0.166624	20.95	13552	41.55	2	43.76548883	0.389	0.753588423	16

optimal_loci_320608_G	1146	0.137519	0	17455	41.53	2	0.034738551	0.365	0.75481103	16
optimal_loci_320616_G	1326	0.137519	5.51	12370	40.42	2	0.034738551	0.199	0.754869388	16
optimal_loci_320619_G	1108	0.137519	6.59	5275	39.8	3	0.228788069	0.39	0.754956395	16
optimal_loci_320642_G	1763	1.273368	18.77	1442	43.5	2	24.81686989	0.341	0.757750803	8
optimal_loci_320664_G	2079	1.609704	7.26	7235	45.59	3	2.720328493	0.423	0.758976861	8
optimal_loci_320730_G	1432	2.692154	2.58	1029	50.76	5	4.857973972	0.311	0.762565944	5
optimal_loci_320772_G	1784	2.479264	13.17	8131	44.84	1	11.09869624	0.305	0.765437199	5
optimal_loci_320809_G	1214	2.445219	34.93	3063	39.45	3	0.130331272	0.177	0.768131513	5
optimal_loci_320824_G	1053	1.97222	10.73	1001	40.17	4	0.087134745	0.1	0.769084736	5
optimal_loci_320866_G	2864	1.908329	5.34	2210	53.03	2	20.98694264	0.499	0.770918771	6
optimal_loci_320947_G	1345	1.484373	9.96	2420	46.84	2	2.086409499	0.338	0.774456065	7
optimal_loci_320988_G	1702	1.73554	0	6567	38.66	1	2.663769899	0.197	0.776838151	7
optimal_loci_321023_G	1969	1.522931	16.1	1001	53.83	2	7.226076205	0.537	0.779751927	8
optimal_loci_321024_G	1278	1.516636	10.56	2003	45.38	3	4.817384137	0.361	0.779858946	9
optimal_loci_321028_G	1131	1.516636	0	5688	43.58	3	4.817384137	0.223	0.779902789	9
optimal_loci_321058_G	1282	1.584927	15.83	2001	45.7	4	51.73064941	0.481	0.781920511	9
optimal_loci_321088_G	1540	1.434257	0	19597	44.48	1	99.99747594	0.385	0.783895295	8
optimal_loci_321094_G	2103	1.902186	31.91	2089	45.55	2	12.14780072	0.348	0.785099342	9
optimal_loci_321106_G	1430	1.911302	0	3426	37.9	4	37.82179591	0.217	0.785804833	8
optimal_loci_321139_G	1286	1.31177	0	7067	34.91	2	6.289900184	0.251	0.78771468	6
optimal_loci_321200_G	1050	1.338515	0	1001	35.52	4	138.3306384	0.137	0.791068406	5
optimal_loci_321267_G	2440	2.929591	14.14	7033	41.59	4	8.566889422	0.323	0.795079199	7
optimal_loci_321299_G	1219	3.42483	13.37	2940	50.12	2	41.16390648	0.489	0.797619094	6
optimal_loci_321300_G	1309	3.42483	0	1598	52.02	2	41.16390648	0.563	0.79763399	6
optimal_loci_321304_G	1111	3.42483	23.58	3992	55.53	2	41.16390648	0.479	0.79780478	6
optimal_loci_321306_G	1627	3.42483	2.52	1001	48	2	41.16390648	0.436	0.797834226	6
optimal_loci_321348_G	1347	3.586915	0	3326	44.54	3	2.491488828	0.229	0.799813591	6
optimal_loci_321482_G	1284	0.849869	0	2001	41.58	1	14.60249388	0.292	0.807781436	4
optimal_loci_321514_G	1438	0.567202	2.5	1001	36.57	3	6.99164687	0.11	0.809941406	4
optimal_loci_321516_G	1048	0.567202	17.56	1001	50.28	3	6.99164687	0.465	0.809964844	4
optimal_loci_321523_G	1408	0.567202	38.28	10122	37.85	2	10.48747031	0.104	0.810147436	4
optimal_loci_321607_G	1173	2.831885	0	1121	54.47	2	2.552893825	0.685	0.816353714	8
optimal_loci_321631_G	2241	3.121521	12.21	4490	47.92	2	0.906814929	0.492	0.817698652	8

optimal_loci_321636_G	1438	2.852818	0	3986	44.5	3	0.406034343	0.234	0.817866586	8
optimal_loci_321638_G	1088	2.749797	0	1725	49.44	5	5.050184236	0.401	0.818007144	8
optimal_loci_321645_G	1955	3.025227	0	2049	48.74	2	14.43811635	0.279	0.818966149	8
optimal_loci_321646_G	1004	3.025227	0	1001	54.08	2	14.43811635	0.494	0.818989932	8
optimal_loci_321647_G	1070	3.025227	0	2001	54.67	2	14.43811635	0.351	0.819056535	8
optimal_loci_321649_G	2210	3.025227	3.08	2001	48.23	2	14.43811635	0.415	0.819074548	8
optimal_loci_321726_G	1070	1.083824	24.77	1001	45.14	2	9.346091276	0.209	0.825141897	4
optimal_loci_321754_G	1070	1.475012	0	4939	34.48	2	2.580020417	0.184	0.826660171	6
optimal_loci_321766_G	2557	1.682756	8.45	2367	31.91	2	3.883005586	0.086	0.827886883	7
optimal_loci_321807_G	2590	3.070717	8.42	3371	44.78	3	4.037645195	0.267	0.829818265	11
optimal_loci_321826_G	1108	7.34823	20.85	2906	42.14	3	5.095230949	0.37	0.832099031	11
optimal_loci_321831_G	2485	7.34823	0	2072	50.9	2	7.261745756	0.337	0.832209571	11
optimal_loci_321841_G	1603	6.193817	13.6	2421	33.43	2	24.29617511	0.242	0.833414094	10
optimal_loci_321861_G	1191	6.193817	4.95	4385	49.7	1	17.89794293	0.538	0.83420545	9
optimal_loci_321862_G	2482	6.193817	8.82	5885	34.48	1	17.89794293	0.206	0.834223296	9
optimal_loci_321863_G	2546	6.193817	0	8452	52.31	1	17.89794293	0.491	0.834253837	9
optimal_loci_321905_G	1546	5.34609	0	9373	41.84	2	23.32972862	0.254	0.835399443	9
optimal_loci_321933_G	1188	5.879969	25.84	1001	43.51	1	3.448471169	0.143	0.836389298	8
optimal_loci_322046_G	1130	1.567718	15.66	11016	34.42	3	10.73111039	0.182	0.845724782	5
optimal_loci_322066_G	2230	1.727719	1.39	2001	43.09	3	7.168736067	0.246	0.846930031	5
optimal_loci_322067_G	1947	1.727719	0	1001	41.96	2	3.524415204	0.329	0.847084592	5
optimal_loci_322069_G	1352	1.727719	13.98	3425	47.04	2	3.524415204	0.394	0.847113432	5
optimal_loci_322081_G	1194	1.717031	0	1001	51.75	3	0.503189522	0.63	0.847879612	5
optimal_loci_322172_G	1429	2.234243	0	2650	46.11	5	3.714299688	0.487	0.8545293	5
optimal_loci_322188_G	1279	1.961015	0	2364	35.41	2	27.3945687	0.165	0.85547743	8
optimal_loci_322190_G	1194	1.961015	0	4483	41.62	2	27.3945687	0.219	0.855502641	8
optimal_loci_322198_G	1388	1.961015	0	2066	37.75	3	27.79211675	0.3	0.85564245	8
optimal_loci_322257_G	2140	2.357228	0	17666	58.59	1	0.02651485	0.696	0.858393634	9
optimal_loci_322305_G	1571	2.495264	5.73	1001	58.62	2	12.58755967	0.627	0.860909509	10
optimal_loci_322306_G	1696	2.495264	19.46	2001	61.49	1	14.2787937	0.607	0.860994005	10
optimal_loci_322310_G	1002	2.495264	12.18	5117	30.53	1	14.2787937	0.136	0.861031078	10
optimal_loci_322317_G	2961	2.695062	9.93	3073	47.78	4	0.715582632	0.402	0.862116221	7
optimal_loci_322347_G	1260	1.302025	32.06	3026	37.38	3	63.59260208	0.112	0.864564255	6

optimal_loci_322364_G	1247	1.551303	23.42	2882	33.92	3	3.150299044	0.117	0.866130904	7
optimal_loci_322449_G	1942	3.195923	17.71	2001	39.13	1	4.268938792	0.242	0.870762739	4
optimal_loci_322501_G	1668	5.608092	0	3412	44.84	3	9.406524089	0.371	0.87302698	5
optimal_loci_322558_G	1169	5.034735	33.79	3098	54.31	1	4.751361258	0.549	0.87615032	8
optimal_loci_322567_G	2288	5.264277	30.38	16605	33.91	1	0.745005332	0.049	0.876932241	7
optimal_loci_322570_G	1152	5.186803	0	12615	36.37	1	0.745005332	0.09	0.876993228	7
optimal_loci_322622_G	2504	5.462885	1.4	1001	38.21	3	5.243981308	0.148	0.880299994	6
optimal_loci_322626_G	1596	5.532646	9.09	10167	55.45	1	1.189930107	0.583	0.880525596	6
optimal_loci_322654_G	1024	5.532646	18.95	13111	39.94	2	1.815319814	0.21	0.881196263	6
optimal_loci_322780_G	2327	4.909868	28.79	5512	39.23	3	7.324260609	0.22	0.888970201	6
optimal_loci_322790_G	1733	5.917721	5.65	2155	40.04	5	10.45814825	0.346	0.889981757	7
optimal_loci_322798_G	1234	5.917721	0	6214	43.03	3	15.18855804	0.348	0.890177627	7
optimal_loci_322827_G	1700	5.183753	0	9711	55.7	2	40.47950642	0.637	0.891735365	7
optimal_loci_322830_G	3145	6.546809	6.61	7351	37.48	2	40.47950642	0.115	0.891772664	7
optimal_loci_322861_G	1321	5.632629	0	2001	58.97	1	4.330945131	0.691	0.893469306	9
optimal_loci_322891_G	1280	4.640352	22.81	2001	37.34	4	1.686908609	0.173	0.895709371	8
optimal_loci_322921_G	2235	3.022196	34	1001	35.7	3	26.29022594	0.066	0.898221033	7
optimal_loci_322928_G	1397	3.022196	19.83	5846	38.51	5	104.7795617	0.158	0.898481888	7
optimal_loci_323030_G	1040	1.485536	10.1	2001	57.4	1	3.137299771	0.694	0.903280991	8
optimal_loci_323038_G	1390	1.476855	0	18349	47.69	1	8.847768067	0.267	0.903552648	8
optimal_loci_323051_G	1030	1.639956	24.95	2504	40.29	2	7.136373091	0.304	0.903922449	8
optimal_loci_323064_G	1471	1.805398	13.19	16956	51.66	1	0.328975394	0.443	0.905103248	7
optimal_loci_323067_G	1528	1.805398	4.91	14582	60.47	1	0.328975394	0.729	0.905130815	7
optimal_loci_323087_G	1228	1.794324	12.21	6306	52.68	2	0.363494635	0.602	0.906636323	8
optimal_loci_323135_G	1259	4.169964	16.84	2934	53.05	4	55.93261272	0.46	0.911002508	10
optimal_loci_323153_G	1587	4.990437	11.97	1083	48.01	3	6.396464691	0.374	0.912355787	9
optimal_loci_323167_G	3016	4.621436	14.03	2609	48.6	3	9.671247734	0.357	0.913159135	8
optimal_loci_323175_G	1231	4.372109	16.73	1382	32.9	3	4.559189803	0.108	0.913435932	8
optimal_loci_323186_G	1843	4.321078	15.74	1443	35.1	4	1.645505895	0.255	0.913984661	8
optimal_loci_323226_G	2150	4.956931	4.33	6625	53.25	3	1.715760371	0.388	0.916398822	9
optimal_loci_323236_G	2234	5.756358	35.68	4386	41.98	3	0.645713928	0.286	0.916782377	9
optimal_loci_323245_G	1125	6.23771	0	1236	38.84	4	10.82339644	0.247	0.91735628	8
optimal_loci_323309_G	1114	3.326698	11.67	7739	40.39	2	1.814048648	0.261	0.922004926	5

optimal_loci_323382_G	2195	3.885517	0	1702	41.54	3	0.351784324	0.197	0.925502851	4
optimal_loci_323504_G	1351	2.844968	12.07	4768	50.77	3	10.00230082	0.306	0.929604089	6
optimal_loci_323506_G	1383	2.844968	23.5	2288	53.21	3	10.00230082	0.519	0.929633215	6
optimal_loci_323572_G	1464	4.20097	5.33	3734	31.96	3	0.56223439	0.096	0.932442733	6
optimal_loci_323576_G	1252	4.233004	9.11	2001	50	3	1.800225381	0.366	0.933055565	6
optimal_loci_323580_G	2576	4.840521	8.04	6877	53.68	4	1.350169035	0.529	0.933207914	6
optimal_loci_323651_G	1322	6.954356	2.34	1001	51.05	3	1.800137555	0.723	0.938340078	11
optimal_loci_323675_G	1090	5.853752	0	2598	47.52	5	23.92852256	0.368	0.939410539	8
optimal_loci_323680_G	1045	5.853752	0	3062	36.65	6	19.65496044	0.096	0.939634404	8
optimal_loci_323682_G	1378	5.853752	0	2574	43.68	6	19.65496044	0.382	0.939658936	8
optimal_loci_323705_G	1125	5.704466	0	1001	47.28	2	11.25071512	0.356	0.9405864	8
optimal_loci_323714_G	1438	5.54673	0	18099	40.95	1	22.50143024	0.356	0.940980793	9
optimal_loci_323732_G	1069	5.044735	2.81	1001	48.26	4	7.418832457	0.357	0.943227651	9
optimal_loci_323751_G	1264	5.735922	5.62	2001	58.06	4	47.850949	0.599	0.944173223	10
optimal_loci_323848_G	1592	4.451572	17.84	2001	40.38	3	0.485544801	0.544	0.946598688	5
optimal_loci_323894_G	1538	4.520713	24.97	13555	37.06	2	3.557473942	0.322	0.949543946	4
optimal_loci_323982_G	1670	5.334292	2.34	19673	35.86	1	5.390425249	0.076	0.95523808	6
optimal_loci_324071_G	1604	7.853501	11.6	2449	47.81	6	7.223509378	0.373	0.960532955	10
optimal_loci_324072_G	1415	7.853501	25.23	1001	46.99	5	8.668211254	0.455	0.960552431	10
optimal_loci_324073_G	1142	7.720317	19.09	2010	47.72	4	11.22037178	0.398	0.960681758	10
optimal_loci_324074_G	1087	7.720317	11.41	1066	36.52	3	14.58505718	0	0.960780068	10
optimal_loci_324094_G	1181	7.562208	0	2001	52.83	5	1.704952667	0.539	0.961588818	9
optimal_loci_324096_G	1122	7.562208	0	2774	55.52	6	1.510310167	0.59	0.961611066	9
optimal_loci_324117_G	1496	8.684325	19.52	6213	39.63	3	9.424860473	0.255	0.962787796	9
optimal_loci_324149_G	1088	6.671873	16.18	8896	51.47	2	37.29099505	0.408	0.964306153	9
optimal_loci_324152_G	1126	6.671873	21.31	13352	47.86	3	29.16261812	0.483	0.964359169	9
optimal_loci_324308_G	1731	2.524393	17.1	2710	45.69	2	39.91583147	0.324	0.976273215	3
optimal_loci_324320_G	1007	2.524393	17.48	1702	35.15	3	36.33755924	0.157	0.976658162	3
optimal_loci_324328_G	1433	2.524393	6.14	16898	29.86	1	37.44619099	0.062	0.976838957	3
optimal_loci_324478_G	3528	2.395895	22	1073	38.8	1	0.350441907	0.224	0.985628723	1
optimal_loci_324826_G	1204	2.114245	0	1001	43.1	2	12.40422428	0.202	0.974311637	1
optimal_loci_324981_G	1534	7.041194	16.88	6702	41	1	23.17788869	0.194	0.951583234	2
optimal_loci_324982_G	1399	7.041194	16.08	5143	33.95	2	27.84361489	0.103	0.951552116	2

optimal_loci_325185_G	1005	0.37251	17.11	15224	32.63	1	1.786227229	0.253	0.920847924	5
optimal_loci_325196_G	1462	3.909597	7.73	5819	42.81	4	6.132933618	0.25	0.920127106	5
optimal_loci_325207_G	2046	3.55228	27.17	3316	34.94	4	5.626063972	0.109	0.919373194	5
optimal_loci_325234_G	1375	9.034325	0	9119	35.27	3	19.10214247	0.096	0.915651038	6
optimal_loci_325313_G	1515	6.95703	29.37	9552	41.71	1	0.21212819	0.15	0.91143519	9
optimal_loci_325362_G	1184	7.529571	7.94	2414	37.58	5	17.5721243	0.232	0.906132056	6
optimal_loci_325381_G	2464	7.496812	8.64	1508	52.15	3	20.14243514	0.456	0.905230818	5
optimal_loci_325392_G	1002	7.418927	2.89	1908	49.4	1	1.549840123	0.556	0.904700579	5
optimal_loci_325401_G	1689	8.280732	10.07	2527	37	1	6.733640138	0.054	0.902808583	5
optimal_loci_325492_G	1614	5.292306	35.01	1001	48.38	5	0.817020615	0.493	0.892378922	3
optimal_loci_325501_G	1160	5.826109	32.33	2453	39.74	4	1.041885882	0.177	0.891318743	4
optimal_loci_325528_G	1024	11.747748	0	18784	40.82	2	1.904401991	0.117	0.887768862	4
optimal_loci_325589_G	1901	8.381072	7.15	1001	43.45	4	4.246644935	0.263	0.882077226	5
optimal_loci_325682_G	2166	7.645182	2.45	1285	50.5	2	2.158471696	0.411	0.872708802	4
optimal_loci_325689_G	1107	7.690927	29	4314	41.82	3	1.937884524	0.417	0.872397725	4
optimal_loci_325727_G	1890	8.142094	27.04	2981	53.75	3	4.380905888	0.447	0.869396806	3
optimal_loci_325839_G	1583	2.935623	0	4925	53.5	3	2.451477642	0.495	0.858019701	2
optimal_loci_325954_G	1387	2.759307	26.89	1377	44.77	3	0.14356208	0.297	0.851546946	3
optimal_loci_326029_G	1086	0.774363	0	2648	45.58	1	16.98290342	0.284	0.841819102	2
optimal_loci_326190_G	1708	1.427801	8.2	2866	36.41	2	282.2351491	0.132	0.823447505	3
optimal_loci_326246_G	1135	1.734735	5.64	1001	33.74	1	39.46332413	0.213	0.817455868	3
optimal_loci_326265_G	1140	1.848281	0	11938	35.96	1	60.52407382	0	0.815599681	3
optimal_loci_326362_G	1206	2.71434	0	9619	51.16	1	0.705894377	0.661	0.802516447	6
optimal_loci_326363_G	1143	2.71434	20.3	8402	35.17	1	0.705894377	0.169	0.802492156	6
optimal_loci_326427_G	1132	2.645696	17.84	8079	61.48	1	10.19447102	0.616	0.79732982	8
optimal_loci_326455_G	1390	3.917178	0	2292	34.31	2	14.4470283	0.031	0.794518882	8
optimal_loci_326460_G	1325	3.787906	4.75	11052	48.07	1	6.096653269	0.346	0.792756347	8
optimal_loci_326465_G	1170	3.785858	31.28	2001	51.53	1	6.096653269	0.668	0.792575689	8
optimal_loci_326491_G	1966	4.024057	24.26	15674	35.3	1	3.967175996	0.042	0.789915609	6
optimal_loci_326516_G	1476	4.024057	7.18	4548	31.09	4	16.99631698	0.037	0.788970699	6
optimal_loci_326617_G	1887	1.626896	12.82	4536	50.55	1	26.27353823	0.482	0.776634691	3
optimal_loci_326665_G	3319	1.323592	5.27	5400	37.45	1	8.211872554	0.235	0.774275808	4
optimal_loci_326723_G	2042	1.298254	17.78	5869	32.81	1	0.380852956	0.102	0.76818495	5

optimal_loci_326752_G	1111	0.843925	12.33	1056	33.39	1	7.148990178	0.156	0.764377086	4
optimal_loci_326763_G	1145	0.880587	10.57	8270	34.58	1	7.148990178	0.111	0.7640601	3
optimal_loci_326869_G	1059	0.578983	9.73	1935	41.17	1	5.988098412	0.369	0.753503014	2
optimal_loci_326876_G	1097	0.578983	21.97	10230	47.94	1	5.988098412	0.317	0.753207385	2
optimal_loci_326971_G	1245	0.856389	12.77	2130	34.85	1	90.17822865	0.091	0.742113593	2
optimal_loci_326987_G	1764	0.887487	38.49	2344	35.65	2	14.91483207	0.173	0.73994495	2
optimal_loci_327208_G	1989	1.768669	28.36	15818	42.43	2	32.67606686	0.204	0.711294371	4
optimal_loci_327214_G	1189	1.649494	0	1001	59.96	2	1.757881426	0.616	0.710638583	4
optimal_loci_327218_G	1043	1.299766	28.38	2001	32.79	4	0.878940713	0.122	0.71010982	4
optimal_loci_327263_G	1149	0.566012	21.93	3596	34.02	1	85.48960449	0.137	0.705412236	4
optimal_loci_327541_G	1606	0.378526	0	7882	42.4	3	2.925653435	0.169	0.670483114	1
optimal_loci_328032_G	1745	1.004216	0	4368	39.02	1	3.330359098	0.155	0.615886946	1
optimal_loci_329014_G	1036	0.247981	0	17284	48.06	1	7.992144397	0.595	0.512441956	2
optimal_loci_329058_G	1620	0.419932	2.28	2085	39.81	1	22.46586144	0.359	0.507843752	3
optimal_loci_329124_G	2602	0.806474	17.45	9662	33.32	2	1.846803169	0.271	0.500604591	2
optimal_loci_329817_G	1179	0.280411	13.57	16303	35.79	1	25.20864427	0.119	0.410787784	1
optimal_loci_336212_G	1048	0.050939	2.77	2001	38.26	1	0.383884526	0.214	0.212900647	3
optimal_loci_336221_G	1376	0.074066	0	1001	34.15	1	45.45797767	0.076	0.213522545	3
optimal_loci_336223_G	2637	0.074066	0	2866	35.3	1	45.45797767	0.197	0.213582081	3
optimal_loci_336589_G	1329	0.15402	3.91	10371	48.3	1	3.709976638	0.343	0.231737386	2
optimal_loci_336618_G	1249	0.107319	16.41	2046	42.43	2	9.854942238	0.216	0.232698696	2
optimal_loci_336861_G	1068	0.819946	0	7748	37.17	3	1.203727542	0	0.246633023	1
optimal_loci_337001_G	1689	3.400151	1.72	1300	56.83	1	2.889518976	0.469	0.253486678	6
optimal_loci_337002_G	1777	3.400151	31.06	3022	48.39	1	2.889518976	0.412	0.253504287	6
optimal_loci_337006_G	1218	3.93113	12.64	10637	43.43	1	63.86359005	0.242	0.254192971	6
optimal_loci_337008_G	1152	3.93113	2.78	8821	55.9	1	63.86359005	0.704	0.254212216	6
optimal_loci_337020_G	2065	3.93113	11.19	17914	49.34	1	63.86359005	0.441	0.254567428	6
optimal_loci_337041_G	1012	4.896046	6.62	11495	32.6	2	10.155477	0.134	0.256278881	6
optimal_loci_337132_G	1098	0.680183	0	1001	36.33	3	18.11862111	0.013	0.263157252	3
optimal_loci_337177_G	1397	0.732142	0	1001	34.57	1	67.47596006	0.068	0.26503633	3
optimal_loci_337179_G	1052	0.732142	0	3791	36.69	2	33.73798003	0.225	0.265244543	3
optimal_loci_337386_G	1067	1.282786	16.4	11023	34.67	2	5.056631506	0.093	0.273274991	3
optimal_loci_337389_G	1004	1.282786	18.43	3365	54.78	2	5.056631506	0.508	0.273353947	3

optimal_loci_337393_G	1161	1.282786	0	3807	34.53	2	5.056631506	0.099	0.273516858	3
optimal_loci_337519_G	1497	1.495248	0	1001	37.4	1	0.065569014	0.271	0.278957047	2
optimal_loci_337594_G	1539	1.797424	4.29	2001	46.13	2	48.04458536	0.273	0.28263681	2
optimal_loci_337903_G	1248	0.376152	0	2081	43.1	1	4.122363313	0.341	0.300888077	3
optimal_loci_337961_G	1766	0.611276	25.54	8176	48.47	1	29.32659711	0.364	0.304478996	3
optimal_loci_337968_G	1199	0.628709	36.95	13479	37.61	1	7.471679274	0.214	0.304637142	3
optimal_loci_338132_G	1053	1.14166	29.82	4999	46.53	2	0.484123419	0.313	0.311442867	2
optimal_loci_338241_G	1097	1.318878	0	1001	52.32	1	8.608126529	0.538	0.316082356	3
optimal_loci_338277_G	1416	1.343304	21.44	1113	34.88	1	32.06987753	0.228	0.319022847	3
optimal_loci_338340_G	1981	2.07936	27.31	2424	40.28	2	0.162797934	0.103	0.323406307	5
optimal_loci_338361_G	3364	1.73802	39.39	2995	32.75	2	7.578490427	0.138	0.324168782	4
optimal_loci_338365_G	1026	1.73802	0	17938	32.94	1	15.08480172	0.091	0.32432159	4
optimal_loci_338377_G	1041	1.706954	0	10045	36.4	2	10.84745231	0.289	0.324940521	4
optimal_loci_338568_G	1689	2.091005	2.96	2179	39.66	2	0.683784676	0.145	0.336596515	7
optimal_loci_338573_G	1032	2.091005	6.69	11728	47.77	2	0.683784676	0.535	0.336772076	7
optimal_loci_338612_G	1835	2.091005	1.53	4772	42.39	2	56.0607852	0.286	0.338532184	8
optimal_loci_338613_G	1157	2.091005	0	6743	41.65	2	56.0607852	0.179	0.33855234	8
optimal_loci_338621_G	1593	1.211457	0	2304	43.81	2	9.29867661	0.212	0.339416431	8
optimal_loci_338629_G	1666	1.209202	39.44	2136	36.73	1	45.01835664	0.126	0.339882483	8
optimal_loci_338640_G	1103	1.173564	9.7	7924	41.61	3	0.042870576	0.523	0.340613186	8
optimal_loci_338701_G	1532	1.088373	21.28	1304	39.55	1	8.557735053	0.209	0.342588512	6
optimal_loci_338876_G	1443	1.909161	0	10786	36.72	1	70.38630753	0.083	0.353537343	5
optimal_loci_338902_G	1841	2.202231	5.7	4035	36.06	1	5.216958681	0.201	0.355124273	5
optimal_loci_338912_G	1266	2.202231	14.3	2001	38.38	3	6.31679992	0.15	0.355489599	5
optimal_loci_338914_G	1326	2.202231	17.72	3439	39.81	3	6.31679992	0.28	0.355514581	5
optimal_loci_338978_G	2153	0.237887	24.34	17422	47.37	1	0.574048026	0.318	0.357911333	5
optimal_loci_340077_G	1471	0.128573	2.31	2501	48.94	1	5.296000175	0.62	0.423558465	2
optimal_loci_340122_G	1214	0.154417	21.83	2081	36.9	2	0.241421113	0.273	0.425736226	2
optimal_loci_340243_G	1285	0.309199	0	16628	41.4	1	5.527961991	0.271	0.432382588	2
optimal_loci_340323_G	1053	0.174844	12.54	18487	38.08	1	18.19269526	0.091	0.436609896	4
optimal_loci_340357_G	1192	0.144962	17.2	1001	39.26	1	1.414277276	0.163	0.43775594	3
optimal_loci_340413_G	1419	0.041357	12.4	6037	34.31	3	5.654404822	0.136	0.441149997	3
optimal_loci_341136_G	1084	0.215859	27.95	5883	38.28	1	35.96070353	0.192	0.48219798	2

optimal_loci_341139_G	1267	0.236897	0	12674	39.62	3	0.644112947	0.387	0.482524804	2
optimal_loci_342099_G	1241	0.157219	27.16	12156	39.8	1	0.792461874	0.332	0.540775412	2
optimal_loci_342106_G	1138	0.167367	22.23	3268	37.87	1	0.792461874	0.231	0.540994505	2
optimal_loci_342209_G	3650	0.160803	0	18044	37.26	3	1.516835931	0.162	0.547051519	3
optimal_loci_342211_G	1425	0.160803	0	14259	56.84	1	4.550507792	0.419	0.547129626	3
optimal_loci_342226_G	1006	0.141847	0	2588	37.87	3	2.133627369	0	0.548944638	3
optimal_loci_342369_G	1036	0.095183	0	4498	41.79	2	4.218925869	0.07	0.557715412	1
optimal_loci_342566_G	1118	0.473228	4.92	11431	33.27	2	33.10073908	0.121	0.569646128	3
optimal_loci_342573_G	1200	0.473228	11.17	3350	41.08	2	33.10073908	0.328	0.569727926	3
optimal_loci_342630_G	1607	0.375029	13.19	2384	46.42	1	7.162532949	0.417	0.573287656	3
optimal_loci_343273_G	2407	0.076746	0	14662	38.55	1	0.657092098	0.235	0.610813274	6
optimal_loci_343298_G	1678	0.106631	0	2176	33.79	1	0.061112868	0.045	0.612554148	6
optimal_loci_343300_G	1112	0.106631	0	2001	32.01	1	0.061112868	0.118	0.612624534	6
optimal_loci_343303_G	1207	0.106631	0	5521	35.04	1	0.061112868	0	0.612660529	6
optimal_loci_343315_G	1372	0.106631	5.61	11649	55.83	1	0.061112868	0.549	0.612723194	6
optimal_loci_343321_G	1693	0.106631	3.84	15889	36.73	1	0.061112868	0.083	0.612766553	6
optimal_loci_343542_G	1775	0.156242	0	2995	39.94	1	7.568580943	0.207	0.621458371	1
optimal_loci_343678_G	1709	0.207311	0	6332	57.98	1	8.346616583	0.685	0.628266182	2
optimal_loci_343764_G	1119	0.131672	0	4673	33.78	2	9.950613683	0.167	0.631995051	2
optimal_loci_344235_G	1868	1.672953	37.9	1001	38.43	1	6.177172177	0.273	0.65663531	2
optimal_loci_344271_G	1641	1.634375	0	15489	36.86	2	4.059852194	0.171	0.658326383	2
optimal_loci_344386_G	1136	0.424254	0	7579	58.53	1	1.594891297	0.655	0.66537018	6
optimal_loci_344413_G	1029	0.256141	31.1	6131	41.1	1	0.098233318	0.232	0.667932625	7
optimal_loci_344414_G	1532	0.256141	0	12907	39.36	1	0.098233318	0.242	0.668001917	7
optimal_loci_344416_G	1305	0.256141	20.46	15425	40.99	1	0.098233318	0.324	0.668027666	7
optimal_loci_344419_G	1415	0.256141	28.83	17616	37.17	1	0.098233318	0.256	0.668050071	7
optimal_loci_344431_G	1089	0.256141	0	9300	32.87	5	5.757567224	0	0.668507268	7
optimal_loci_344494_G	1510	0.03608	34.64	1102	33.7	2	17.08190378	0.182	0.672298362	6
optimal_loci_344662_G	2289	0.068676	9.44	3682	45.47	1	0.116423696	0.275	0.682401601	4
optimal_loci_344663_G	1629	0.068676	0	15182	46.71	1	0.116423696	0.579	0.682519201	4
optimal_loci_344664_G	1905	0.068676	16.33	16961	38.16	1	0.116423696	0.204	0.682537393	4
optimal_loci_344722_G	1027	0.089344	0	3221	40.4	2	10.88466882	0.136	0.685327449	7
optimal_loci_344806_G	1008	0.087016	15.58	1347	39.48	1	2.111736446	0.326	0.688841407	4

optimal_loci_344833_G	1874	0.092015	37.99	6794	35.64	2	13.68300478	0.113	0.690085754	4
optimal_loci_344835_G	2272	0.092015	15.62	2558	36.35	2	13.68300478	0.15	0.690125002	4
optimal_loci_345075_G	1050	0.941624	4.29	4087	48.19	2	10.38812578	0.425	0.705662232	2
optimal_loci_345130_G	1900	0.24741	0	1001	51.89	3	0.410768222	0.565	0.709167304	2
optimal_loci_345196_G	1104	14.806378	19.38	6684	38.94	1	14.28864324	0.17	0.714446402	4
optimal_loci_345197_G	1396	14.806378	18.7	8064	50.57	1	14.28864324	0.339	0.714460514	4
optimal_loci_345198_G	1676	14.806378	0	9756	56.44	1	14.28864324	0.631	0.714477817	4
optimal_loci_345199_G	1862	14.806378	1.5	11736	53.92	1	14.28864324	0.46	0.714498064	4
optimal_loci_345383_G	1122	1.235223	0	1363	56.5	2	23.52732126	0.535	0.727801526	3
optimal_loci_345436_G	2173	1.098005	11.04	7163	47.99	1	0.116197645	0.424	0.730613476	4
optimal_loci_345445_G	1099	1.042066	2.55	3672	48.04	2	0.058098823	0.441	0.730902873	4
optimal_loci_345504_G	1155	1.204393	14.37	2106	45.02	2	1.0430207	0.562	0.734025777	4
optimal_loci_345609_G	1251	1.076506	14.15	9092	29.73	1	0.936554406	0.107	0.739072559	4
optimal_loci_345673_G	1013	0.646583	39.98	3678	38.49	5	2.441620813	0.114	0.74335658	3
optimal_loci_345674_G	1631	0.646583	2.02	4862	34.7	5	2.441620813	0.123	0.743368688	3
optimal_loci_345796_G	1690	1.42621	0	1598	62.84	3	2.616585699	0.84	0.75210274	1
optimal_loci_345891_G	1983	1.686875	20.68	2001	37.31	4	4.504764772	0.169	0.758411428	2
optimal_loci_345972_G	1241	1.833879	8.62	2651	45.93	1	13.10490254	0.294	0.762626699	4
optimal_loci_346030_G	1300	2.17728	34.69	1111	34.53	5	20.83172464	0.125	0.765615764	4
optimal_loci_346043_G	1159	2.17728	0	1001	48.57	4	11.64341783	0.34	0.766627601	4
optimal_loci_346091_G	1290	3.195069	2.64	3689	51.7	5	6.222244486	0.473	0.768947668	3
optimal_loci_346310_G	1275	1.725889	33.65	2433	43.29	3	0.003698196	0.341	0.783249837	1
optimal_loci_346552_G	1165	1.17696	16.48	5821	34.42	3	2.822765442	0.289	0.797273744	2
optimal_loci_346615_G	1008	1.717574	0	1001	34.72	2	9.751905875	0.17	0.80090022	3
optimal_loci_346640_G	1159	1.62171	37.19	2001	43.39	2	21.33437173	0.334	0.80419216	2
optimal_loci_346775_G	1172	2.787966	0	2101	34.47	4	0.005941032	0.059	0.812911988	6
optimal_loci_346796_G	1004	2.831904	0	6698	43.02	2	32.32774238	0.178	0.81377703	6
optimal_loci_346825_G	1083	2.985857	0	5724	48.29	3	5.555527825	0.283	0.815711114	6
optimal_loci_346833_G	1027	2.985857	0	8254	34.85	3	5.555527825	0.214	0.815986359	6
optimal_loci_346851_G	3006	2.432021	2.5	18964	47.03	1	2.899378136	0.398	0.817534133	6
optimal_loci_346854_G	1384	2.432021	0	15933	46.53	1	2.899378136	0.435	0.817581715	6
optimal_loci_347091_G	1541	1.80067	0	4366	39.58	1	0.241309511	0.329	0.828366449	6
optimal_loci_347093_G	1392	1.80067	6.97	2303	48.2	1	0.241309511	0.561	0.828389069	6

optimal_loci_347106_G	1570	1.887376	17.26	8488	39.74	1	2.94065212	0.3	0.829250777	6
optimal_loci_347126_G	1699	1.400582	3.94	1001	42.67	2	1.098249362	0.283	0.830190623	9
optimal_loci_347203_G	1977	1.391817	39.25	5759	35.4	3	8.394905657	0.153	0.831897219	9
optimal_loci_347237_G	1372	1.412704	30.1	2477	45.69	3	2.956389188	0.394	0.83253378	9
optimal_loci_347272_G	1825	1.414807	0	2018	42.41	5	13.8434027	0.134	0.834939572	8
optimal_loci_347273_G	1207	1.41619	7.62	2001	41.83	5	13.8434027	0.208	0.834959676	8
optimal_loci_347279_G	1907	1.507004	2.73	14568	35.86	3	21.81147934	0.099	0.835240361	8
optimal_loci_347340_G	1332	2.644378	0	2765	44.81	3	11.65346402	0.393	0.838574055	12
optimal_loci_347343_G	1322	2.644378	14.22	2001	36.68	3	11.65346402	0.089	0.838608475	12
optimal_loci_347361_G	1358	2.952167	28.13	1968	32.98	4	0.244773727	0.18	0.840458369	11
optimal_loci_347362_G	1084	2.952167	0	3510	36.99	4	0.244773727	0	0.840474137	11
optimal_loci_347363_G	1170	2.952167	0	4682	44.52	4	0.244773727	0.34	0.840486122	11
optimal_loci_347364_G	1314	2.952167	18.65	6025	35.54	4	0.244773727	0	0.840499856	11
optimal_loci_347368_G	1032	3.831114	2.71	2513	40.79	2	0.278539843	0.222	0.840730382	11
optimal_loci_347380_G	1599	3.77019	2.56	1001	37.27	2	15.82739769	0.162	0.841199328	11
optimal_loci_347406_G	1861	3.73933	15.26	11254	48.03	1	2.978987118	0.246	0.84240679	11
optimal_loci_347453_G	1218	3.479554	31.61	7612	38.17	2	17.93918215	0.211	0.845346637	12
optimal_loci_347454_G	1005	3.479554	8.96	9044	50.14	2	17.93918215	0.28	0.845361281	12
optimal_loci_347483_G	1182	4.066077	18.44	1001	40.01	3	0.571701642	0.314	0.848075899	13
optimal_loci_347484_G	1193	4.066077	13.75	2269	40.31	3	0.571701642	0.127	0.848088866	13
optimal_loci_347485_G	1669	4.066077	0	3625	43.73	3	0.571701642	0.148	0.848102732	13
optimal_loci_347516_G	1364	3.168465	16.72	12976	32.4	2	3.967507493	0.152	0.850754869	14
optimal_loci_347526_G	1623	3.462814	0	10517	39.92	2	2.64174173	0.284	0.851032374	14
optimal_loci_347529_G	1621	3.462814	33.81	7650	44.29	2	2.64174173	0.364	0.851061712	14
optimal_loci_347531_G	1848	3.462814	19.91	5221	39.33	2	2.64174173	0.239	0.85108423	14
optimal_loci_347544_G	1312	3.483227	0	3175	60.51	2	13.88470493	0.68	0.851552921	15
optimal_loci_347547_G	1139	3.541865	0	1001	47.14	2	13.88470493	0.659	0.851657871	15
optimal_loci_347549_G	1519	3.541865	2.57	3632	57.01	2	13.88470493	0.532	0.851744271	15
optimal_loci_347553_G	1033	3.541865	0	7678	49.17	2	13.88470493	0.353	0.851785645	15
optimal_loci_347607_G	1140	2.7789	0	3943	51.49	2	9.449458974	0.799	0.854916147	14
optimal_loci_347614_G	1663	2.7789	2.1	1305	49.84	2	9.449458974	0.52	0.854991912	14
optimal_loci_347616_G	1737	2.7789	7.83	3370	41.96	2	9.449458974	0.465	0.855016536	14
optimal_loci_347658_G	1665	2.796677	0	13195	51.11	1	1.041656361	0.512	0.856247324	11

optimal_loci_347678_G	1340	2.156062	3.21	4022	41.94	2	4.682364815	0.178	0.857736186	8
optimal_loci_347715_G	1444	2.583486	7.41	3442	37.04	1	0.899716531	0.166	0.859737527	8
optimal_loci_347747_G	1207	2.106643	13.67	3401	35.87	1	3.676816505	0.199	0.861244949	5
optimal_loci_347758_G	1158	1.943157	5.18	2498	58.63	3	7.67055426	0.534	0.861997331	5
optimal_loci_347876_G	2456	3.666985	8.14	13811	45.23	2	15.34132498	0.321	0.867005919	2
optimal_loci_348005_G	1062	2.693711	8.38	1950	50.09	2	19.17872766	0.353	0.872777678	6
optimal_loci_348016_G	2139	2.788758	11.59	19728	37.02	1	32.03601785	0.188	0.873040232	6
optimal_loci_348032_G	1226	3.005753	2.77	6254	37.11	1	4.412847994	0.28	0.87370919	6
optimal_loci_348043_G	1097	3.069975	0	8474	36.82	1	0.049762134	0.213	0.874597343	6
optimal_loci_348058_G	1290	1.337936	0	2001	45.42	4	1.65432059	0.197	0.875655514	6
optimal_loci_348059_G	1334	1.337936	3.07	2662	47.15	4	1.65432059	0.311	0.875767101	6
optimal_loci_348161_G	1144	3.040134	2.45	1417	44.58	1	0.361281125	0.363	0.8828381	5
optimal_loci_348184_G	1066	2.863646	23.26	2001	45.77	2	56.2044163	0.389	0.883627848	9
optimal_loci_348197_G	1217	2.845614	10.93	6298	56.94	5	41.31908622	0.483	0.884279605	11
optimal_loci_348220_G	1850	2.845614	6.65	1001	35.94	3	0.13339265	0.366	0.885521161	11
optimal_loci_348227_G	1832	2.667096	12.61	8139	40.44	2	0.1780472	0.16	0.886027719	11
optimal_loci_348258_G	1486	2.596544	4.24	17508	41.58	1	5.082916781	0.268	0.888613704	12
optimal_loci_348259_G	1427	2.599896	0	15784	58.93	1	5.082916781	0.68	0.888631937	12
optimal_loci_348260_G	1283	2.599896	2.57	13792	50.11	1	5.082916781	0.231	0.888653779	12
optimal_loci_348267_G	2868	2.596465	0	3611	46.79	2	2.54145839	0.351	0.888741683	12
optimal_loci_348273_G	1231	2.615721	0	1800	57.59	2	2.54145839	0.578	0.888861706	11
optimal_loci_348274_G	1580	2.615721	0	2721	54.68	2	2.54145839	0.657	0.888877505	11
optimal_loci_348345_G	1220	3.3713	16.39	3000	62.7	2	5.07488221	0.695	0.893053222	11
optimal_loci_348351_G	2074	3.3713	0	1001	54.05	2	5.07488221	0.66	0.893161465	11
optimal_loci_348380_G	1540	3.565892	0	4470	49.41	1	36.07055948	0.244	0.894599043	5
optimal_loci_348407_G	1589	3.230191	7.55	2001	42.85	4	17.43376553	0.6	0.895695747	5
optimal_loci_348413_G	1671	3.44357	2.27	2055	47.99	1	2.161154705	0.282	0.896261841	5
optimal_loci_348595_G	1011	2.539148	0	7328	46.88	3	0.028788209	0.375	0.904423929	4
optimal_loci_348625_G	1075	3.582338	0	3076	46.6	2	20.09546476	0.385	0.906875564	9
optimal_loci_348638_G	1152	3.920426	0	2488	51.56	2	3.616144401	0.635	0.908384295	11
optimal_loci_348650_G	1119	4.096453	2.5	1001	51.83	2	5.365697512	0.744	0.90882286	11
optimal_loci_348656_G	2157	4.461142	0	2001	39.08	3	20.25791153	0.167	0.909573033	11
optimal_loci_348673_G	2970	5.024853	6.84	6116	39.42	1	13.86061	0.184	0.910822647	11

optimal_loci_348674_G	2293	5.057041	16.69	3513	44.43	1	13.86061	0.235	0.910856188	11
optimal_loci_348681_G	1417	4.497635	0	18662	51.58	1	2.079394239	0.626	0.911440515	11
optimal_loci_348686_G	1424	4.497635	2.81	16355	39.81	2	0.8895862	0.199	0.911494693	11
optimal_loci_348706_G	1141	5.43254	0	8742	47.15	4	21.3686937	0.433	0.91218445	11
optimal_loci_348718_G	1357	5.43254	0	7397	37.65	2	17.10132252	0.26	0.912589443	11
optimal_loci_348745_G	1164	5.745961	0	3447	47.76	3	5.059831491	0.281	0.914409476	11
optimal_loci_348776_G	1214	5.746945	0	2105	42.91	1	18.37228919	0.266	0.91725236	6
optimal_loci_348782_G	1856	5.867621	15.73	2951	39.33	3	15.14856851	0.205	0.917991028	4
optimal_loci_348789_G	1148	5.916206	0	10662	35.62	2	20.4015402	0.125	0.918359862	4
optimal_loci_348891_G	1099	4.25654	0	4189	44.94	3	7.39008604	0.301	0.924188109	3
optimal_loci_348915_G	1370	4.455138	0	1001	54.74	3	16.52912743	0.585	0.924626878	3
optimal_loci_348938_G	1377	4.043273	37.11	6377	38.27	2	9.716383878	0.219	0.924971803	3
optimal_loci_349019_G	1035	3.725938	0	1001	36.71	2	3.407436887	0.095	0.930388533	2
optimal_loci_349021_G	1126	3.725938	0	1077	39.34	2	3.407436887	0.308	0.93040465	2
optimal_loci_349151_G	1746	1.373769	3.44	2313	38.25	2	7.831958663	0.116	0.937850311	3
optimal_loci_349158_G	1378	1.366749	39.4	13258	38.53	2	4.073104678	0.276	0.938346315	4
optimal_loci_349253_G	1486	2.258055	0	6240	47.57	1	20.06237141	0.495	0.941973139	8
optimal_loci_349271_G	1018	2.000822	38.51	5239	39.29	3	61.14234665	0.214	0.943145627	8
optimal_loci_349305_G	2010	2.33217	33.58	2266	35.77	3	13.76919714	0.122	0.944319159	7
optimal_loci_349349_G	2262	3.346904	0	2001	52.07	2	9.889886846	0.558	0.946231625	11
optimal_loci_349362_G	1459	3.58563	0	6662	37.62	2	0.498581974	0.196	0.947045302	12
optimal_loci_349363_G	4006	3.58563	9.66	2001	52.09	2	0.498581974	0.53	0.94706692	12
optimal_loci_349390_G	1993	4.318857	9.98	8517	47.81	2	0.802530329	0.413	0.948007615	12
optimal_loci_349407_G	2870	4.200413	0	1559	52.22	3	11.56226082	0.572	0.949603912	11
optimal_loci_349408_G	2531	4.200413	0	2001	59.77	2	17.26865884	0.668	0.949829355	11
optimal_loci_349412_G	1052	4.200413	8.27	9222	43.15	2	17.26865884	0.22	0.949903198	11
optimal_loci_349425_G	2394	4.200413	8.69	1001	32.83	4	1.920441865	0.249	0.950550834	12
optimal_loci_349453_G	1831	3.431716	6.01	2239	47.18	3	42.19195226	0.394	0.951795345	12
optimal_loci_349462_G	1679	3.542513	3.77	17267	47.64	1	0.035765603	0.352	0.952257368	10
optimal_loci_349477_G	1348	3.617395	0	2294	46.95	1	10.01923708	0.344	0.953174727	9
optimal_loci_349522_G	1208	3.713899	28.06	5699	36.25	1	7.704761407	0.228	0.955157927	8
optimal_loci_349552_G	1258	3.508849	0	1095	43.16	4	106.4541469	0.328	0.956661341	7
optimal_loci_349573_G	1492	3.276621	0	2001	50.13	3	56.55013716	0.507	0.958958092	5

optimal_loci_349575_G	1668	3.219831	19.78	1394	39.86	2	84.06388097	0.263	0.959080856	5
optimal_loci_349654_G	3871	4.404321	16.84	1184	38.23	3	2.50295472	0.112	0.962606574	4
optimal_loci_349709_G	1770	4.581153	1.92	1487	52.82	3	10.93455437	0.555	0.967424303	3
optimal_loci_349752_G	1307	5.253267	13.39	2025	42.46	5	7.349571716	0.213	0.968726305	2
optimal_loci_349833_G	1486	5.070585	11.71	4425	68.3	2	5.397766908	0.752	0.975672096	3
optimal_loci_349870_G	1043	4.807157	39.41	2209	31.73	2	116.3099406	0.075	0.976961438	3
optimal_loci_349892_G	1322	4.261222	33.21	2119	33.2	5	4.920594328	0.204	0.978862717	4
optimal_loci_349951_G	1866	4.353167	0	2208	38.58	4	8.453758358	0.143	0.983696214	6
optimal_loci_349983_G	1294	3.856244	10.43	15034	49.22	1	0.676290675	0.301	0.984917573	5
optimal_loci_350036_G	1230	3.612129	0	1001	39.75	6	29.17479431	0.186	0.986105861	5
optimal_loci_350037_G	1007	3.612129	0	2068	46.97	6	38.23342096	0.414	0.986160376	5
optimal_loci_350039_G	1366	3.612129	8.2	4032	35.94	5	20.5134294	0.351	0.98618046	5

WHAT IS CLAIMED IS:

1. A recombinant sequence, said recombinant sequence comprising:

a nucleic acid sequence of at least 1 Kb and having at least 90% sequence identity with a

- 5 nongenic sequence selected from the group consisting of loci_137693_G1 (SEQ ID NO:387),
loci_265551_G1 (SEQ ID NO:463),
loci_128078_G1 (SEQ ID NO:560),
loci_168286_G1 (SEQ ID NO:573),
loci_3733_G1 (SEQ ID NO:1268),
10 loci_203075_G1 (SEQ ID NO:2030),
loci_232484_G1 (SEQ ID NO:2053),
loci_136086_G1 (SEQ ID NO:4425),
loci_203704_G1 (SEQ ID NO:2033),
loci_127268_G1 (SEQ ID NO:2709),
15 loci_204637_G1 (SEQ ID NO:2731),
loci_291068_G1 (SEQ ID NO:3230),
loci_232222_G1 (SEQ ID NO:3357),
loci_43577_G1 (SEQ ID NO:3428),
loci_204726_G1 (SEQ ID NO:424),
20 loci_232228_G1 (SEQ ID NO: 4529); and,

a DNA of interest, wherein the DNA of interest is inserted into said nongenic sequence to produce said recombinant sequence.

2. The recombinant sequence of claim 1 wherein said DNA of interest is inserted proximal
25 to a zinc finger target site specific for said nongenic sequence.

3. The recombinant sequence of claim 1, wherein said DNA of interest is inserted between a pair of zinc finger target sites specific for said nongenic sequence.

30 4. The recombinant sequence of claim 1, wherein said DNA of interest comprises an analytical domain.

5. The recombinant sequence of claim 1, wherein said DNA of interest does not encode a peptide.

35

6. The recombinant sequence of claim 1, wherein said DNA of interest encodes a peptide.

7. The recombinant sequence of claim 1, wherein said DNA of interest comprises a gene expression cassette comprising an insecticidal resistance gene, herbicide tolerance gene,
5 nitrogen use efficiency gene, water use efficiency gene, nutritional quality gene, DNA binding gene, and selectable marker gene.

8. The recombinant sequence of claim 1, wherein said DNA of interest comprises two or more gene expression cassettes.

9. The recombinant sequence of claim 1, wherein two or more of said nongenic sequences each comprise an inserted DNA of interest to produce two or more recombinant sequences wherein the two or more recombinant sequences are located on a same chromosome.

10. The recombinant sequence of claim 1, wherein said DNA of interest and/or said nongenic sequence are modified during insertion of said DNA of interest into said nongenic sequence.

11. The recombinant sequence of any of one of claims 1-10 wherein said nongenic sequence
20 is selected from the group consisting of optimal loci_ 204637 (SEQ ID NO:2731), optimal_loci_136086 (SEQ ID NO:4425), optimal_loci_232484 (SEQ ID NO:2053), optimal_loci_203075 (SEQ ID NO:2030), optimal_loci_3733 (SEQ ID NO:1268), optimal_loci_168286 (SEQ ID NO:573), optimal_loci_128078 (SEQ ID NO:560), optimal_loci_265551 (SEQ ID NO:463), optimal_loci_127268 (SEQ ID NO:2709),
25 optimal_loci_204726 (SEQ ID NO:424), and optimal_loci_232222 (SEQ ID NO:3357).

12. The recombinant sequence of any of one of claims 1-10 wherein said nongenic sequence is selected from the group consisting of optimal loci_ 204637 (SEQ ID NO:2731), optimal_loci_136086 (SEQ ID NO:4425), optimal_loci_232484 (SEQ ID NO:2053),
30 optimal_loci_203075 (SEQ ID NO:2030), optimal_loci_3733 (SEQ ID NO:1268), optimal_loci_168286 (SEQ ID NO:573), optimal_loci_128078 (SEQ ID NO:560) and optimal_loci_265551 (SEQ ID NO:463).

13. The recombinant sequence of any of one of claims 1-10 wherein said nongenic sequence is selected from the group consisting of optimal loci_ 204637 (SEQ ID NO:2731), optimal_loci_ 203075 (SEQ ID NO:2030) and optimal_loci_ 128078 (SEQ ID NO:560).

14. The recombinant sequence of any of one of claims 1-10 wherein said nongenic sequence is selected from the group consisting of optimal_loci_ 137693_G1 (SEQ ID NO:387), optimal_loci_ 265551_G1 (SEQ ID NO:463), optimal_loci_ 128078_G1 (SEQ ID NO:560), optimal_loci_ 168286_G1 (SEQ ID NO:573), optimal_loci_ 3733_G1 (SEQ ID NO:1268), optimal_loci_ 203075_G1 (SEQ ID NO:2030), optimal_loci_ 232484_G1 (SEQ ID NO:2053), and optimal_loci_ 204637_G1 (SEQ ID NO:2731).

15. A maize plant, maize plant part, or maize plant cell comprising a recombinant sequence of any one of claims 1-10.

16. A method of making a transgenic plant cell comprising a DNA of interest, the method comprising:

a. selecting a target nongenic maize genomic locus having at least 90% sequence identity from the group consisting of loci_ 137693_G1 (SEQ ID NO:387), loci_ 265551_G1 (SEQ ID NO:463), loci_ 128078_G1 (SEQ ID NO:560), loci_ 168286_G1 (SEQ ID NO:573), loci_ 3733_G1 (SEQ ID NO:1268), loci_ 203075_G1 (SEQ ID NO:2030), loci_ 232484_G1 (SEQ ID NO:2053), loci_ 136086_G1 (SEQ ID NO:4425), loci_ 203704_G1 (SEQ ID NO:2033), loci_ 127268_G1 (SEQ ID NO:2709), loci_ 204637_G1 (SEQ ID NO:2731), loci_ 291068_G1 (SEQ ID NO:3230), loci_ 232222_G1 (SEQ ID NO:3357), loci_ 43577_G1 (SEQ ID NO:3428), loci_ 204726_G1 (SEQ ID NO:424), and loci_ 232228_G1 (SEQ ID NO: 4529);

b. selecting a site specific nuclease that specifically binds and cleaves said target nongenic maize genomic locus

c. introducing said site specific nuclease into a maize plant cell;

d. introducing the DNA of interest into the plant cell;

e. inserting the DNA of interest into said target nongenic maize genomic loci; and,

f. selecting transgenic plant cells comprising the DNA of interest targeted to said nongenic locus.

17. The method of making a transgenic plant cell of claim 16, wherein said DNA of interest comprises an analytical domain.

18. The method of making a transgenic plant cell of claim 16, wherein said DNA of interest does not encode a peptide.

5 19. The method of making a transgenic plant cell of claim 16, wherein said DNA of interest encodes a peptide.

20. The method of making a transgenic plant cell of claim 16, wherein said DNA of interest comprises a gene expression cassette comprising a transgene.

10

21. The method of making a transgenic plant cell of claim 16, wherein said DNA of interest comprises two or more gene expression cassettes.

22. The method of making a transgenic plant cell of claim 16, wherein said site specific
15 nuclease is selected from the group consisting of a zinc finger nuclease, a CRISPR nuclease, a TALEN, a homing endonuclease or a meganuclease.

23. The method of making a transgenic plant cell of claim 16, wherein said DNA of interest is integrated within said nongenic locus via a homology directed repair integration method.

20

24. The method of making a transgenic plant cell of claim 16, wherein said DNA of interest is integrated within said nongenic locus via a non-homologous end joining integration method.

25. The method of making a transgenic plant cell of claim 16, wherein two or more of said
25 DNA of interest are inserted into two or more of said target nongenic maize genomic loci.

26. The method of making a transgenic plant cell of claim 25, wherein two or more of said target nongenic maize genomic loci are located on a same chromosome.

30 27. The method of making a transgenic plant cell of claim 16, wherein said DNA of interest and/or said target nongenic maize genomic loci are modified during insertion of said DNA of interest into said target nongenic maize genomic loci.

28. A purified nongenic maize genomic loci of at least 1 Kb and having at least 90% sequence identity with a nongenic sequence selected from the group consisting of loci_137693_G1 (SEQ ID NO:387), loci_265551_G1 (SEQ ID NO:463), loci_128078_G1 (SEQ ID NO:560), loci_168286_G1 (SEQ ID NO:573),
5 loci_3733_G1 (SEQ ID NO:1268), loci_203075_G1 (SEQ ID NO:2030), loci_232484_G1 (SEQ ID NO:2053), loci_136086_G1 (SEQ ID NO:4425), loci_203704_G1 (SEQ ID NO:2033), loci_127268_G1 (SEQ ID NO:2709), loci_204637_G1 (SEQ ID NO:2731), loci_291068_G1 (SEQ ID NO:3230), loci_232222_G1 (SEQ ID NO:3357), loci_43577_G1 (SEQ ID NO:3428),
10 loci_204726_G1 (SEQ ID NO:424), and loci_232228_G1 (SEQ ID NO: 4529).
29. The purified nongenic maize genomic loci of claim 28 wherein said nongenic sequence is selected from the group consisting of optimal loci_204637 (SEQ ID NO:2731), optimal_loci_136086 (SEQ ID NO:4425), optimal_loci_232484 (SEQ ID NO:2053),
15 optimal_loci_203075 (SEQ ID NO:2030), optimal_loci_3733 (SEQ ID NO:1268), optimal_loci_168286 (SEQ ID NO:573), optimal_loci_128078 (SEQ ID NO:560) and optimal_loci_265551 (SEQ ID NO:463).
30. The purified nongenic maize genomic loci of claim 28 wherein said nongenic sequence
20 is selected from the group consisting of optimal loci_204637 (SEQ ID NO:2731), optimal_loci_203075 (SEQ ID NO:2030) and optimal_loci_128078 (SEQ ID NO:560).
31. The purified nongenic maize genomic loci of claims 28 wherein said nongenic sequence is selected from the group consisting of optimal_loci_137693_G1 (SEQ ID NO:387),
25 optimal_loci_265551_G1 (SEQ ID NO:463), optimal_loci_128078_G1 (SEQ ID NO:560), optimal_loci_168286_G1 (SEQ ID NO:573), optimal_loci_3733_G1 (SEQ ID NO:1268), optimal_loci_203075_G1 (SEQ ID NO:2030), optimal_loci_232484_G1 (SEQ ID NO:2053), and optimal_loci_204637_G1 (SEQ ID NO:2731).
- 30 32. The purified nongenic maize genomic loci of any one of claims 28 to 31, further comprising a DNA of interest, wherein said DNA of interest is inserted into said nongenic sequence.
33. The purified nongenic maize genomic loci of claim 32, wherein said DNA of interest is
35 inserted proximal to a zinc finger target site specific for said nongenic sequence.

34. The purified nongenic maize genomic loci of claim 32, wherein said DNA of interest is inserted between a pair of zinc finger target sites specific for said nongenic sequence.

35. The purified nongenic maize genomic loci of claim 32, wherein said DNA of interest comprises an analytical domain.

36. The purified nongenic maize genomic loci of claim 32, wherein said DNA of interest does not encode a peptide.

37. The purified nongenic maize genomic loci of claim 32, wherein said DNA of interest encodes a peptide.

38. The purified nongenic maize genomic loci of claim 32, wherein said DNA of interest comprises a gene expression cassette comprising an insecticidal resistance gene, herbicide tolerance gene, nitrogen use efficiency gene, water use efficiency gene, nutritional quality gene, DNA binding gene, and selectable marker gene.

39. The purified nongenic maize genomic loci of any one of claims 32, 37 or 38, wherein said DNA of interest comprises two or more gene expression cassettes.

40. The purified nongenic maize genomic loci of any one of claims 32 to 39, wherein two or more of said nongenic sequences each comprise an inserted DNA of interest to produce two or more recombinant sequences wherein the two or more recombinant sequences are located on a same chromosome.

41. The purified nongenic maize genomic loci of any one of claims 32 to 40, wherein said DNA of interest and/or said nongenic sequence are modified during insertion of said DNA of interest into said nongenic sequence.

42. The purified nongenic maize genomic loci of any one of claims 32 to 41, wherein said DNA of interest is inserted via a homology directed repair or a non-homologous end joining repair mechanism.

43. A plant comprising a recombinant sequence, said recombinant sequence comprising:
a nucleic acid sequence having at least 90% sequence identity with a nongenic
sequence, and
a DNA of interest, wherein the DNA of interest is inserted into said nongenic sequence.

5

44. The plant of claim 43, wherein said nongenic sequence is selected from the group
consisting of

loci_137693_G1 (SEQ ID NO:387), loci_265551_G1 (SEQ ID NO:463),

loci_128078_G1 (SEQ ID NO:560), loci_168286_G1 (SEQ ID NO:573),

10 loci_3733_G1 (SEQ ID NO:1268), loci_203075_G1 (SEQ ID NO:2030),

loci_232484_G1 (SEQ ID NO:2053), loci_136086_G1 (SEQ ID NO:4425),

loci_203704_G1 (SEQ ID NO:2033), loci_127268_G1 (SEQ ID NO:2709),

loci_204637_G1 (SEQ ID NO:2731), loci_291068_G1 (SEQ ID NO:3230),

loci_232222_G1 (SEQ ID NO:3357), loci_43577_G1 (SEQ ID NO:3428),

15 loci_204726_G1 (SEQ ID NO:424), and loci_232228_G1 (SEQ ID NO: 4529).

45. The plant of claim 43, comprising two or more of said recombinant sequences.

46. The plant of claim 43, wherein said recombinant sequence are located on the same
20 chromosome.

47. The plant of claim 43, wherein said DNA of interest is inserted proximal to a zinc finger
target site specific for said nongenic sequence.

- 25 48. The plant of claim 43, wherein said DNA of interest is inserted between a pair of zinc
finger target sites specific for said nongenic sequence.

49. The plant of claim 43, wherein said DNA of interest comprises an analytical domain.

- 30 50. The plant of claim 43, wherein said DNA of interest does not encode a peptide.

51. The plant of claim 43, wherein said DNA of interest encodes a peptide.

52. The plant of claim 43, wherein said DNA of interest comprises a gene expression
35 cassette comprising an insecticidal resistance gene, herbicide tolerance gene, nitrogen use

efficiency gene, water use efficiency gene, nutritional quality gene, DNA binding gene, and selectable marker gene.

53. The plant of claim 43, wherein said DNA of interest and/or said nongenic sequence are
5 modified during insertion of said DNA of interest into said nongenic sequence.

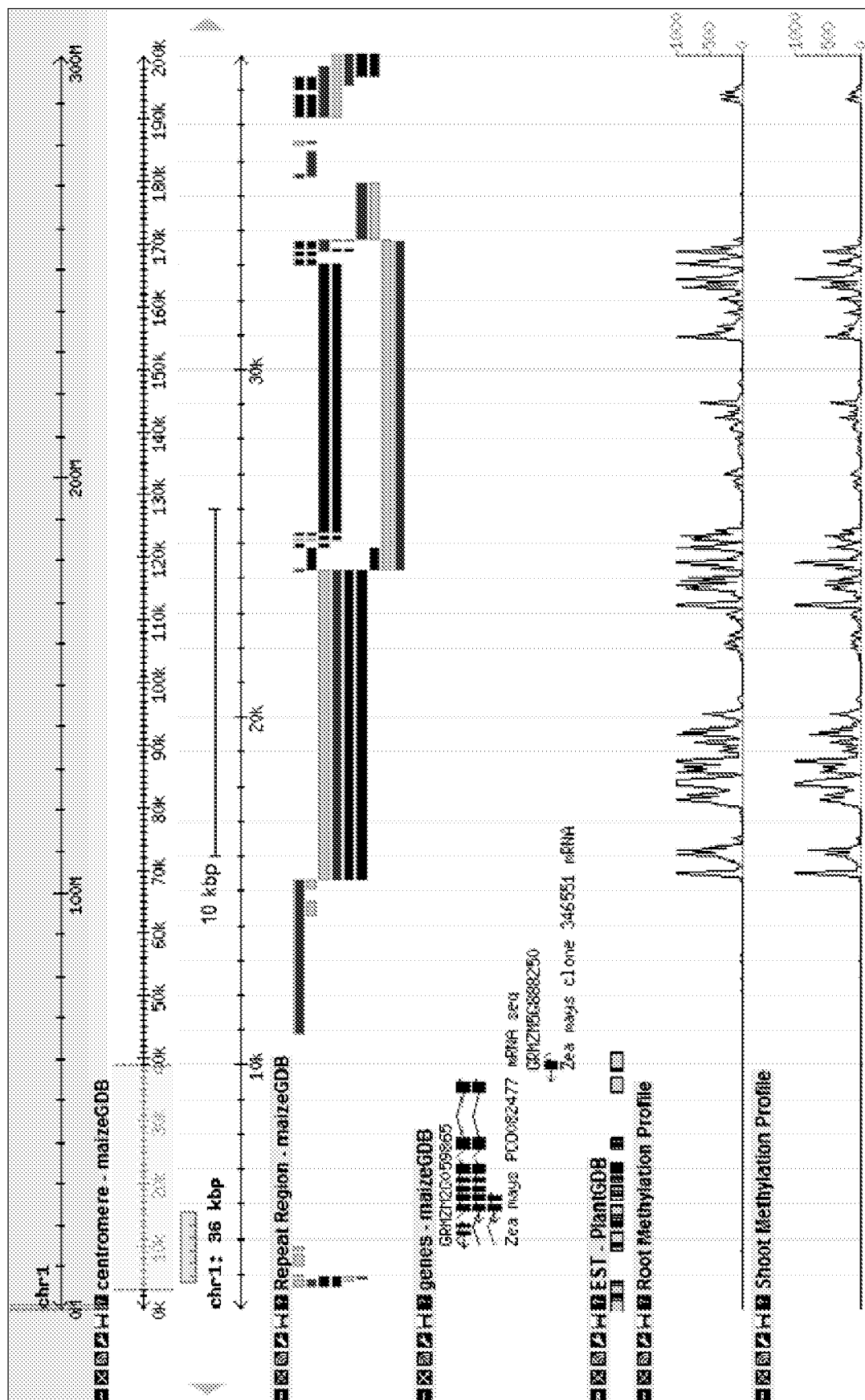


Fig. 1

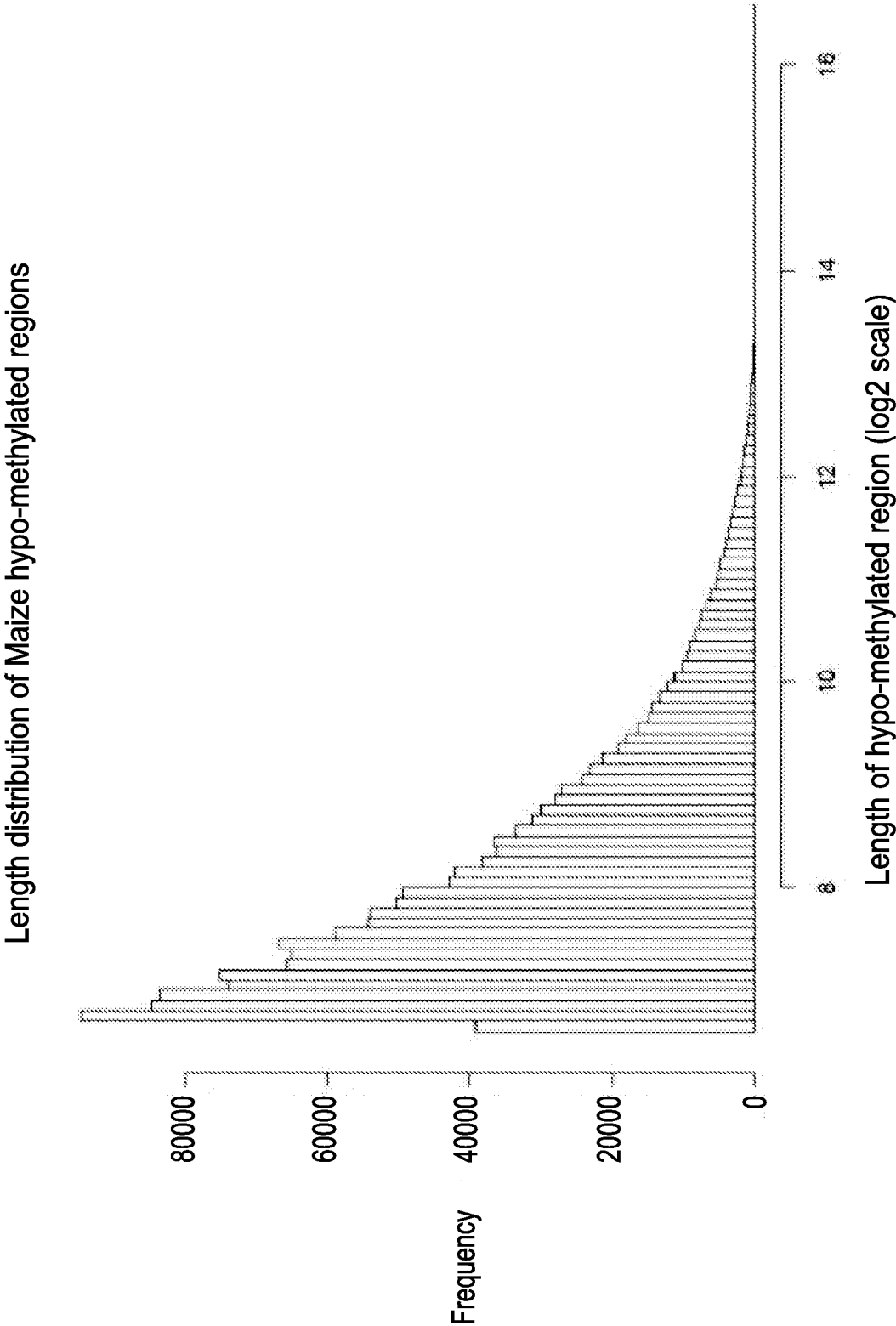


Fig. 2

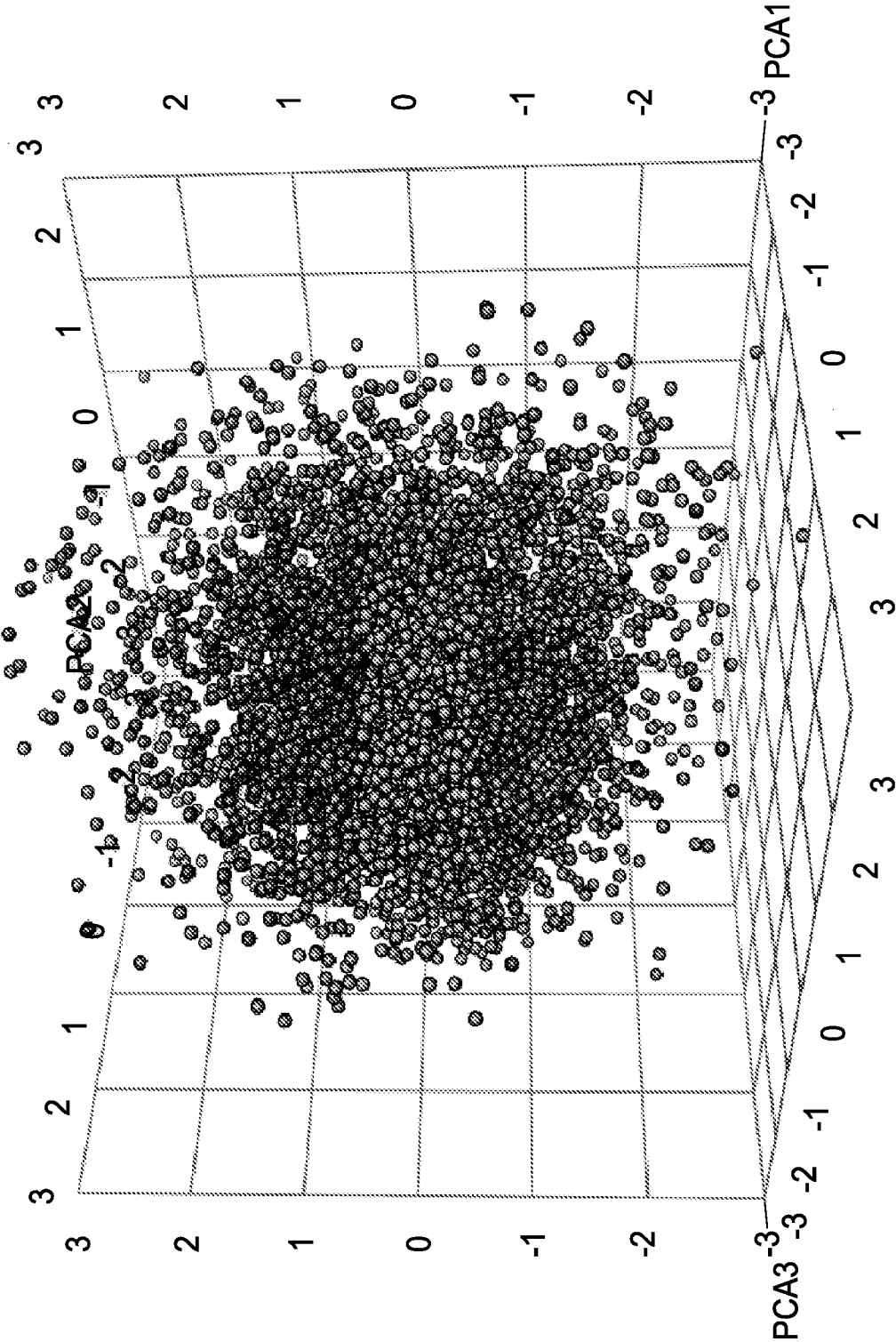


Fig. 3

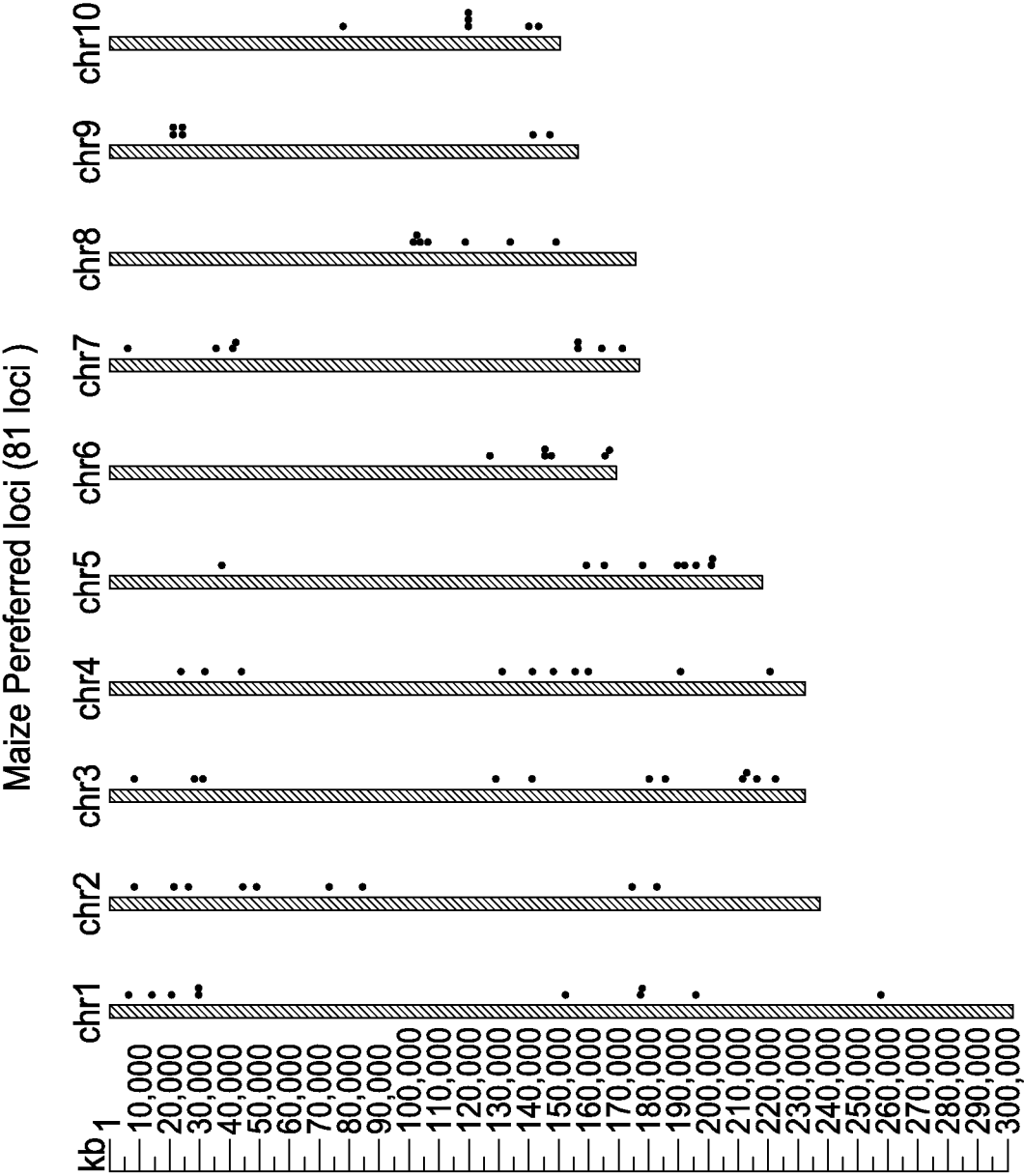


Fig. 4

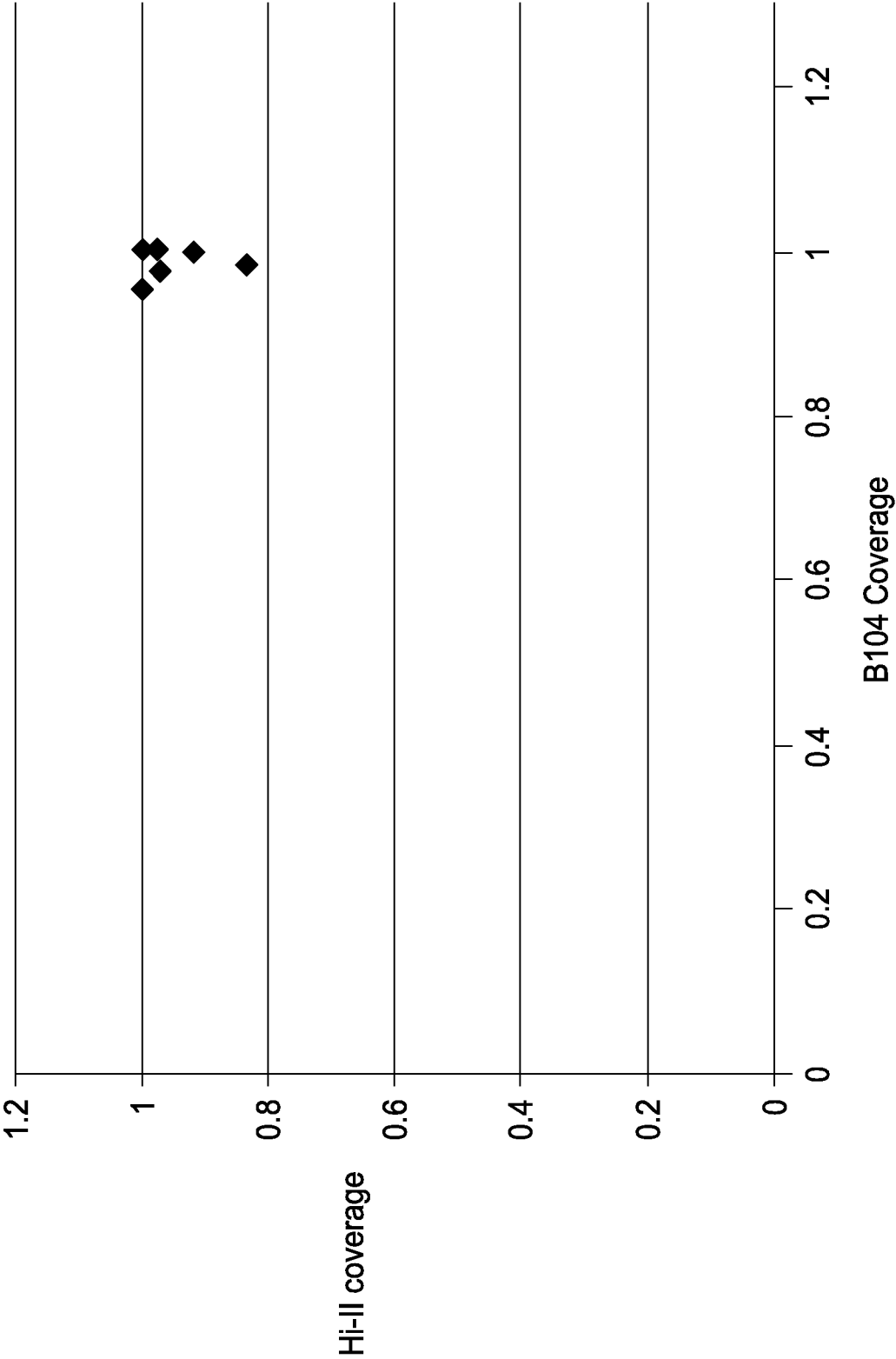


Fig. 5

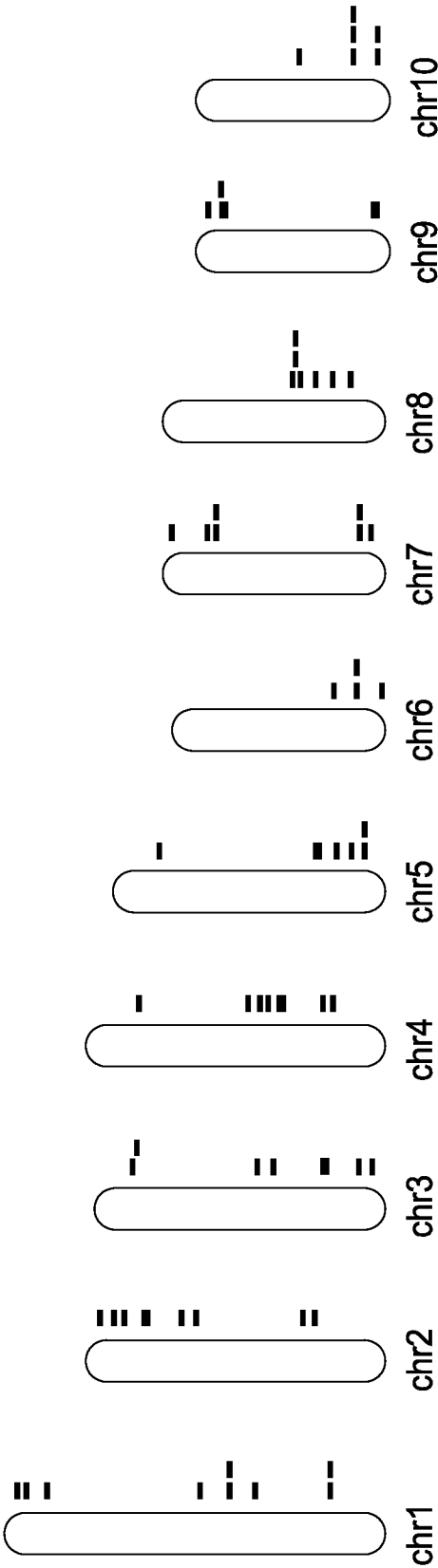


Fig. 6

7/28

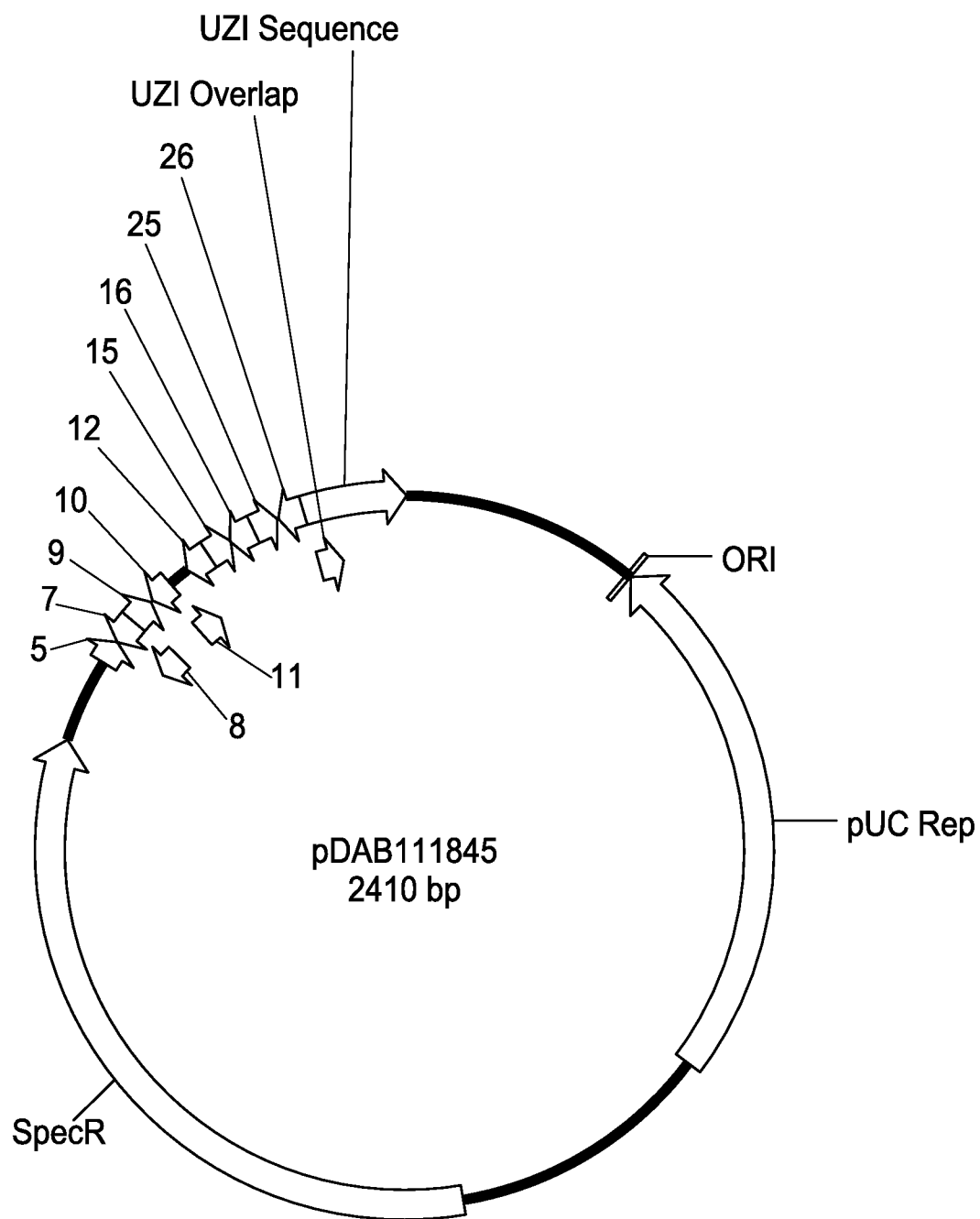


Fig. 7

8/28

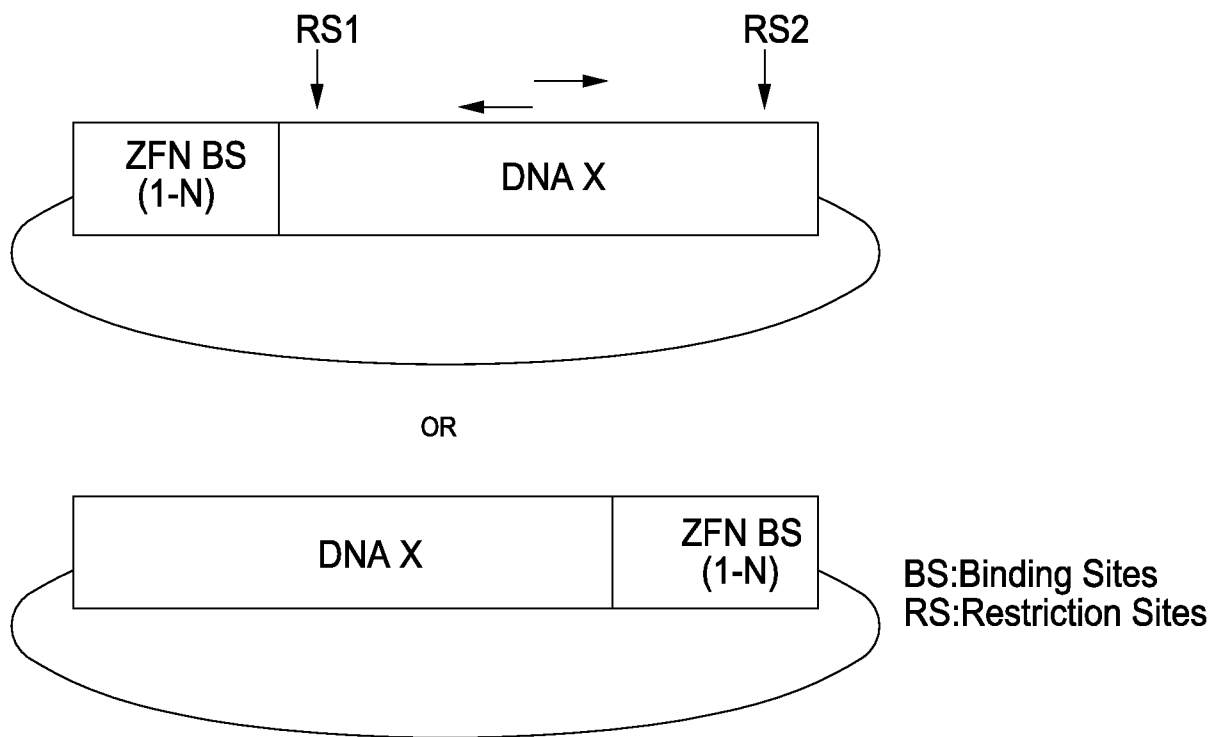


Fig. 8

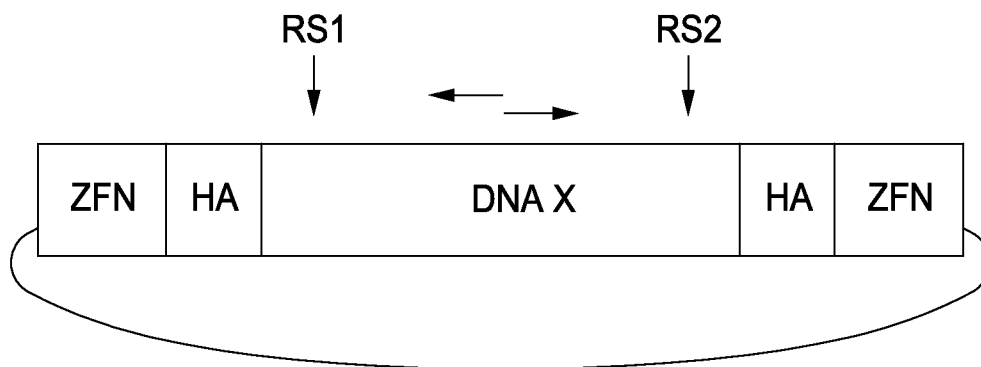


Fig. 9

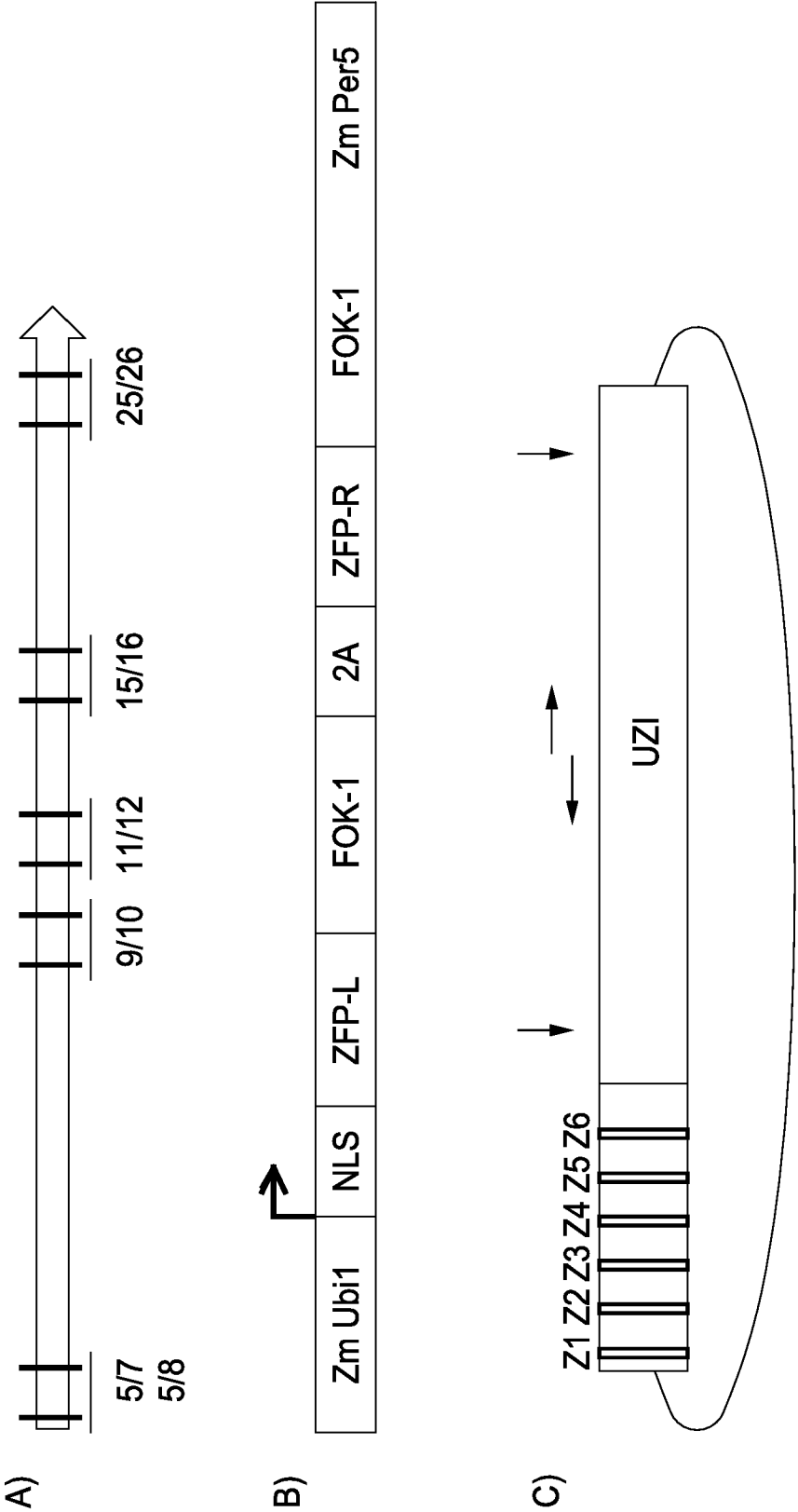


Fig. 10

10/28

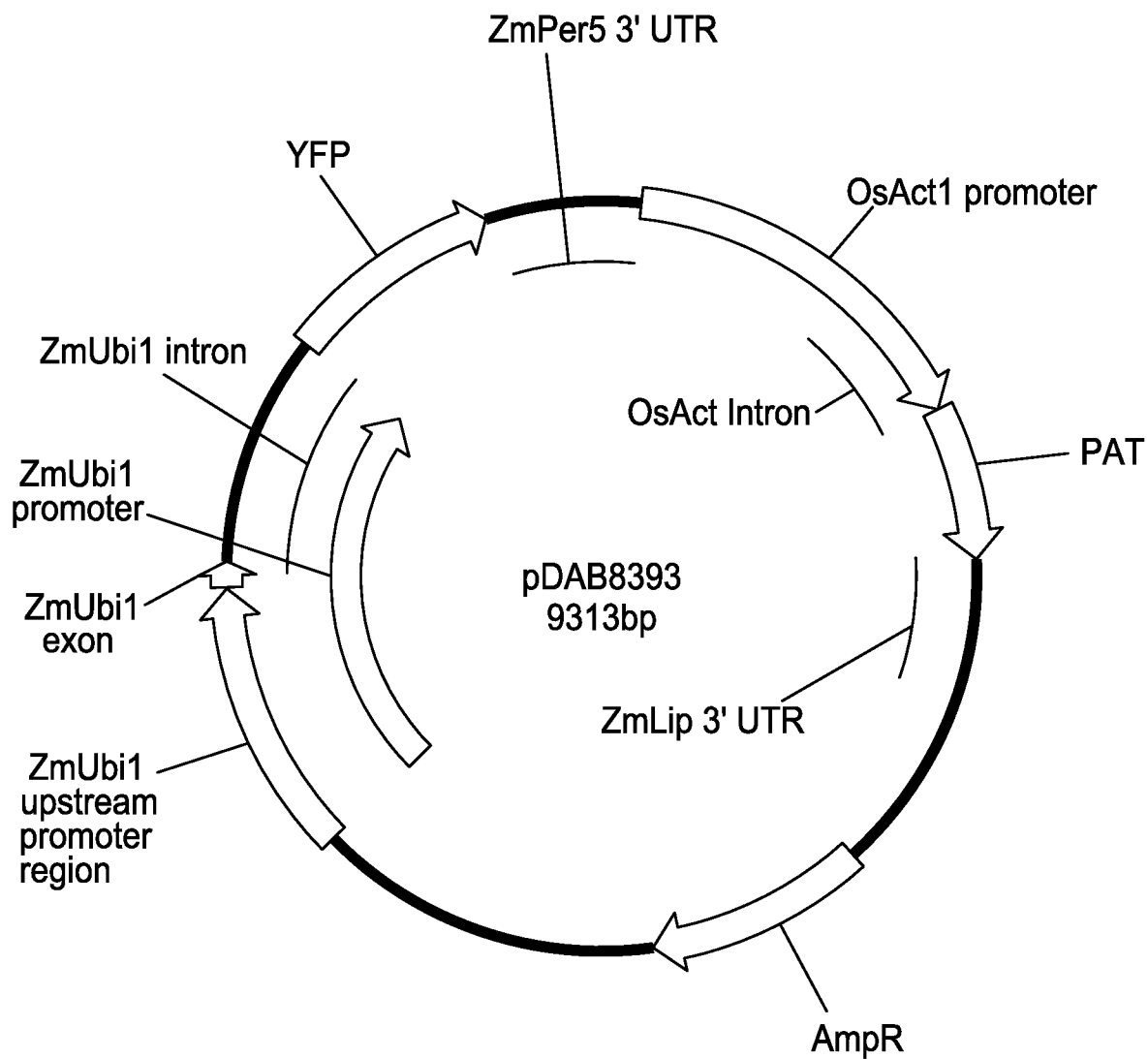
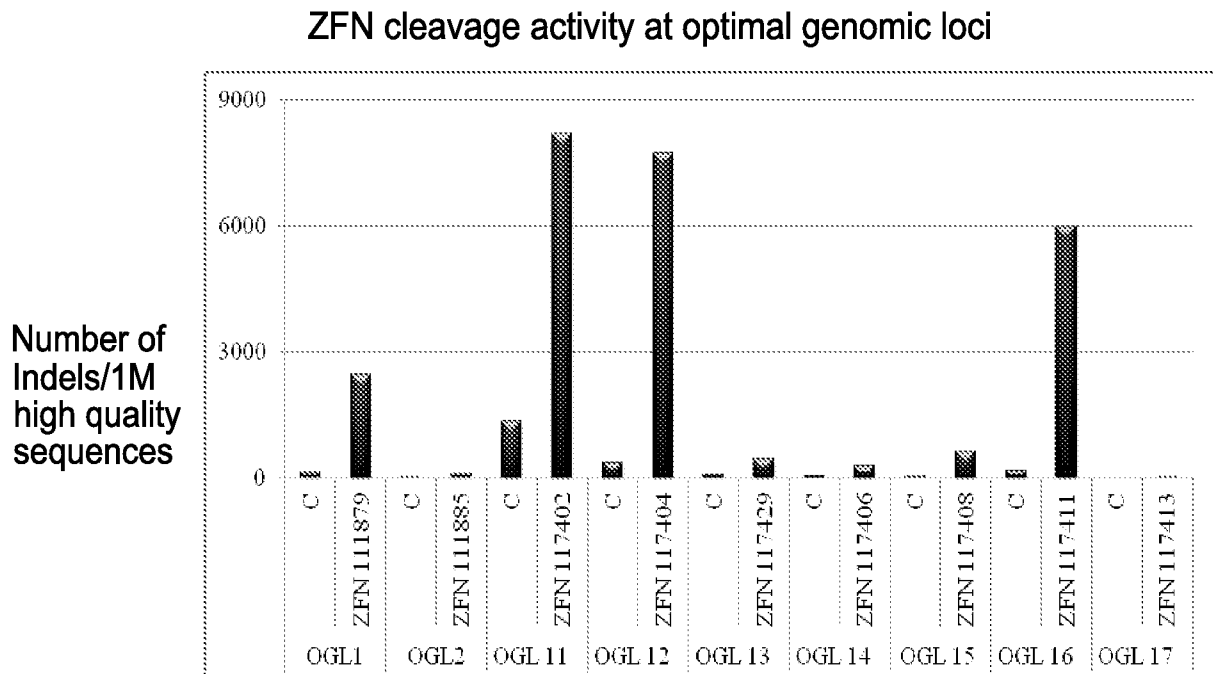


Fig. 11

11/28



ID	Name	Treatment	# Indels/1M reads α	HQ
optimal_loci_204637	OGL1	C	115.1827783	
		ZFN 111879	2458.971273	
optimal_loci_204726	OGL2	C	10.86457474	
		ZFN 111885	102.9851891	
optimal_loci_31710	OGL11	C	1359.364352	
		ZFN 117402	8209.320688	
optimal_loci_156393	OGL12	C	368.6331485	
		ZFN 117404	7748.53473	
optimal_loci_157315	OGL13	C	79.11178495	
		ZFN 117429	453.3253803	
optimal_loci_197372	OGL14	C	48.99318995	
		ZFN 117406	277.1403482	
optimal_loci_198387	OGL15	C	45.49262935	
		ZFN 117408	622.2166624	
optimal_loci_232228	OGL16	C	163.1649867	
		ZFN 117411	5980.912998	
optimal_loci_285621	OGL17	C	0 α	
		ZFN 117413	4.815941547	

Fig. 12

12/28

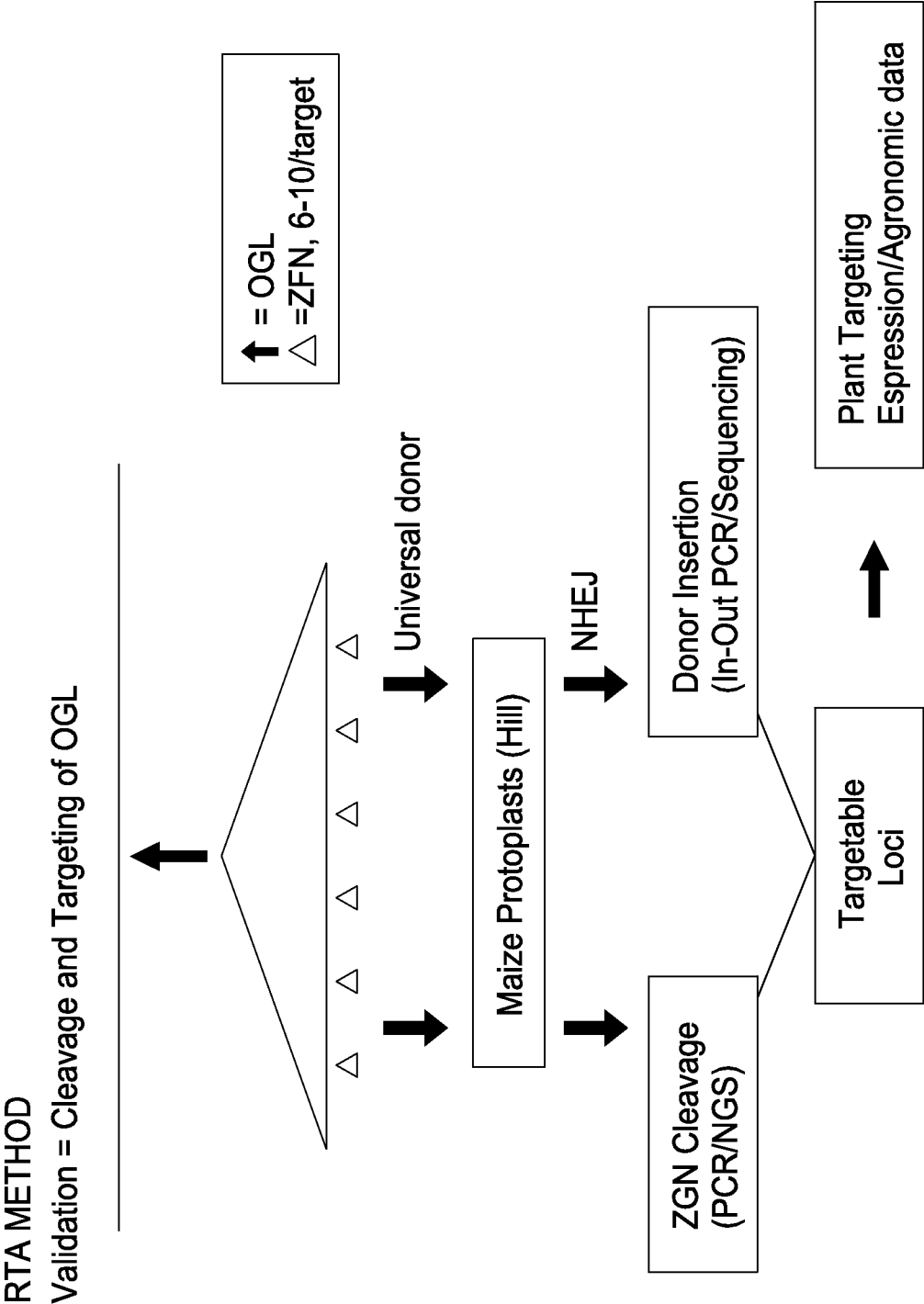


Fig. 13

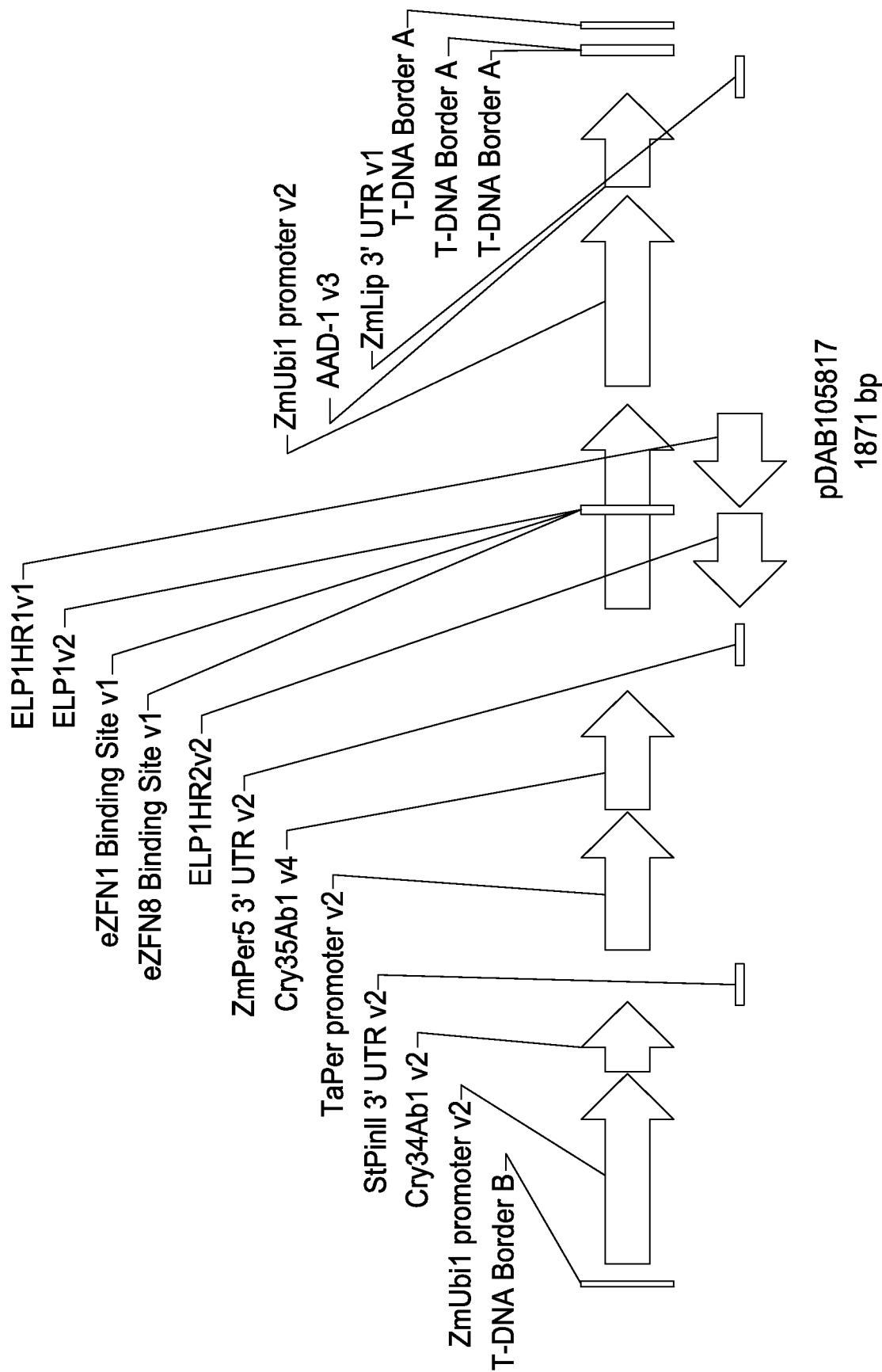


Fig. 14

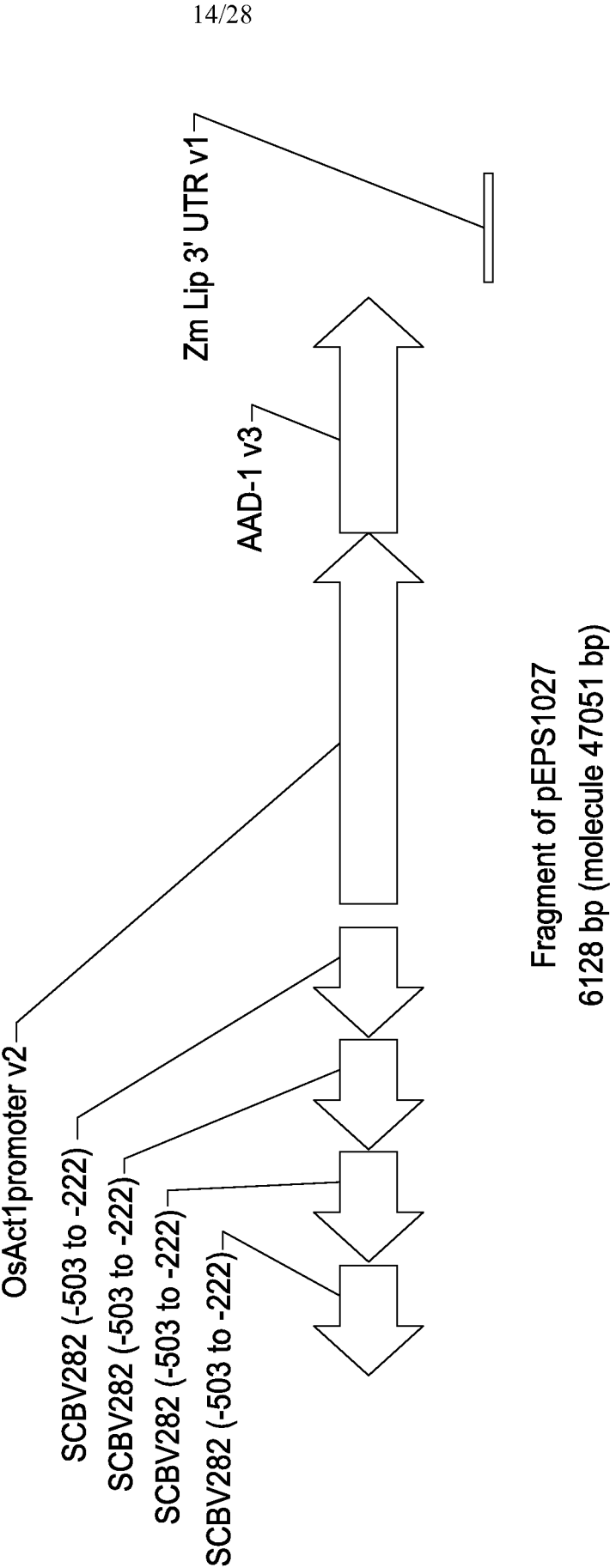
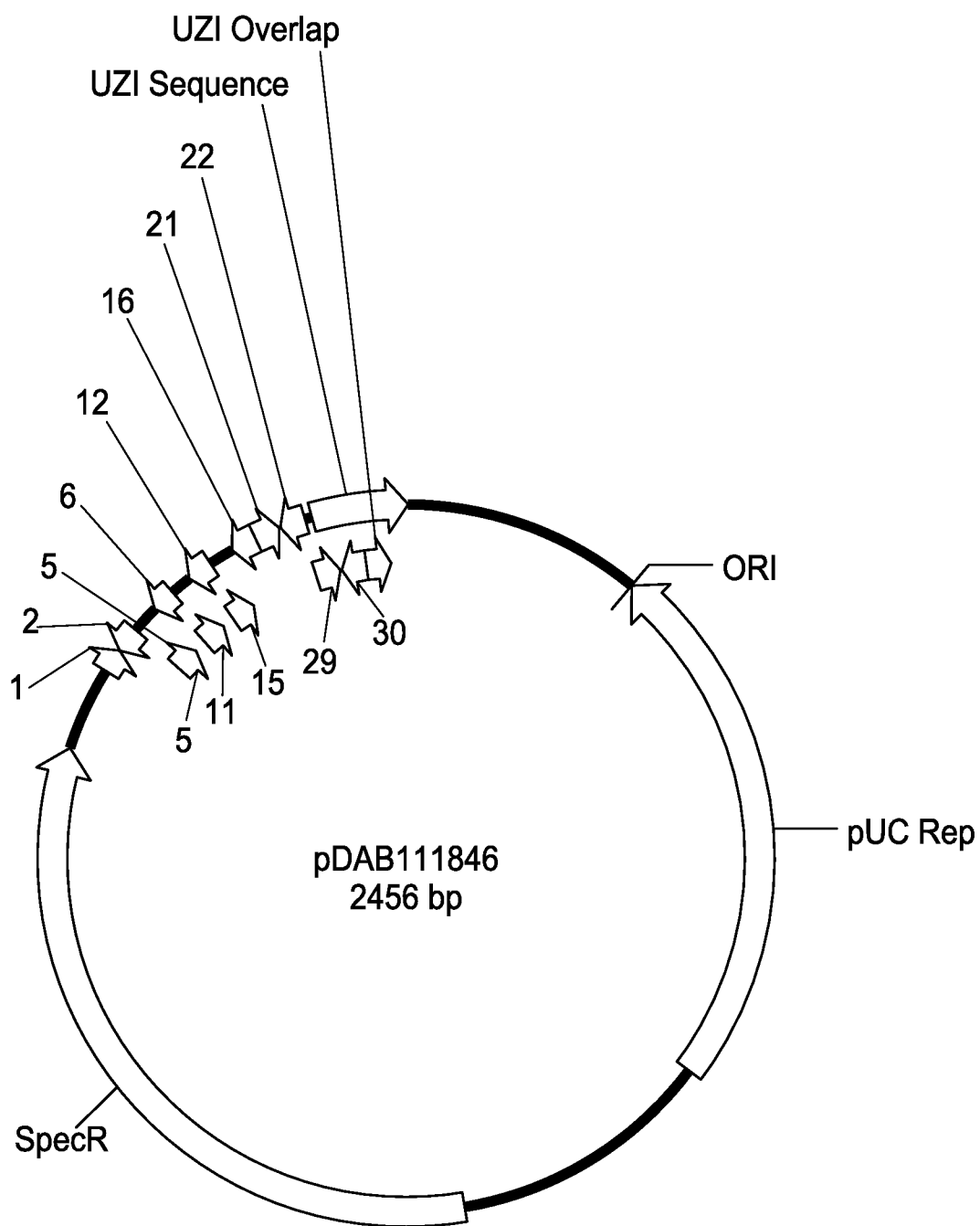
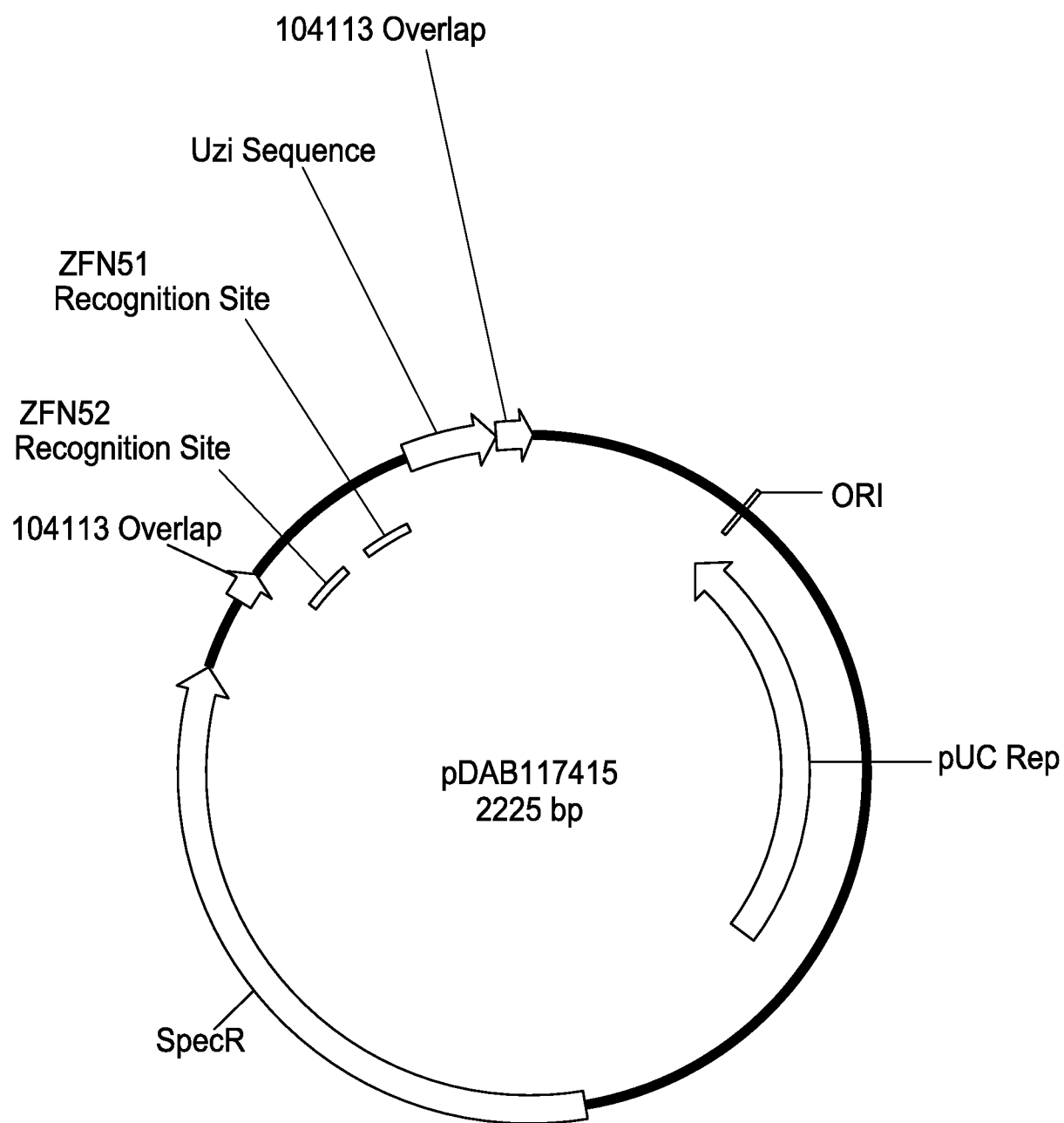


Fig. 14B

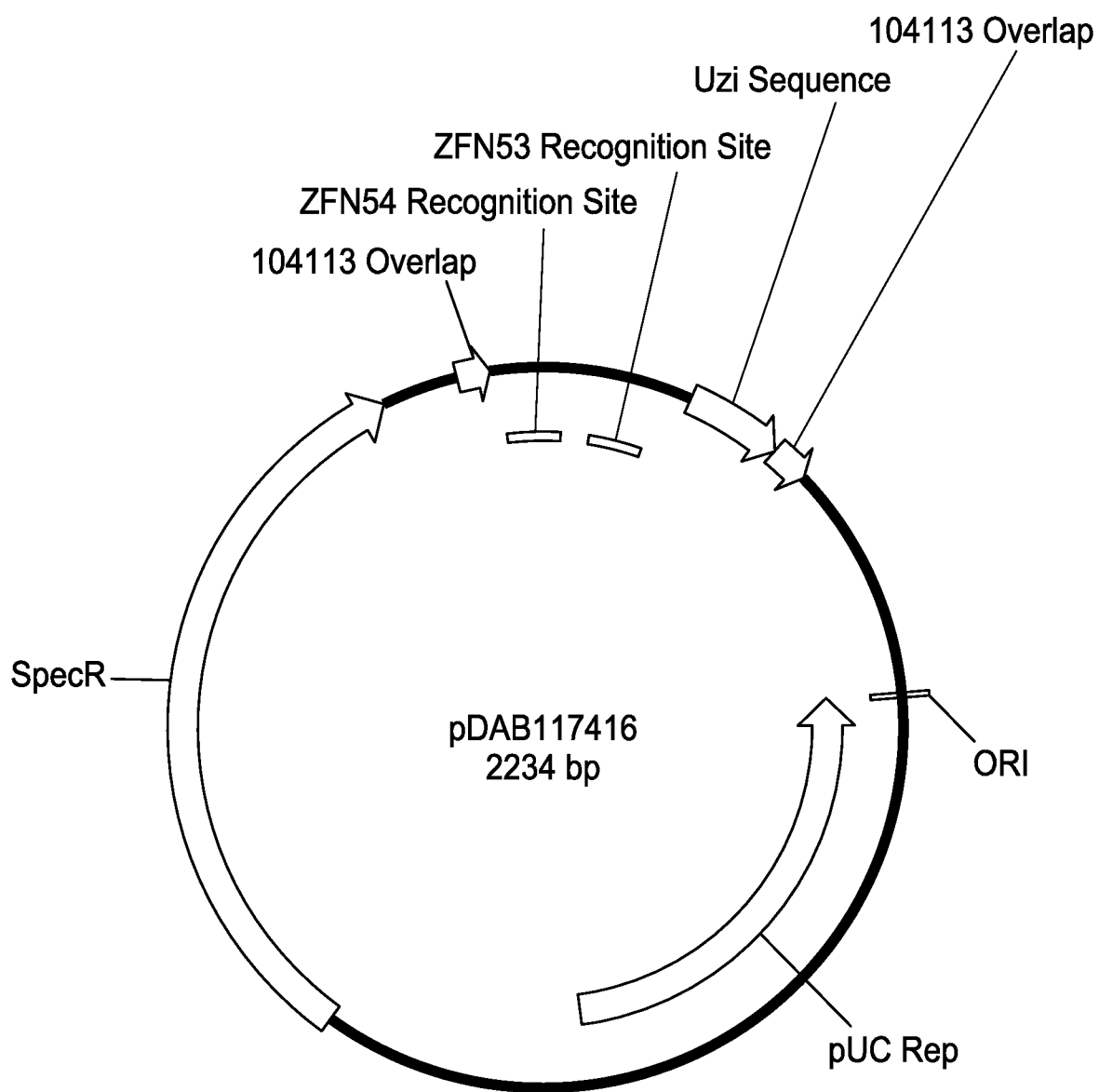
15/28

**Fig. 15**

16/28

**Fig. 16**

17/28

**Fig. 17**

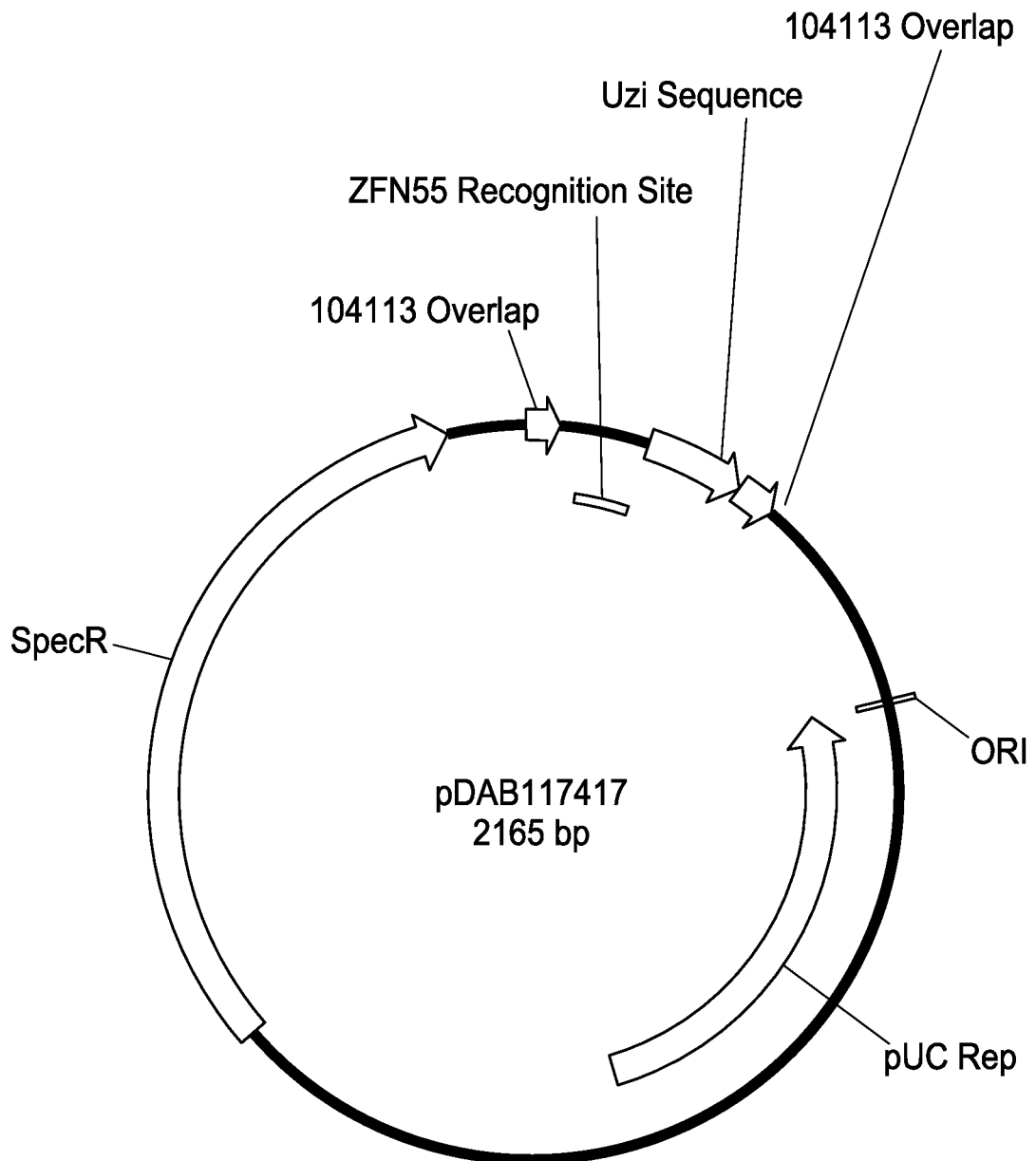
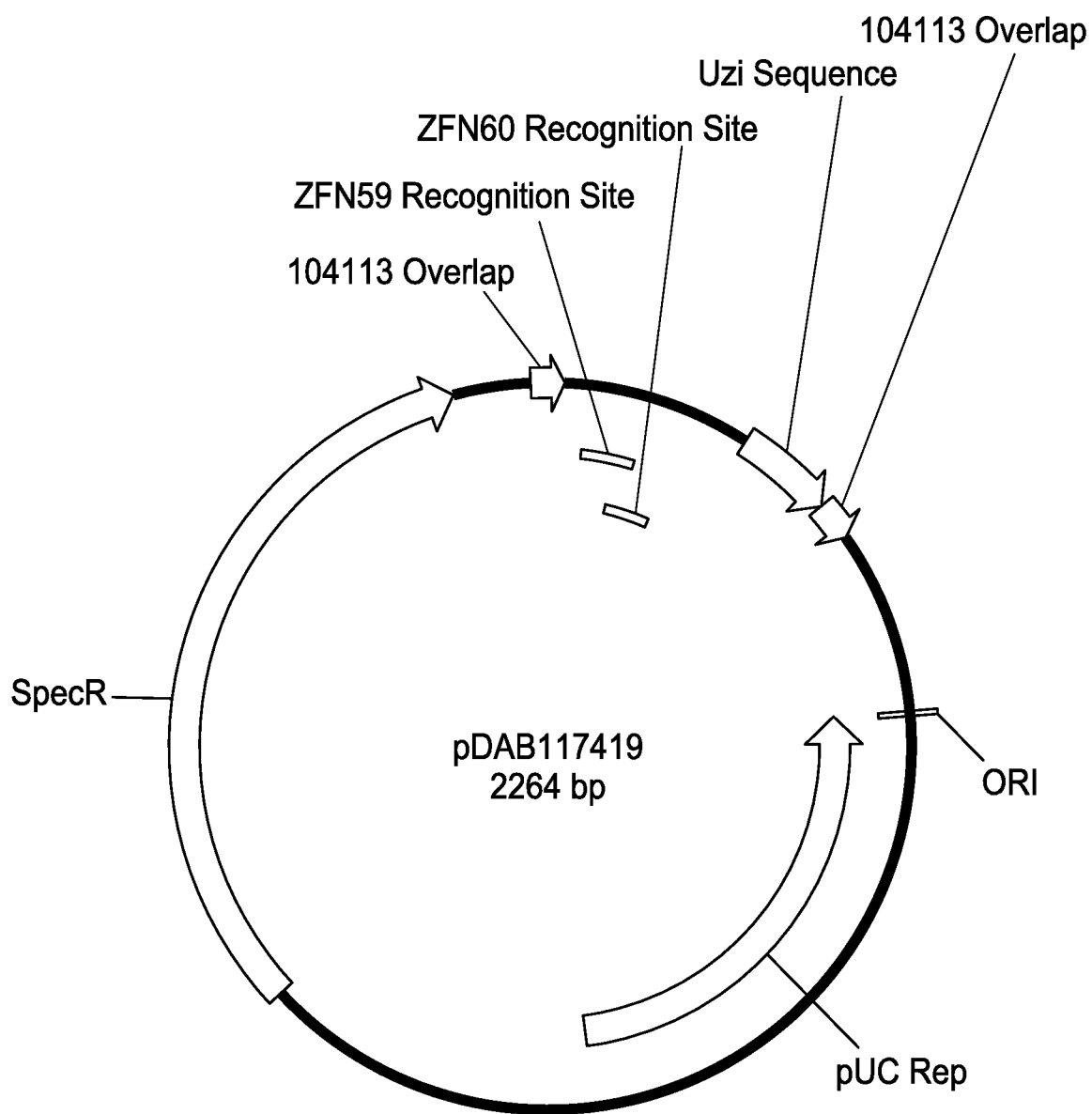
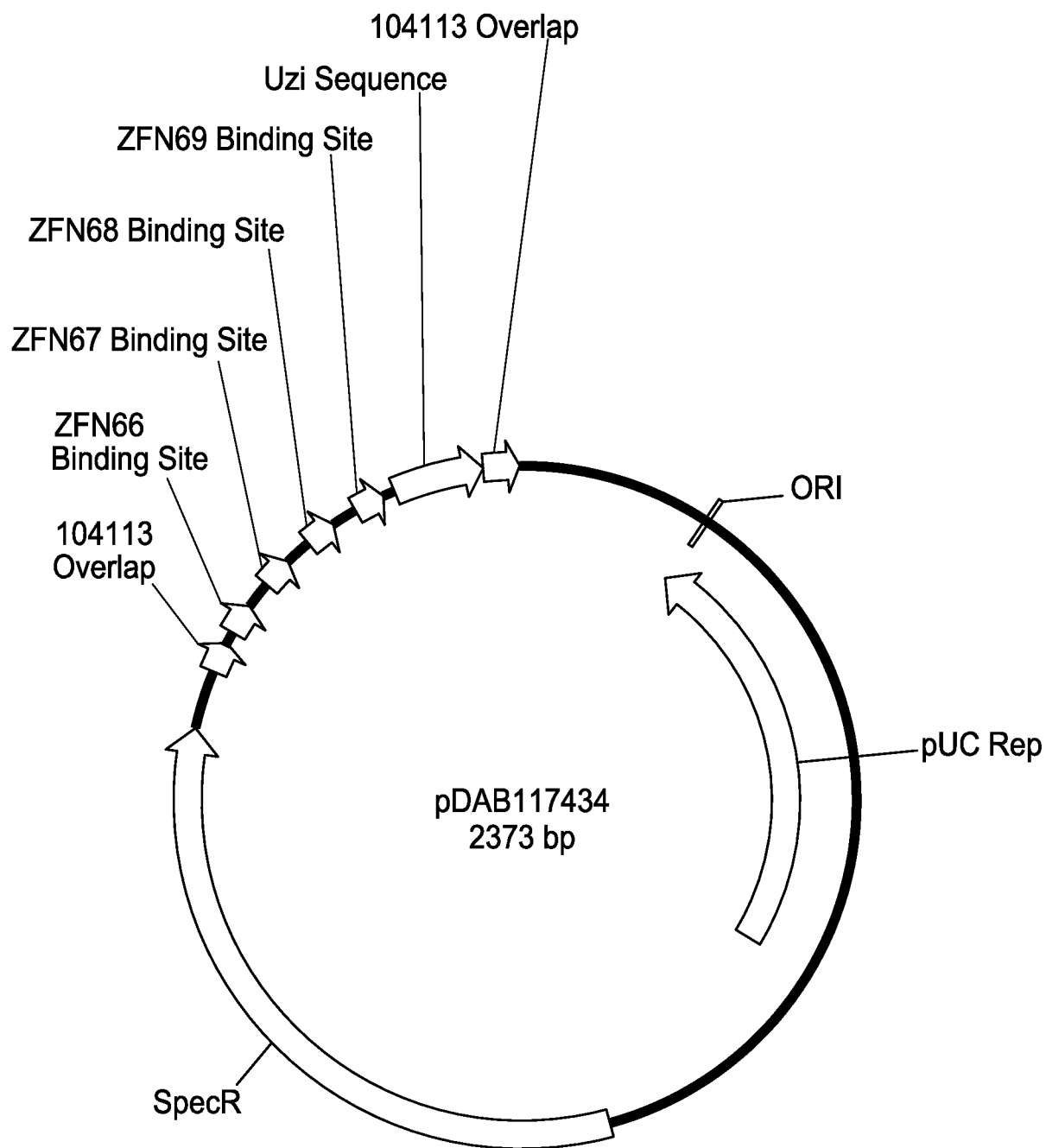


Fig. 18

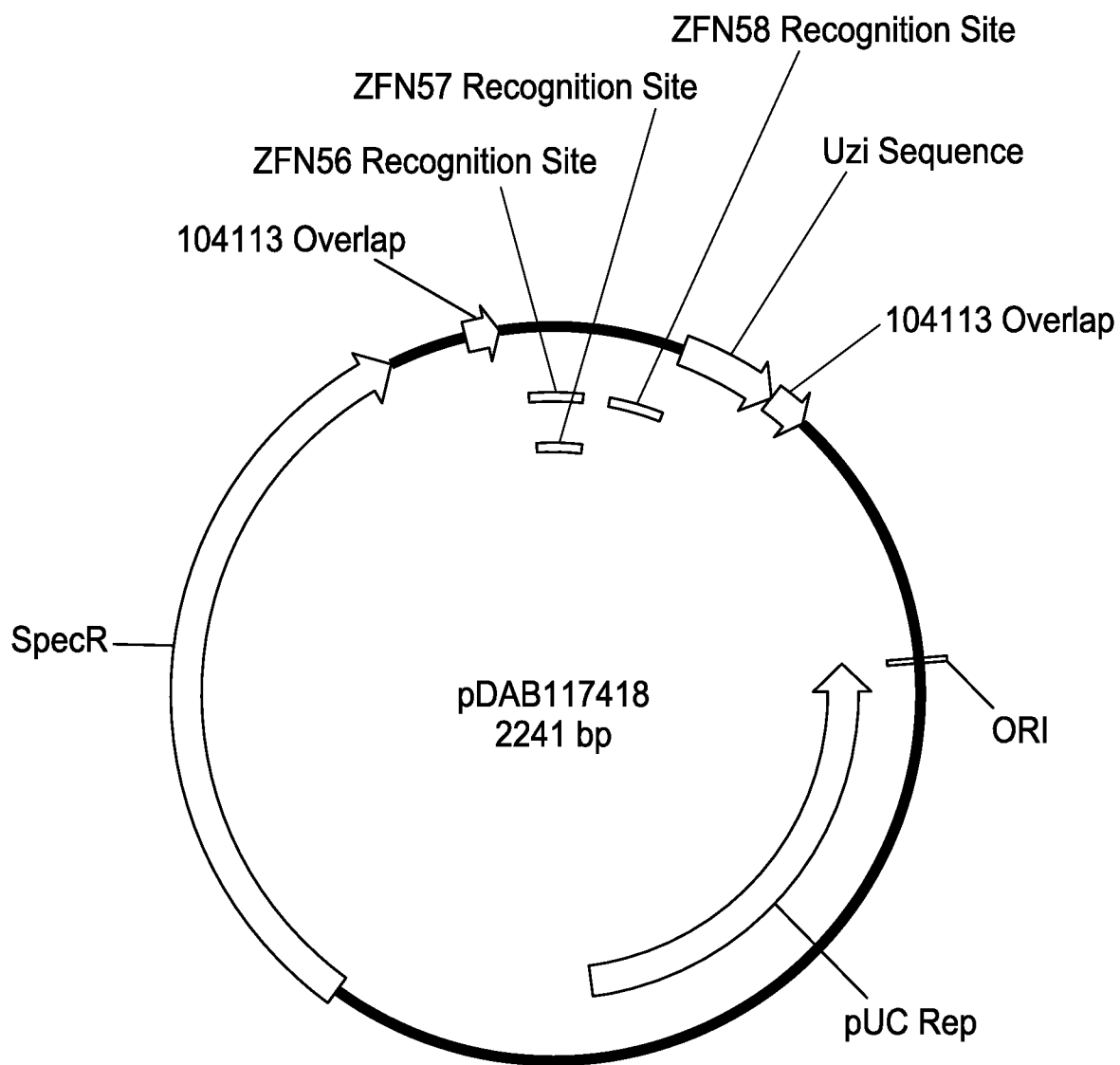
19/28

**Fig. 19**

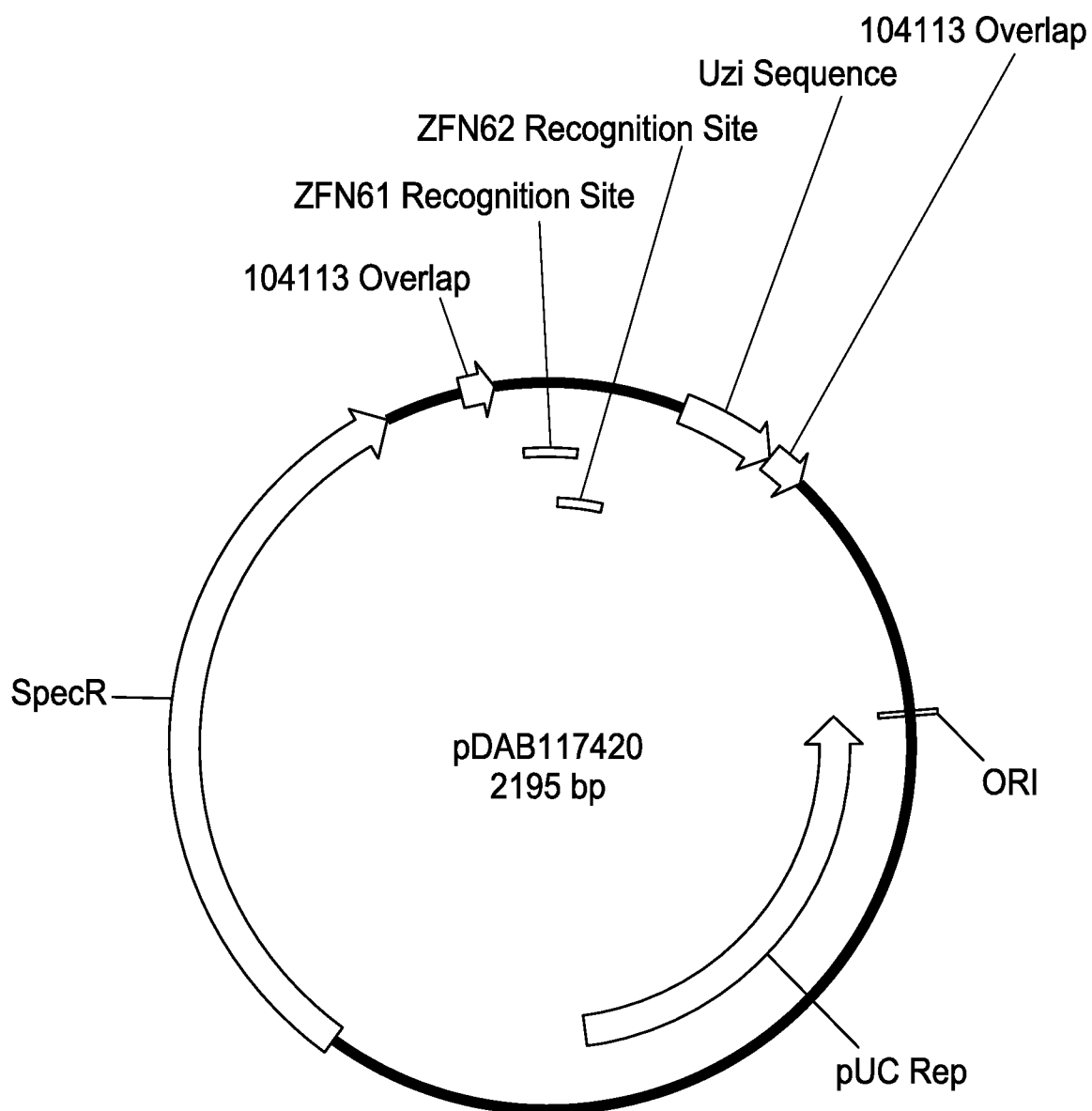
20/28

**Fig. 20**

21/28

**Fig. 21**

22/28

**Fig. 22**

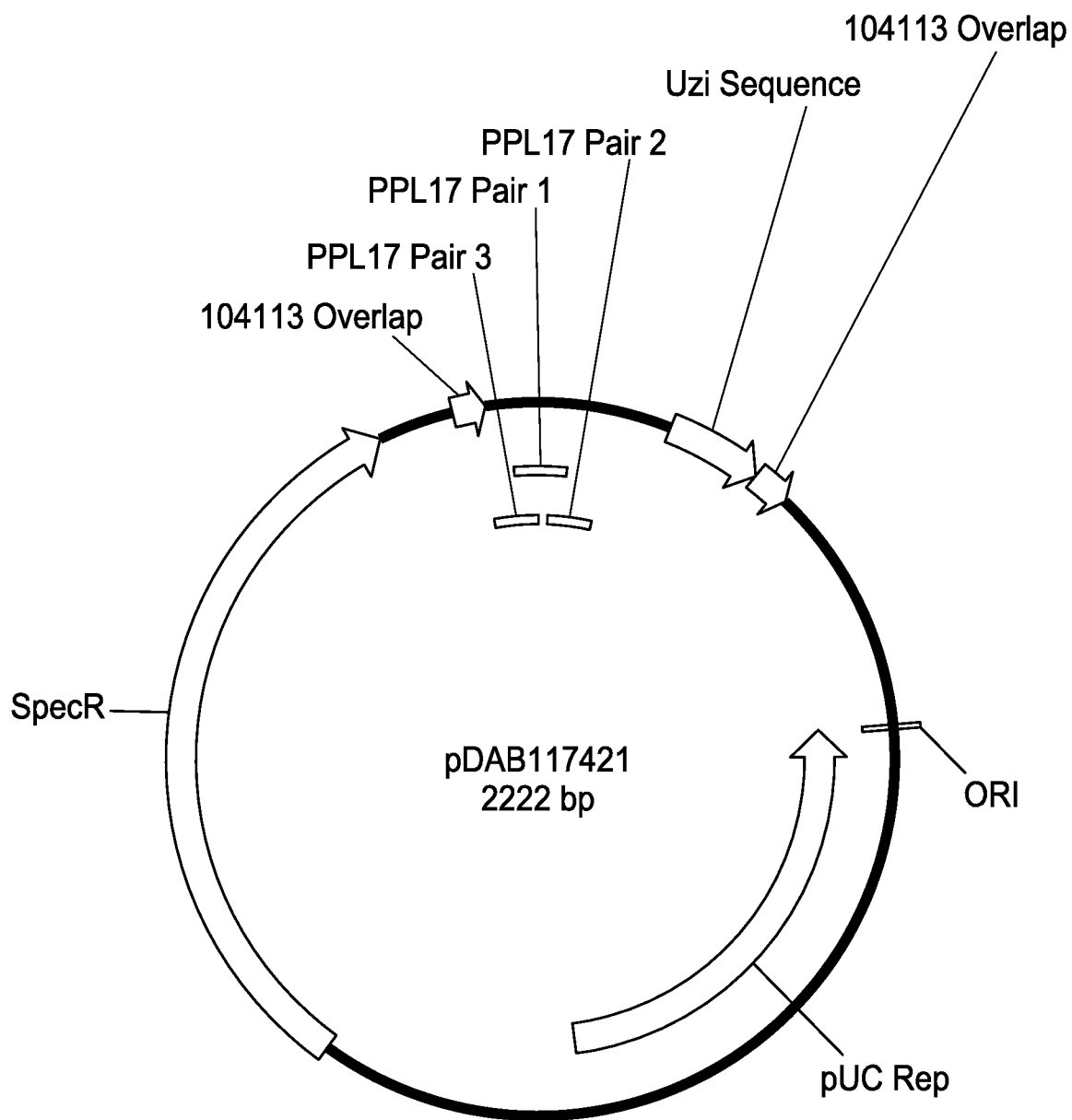


Fig. 23

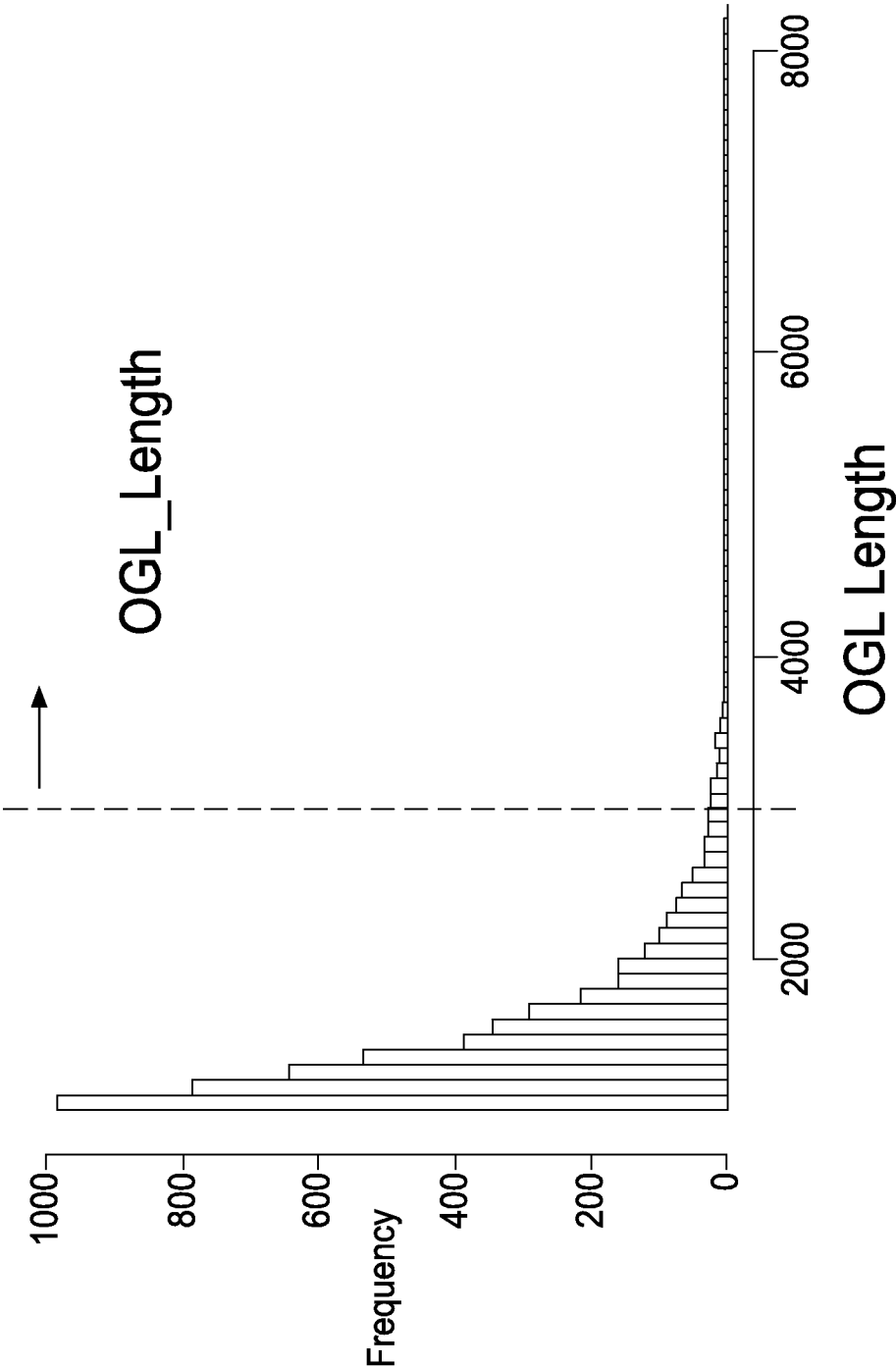


Fig. 24A

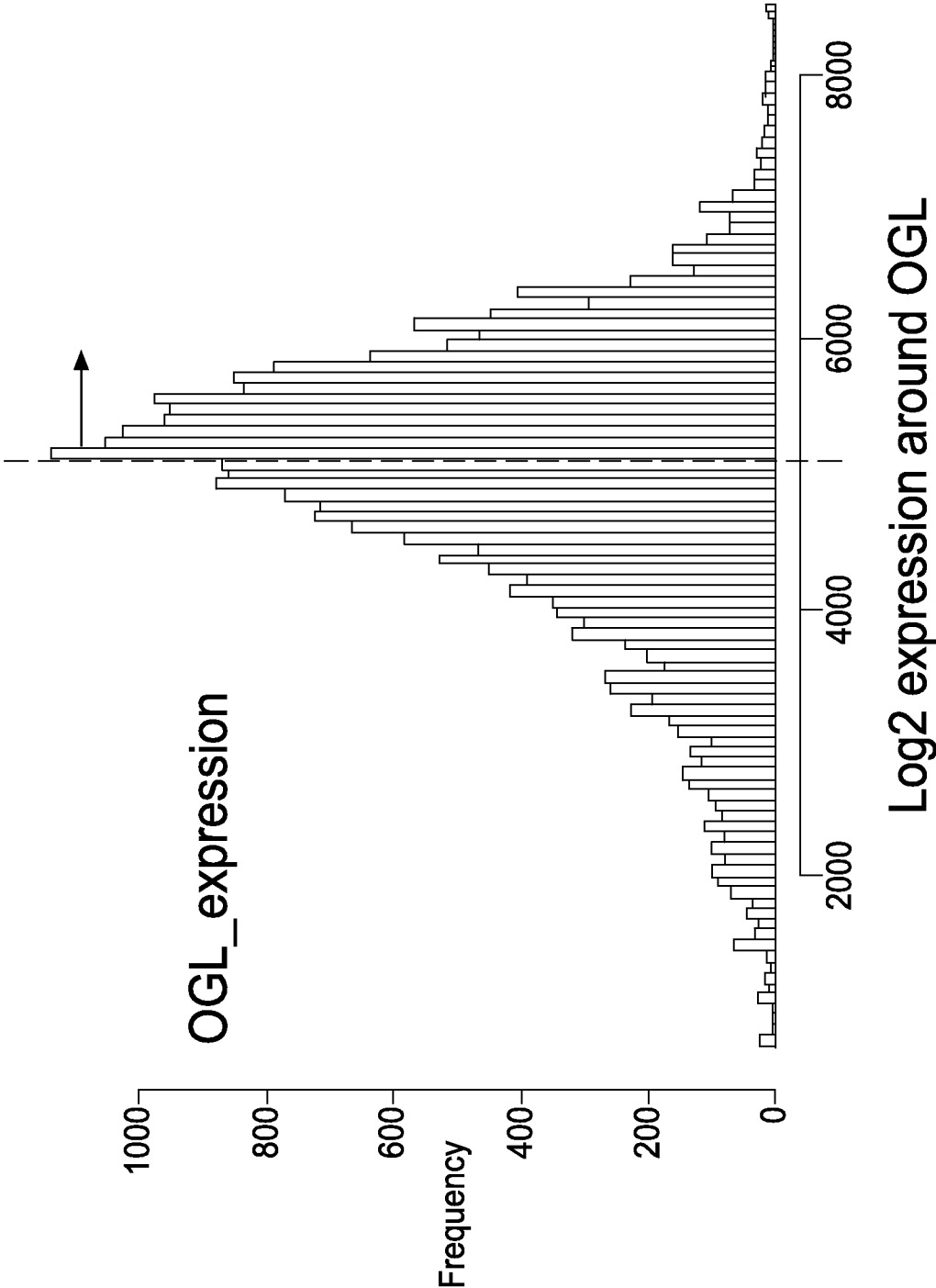


Fig. 24B

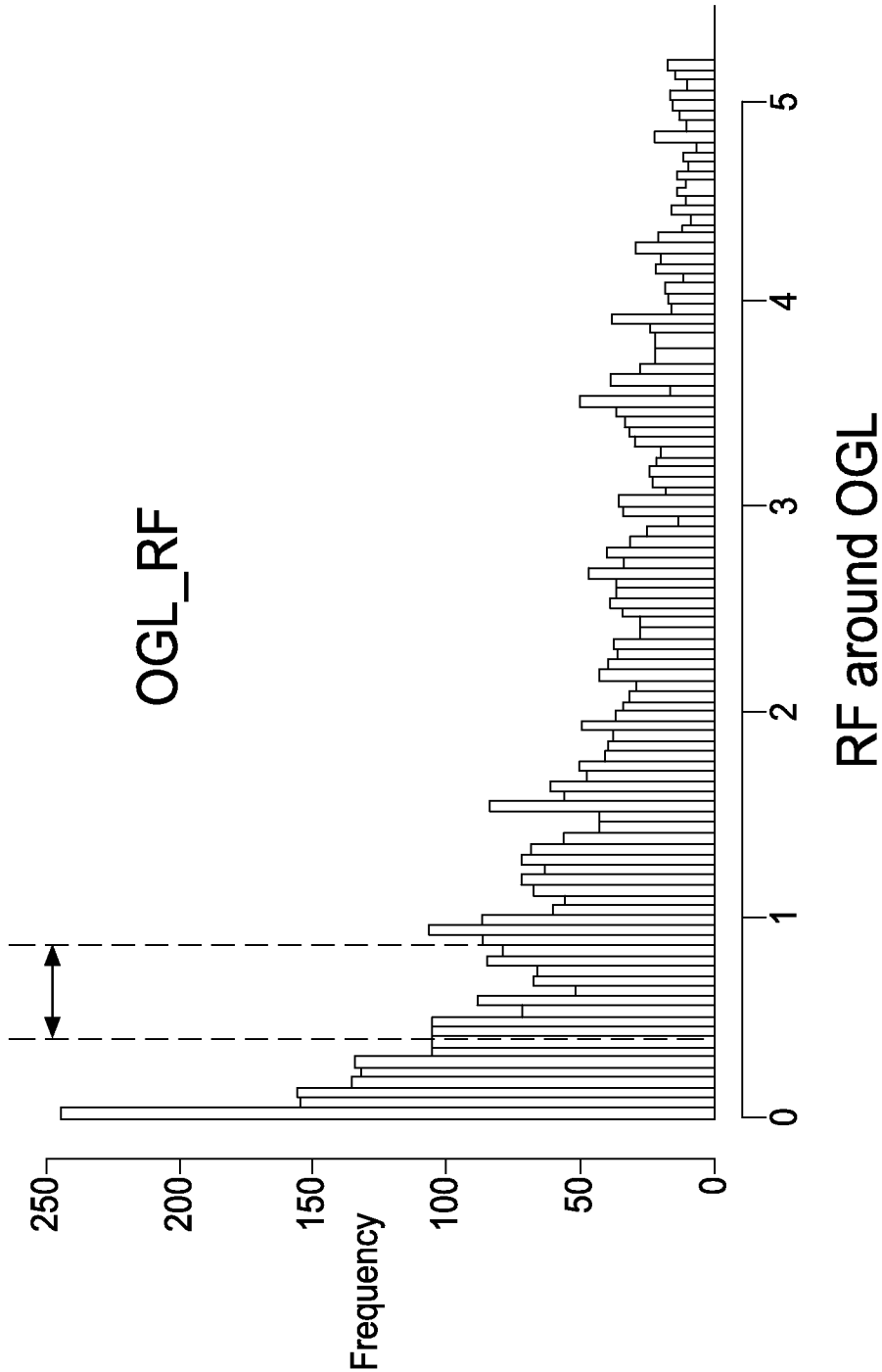
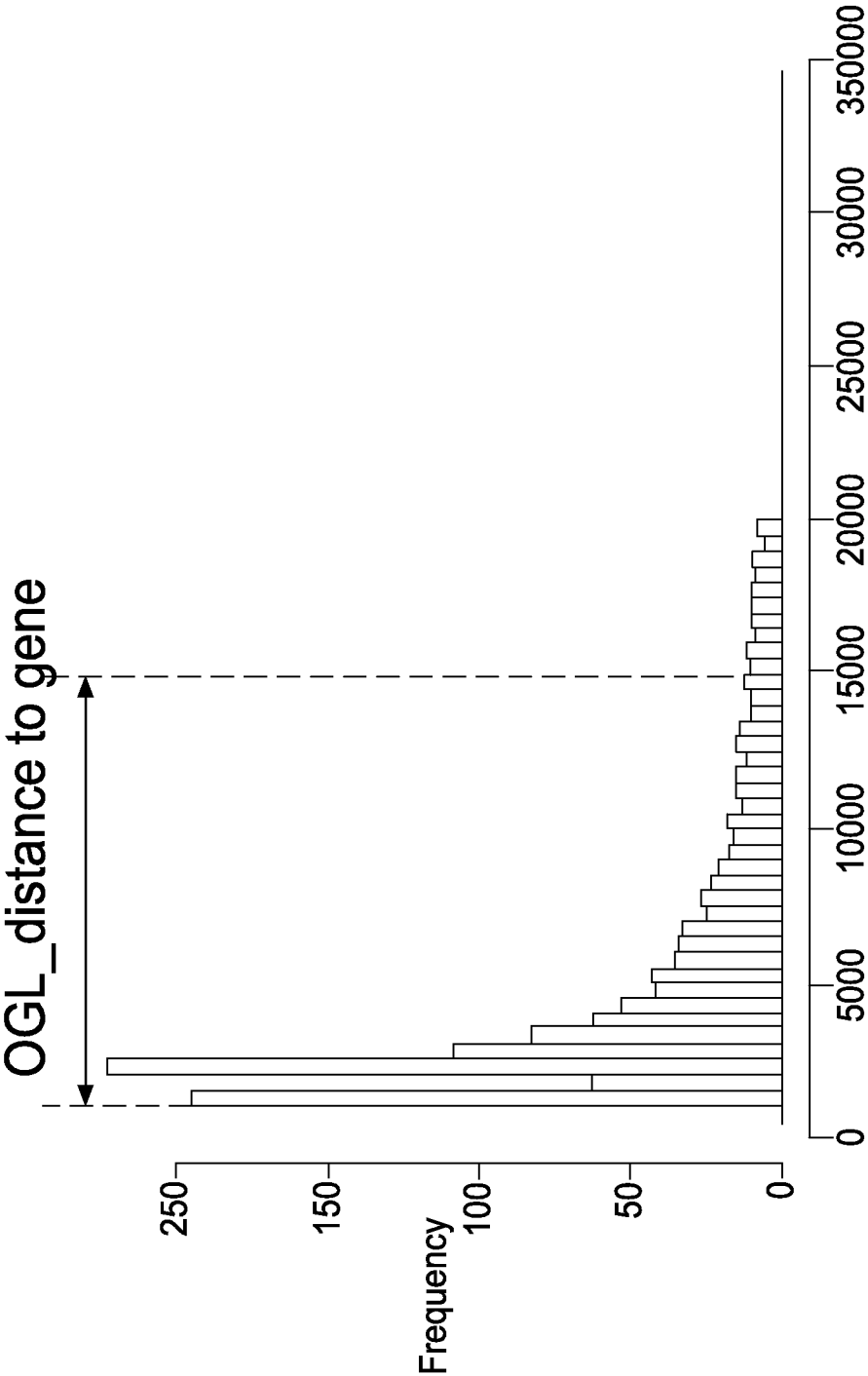


Fig. 24C



Distance to Gene

Fig. 25A

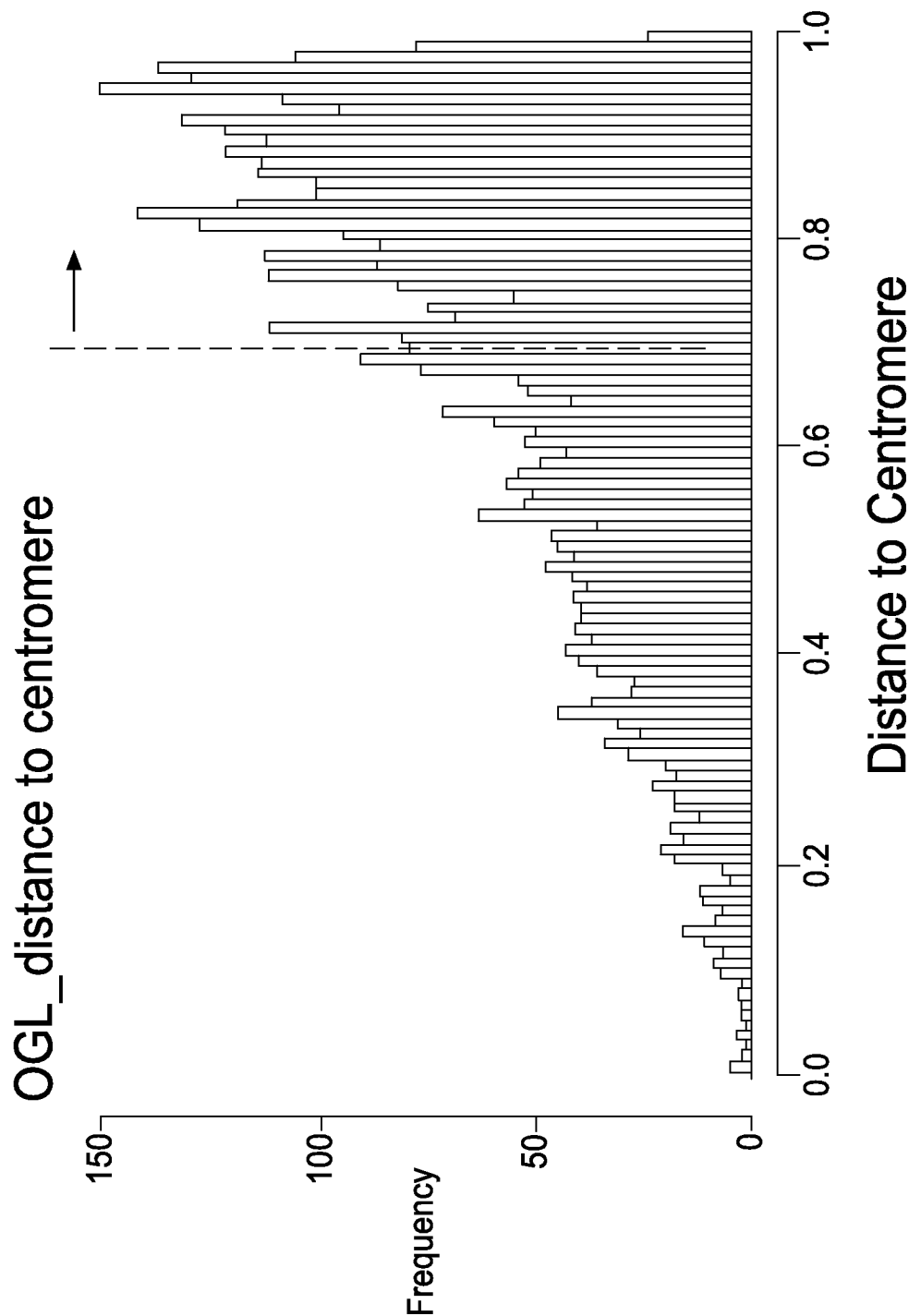


Fig. 25B