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(71) Applicant(s)
Dow AgroSciences LLC

(72) Inventor(s)
Sastry-Dent, Lakshmi;Cao, Zehui;Sriram, Shreedharan;Webb, Steven R.;Camper, Debra L.

(74) Agent / Attorney
FPA Patent Attorneys Pty Ltd, Level 43 101 Collins Street, Mebourne, VIC, 3000, AU

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(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, Indianapolis, Indiana 46240 (US). **WEBB, Steven R.**; 15416 Bloomfield Court, Westfield, Indiana 46074 (US). **CAMPER, Debra L.**; 5340 North Delaware Street, Indianapolis, Indiana 46220 (US).

(74) Agents: **ADDISON, Bradford, G.** et al.; Barnes & Thornburg LLP, 11South Meridian Street, Indianapolis, Indiana 46204 (US).

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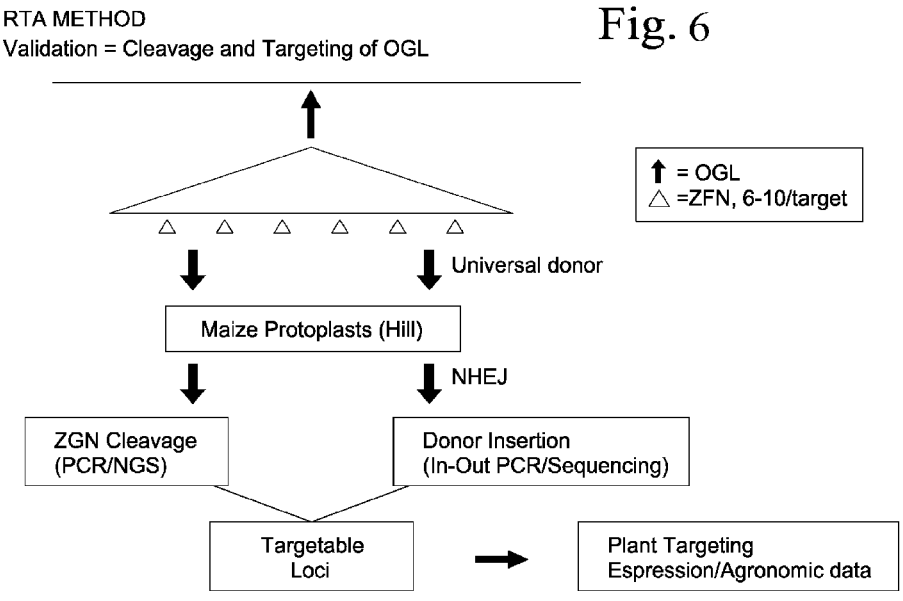


Fig. 6

(57) Abstract: As disclosed herein, optimal native genomic loci have been identified in dicot plants, such as soybean plants, that represent best sites for targeted insertion of exogenous sequences.

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CROSS-REFENCE TO RELATED APPLICATIONS

This application claims the benefit, under 35 U.S.C. §119(e), to U.S. Provisional Patent Application No. 61/899,566, filed on November 4, 2013 and U.S. Provisional Patent Application No.61/889,587, 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 "74892232308seqlist.txt", created on November 3, 2014, and having a size of 13.4 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.

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BACKGROUND

Reference to any prior art in the specification is not an acknowledgment or suggestion that this prior art forms part of the common general knowledge in any jurisdiction or that this prior art could reasonably be expected to be understood, regarded as relevant, and/or combined with other pieces of prior art by a skilled person in the art.

The genome of numerous types of dicot plants, for example soybean plants, was successfully transformed with transgenes in the early 1990's. Over the last twenty years, numerous methodologies have been developed for transforming the genome of dicot plants, like soybean, wherein a transgene is stably integrated into the genome of dicot plants. This evolution of dicot transformation methodologies has resulted in the capability to successfully

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introduce a transgene comprising an agronomic trait within the genome of dicot plants, such as soybean. The introduction of insect resistance and herbicide tolerant traits within dicot 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 dicot plants are commercially available throughout the

world, and new transgenic products such as Enlist™ Soybean offer improved solutions for ever-increasing weed challenges. The utilization of transgenic dicot plants in modern agronomic practices would not be possible, but for the development and improvement of transformation methodologies.

However, current transformation methodologies rely upon the random insertion of transgenes within the genome of dicot plants, such as soybean. 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 plant. In addition, the transgenic events may indiscriminately integrate into locations of the 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 plants. Finally, the random integration of transgenes within the plant 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 soybean transgenic event. The random nature of plant transformation methodologies results in a "position-effect" of the integrated transgene, which hinders the effectiveness and efficiency of 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 genome of diot plants, such as soybean plants, 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 trangenes 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 Nucelases (TALENS) and Clustered Regularly Interspaced Short Palindromic Repeats/CRISPR-associated nuclease (CRISPR/Cas) with an engineered crRNA/tracr RNA), 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 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 genome of dicot plants like soybean. In recent years, several technologies have been developed and applied to plant cells for the targeted delivery of a transgene within the genome of dicot plants like soybean. 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 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 genome of dicot plants, for example soybean plants, for targeted transgene integration.

SUMMARY

One embodiment of the present disclosure is directed to methods of identifying optimal sites in a dicot genome, including for example the soybean genome for the insertion of exogenous sequences. There is documentation in the literature that suggests that plant chromosomal regions are targetable and support expression. Applicants have constructed a set of criteria for identifying regions of native soybean genomic sequences that are optimal sites for site directed targeted insertion. More particularly, in accordance with one embodiment, an optimal locus should be nongenic, targetable, support gene expression, agronomically neutral, and have evidence of recombination. As disclosed herein, applicants have discovered a number of loci in the soybean genome that meet these criteria and thus represent optimal sites for the insertion of exogenous sequences.

In accordance with one embodiment a recombinant soybean sequence is disclosed herein wherein the recombinant sequence comprises a nongenic soybean genomic sequence of at least 1 Kb, and a DNA of interest inserted into the nongenic soybean genomic sequence, wherein the nongenic soybean genomic sequence has been modified by the insertion of the DNA of interest. In one embodiment the native nongenic soybean sequence is hypomethylated, expressable, exemplifies evidence of recombination and is located in proximal location to a genic region in the soybean genome. In one embodiment the nongenic sequence has a length ranging from about 1 Kb to about 5.7 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 accordance with one embodiment a recombinant sequence is provided comprising an optimal nongenic soybean genomic sequence of about 1 Kb to about 5.7 Kb and a DNA of interest wherein the nongenic soybean genomic sequence has 1, 2, 3, 4 or 5 of the following properties or characteristics:

a) has a known or predicted soybean coding sequence within 40 Kb of said soybean genomic sequence;

b) has a sequence comprising a 2 Kb upstream and/or 1 Kb downstream of a known soybean gene within 40 Kb of one end of said soybean genomic sequence;

c) does not contain greater than 1% DNA methylation within the sequence; d) does not contain a 1 Kb sequence having greater than 40% sequence identity to any other sequence within the soybean genome; and

e) exemplifies evidence of recombination at a recombination frequency of greater than 0.01574 cM/Mb.

In accordance with one embodiment a soybean plant, soybean plant part, or soybean plant cell is provided, comprising a DNA of interest inserted into an identified and targeted nongenic soybean genomic sequence of the soybean plant, soybean plant part, or soybean plant cell. In one embodiment the nongenic soybean genomic sequence of the soybean plant, soybean plant part, or soybean plant cell is hypomethylated, expressable, exemplifies evidence of recombination and is located in proximal location to an genic region in the soybean genome. In one embodiment the nongenic soybean genomic sequence of the soybean plant, soybean plant part, or soybean plant cell is about 1 Kb to about 5.7 Kb in length, is hypomethylated and has 1, 2, 3 or 4 of the following properties or characteristics:

a) has a known or predicted soybean coding sequence within 40 Kb of said soybean genomic sequence;

b) has a sequence comprising a 2 Kb upstream and/or 1 Kb downstream of a known soybean gene within 40 Kb of one end of said soybean genomic sequence;

c) does not contain greater than 1% DNA methylation within the sequence ;

d) does not comprise a 1 Kb sequence having greater than 40% sequence identity to any other sequence within the soybean genome; and

e) exemplifies evidence of recombination at a recombination frequency of greater than 0.01574 cM/Mb.

In one embodiment a method of making a transgenic plant cell comprising a DNA of interest targeted to a nongenic soybean genomic sequence is provided, the method comprising:

a) selecting an optimal nongenic soybean genomic locus;

b) introducing a site specific nuclease into a plant cell, wherein the site specific nuclease cleaves said nongenic sequence;

c) introducing the DNA of interest into the plant cell;

d) targeting the DNA of interest into said nongenic sequence, wherein the cleavage of said nongenic sequence stimulates integration of the polynucleotide sequence into said nongenic sequence; and

e) selecting transgenic plant cells comprising the DNA of interest targeted to said nongenic sequence.

In accordance with one embodiment the selected nongenic sequence comprises 2, 3, 4, 5, 6, 7 or 8 of the following characteristics:

a) the nongenic sequence does not contain a methylated polynucleotide;

b) the nongenic sequence exhibits a 0.01574 to 83.52 cM/Mb rate of recombination within the soybean genome;

c) the nongenic sequence exhibits a 0 to 0.494 level of nucleosome occupancy of the soybean genome;

d) the nongenic sequence shares less than 40% sequence identity with any other 1 Kb sequence contained in the soybean genome;

e) the nongenic sequence has a relative location value from 0 to 0.99682 ratio of genomic distance from a soybean chromosomal centromere;

f) the nongenic sequence has a guanine/cytosine percent content range of 14.36 to 45.9%;

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

h) a 1 Mb region of soybean genomic sequence comprising said nongenic sequence, comprises one or more nongenic sequences.

An embodiment of the present disclosure is directed to methods of identifying a nongenic soybean genomic sequence, comprising the steps of:

a) identifying soybean genomic sequences of at least 1 Kb in length that do not contain greater than a 1% level of methylation to generate a first pool of sequences;

b) eliminating any soybean genomic sequences that encode soybean transcripts from the first pool of sequences;

c) eliminating any soybean genomic sequences that do not provide evidence of recombination from the first pool of sequences;

d) eliminating any soybean genomic sequences that comprise a 1 Kb sequence that shares 40% or higher sequence identity with another 1 Kb sequence contained in the soybean genome from the first pool of sequences;

e) eliminating any soybean genomic sequence that do not have a known soybean gene within 40 Kb of the identified sequence from the first pool of sequences; and,

f) identifying the remaining soybean genomic sequences in the pool of sequences as nongenic soybean genomic sequence. Once the sequences have been identified they can be manipulated using recombinant techniques to target the insertion of nucleic acid sequences not found in the loci in the native genome.

In accordance with an embodiment, any soybean genomic sequences that do not have a known soybean gene, or at least a 2 Kb upstream or 1 Kb downstream sequence of a known gene located within 40 Kb of the soybean genomic sequence are eliminated from the pool of nongenic soybean genomic sequences.

In accordance with an embodiment, any soybean genomic sequences that do not have a gene expressing a soybean protein located within 40 Kb of the soybean genomic sequence are eliminated from the pool of nongenic soybean genomic sequences.

In accordance with one embodiment a purified soybean polynucleotide sequence is disclosed herein wherein the purified sequence comprises a nongenic soybean genomic sequence of at least 1 Kb. In one embodiment the nongenic soybean sequence is hypomethylated, expressable, exemplifies evidence of recombination and is located in proximal location to a genic region in the soybean genome. In one embodiment the nongenic sequence has a length ranging from about 1 Kb to about 5.7 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 accordance with one embodiment a purified soybean polynucleotide sequence is provided comprising an optimal nongenic soybean genomic sequence of about 1 Kb to about 5.7 Kb and a DNA of interest wherein the nongenic soybean genomic sequence has 1, 2, 3, 4 or 5 of the following properties or characteristics:

a) has a known or predicted soybean coding sequence within 40 Kb of said recombinant sequence;

b) has a sequence comprising a 2 Kb upstream and/or 1 Kb downstream of a known soybean gene within 40 Kb of one end of said nongenic;

c) does not contain a methylated polynucleotide;

d) does not contain a 1 Kb sequence having greater than 40% sequence identity to any other sequence within the soybean genome; and

e) exemplifies evidence of recombination at a recombination frequency of greater than 0.01574 cM/Mb.

In accordance with one embodiment, a purified soybean polynucleotide sequence is provided comprising a selected nongenic sequence. The selected nongenic sequence comprises 2, 3, 4, 5, 6, 7 or 8 of the following characteristics:

a) the nongenic sequence does not contain a methylated polynucleotide;

b) the nongenic sequence exhibits a 0.01574 to 83.52 cM/Mb rate of recombination within the soybean genome;

c) the nongenic sequence exhibits a 0 to 0.494 level of nucleosome occupancy of the soybean genome;

d) the nongenic sequence shares less than 40% sequence identity with any other 1 Kb sequence contained in the soybean genome;

e) the nongenic sequence has a relative location value from 0 to 0.99682 ratio of genomic distance from a soybean chromosomal centromere;

f) the nongenic sequence has a guanine/cytosine percent content range of 14.36 to 45.9%;

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

h) a 1 Mb region of soybean genomic sequence comprising said nongenic sequence, comprises one or more nongenic sequences.

In accordance with an embodiment, any soybean genomic sequences that do not provide evidence of recombination at a recombination frequency of greater than 0.01574 cM/Mb are eliminated from the pool of nongenic soybean genomic sequences.

In accordance with one embodiment the selected nongenic sequence comprise 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 0.211 to 0.976 ratio of genomic distance from a soybean chromosomal centromere;

c) the nongenic sequence has a guanine/cytosine percent content range of 25.62 to 43.76 %; and,

d) the nongenic sequence is from about 1 Kb to about 4.4 Kb in length.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1. Represents a three dimensional graph of the 7,018 select genomic loci clustered into 32 clusters. The clusters can be graphed three dimensionally and distinguished by color or other indicators. Each cluster was assigned a unique identifier for ease of visualization, wherein all select genomic loci with the same identifier belonging to the same cluster. After the clustering process, a representative select genomic loci was chosen from each cluster. This was performed by choosing a select genomic loci, within each cluster, that was closest to the centroid of that cluster.

Fig. 2. Provides a schematic drawing indicating the chromosomal distribution of the optimal genomic loci, selected for being closest to the centroid of each of the 32 respective clusters.

Fig. 3. Provides a schematic drawing indicating the soybean chromosomal location of the optimal genomic loci selected for targeting validation.

Fig. 4. 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 arrows represent potential PCR primer sites.

Fig. 5. 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 sites and horizontal arrows represent potential PCR primer sites.

Fig. 6. Validation of soybean selected genomic loci targets using NHEJ based Rapid Targeting Analysis (RTA) method.

Fig. 7. Plasmid map of pDAB124280 (SEQ ID NO:7561). The numbered elements (i.e., GmPPL01ZF391R and GMPPL01ZF391L) 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. 8. Plasmid map of pDAB124281 (SEQ ID NO:7562). The numbered elements (i.e., GmPPL02ZF411R and GMPPL02ZF411L) 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. 9. Plasmid map of pDAB121278 (SEQ ID NO:7563). The numbered elements (i.e., GmPPL18_4 and GMPPL18_3) 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. 10. Plasmid map of pDAB123812 (SEQ ID NO:7564). The numbered elements (i.e., ZF538R and ZF538L) 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. 11. Plasmid map of pDAB121937 (SEQ ID NO:7565). The numbered elements (i.e., GmPPL34ZF598L, GmPPL34ZF598R, GmPPL36ZF599L, GmPPL36ZF599R, GmPPL36ZF600L, and GmPPL36ZF600R) 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. 12. Plasmid map of pDAB123811 (SEQ ID NO:7566). The numbered elements (i.e., ZF 560L and ZF 560R) 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. 13. Plasmid map of pDAB124864 (SEQ ID NO:7567). The numbered elements (i.e., ZF631L and ZF631R) 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

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

Fig. 14. Plasmid map of pDAB7221 (SEQ ID NO:7569). This plasmid contains the Cassava Vein Mosaic Virus Promoter (CsVMV) driving the GFP protein and flanked by the Agrobacterium tumefaciens (AtuORF 24 3'UTR).

Figs. 15A-15C. Histrogram of characteristics (length, expression of coding region within 40 Kb of loci, and recombination frequency) for the identified optimal nongenic soybean loci. Fig. 15A illustrates a distribution of the polynucleotide sequence lengths of the optimal genomic loci (OGL). Fig. 15B illustrates the distribution of the optimal nongenic maize loci relative to their recombination frequency. Fig. 15C illustrates the distribution of expressed nucleic acid sequences relative to their proximity (log scale) to the optimal genomic loci (OGL).

DETAILED DESCRIPTION

DEFINITIONS

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

As used herein, except where the context requires otherwise, the term "comprise" and variations of the term, such as "comprising", "comprises" and "comprised", are not intended to exclude other additives, components, integers or steps.

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

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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 an "optimal dicot genomic loci", "optimal nongenic dicot loci", "optimal nongenic loci", or "optimal genomic loci (OGL)" is a native DNA sequence found in the nuclear genome of a dicot plant that has the following properties: nongenic, hypomethylated, targetable, and in proximal location to a genic region, wherein the genomic region around the optimal dicot genomic loci exemplifies evidence of recombination.

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

As used herein, the terms "nongenic dicot sequence" or "nongenic dicot genomic sequence" are used interchangably to designatea native DNA sequence found in the nuclear genome of a dicot 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 dicot 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, the terms "nongenic soybean sequence" or "nongenic soybean genomic sequence" are used interchangably to designatea native DNA sequence found in the nuclear genome of a soybean 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 soybean 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 dicot genome, like a soybean 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 dicot genome of soybean for example, the inserted sequences are referred to as the "inserted DNA of interest". Further, the nucleic acid of interest 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.

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 example, U.S. Patent Publication No 20110191899, incorporated herein by reference in its entirety.

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

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

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 genome of a dicot plant like a soybean plant.

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 1 Kb in length that shares less than 40% identity to any other sequence within the genome of a dicot plant, like soybean. Calculations of sequence identity can be determined using any standard technique known to those skilled in the art including, for example, scanning a selected genomic sequence against the dicot genome, e.g., soybean c.v. Williams82 genome, using a BLAST™ based homology search using the NCBI BLAST™+ software (version 2.2.25) 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 soybean sequences (from the *Glycine max* c.v. Williams82 genome) were analyzed, the first BLAST™ hit identified from such a search represents the dicot sequence, e.g., soybean c.v. Williams82 sequence, itself. The second BLAST™ hit for each selected soybean sequence was identified and the alignment coverage (represented as the percent of the selected soybean sequence covered by the BLAST™ hit) of the hit was used as a measure of uniqueness of the selected soybean sequence within the genome of a dicot plant, such as soybean. These alignment coverage values for the second BLAST™ hit ranged from a minimum of 0% to a maximum of 39.97% sequence identity. Any sequences that aligned at 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 soybean genomic loci sequence) is analyzed. This analysis was completed by assaying gene annotation information and the locations of known genes in the genome of a known dicot, such as soybean, that were extracted froma moncot genome database, for example

the Soybean Genome Database. For each of the optimal nongenic soybean genomic loci, e.g., 7,018 optimal nongenic soybean 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 18 genes within the 40 Kb neighborhood.

The term "known soybean coding sequence" as used herein relates to any polynucleotide sequence identified from any dicot genomic database, including the Soybean Genomic Database (www.soybase.org, Shoemaker, R.C. et al. SoyBase, the USDA-ARS soybean genetics and genomics database. *Nucleic Acids Res.* 2010 Jan;38(Database issue):D843-6.) that comprise an open 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 soybean coding sequence can be a cDNA sequence or a genomic sequence. In some instances, the known soybean coding sequence can be annotated as a functional protein. In other instances, the known soybean coding sequence may not be annotated.

The term "predicted dicot coding sequence" as used herein relates to any Expressed Sequence Tag (EST) polynucleotide sequences described in a dicot genomic database, for example the the Soybean 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 dicot genomic database, e.g., Soybean Genomic Database and can be searched via bioinformatics methods to predict corresponding 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 "predicted soybean coding sequence" as used herein relates to any Expressed Sequence Tag (EST) polynucleotide sequences described in a soybean genomic database, for example the the Soybean 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 soybean genomic database, e.g., Soybean Genomic

Database and can be searched via bioinformatics methods to predict corresponding 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 dicot genomic markers, e.g., soybean genomic markers, across a chromosome region comprising the selected soybean 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 soybean sequence to have evidence of recombination, the selected soybean sequence must contain at least one recombination event between two markers flanking the selected soybean sequence as detected using a high resolution marker dataset generated from multiple mapping populations.

As used herein the term "relative location value" is a calculated value defining the distance of a genomic locus from its corresponding chromosomal centromere. For each selected soybean sequence, the genomic distance from the native location of the selected soybean sequence to the centromere of the chromosome that it is located on, is measured (in Bp). The relative location of selected soybean 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 (measured in Bp) that it lies on. These relative location values for the optimal nongenic soybean genomic loci can be generated for different dicot plants, the relative location values for the soybean dataset ranged from a minimum of 0 to a maximum of 0.99682 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 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 (Kd). "Affinity" refers to the strength of binding: increased binding affinity being correlated with a lower binding constant (Kd).

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 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.

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 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 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 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 concer 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.

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 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 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. 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 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 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): 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.

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 polynucelotide sequences do not necessarily descend from a common ancestral DNA sequence. Those with skill in the art are aware of the interchangeably 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 7,018 optimal genomic loci.

As an embodiment, the identified optimal genomic loci comprising 7,018 individual 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 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 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 7,018 individual optimal genomic loci sequences.

Operably linked: A first nucleotide sequence is "operably linked" with a second 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, 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 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 soybean 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 genome of dicot plants, like a soybean plant, 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 trangenes 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 dicot genome, like the soybean 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 genome of a dicot plant, like a soybean plant. 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 genome of a soybean plant 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 an inserted coding sequence.

I. Identification of Nongenic Soybean Genomic Loci

In accordance with one embodiment a method is provided for identifying optimal nongenic soybean genomic sequence for insertion of exogenous sequences. The method comprises the steps of first identifying soybean 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 5.7 Kb 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 soybean 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 cytocine based followed by guanine. More particularly, in one embodiment the selected soybean sequence has less than 1, 2 or 3 methylated nucleotides per 500 nucleotides of the selected soybean sequence. In one embodiment the selected soybean sequence has less than one, two, or three 5-methylcytosines at CpG dinucleotides per 500 nucleotides of the selected soybean sequence. In one embodiment the selected soybean sequence is 1 to 4 Kb in length and comprises a 1 Kb sequence devoid of 5-methylcytosines. In one embodiment the selected soybean sequence is 1, 1.5, 2, 2.5, 3, 3.5, 4, 4.5, 5, 5.5, or 6, Kb in length and contains 1 or 0 methylated nucleotides in its entire length. In one embodiment the selected soybean sequence is 1, 1.5, 2, 2.5, 3, 3.5, 4, 4.5, 5, 5.5, or 6, Kb in length and contains no 5-methylcytosines at CpG dinucleotides within in its entire length. In accordance with one embodiment the methylation of a selected soybean 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 soybean 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 soybean genomic locus of the present disclosure.

Optimal nongenic soybean genomic loci must also be sequences that have demonstrated evidence of recombination. In one embodiment the selected soybean sequence must be one

where at least one recombination event has been detected between two markers flanking the selected soybean 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 dicot genomic sequence, such as a soybean genomic sequence, comprising the selected soybean sequence are used to calculate the recombinant frequency for the selected soybean 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 0.0157 cM/Mb. In one embodiment the recombination frequency for a 1 Mb soybean genomic sequence comprising the selected soybean sequence ranges from about 0.01574 cM/Mb to about 83.52 cM/Mb. In one embodiment an optimal genomic loci is one where recombination events have been detected within the selected soybean sequence.

An optimal nongenic soybean genomic loci will also be a targetable sequence, i.e., a sequence that is relatively unique in the soybean genome such that a gene targeted to the selected soybean sequence will only insert in one location of the soybean 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 soybean genome. Accordingly, in one embodiment the selected soybean sequence cannot comprise a 1 Kb sequence that share more than 25%, 30%, 35%, or 40% sequence identity with another 1 Kb sequence contained in the soybean genome. In a further embodiment the selected soybean sequence cannot comprise a 500 bp sequence that share more than 30%, 35%, or 40% sequence identity with another 500 bp sequence contained in the soybean genome. In one embodiment the selected soybean sequence cannot comprise a 1 Kb sequence that share more than 40% sequence identity with another 1 Kb sequence contained in the genome of a dicot plant, like a soybean plant.

An optimal nongenic soybean genomic loci will also be proximal to a genic region. More particularly, a selected soybean sequence must be located in the vicinity of a genic region (e.g., a genic region must be located within 40 Kb of genomic sequence flanking and contiguous with either end of the selected soybean 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 soybean sequence as found in the native soybean 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 soybean sequence. In one embodiment 1-18 genic regions are located within 10, 20, 30 or 40 Kb of contiguous genomic sequence flanking the two ends of the selected soybean sequence. In one embodiment

two or more genic regions are located within a 20, 30 or 40 Kb genomic sequence comprising the selected soybean sequence. In one embodiment 1-18 genic regions are located within a 40 Kb genomic sequence comprising the selected soybean sequence. In one embodiment the genic region located within a 10, 20, 30 or 40 Kb of contiguous genomic sequence flanking the selected soybean sequence comprises a known gene in the genome of a dicot plant, such as a soybean plant.

In accordance with one embodiment a modified nongenic soybean genomic loci is provided wherein the loci is at least 1 Kb in length, is nongenic, comprises no methylated cytosine residues, has a recombination frequency of greater than 0.01574 cM/Mb over a 1Mb genomic region encompassing the soybean genomic loci and a 1 Kb sequence of the soybean genomic loci shares less than 40% sequence identity with any other 1 Kb sequence contained in the dicot genome, wherein the nongenic soybean genomic loci is modified by the insertion of a DNA of interest into the nongenic soybean genomic loci.

In accordance with one embodiment a method for identifying optimal nongenic dicot genomic loci, including for example, soybean genomic loci is provided. In some embodiments, the method first comprises screening the dicot genome to create a first pool of selected soybean sequences that have a minimal length of 1 Kb and are hypomethylated, optionally wherein the genomic sequence has less than 1% methylation, optionally wherein the genomic sequence is devoid of any methylated cytosine residues. This first pool of selected soybean sequences can be further screened to eliminate loci that do not meet the requirements for optimal nongenic soybean genomic loci. Dicot genomic sequences, such as those obtained from soybean, that encode dicot 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 40 Kb of the selected soybean sequence, are eliminated from the first pool of sequences, leaving a second pool of sequences that qualify as optimal nongenic soybean loci. In one embodiment any selected soybean sequences that do not have a known dicot gene (i.e., a soybean gene), or a sequence comprising a 2 Kb upstream and/or 1 Kb downstream region of a known dicot gene, within 40 Kb of one end of said nongenic sequence are eliminated from the first pool of sequences. In one embodiment any selected soybean sequences that do not contain a known gene that expresses a protein within 40 Kb of the selected soybean sequence are eliminated. In one embodiment any selected soybean sequences that do not have a recombination frequency of greater than 0.01574 cM/Mb are eliminated.

Using these selection criteria applicants have identified select optimal genomic loci of dicot, such as soybean, that serve as optimal nongenic soybean genomic loci, the sequences of

which are disclosed as SEQ ID NO: 1-SEQ ID NO: 7,018. The present disclosure also encompasses natural variants or modified derivatives of the identified optimal nongenic soybean genomic loci wherein the variant or derivative loci comprise a sequence that differs from any sequence of SEQ ID NO: 1-SEQ ID NO: 7,018 by 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 nucleotides. In one embodiment optimal nongenic soybean genomic loci for use in accordance with the present disclosure comprise sequences selected from SEQ ID NO: 1-SEQ ID NO: 7,018 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: 7,018.

In another embodiment, dicot plants for use in accordance with the present disclosure comprise any plant selected from the group consisting of a soybean plant, a canola plant, a rape plant, a *Brassica* plant, a cotton plant, and a sunflower plant. Examples of dicot plants that can be used include, but are not limited to, canola, cotton, potato, quinoa, amaranth, buckwheat, safflower, soybean, sugarbeet, sunflower, canola, rape, tobacco, *Arabidopsis*, *Brassica*, and cotton.

In another embodiment, optimal nongenic soybean genomic loci for use in accordance with the present disclosure comprise sequences selected from soybean plants. In a further embodiment, optimal nongenic soybean genomic loci for use in accordance with the present disclosure comprise sequences selected from *Glycine max* inbreds. Accordingly, a *Glycine max* inbred includes agronomically elite varieties thereof. In a subsequent embodiment, optimal nongenic soybean genomic loci for use in accordance with the present disclosure comprise sequences selected from transformable soybean lines. In an embodiment, representative transformable soybean lines include; Maverick, Williams82, Merrill JackPeking, Suzuyutaka, Fayette, Enrei, Mikawashima, WaseMidori, Jack, Leculus, Morocco, Serena, Maple prest, Thorne, Bert, Jungery, A3237, Williams, Williams79, AC Colibri, Hefeng 25, Dongnong 42, Hienong 37, Jilin 39, Jiyu 58, A3237, Kentucky Wonder, Minidoka, and derivatives thereof. One of skill in the art will appreciate that as a result of phylogenetic divergence, various types of soybean 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 soybean genomic loci wherein the polymorphisms or allelic variation comprise a sequence that differs from any sequence with SEQ ID NO: 1-SEQ ID NO: 7,018 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 soybean genomic loci wherein the sequences comprising the polymorphisms or allelic variation share 90%, 91%,

92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity with any sequence of SEQ ID NO: 1-SEQ ID NO: 7,018.

The identified optimal genomic loci comprising 7,018 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 soybean 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 soybean 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 7,018 optimal soybean genomic loci using the following 10 features for each identified optimal soybean genomic loci:

1. Length of the hypo-methylated region around the optimal soybean genomic loci (OGL)
    a. DNA methylation profiles of root and shoot tissues isolated from a dicot plant, e.g., *Glycine Max* cultivar Williams82, were constructed using a high throughput whole genome sequencing approach. Extracted DNA was subjected to bisulphite treatment that converts unmethylated cytosines to uracils, but does not affect methylated cytosines, and then sequenced using Illumina HiSeq technology (Krueger, F. et al. DNA methylome analysis using short bisulfite sequencing data. Nature Methods 9, 145–151 (2012)). The raw sequencing reads were mapped to the dicot reference sequence, e.g., *Glycine max* reference sequence, 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 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 OGLsequence uniqueness
    a. For each OGL, the nucleotide sequence of the OGL was scanned against the genome of a dicot plant, e.g., soybean c.v. Williams82 genome, using a BLAST based homology search. As these OGL sequences are identified from the genome of a dicot plant, e.g., soybean c.v. Williams82 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 dicot genome, e.g., soybean genome.
4. Distance from the OGLto the closest gene in its neighborhood
    a. Gene annotation information and the location of known genes in the dicot genome, e.g., soybean c.v. Williams82 genome, were extracted from a known dicot genome database, e.g., Soybean Genome Database (www.soybase.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 OGL neighborhood
    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 dicot genome, e.g., soybean c.v. Williams82 genome, were extracted from a known dicot genomic database, e.g., Soybean Genome Database (www.soybase.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 dicot genes, e.g., soybean genes, was measured by analyzing transcriptome profiling data generated from dicot plant tissues, e.g., soybean c.v. Williams82 root and shoot tissues, using RNAseq technology. For each OGL, annotated genes within the dicot genome, soybean c.v. Williams82 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 dicot chromosomes, e.g., soybean chromosomes, and the lengths of the chromosome arms was extracted from a dicot genomic database, e.g., Soybean Genome Databae (www.soybase.org). For each OGL, the genomic distance from the OGL sequence 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 1 Mb region around the OGL
    a. For each OGL, a 1 Mb genomic window around the OGL location is defined and the number of OGLs, in the dicot 1 Kb 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 nongenic soybean genomic loci are further described in Table 3 of Example 2. The resulting dataset was used in the PCA statistical method to cluster the 7,018 identified optimal nongenic soybean 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 7,018 optimal soybean 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. 1). 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 soybean chromosomes as shown in Fig. 2.

In an embodiment an isolated or purified optimal nongenic soybean genomic loci sequence is provided selected from any cluster described in Table 6 of Example 2. In one embodiment the isolated or purified optimal nongenic soybean genomic loci sequence is a genomic sequence selected from cluster 1. In one embodiment the isolated or purified optimal nongenic soybean genomic loci sequence is a genomic sequence selected from cluster 2. In one embodiment the isolated or purified optimal nongenic soybean genomic loci sequence is a genomic sequence selected from cluster 3. In one embodiment the isolated or purified optimal nongenic soybean genomic loci sequence is a genomic sequence selected from cluster 4. In one embodiment the isolated or purified optimal nongenic soybean genomic loci sequence is a genomic sequence selected from cluster 5. In one embodiment the isolated or purified optimal nongenic soybean genomic loci sequence is a genomic sequence selected from cluster 6. In one embodiment the isolated or purified optimal nongenic soybean genomic loci sequence is a genomic sequence selected from cluster 7. In one embodiment the isolated or purified optimal nongenic soybean genomic loci sequence is a genomic sequence selected from cluster 8. In one embodiment the isolated or purified optimal nongenic soybean genomic loci sequence is a genomic sequence selected from cluster 9. In one embodiment the isolated or purified optimal nongenic soybean genomic loci sequence is a genomic sequence selected from cluster 10. In one embodiment the isolated or purified optimal nongenic soybean genomic loci sequence is a

genomic sequence selected from cluster 11. In one embodiment the isolated or purified optimal nongenic soybean genomic loci sequence is a genomic sequence selected from cluster 12. In one embodiment the isolated or purified optimal nongenic soybean genomic loci sequence is a genomic sequence selected from cluster 13. In one embodiment the isolated or purified optimal nongenic soybean genomic loci sequence is a genomic sequence selected from cluster 14. In one embodiment the isolated or purified optimal nongenic soybean genomic loci sequence is a genomic sequence selected from cluster 15. In one embodiment the isolated or purified optimal nongenic soybean genomic loci sequence is a genomic sequence selected from cluster 16. In one embodiment the isolated or purified optimal nongenic soybean genomic loci sequence is a genomic sequence selected from cluster 17. In one embodiment the isolated or purified optimal nongenic soybean genomic loci sequence is a genomic sequence selected from cluster 18. In one embodiment the isolated or purified optimal nongenic soybean genomic loci sequence is a genomic sequence selected from cluster 19. In one embodiment the isolated or purified optimal nongenic soybean genomic loci sequence is a genomic sequence selected from cluster 20. In one embodiment the isolated or purified optimal nongenic soybean genomic loci sequence is a genomic sequence selected from cluster 21. In one embodiment the isolated or purified optimal nongenic soybean genomic loci sequence is a genomic sequence selected from cluster 22. In one embodiment the isolated or purified optimal nongenic soybean genomic loci sequence is a genomic sequence selected from cluster 23. In one embodiment the isolated or purified optimal nongenic soybean genomic loci sequence is a genomic sequence selected from cluster 24. In one embodiment the isolated or purified optimal nongenic soybean genomic loci sequence is a genomic sequence selected from cluster 25. In one embodiment the isolated or purified optimal nongenic soybean genomic loci sequence is a genomic sequence selected from cluster 26. In one embodiment the isolated or purified optimal nongenic soybean genomic loci sequence is a genomic sequence selected from cluster 27. In one embodiment the isolated or purified optimal nongenic soybean genomic loci sequence is a genomic sequence selected from cluster 28. In one embodiment the isolated or purified optimal nongenic soybean genomic loci sequence is a genomic sequence selected from cluster 29. In one embodiment the isolated or purified optimal nongenic soybean genomic loci sequence is a genomic sequence selected from cluster 30. In one embodiment the isolated or purified optimal nongenic soybean genomic loci sequence is a genomic sequence selected from cluster 31. In one embodiment the isolated or purified optimal nongenic soybean genomic loci sequence is a genomic sequence selected from cluster 32.

In accordance with one embodiment a modified optimal nongenic soybaen genomic loci is provided wherein the optimal nongenic soybean genomic loci has been modified and

comprise one or more nucleotide substitutions, deletions or insertions. In one embodiment the optimal nongenic soybean 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 soybean genomic loci to be modified is a genomic sequence selected from any cluster described in Table 6 of Example 2. In one embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1. In one embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 2. In one embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 3. In one embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 4. In one embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 5. In one embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 6. In one embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 7. In one embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 8. In one embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 9. In one embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 10. In one embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 11. In one embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 12. In one embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 13. In one embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 14. In one embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 15. In one embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 16. In one embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 17. In one embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 18. In one embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 19. In one embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 20. In one embodiment the optimal nongenic soybean genomic loci to be

modified is a genomic sequence selected from cluster 21. In one embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 22. In one embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 23. In one embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 24. In one embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 25. In one embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 26. In one embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 27. In one embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 28. In one embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 29. In one embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 30. In one embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 31. In one embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 32.

In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or 31. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, or 29. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or 28. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, or 27. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, or 26. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence

selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, or 24. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, or 23. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, or 22. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 21. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, or 19. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or 18. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, or 14. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, or 13. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, or 9. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, or 8. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, or 7. In a further embodiment the optimal nongenic

soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, or 6. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, or 5. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, or 4. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, or 3. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1 or 2.

In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is

a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 25, 26, 27, 28, 29, 30,

31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, or 32.

In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a

genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further

embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 25, 26, 27, 28, 29, 30, 31 or 32.In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 or 32.

In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 8, 9, 10, 11,

12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1,

2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, or 32.

In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a

genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, or 27. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 9, 10, 11, 12, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 15, 16, 17, 18, 25, 26, 27, 28, 29, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 21, 22, 23, 24, 30, 31 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30 or 32. In a further embodiment the optimal nongenic soybean genomic loci to be modified is a genomic sequence selected from cluster 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29 or 31.

In one embodiment the optimal nongenic soybean genomic loci is selected from the genomic sequences of soy_ogl_2474 (SEQ ID NO: 1), soy_ogl_768 (SEQ ID NO: 506), soy_ogl_2063 (SEQ ID NO: 2063), soy_ogl_1906 (SEQ ID NO: 1029), soy_ogl_1112 (SEQ ID NO: 1112), soy_ogl_3574 (SEQ ID NO: 1452), soy_ogl_2581 (SEQ ID NO: 1662), soy_ogl_3481 (SEQ ID NO: 1869), soy_ogl_1016 (SEQ ID NO: 2071), soy_ogl_937 (SEQ ID NO: 2481), soy_ogl_6684 (SEQ ID NO: 2614), soy_ogl_6801 (SEQ ID NO: 2874), soy_ogl_6636 (SEQ ID NO: 2970), soy_ogl_4665 (SEQ ID NO: 3508), soy_ogl_3399 (SEQ ID NO: 3676), soy_ogl_4222 (SEQ ID NO: 3993), soy_ogl_2543 (SEQ ID NO: 4050), soy_ogl_275 (SEQ ID NO: 4106), soy_ogl_598 (SEQ ID NO: 4496), soy_ogl_1894 (SEQ ID NO: 4622),

soy_ogl_5454 (SEQ ID NO: 4875), soy_ogl_6838 (SEQ ID NO: 4888), soy_ogl_4779 (SEQ ID NO: 5063), soy_ogl_3333 (SEQ ID NO: 5122), soy_ogl_2546 (SEQ ID NO: 5520), soy_ogl_796 (SEQ ID NO: 5687), soy_ogl_873 (SEQ ID NO: 6087), soy_ogl_5475 (SEQ ID NO: 6321), soy_ogl_2115 (SEQ ID NO: 6520), soy_ogl_2518 (SEQ ID NO: 6574), soy_ogl_5551 (SEQ ID NO: 6775), and soy_ogl_4563 (SEQ ID NO: 6859).

In one embodiment the optimal nongenic soybean genomic loci is selected from the genomic sequences of soy_ogl_308 (SEQ ID NO: 43), soy_ogl_307 (SEQ ID NO: 566), soy_ogl_2063 (SEQ ID NO: 748), soy_ogl_1906 (SEQ ID NO: 1029), soy_ogl_262 (SEQ ID NO: 1376), soy_ogl_5227 (SEQ ID NO: 1461), soy_ogl_4074 (SEQ ID NO: 1867), soy_ogl_3481 (SEQ ID NO: 1869), soy_ogl_1016 (SEQ ID NO: 2071), soy_ogl_937 (SEQ ID NO: 2481), soy_ogl_5109 (SEQ ID NO: 2639), soy_ogl_6801 (SEQ ID NO: 2874), soy_ogl_6636 (SEQ ID NO: 2970), soy_ogl_4665 (SEQ ID NO: 3508), soy_ogl_6189 (SEQ ID NO: 3682), soy_ogl_4222 (SEQ ID NO: 3993), soy_ogl_2543 (SEQ ID NO: 4050), soy_ogl_310 (SEQ ID NO: 4326), soy_ogl_2353 (SEQ ID NO: 4593), soy_ogl_1894 (SEQ ID NO: 4622), soy_ogl_3669 (SEQ ID NO: 4879), soy_ogl_3218 (SEQ ID NO: 4932), soy_ogl_5689 (SEQ ID NO: 5102), soy_ogl_3333 (SEQ ID NO: 5122), soy_ogl_2546 (SEQ ID NO: 5520), soy_ogl_1208 (SEQ ID NO: 5698), soy_ogl_873 (SEQ ID NO: 6087), soy_ogl_5957 (SEQ ID NO: 6515), soy_ogl_4846 (SEQ ID NO: 6571), soy_ogl_3818 (SEQ ID NO: 6586), soy_ogl_5551 (SEQ ID NO: 6775), soy_ogl_7 (SEQ ID NO: 6935), soy_OGL_684 (SEQ ID NO: 47), soy_OGL_682 (SEQ ID NO: 2101), soy_OGL_685 (SEQ ID NO: 48), soy_ OGL _1423 (SEQ ID NO: 639), soy_ OGL _1434 (SEQ ID NO: 137), soy_ OGL _4625 (SEQ ID NO: 76), and soy_ OGL _6362 (SEQ ID NO: 440).

In one embodiment the optimal nongenic soybean 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: SEQ ID NO: 7363 and SEQ ID NO: 7364, SEQ ID NO: 7365 and SEQ ID NO: 7366, SEQ ID NO: 7367 and SEQ ID NO: 7368, SEQ ID NO: 7369 and SEQ ID NO: 7370, SEQ ID NO: 7371 and SEQ ID NO: 7372, SEQ ID NO: 7373 and SEQ ID NO: 7374, SEQ ID NO: 7375 and SEQ ID NO: 7376, SEQ ID NO: 7377 and SEQ ID NO: 7378, SEQ ID NO: 7379 and SEQ ID NO: 7380, SEQ ID NO: 7381 and SEQ ID NO: 7382, SEQ ID NO: 7383 and SEQ ID NO: 7384, SEQ ID NO: 7385 and SEQ ID NO: 7386, SEQ ID NO: 7387 and SEQ ID NO: 7388, SEQ ID NO: 7389 and SEQ ID NO: 7390, SEQ ID NO: 7391 and SEQ ID NO: 7392, SEQ ID NO: 7393 and SEQ ID NO: 7394, SEQ ID NO: 7395 and

SEQ ID NO: 7396, SEQ ID NO: 7397 and SEQ ID NO: 7398, SEQ ID NO: 7399 and SEQ ID NO: 7400, SEQ ID NO: 7401 and SEQ ID NO: 7402, SEQ ID NO: 7403 and SEQ ID NO: 7404, SEQ ID NO: 7405 and SEQ ID NO: 7406, SEQ ID NO: 7407 and SEQ ID NO: 7408, SEQ ID NO: 7409 and SEQ ID NO: 7410, SEQ ID NO: 7411 and SEQ ID NO: 7412, SEQ ID NO: 7413 and SEQ ID NO: 7414, SEQ ID NO: 7415 and SEQ ID NO: 7416, SEQ ID NO: 7417 and SEQ ID NO: 7418, SEQ ID NO: 7419 and SEQ ID NO: 7420, SEQ ID NO: 7421 and SEQ ID NO: 7422, SEQ ID NO: 7423 and SEQ ID NO: 7424, SEQ ID NO: 7425 and SEQ ID NO: 7426.

In accordance with an embodiment, the zinc finger nuclease binds to the zinc finger target site and cleaves the unique soybean genomic polynucleotide target sites, whereupon the DNA of interest integrates within or proximal to the soybean genomic polynucleotide target sites. In an embodiment, integration of the DNA of interest 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 2 Kb, 1.75 Kb, 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 0.211 to 0.976 ratio of genomic distance from a soybean chromosomal centromere;

c) the nongenic sequence has a guanine/cytosine percent content range of 25.62 to 43.76 %; and,

d) the nongenic sequence is from about 1 Kb to about 4.4 Kb in length.

II. Recombinant Derivatives of Identified Optimal Nongenic Soybean Genomic Loci

In accordance with one embodiment, after having identified a genomic loci of a dicot plant, such as a soybean plant, 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 a dicot plant, such as a soybean plant, as a highly desirable location for inserting polynucleotide donor sequences, one or more nucleic acids of interest of the optimal nongenic soybean 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 soybean 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 soybean genomic locus using ZFNs and a polynucleotide donor construct. The methods for inserting a nucleic acid sequence of interest into the optimal nongenic soybean 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 Soybean 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, *Sinorhizoboium 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 (Kaeppler 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 dicot genomic sequence, such as a genomic sequence from soybean, 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 Cys_2His_2 (as well as non-canonical Cys_3His) 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 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, 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 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 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 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 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. 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 ued 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 (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, 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 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 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 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 entireties 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 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 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. 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 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 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 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 the 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 dicot plant, such as a soybean plant, is provided wherein a DNA of interest has been inserted into an optimal nongenic soybean genomic locus. The method comprises the steps of :

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

b. introducing a site specific nuclease into a dicot plant cell, such as a soybean 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 nongenic sequence.

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

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

b. introducing a site specific nuclease into a dicot protoplast cell, like a soybean protoplast cell, wherein the site specific nuclease cleaves the nongenic sequence;

c. introducing the DNA of interest into the dicot protoplast cell, like a soybean protoplast cell; and

d. selecting the transgenic dicot protoplast cell, like a soybean protoplast cell, comprising the DNA of interest 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 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 soybean genomic locus for 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 0.01574 to 83.52 cM/Mb rate of recombination within the dicot genome, like a soybean genome;

c. the nongenic sequence exhibits a 0 to 0.494 level of nucleosome occupancy of the dicot genome, like a soybean genome;

d. the nongenic sequence shares less than 40% sequence identity with any other sequence contained in the dicot genome, like a soybean genome;

e. the nongenic sequence has a relative location value from 0 to 0.99682 ratio of genomic distance from a dicot chromosomal centromere, like soybean;

f. the nongenic sequence has a guanine/cytosine percent content range of 14.4 to 45.9%;

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

h. a 1 Mb region of dicot genomic sequence, like a soybean genomic sequence, comprising said nongenic sequence comprises one or more additional nongenic sequences. In one embodiment the optimal nongenic soybean 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, 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 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; 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 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 genomic locus of a dicot plant, like a soybean plant, 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.

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.

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 genome of a dicot plant, like a soybean plant, 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 induce the insertion of a DNA of interest into an optimal nongenic genomic locus of a dicot plant, like a soybean plant. Either the first nucleic acid sequence comprises a ZFN specific to the optimal nongenic soybean 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 soybean genomic locus and the nucleic acid of interest. The resulting double stranded break in the 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 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 soybean 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 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 genomic locus of a dicot plant, like a soybean plant.

Exemplary exogenous sequences that can be inserted into an optimal nongenic soybean 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; 3.sup.rd 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 soybean genomic loci. This is useful inasmuch as expression of an introduced transgene into the soybean 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 soybean 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 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 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 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 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 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 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. US Patent 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 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 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 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 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 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 soybean, diketonitriles (EP496630, EP496631), in particular 2-cyano-3-cyclopropyl-1-(2-SO2CH3-4-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 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. 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 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 soybean 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 dicots, this, for example, could be accomplished by cloning and then reintroducing DNA associated with the single allele which is responsible for soybean 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 soybean 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 soybean 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 soybean 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 5.7 Kb in length and does not contain a methylated polynucleotide;

b. the nongenic sequence exhibits a 0.01574 to 83.52 cM/Mb rate of recombination within the genome of a dicot plant, like a soybean plant;

c. the nongenic sequence exhibits a 0 to 0.494 level of nucleosome occupancy of the dicot genome, like a soybean genome;

d. the nongenic sequence shares less than 40% sequence identity with any other sequence contained in the dicot genome, like a soybean genome;

e. the nongenic sequence has a relative location value from 0 to 0.99682 ratio of genomic distance from a dicot chromosomal centromere, like a soybean chromosomal center;

f. the nongenic sequence has a guanine/cytosine percent content range of 14.4 to 45.9%;

g. the nongenic sequence is located proximally to an genic sequence, comprising a known or predicted dicot coding sequence, such as a soybean 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 dicot genomic sequence, such as a genomic sequence, that comprises at least a second nongenic sequence.

In one embodiment the optimal nongenic soybean genomic sequence is further characterized as having a genic region comprisings 1 to 18 known or predicted soybean coding sequence within 40 Kb of contiguous genomic DNA comprising the native nongenic sequence. In one embodiment the optimal nongenic soybean 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.

IV. Transgenic Plants

Transgenic plants comprising the recombinant optimal nongenic soybean 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.

A transformed dicot cell, callus, tissue or plant (i.e., a soybean 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 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.

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-12 (aryloxyalkanoate dioxygenase; see WO 2011/066360) and PAT (phosphinothricin-N-acetyl-transferase (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 dicot protoplast (i.e., a soybean protoplast) is provided comprising a recombinant optimal nongenic soybean locus. More particularly, a dicot protoplast, such as a soybean protoplast, is provided comprising a DNA of interest inserted into an optimal nongenic soybean genomic loci of the dicot protoplast (i.e, a soybean protoplast), wherein said nongenic soybean genomic loci is about 1 Kb to about 5.7 Kb in length and lacks any methylated nucleotides. In one embodiment the transgenic dicot protoplast (i.e., a transgenic soybean protoplat), comprises a DNA of interest inserted into the optimal nongenic soybean 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 dicot plant, dicot plant part, or dicot plant cell (i.e., a transgenic soybean plant, soybean plant part, or soybean plant cell) is provided comprising a recombinant optimal nongenic soybean locus. More particularly, a dicot plant, dicot plant part, or dicot plant cell (i.e., a soybean plant, soybean plant part, or soybean plant cell) is provided comprising a DNA of interest inserted into an optimal nongenic soybean genomic loci of the dicot plant, dicot plant part, or dicot plant cell (i.e., a soybean plant, soybean plant part, or soybean plant cell), wherein said nongenic soybean genomic loci is about 1 Kb to about 5.7 Kb in length and lacks any methylated nucleotides. In one embodiment the transgenic dicot plant, dicot plant part, or dicot plant cell (i.e., a transgenic soybean plant, soybean plant part, or soybean plant cell) comprises a DNA of interest inserted into the optimal nongenic soybean 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 a nongenic soybean genomic sequence of at least 1 Kb, said nongenic sequence being hypomethylated, targetable, located proximal to a genic region within a soybean genome, and exemplifying evidence of recombination further comprises a DNA of interest inserted into said

nongenic sequence. In accordance with embodiment 2, the recombinant sequence of embodiment 1 has the following characterstics:

a. the level of methylation of said nongenic sequence is 1% or less

b. said nongenic sequence shares less than 40% sequence identity with any other sequence contained in the soybean genome;

c. said nongenic sequence is located within a 40 Kb region of a known or predicted expressive soybean coding sequence; and

d. said nongenic sequence exhibits a recombination frequency within the soybean genome of greater than 0.01574 cM/Mb. In accordance with embodiment 3 the recombinant sequence of embodiment 1 or 2 is provided wherein said nongenic sequence comprises a maximum length of 5.73 Kb. In accordance with embodiment 4 the recombinant sequence of any of embodiments 1-3 is provided, wherein said nongenic sequence comprises 1% or less nucleotide methylation. In accordance with embodiment 5 the recombinant sequence of any of embodiments 1-4 is provided, wherein said nongenic sequence is 1 Kb to 5.73 Kb in length and contains no methylated cytosine residues. In accordance with embodiment 6 the recombinant sequence of any of embodiments 1-5 is provided, wherein said nongenic sequence does not align with greater than 40% sequence identity to any other sequence within the soybean genome.

In accordance with embodiment 7 the recombinant sequence of any of claims 1-6 is provided, wherein said nongenic sequence exemplifies evidence of recombination at a recombination frequency of greater than 0.01574 cM/Mb. In accordance with embodiment 8 the recombinant sequence of any of claims 1-7 is provided, wherein a 40 Kb region of native soybean genome comprising said nongenic sequence also comprises at least one known or predicted soybean coding sequence, or a sequence comprising a 2 Kb upstream and/or 1 Kb downstream sequence of a known soybean gene. In accordance with embodiment 9 the recombinant sequence of any of claims 1-8 is provided, wherein said known or predicted soybean coding sequence expresses a soybean protein. In accordance with embodiment 10 the recombinant sequence of any of claims 1-9 is provided, wherein said nongenic sequence does not contain a methylated polynucleotide. In accordance with embodiment 11 the recombinant sequence of any of claims 1-10 is provided, wherein one end of said nongenic sequence is within 40 Kb of an expressed endogenous gene. In accordance with embodiment 12 the recombinant sequence of any of claims 1-11 is provided, wherein said DNA of interest comprises an analytical domain. In accordance with embodiment 13 the recombinant sequence of any of claims 1-12 is provided, wherein said DNA of interest does not encode a peptide. In accordance with embodiment 14

the recombinant sequence of any of claims 1-12 is provided, wherein said DNA of interest encodes a peptide, optionally encoding an insecticidal resistance gene, herbicide tolerance gene, nitrogen use efficiency gene, water use efficiency gene, nutritional quality gene, DNA binding gene, or selectable marker gene. In accordance with embodiment 16 the recombinant sequence of any of claims 1-14 is provided, wherein said recombinant sequence comprises the following characteristics:

a. said nongenic sequence contains less than 1% DNA methylation

b. said nongenic sequence exhibits a 0.01574 to 83.52 cM/Mb recombination frequency within the soybean genome;

c. said nongenic sequence exhibits a 0 to 0.494 level of nucleosome occupancy of the soybean genome;

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

e. said nongenic sequence has a relative location value from 0 to 0.99682 ratio of genomic distance from a soybean chromosomal centromere;

f. said nongenic sequence has a guanine/cytosine percent content range of 14.36 to 45.9%;

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

h. said nongenic sequence is located in a 1 Mb region of soybean genomic sequence that comprises one or more additional nongenic sequences.

In accordance with embodiment 17 a soybean plant, soybean plant part, or soybean plant cell comprising a recombinant sequence of any one of embodiments 1-14 and 16. In accordance with embodiment 18 the soybean plant, soybean plant part, or soybean plant cell of embodiment 17 is provided, wherein said known or predicted soybean coding sequence expresses at a level ranging from 0.000415 to 872.7198. In accordance with embodiment 19 the recombinant sequence of any of claims 1-14, 16 or 17 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 20 a method of making a transgenic plant cell comprising a DNA of interest targeted to one nongenic soybean genomic sequenceis provided wherein the method comprises:

a. selecting an optimal nongenic soybean genomic locus;

b. introducing a site specific nuclease into a plant cell, wherein the site specific nuclease cleaves said nongenic soybean genomic sequence;

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

d. targeting the DNA of interest into said nongenic locus, wherein the cleavage of said nongenic sequence facilitates integration of the polynucleotide sequence into said nongenic locus; and

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

EXAMPLES

Example 1: Identification of Targetable Genomic Loci in Soybean

The soybean 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 soybean 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 7,018 genomic loci (SEQ ID NO:1 – SEQ ID NO:7,018) were identified using these specific criteria. The specific criteria are further described in detail below.

Hypomethylation

The soybean genome was scanned to select optimal genomic loci larger than 1 Kb that were DNA hypomethylated. DNA methylation profiles of root and shoot tissues isolated from Glycine Max cultivar Williams82 were constructed using a high throughput whole genome sequencing approach. Extracted DNA was subjected to bisulphite treatment that converts unmethylated cytosines to uracils, but does not affect methylated cytosines, and then sequenced using Illumina HiSeq technology (Krueger, F. et al. DNA methylome analysis using short bisulfite sequencing data. Nature Methods 9, 145–151 (2012)). The raw sequencing reads were collected and mapped to the soybean c.v. Williams82 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).

Since, during the bisulphite conversion process, cytosines in the DNA sequence that are methylated do not get converted to uracils, occurence of cytosine bases in the sequencing data indicate the presence of DNA methylation. The reads that are mapped to the reference sequence were analyzed to identify genomic positions of cytosine residues with support for DNA methylation. 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 soybean genome. For example, consider that there is a cytosine base at position 100 in chromosome 1 of the soybean c.v. Williams82 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 soybean was calculated. The reads that could not be correctly mapped to unique locations in the soybean genome matched repetitive sequences that are widespread in the soybean genome, and are known in the art to be predominantly methylated.

Using the above described protocol, the methylation levels for the soybean c.v. Williams82 genome were measured. As such, regions of the soybean genome containing methylated reads indicated that these regions of the soybean genome were methylated. Conversely, the regions of the soybean genome that were absent of methylated reads indicated these regions of the soybean genome were non-methylated. The regions of the soybean 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 soybean c.v. Williams82 chromosomes.

After obtaining the DNA methylation level at the resolution of a single base pair in root and shoot tissues, as described above, the soybean genome was screened using 100 bp windows to identify genomic regions that are methylated. For each window screened in the genome, a DNA methylation level was obtained by calculating the average level of methylation at every cytosine base in that window. Genomic windows with a DNA methylation level greater than 1% were termed as genomic regions that were methylated. The methylated windows identified

in root and shoot profiles were combined to create a consensus methylation profile. Conversely, regions in the genome that did not meet these criteria and were not identified as methylated regions in the consensus profile were termed as hypo-methylated regions. Table 1 summarizes the identified hypo-methylated regions.

Table 1. Hypomethylation profile of soybean c.v. Williams82 genome.

Total soybean c.v. Williams82 genome size	~970 Mb
Total combined length of hypomethylated region	~354 Mb (36.5% of the soybean c.v. Williams82 genome)
Number of hypomethylated regions above 100 Bp	763,709
Number of hypomethylated regions above 1 Kb	94,745
Number of hypomethylated regions above 2 Kb	19,369
Number of hypomethylated regions above 10 Kb	354
Minimum length of hypomethylated region	100 Bp
Maximum length of hypomethylated region	84,100 Bp

These hypomethylated regions of the soybean c.v. WILLIAMS82 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 conducted on the identified hypomethylated regions.

Targetability

The hypomethylated sites identified in the soybean c.v. WILLIAMS82 were further analyzed to determine which sites were targetable *via* site specific nuclease-mediated integration of a polynucleotide donor. *Glycine max* is known to be a paleopolyploid crop which has undergone genome duplications in its genomic history (Jackson et al Genome sequence of the palaeopolyploid soybean, *Nature* 463, 178-183 (2010)). The soybean 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 soybean genome was collected from the Soybean Genome Database (www.soybase.org, Shoemaker, R.C. et al. SoyBase, the USDA-ARS soybean genetics and genomics database. Nucleic Acids Res. 2010 Jan;38(Database issue):D843-6.).

Accordingly, the hypomethylated sites identified above were screened to remove any sites that aligned with known repetitive regions annotated on the soybean genome. The remaining hypomethylated sites that passed this first screen were subsequently scanned using a BLAST™ based homology search of a soybean genomic database *via* the NCBI BLAST™+ software (version 2.2.25) 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%, were removed from further analyses.

Agronomically Neutral or Nongenic

The hypomethylated sites identified in the soybean c.v. William82 were further analyzed to determine which sites were agronomically neutral or nongenic. As such, the hypomethylated sites described above were screened to remove any sites that overlapped or contained any known or predicted endogenous soybean c.v. William82 coding sequences. For this purpose, annotation data of known genes and mapping information of expressed sequence tag (EST) data were collected from Soybean Genomic Database (www.soybase.org - version 1.1 gene models were used, Jackson et al Genome sequence of the palaeopolyploid soybean Nature 463, 178-183 (2010)). Any genomic region 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 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 soybean c.v. Williams82 were further analyzed to determine which sites were within proximity to an expressed soybean gene. The transcript level expression of soybean genes was measured by analyzing transcriptome profiling data generated from soybean c.v. Williams82 root and shoot tissues using RNAseq™ technology as described in Mortazavi *et al.,* Mapping and quantifying mammalian transcriptomes by RNA-Seq. *Nat Methods.* 2008;5(7):621-628, and Shoemaker RC *et al.,* RNA-Seq Atlas of

Glycine max: a guide to the soybean Transcriptome. *BMC Plant Biol.* 2010 Aug 5;10:160. 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 soybean gene and were removed from further analyses.

Recombination

The hypomethylated sites identified in the soybean c.v. Williams82 were further analyzed to determine which sites had evidence of recombination and could facilitate introgression of the optimal genomic loci into other lines of soybean via conventional breeding. Diverse soybean genotypes are routinely crossed during conventional breeding to develop new and improved soybean lines containing traits of agronomic interest. As such, agronomic traits that are introgressed into optimal genomic loci within a soybean line via plant-mediated transformation of a transgene should be capable of further being introgressed into other soybean 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 soybean, these cold spots were defined using a marker dataset generated from recombinant inbred mapping population (Williams 82 x PI479752). This dataset consisted of ~16,600 SNP markers that could be physically mapped to the Glycine max reference genome sequence.

The meiotic recombination frequencies between any pair of soybean 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 cM/Mb were identified and removed from further analysis. The remaining hypomethylated regions comprising a recombination frequency greater than 0 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 90,325 optimal genomic loci from the soybean 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 1 Kb 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 optiml genomic loci are disclosed as SEQ ID NO:1 – SEQ ID NO:7,018. Collectively, these optimal genomic loci are locations within the soybean 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 soybean 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	90,325
Number of optimal genomic loci larger than 1 Kb	7,018
Number of optimal genomic loci larger than 2 Kb	604
Number of optimal genomic loci larger than 4 Kb	9

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

The 7,018 identified optimal genomic loci (SEQ ID NO: 1- SEQ ID NO: 7,018) 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 7,018 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. 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 7,018 optimal genomic loci, and that the number of optimal genomic loci sampled is 10% or less of the total population of 7,018 optimal genomic loci.

The F-distribution analysis indicated that 32 of the 7,018 optimal genomic loci provided a representative number of the 7,018 optimal genomic loci, at a 95% confidence level. Accordingly, the F-distribution analysis showed that if 32 optimal genomic loci were tested and all were targetable with a donor polynucleotide sequence, then these results would indicate that 91 or more of the 7,018 optimal genomic loci are positive at the 95% confidence level. The best estimate of validating the total percentage of the 7,018 optimal genomic loci would be if 100% of the 32 tested optimal genomic loci were targetable. Accordingly, 91% 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, 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 assess and visualize similarities and differences of the data set comprising the 7,018 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 7,018 identified optimal genomic loci by generating a set of calculable features or attributes that could be used to describe the 7,018 identified optimal genomic loci. Each feature is numerically calculable and is defined specifically to capture the

genomic and epigenomic context of the 7,018 identified optimal genomic loci. A set of 10 features for each soybean 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 5,713 Bp.
2. Recombination frequency in a 1 MB region around the optimal genomic loci
    a. In soybean, recombination frequency for a chromosomal location was defined using an internal high resolution marker dataset generated from multiple mapping populations .
    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 0.01574 cM/Mb to a maximum of 83.52 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 soybean c.v. Williams82 genome using a BLAST™ based homology search using the NCBI BLAST™+ software (version 2.2.25) 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 soybean c.v. Williams82 genome, the first BLAST™ hit identified through this search represents the soybean c.v. Williams82 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 soybean genome. These alignment coverage values for the second BLAST™ hit ranged from a minimum of 0% to a maximum of 39.97% 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 *Soybean* genome were extracted from Soybean Genome Database (available at, www.soybase.org - version 1.1 gene models were used, Jackson et al Genome sequence of the palaeopolyploid soybean, *Nature* 463, 178-183 (2010)). 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 Gm01 from position 2,500 to position 3,500, and the closest gene to this optimal genomic locus is located in chromosome Gm01 from position 5,000 to position 6,000, the distance from the optimal genomic loci to this closest gene is calculated to be 1500 Bp. These values for all 7,018 of the optimal genomic loci dataset ranged from a minimum of 1,001 Bp to a maximum of 39,482 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 soybean optimal genomic loci dataset range from 14.4% to 45.9%.
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 soybean c.v. Williams82 genome were extracted from Soybean Genome Database. For each of the 7,018 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 18 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 soybean genes was measured by analyzing available transcriptome profiling data generated from soybean c.v. Williams82 root and shoot tissues using RNAseq™ technology. Gene annotation information and the location of known genes in the soybean c.v. Williams82 genome were

extracted from Soybean Genome Database For each optimal genomic locus, annotated genes within the soybean c.v. Williams82 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 soybean vary greatly. The average expression values for all of the 7,018 optimal genomic loci dataset ranged from a minimum of 0.000415 to a maximum of 872.7198.

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-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 of the 7,018 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 soybean optimal genomic loci dataset ranged from a minimum of 0 to a maximum of 0.494.
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 20 Soybean chromosomes were identified in the published soybean c.v. Williams82 reference sequence (Jackson et al Genome sequence of the palaeopolyploid soybean *Nature* 463, 178-183 (2010)). Information on the position of the centromere in each of the *Soybean* chromosomes and the lengths of the chromosome arms was extracted from Soybean 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 soybean optimal genomic loci dataset ranged from a minimum of 0 to a maximum of 0.99682 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 49.

All of the 7,018 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 7,018 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 7,018 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 (Fig. 1). 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 20 soybean chromosomes and are not biased toward any particular genomic location, as shown in Fig. 2.

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

Optimal Genomic Loci Name	Genomic Location	Length (Bp)	Cluster Number	SEQ ID NO:
soy_ogl_2474	Gm08:2764201..2766752	2552	1	1
soy_ogl_768	Gm03:339101..341100	2000	2	506
soy_ogl_2063	Gm06:43091928..43094600	2673	3	748
soy_ogl_1906	Gm06:11576991..11578665	1675	4	1029
soy_ogl_1112	Gm03:46211408..46213400	1993	5	1166
soy_ogl_3574	Gm10:46279901..46281026	1126	6	1452
soy_ogl_2581	Gm08:9631801..9632800	1000	7	1662
soy_ogl_3481	Gm10:40763663..40764800	1138	8	1869
soy_ogl_1016	Gm03:41506001..41507735	1735	9	2071
soy_ogl_937	Gm03:37707001..37708600	1600	10	2481
soy_ogl_6684	Gm20:1754801..1755800	1000	11	2614
soy_ogl_6801	Gm20:36923690..36924900	1211	12	2874
soy_ogl_6636	Gm19:49977101..49978357	1257	13	2970
soy_ogl_4665	Gm14:5050547..5051556	1010	14	3508
soy_ogl_3399	Gm10:6612501..6613500	1000	15	3676
soy_ogl_4222	Gm13:23474923..23476100	1178	16	3993
soy_ogl_2543	Gm08:7532001..7534800	2800	17	4050
soy_ogl_275	Gm01:51869201..51870400	1200	18	4106
soy_ogl_598	Gm02:41665601..41667900	2300	19	4496
soy_ogl_1894	Gm06:10540801..10542300	1500	20	4622
soy_ogl_5454	Gm17:1944101..1945800	1700	21	4875
soy_ogl_6838	Gm20:38263922..38265300	1379	22	4888
soy_ogl_4779	Gm14:45446301..45447700	1400	23	5063
soy_ogl_3333	Gm10:2950701..2951800	1100	24	5122
soy_ogl_2546	Gm08:7765875..7767500	1626	25	5520
soy_ogl_796	Gm03:1725501..1726600	1100	26	5687
soy_ogl_873	Gm03:33650665..33653000	2336	27	6087
soy_ogl_5475	Gm17:3403108..3404200	1093	28	6321
soy_ogl_2115	Gm07:1389701..1390900	1200	29	6520
soy_ogl_2518	Gm08:5229501..5230667	1167	30	6574
soy_ogl_5551	Gm17:6541901..6543200	1300	31	6775
soy_ogl_4563	Gm13:38977701..38978772	1072	32	6859

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

A total of 32 genomic loci were identified and selected for targeting with a donor polynucleotide sequence from the 7,018 genomic loci that were clustered within 32 distinct clusters. For each of the 32 clusters, a representative genomic locus (closest to the centroid of the cluster as described above in Table 4) or an additional locus with homology to targeting line were chosen. The additional optimal genomic loci were selected by first screening all of the

7,018 selected optimal genomic sequences against a whole genome database consisting of genomic DNA sequence data for both *Glycine max* c.v. Maverick (transformation and targeting screening line) and *Glycine max* c.v. Williams82 (reference 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 optimal genomic loci with 100% coverage (the entire sequence length of the optimal loci aligned between both genomes) and 100% identity in the Williams82 genomic databases were selected for targeting validation. 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 32 selected optimal genomic loci and the specific genomic configuration of each soybean optimal genomic loci are shown in Fig. 3 and Table 5, respectively.

Table 5. Table 5. Description of the 32 soybean selected optimal genomic loci chosen for targeting validation. From these optimal genomic loci listed in this table, exemplification of cleavage and targeting of 32 soybean optimal genomic loci are representative of the identified total of 7,018 soybean selected optimal genomic loci.

Optimal Genomic Loci Name	Genomic Location	Length (Bp)	Cluster Number	SEQ ID NO:
soy_ogl_308	Gm02:1204801..1209237	4437	1	43
soy_ogl_307	Gm02:1164701..1168400	3700	2	566
soy_ogl_2063	Gm06:43091928..43094600	2673	3	748
soy_ogl_1906	Gm06:11576991..11578665	1675	4	1029
soy_ogl_262	Gm01:51061272..51062909	1638	5	1376
soy_ogl_5227	Gm16:1298889..1300700	1812	6	1461
soy_ogl_4074	Gm12:33610401..33611483	1083	7	1867
soy_ogl_3481	Gm10:40763663..40764800	1138	8	1869
soy_ogl_1016	Gm03:41506001..41507735	1735	9	2071
soy_ogl_937	Gm03:37707001..37708600	1600	10	2481
soy_ogl_5109	Gm15:42391349..42393400	2052	11	2639
soy_ogl_6801	Gm20:36923690..36924900	1211	12	2874
soy_ogl_6636	Gm19:49977101..49978357	1257	13	2970
soy_ogl_4665	Gm14:5050547..5051556	1010	14	3508
soy_ogl_6189	Gm18:55694401..55695900	1500	15	3682
soy_ogl_4222	Gm13:23474923..23476100	1178	16	3993
soy_ogl_2543	Gm08:7532001..7534800	2800	17	4050
soy_ogl_310	Gm02:1220301..1222300	2000	18	4326
soy_ogl_2353	Gm07:17194522..17196553	2032	19	4593
soy_ogl_1894	Gm06:10540801..10542300	1500	20	4622

soy_ogl_3669	Gm11:624301..626200	1900	21	4879
soy_ogl_3218	Gm09:40167479..40168800	1322	22	4932
soy_ogl_5689	Gm17:15291601..15293400	1800	23	5102
soy_ogl_3333	Gm10:2950701..2951800	1100	24	5122
soy_ogl_2546	Gm08:7765875..7767500	1626	25	5520
soy_ogl_1208	Gm04:4023654..4025650	1997	26	5698
soy_ogl_873	Gm03:33650665..33653000	2336	27	6087
soy_ogl_5957	Gm18: 6057701..6059100	1400	28	6515
soy_ogl_4846	Gm15:924901..926200	1300	29	6571
soy_ogl_3818	Gm11:10146701..10148200	1500	30	6586
soy_ogl_5551	Gm17:6541901..6543200	1300	31	6775
soy_ogl_7	Gm05:32631801..32633200	1400	32	6935
soy_OGL_684	Gm02:45903201..45907300	4100	1	47
soy_OGL_682	Gm02:45816543..45818777	2235	9	2101
soy_OGL_685	Gm02:45910501..45913200	2700	1	48
soy_ OGL _1423	Gm04:45820631..45822916	2286	2	639
soy_ OGL _1434	Gm04:46095801..46097968	2168	1	137
soy_ OGL _4625	Gm14:3816738..3820070	3333	1	76
soy_ OGL _6362	Gm19:5311001..5315000	4000	1	440

A large suite of 7,018 genomic locations have been identified in the soybean 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 7,018 selected genomic loci into 32 clusters with similar genomic contexts, and to identify a subset of 32 selected genomic loci representative of the set of 7,018 selected genomic loci. The 32 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.

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:7,018) 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:505)	Cluster2 (SEQ ID NO:506 - - SEQ ID NO:747)	Cluster3 (SEQ ID NO:748-- SEQ ID NO:1028)	Cluster4 (SEQ ID NO: 1029-- SEQ ID NO:1165)	Cluster5 (SEQ ID NO: 1166-- SEQ ID NO:1451)	Cluster6 (SEQ ID NO: 1452-- SEQ ID NO:1661)	Cluster7 (SEQ ID NO: 1662-- SEQ ID NO:1868)	Cluster8 (SEQ ID NO: 1869-- SEQ ID NO:2070)	Cluster9 (SEQ ID NO:2071-- SEQ ID NO:2480)	Cluster10 (SEQ ID NO: 2481-- SEQ ID NO:2613)	Cluster11 (SEQ ID NO:2614 -- SEQ ID NO:2873)
PCA1	Min	-1.70227	0.022046	-4.54911	-1.72266	-0.36976	0.287697	-3.34863	-1.0806	-1.5084417	-0.06921	-4.85854
	Mean	0.349775	0.812634	-1.47305	-0.00185	0.540899	0.967917	-0.58528	0.313491	0.178145825	0.746656	-1.77485
	Median	0.363103	0.796321	-1.18164	0.049082	0.52498	0.918269	-0.34364	0.291582	0.204892845	0.729936	-1.59613
	Max	1.507894	1.834871	0.032399	2.027233	1.499719	2.461219	0.417058	1.718384	1.4452823	2.258209	-0.10335
PCA2	Min	-0.65485	-0.6907	-1.37642	-1.15246	-2.2623	-2.69847	-2.33499	-2.05394	-0.85615188	-1.07918	-1.48917
	Mean	0.803591	0.805611	0.42863	0.549053	-0.97646	-0.63594	-1.07926	-0.67684	0.0131018	0.201017	-0.12584
	Median	0.640172	0.690953	0.30208	0.435896	-0.92946	-0.51848	-1.03176	-0.62625	-0.061526693	0.165577	-0.16842
	Max	6.750318	4.21356	3.492035	2.037537	0.224862	0.316075	0.014994	0.262266	2.8737593	1.883538	2.389063
PCA3	Min	-4.63386	-6.20928	-3.64977	-7.46971	-2.4347	-3.28026	-2.79672	-2.36222	-1.7842444	-3.17428	-2.64864
	Mean	-1.0374	-0.87017	-1.09511	-1.21149	-0.49711	-0.30392	-0.4893	-0.36718	-0.137149779	-0.20772	-0.28997
	Median	-0.94654	□0.7282	-0.92816	-0.96309	-0.45901	-0.19996	-0.43677	-0.27515	-0.068803158	-0.04455	-0.18716
	Max	0.240454	0.010148	-0.11534	-0.13414	0.476554	0.457804	0.452481	0.453505	0.9092167	0.928412	0.782125
PCA4	Min	-2.22011	-1.02405	-1.33923	0.069312	-1.70627	-0.80904	-1.29231	0.360563	-2.9615474	-2.44418	-2.7613
	Mean	-0.71495	0.283541	0.212841	1.084988	-0.35855	0.479481	0.459736	1.348666	-1.407512305	-0.75615	-0.85361
	Median	-0.70787	0.306108	0.209055	1.116651	-0.35772	0.435449	0.436138	1.307628	-1.38790425	-0.78738	-0.81593
	Max	0.786678	1.575184	2.221794	2.571196	0.755949	2.664817	2.193427	3.122114	-0.40942505	0.783523	0.985444
PCA5	Min	-0.17971	-3.06393	-0.53749	-4.5557	0.159064	-2.0539	-0.70289	-1.90857	-1.897981	-4.47156	-2.35152
	Mean	0.943093	0.368965	0.713771	-0.21905	0.876745	0.463248	0.768677	0.285719	-0.029561107	-0.90424	-0.18625
	Median	0.854279	0.3771	0.670629	-0.10817	0.846543	0.459296	0.763885	0.338391	0.034177913	-0.68409	-0.12264
	Max	3.583402	2.613815	2.279238	2.341478	1.913726	1.633977	2.164417	1.422805	0.84937429	0.242494	0.940019

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		Cluster12 (SEQ ID NO: 2874-- SEQ ID NO:2969)	Cluster13 (SEQ ID NO:2970 -- SEQ ID NO:3507)	Cluster14 (SEQ ID NO:3508 -- SEQ ID NO:3675)	Cluster15 (SEQ ID NO:3676 -- SEQ ID NO:3992)	Cluster16 (SEQ ID NO:3993 -- SEQ ID NO:4049)	Cluster17 (SEQ ID NO:4050-- SEQ ID NO:4105)	Cluster18 (SEQ ID NO:4106 -- SEQ ID NO:4495)	Cluster19 (SEQ ID NO: 4496-- SEQ ID NO:4621)	Cluster20 (SEQ ID NO: 4622-- SEQ ID NO:4874)	Cluster21 (SEQ ID NO:4875 -- SEQ ID NO:4887)
PCA1	Min	-2.10567	-0.78413	-0.1362	-3.50478	-1.06581	-0.48995	-0.12394	-3.44417	-2.5926	0.041919
	Mean	0.215254	0.402511	0.841125	-0.99405	0.054644	0.218477	0.705185	-1.60324	-0.21989	0.498017
	Median	0.167943	0.421486	0.793343	-0.86435	0.043314	0.186449	0.69823	-1.62442	-0.07645	0.530588
	Max	2.638122	1.521265	2.011089	0.254192	1.078006	1.212386	1.894809	-0.14778	1.10593	0.937608
PCA2	Min	-3.24885	-2.49287	-2.07915	-2.50642	-2.60289	0.060129	0.131404	-0.33368	-0.05632	-1.56352
	Mean	-0.53611	-1.09247	-0.94959	-1.29395	-1.20352	1.419729	1.150768	1.001573	0.843814	-0.4111
	Median	-0.33651	-1.08189	-0.91699	-1.24996	-1.17679	1.280417	1.065186	0.789798	0.776486	-0.28559
	Max	2.608386	-0.24001	0.020389	-0.4655	-0.31958	3.913198	3.040107	6.340514	2.929741	0.123387
PCA3	Min	-14.6314	-1.01198	-1.91077	-1.7135	-2.73956	-1.73844	-1.13076	-1.78506	-0.92532	0.00053
	Mean	-3.0284	0.137956	0.208329	0.071922	-0.21452	-0.27811	0.161876	-0.14195	0.233953	0.437291
	Median	-1.93463	0.177648	0.306399	0.132791	-0.00072	-0.15148	0.163129	-0.06546	0.23185	0.450869
	Max	0.72284	1.034171	1.086972	0.996862	0.765974	0.427866	1.323874	0.948736	1.409277	0.918483
PCA4	Min	-1.00771	-2.10637	-1.17239	-1.48955	-0.78727	-1.60097	-0.69878	-1.09012	0.172103	-0.51316
	Mean	0.594551	-0.85746	-0.33529	-0.37717	0.438916	-0.23831	0.47476	0.670052	1.210219	0.100213
	Median	0.392421	-0.86062	-0.4333	-0.47105	0.356632	-0.21174	0.451745	0.638494	1.196036	0.075167
	Max	4.86024	0.27396	0.580863	0.978394	2.500934	0.871996	1.775638	2.468554	2.614263	0.536589
PCA5	Min	-18.7726	-0.77506	-3.53913	-1.20206	-3.51125	0.008136	-0.77069	-0.62934	-1.42543	0.258308
	Mean	-4.21943	0.229577	-0.3992	0.08327	-0.93398	0.701934	0.233117	0.369827	-0.02377	0.648857
	Median	-2.90093	0.240883	-0.33338	0.087451	-0.70513	0.602369	0.225125	0.29277	-0.01138	0.603284
	Max	-0.33401	1.115681	0.396515	1.044241	0.040091	2.01268	1.665714	1.937356	1.791794	1.079582

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		Cluster22 (SEQ ID NO: 4888--SEQ ID NO:5062)	Cluster23 (SEQ ID NO:5063 --SEQ ID NO:5121)	Cluster24 (SEQ ID NO:5122 --SEQ ID NO:5519)	Cluster25 (SEQ ID NO:5520 --SEQ ID NO:5686)	Cluster26 (SEQ ID NO:5687 --SEQ ID NO:6086)	Cluster27 (SEQ ID NO:6087 --SEQ ID NO:6320)	Cluster28 (SEQ ID NO:6321 --SEQ ID NO:6519)	Cluster29 (SEQ ID NO:6520 --SEQ ID NO:6573)	Cluster30 (SEQ ID NO:6574 --SEQ ID NO:6774)	Cluster31 (SEQ ID NO:6775 --SEQ ID NO:6588)	Cluster32 (SEQ ID NO:6589--SEQ ID NO:7018)
PCA1	Min	0.192262	-3.01097	-2.17545	-1.47203	-0.82652	-4.22215	-2.8128	-0.55955	-0.14823	-3.68328	-2.1948
	Mean	0.919859	-1.10273	0.189203	0.026625	0.609339	-1.7704	-0.5307	0.365085	0.695365	-1.17291	-0.20762
	Median	0.860249	-1.05343	0.274006	0.000548	0.622131	-1.68559	-0.44093	0.372341	0.679272	-1.05591	-0.07481
	Max	1.90419	0.215051	1.539568	1.204076	2.040596	-0.20599	1.026142	1.082778	1.542552	-0.04543	1.044939
PCA2	Min	-1.38005	-1.37504	-1.29996	-0.49733	-0.35268	-0.8685	-0.39322	-1.70938	-1.71589	-1.7904	-1.39851
	Mean	-0.07498	-0.52564	-0.24039	0.701345	0.996746	0.520887	0.744232	-0.66621	-0.41853	-0.82975	-0.40126
	Median	-0.02529	-0.48207	-0.18651	0.497651	0.817435	0.384759	0.686377	-0.69103	-0.33802	-0.8047	-0.39539
	Max	0.788801	0.176255	0.87503	3.880586	4.311936	3.021218	3.474901	0.015191	0.704506	-0.11251	0.595757
PCA3	Min	-0.17801	-0.26777	-0.37688	-0.16467	-0.23246	-0.47501	-0.00111	0.538379	0.435168	0.337445	0.222405
	Mean	0.567525	0.293	0.505379	0.71742	1.077263	0.78187	1.005429	1.055894	1.156804	1.045676	1.227425
	Median	0.560588	0.264634	0.473588	0.674781	1.053549	0.727749	1.007761	1.085427	1.14325	1.036725	1.200613
	Max	1.635718	0.932042	1.841691	2.234525	2.790854	2.556613	2.483974	1.565017	3.16182	1.973707	2.509435
PCA4	Min	-0.24073	0.213129	0.305131	-3.03078	-3.22656	-2.78298	-0.8606	-1.61996	-1.16215	-1.17888	-0.50044
	Mean	0.936613	1.158602	1.628149	-1.25321	-0.49661	-0.42577	0.564935	-0.67182	-0.02267	0.109856	0.973061
	Median	0.954165	1.088302	1.633074	-1.21889	-0.46274	-0.40653	0.537203	-0.72684	-0.03125	0.201603	0.930979
	Max	2.449815	2.046121	2.833294	-0.00705	1.301237	1.30015	2.491648	0.122389	1.218455	1.682597	2.614142
PCA5	Min	-0.57322	-0.00876	-1.17026	-2.49874	-3.23886	-2.76649	-4.07782	-0.9589	-1.70771	-1.41474	-2.02076
	Mean	0.282176	0.59606	0.172591	-0.46655	-0.94402	-0.73067	-1.02591	-0.15265	-0.47755	-0.34837	-0.70651
	Median	0.263371	0.577423	0.151654	-0.39547	-0.84381	-0.69992	-0.89159	-0.17176	-0.40794	-0.32927	-0.61785
	Max	1.412132	1.322481	1.497953	0.404344	0.182532	0.480085	-0.10675	0.562286	0.446026	0.347785	-0.0103

Example 3: Design of Zinc Fingers to Bind Genomic Loci in Soybean

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 32 selected optimal genomic loci. Numerous ZFP designs were developed and tested to identify the fingers which bound with the highest level of efficiency with 32 different representative genomic loci target sites which were identified and selected in soybean 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 soybean genome.

Table 7. zinc finger designs for the soybean selected genomic loci (N/A indicates "not applicable").

pDAB Number	ZFP Number	F1	F2	F3	F4	F5	F6
124201	391	SEQ ID NO: 7019 QSANRTK	SEQ ID NO: 7020 HRSSLRR	SEQ ID NO: 7021 QSANRTK	SEQ ID NO: 7022 DSSDRKK	SEQ ID NO: 7023 DRSNRTT	SEQ ID NO: 7024 DNSNRIK
		SEQ ID NO: 7025 RSDNLSV	SEQ ID NO: 7026 QKATRIN	SEQ ID NO: 7027 RSDHLSE	SEQ ID NO: 7028 RNDNRKN	SEQ ID NO: 7029 DRSNRTT	SEQ ID NO: 7030 RKYYLAK
124221	411	SEQ ID NO: 7031 DRSNRTT	SEQ ID NO: 7032 QSAHRIT	SEQ ID NO: 7033 HAQGLRH	SEQ ID NO: 7034 QSGHLSR	SEQ ID NO: 7035 QSGHLSR	N/A
		SEQ ID NO: 7036 QSGSLTR	SEQ ID NO: 7037 RLDWLPM	SEQ ID NO: 7038 RPYTLRL	SEQ ID NO: 7039 DNSNRIK	N/A	N/A

125332		SEQ ID NO: 7040 TSGNLTR	SEQ ID NO: 7041 TSGNLTR	SEQ ID NO: 7042 QSGDLTR	SEQ ID NO: 7043 HKWVLRQ	N/A	N/A
	651	SEQ ID NO: 7044 QSGHLAR	SEQ ID NO: 7045 TSSNRKT	SEQ ID NO: 7046 DSSDRKK	SEQ ID NO: 7047 QSGNLAR	SEQ ID NO: 7048 HNSSLKD	N/A
125309		SEQ ID NO: 7049 TSGSLSR	SEQ ID NO: 7050 QLNNLKT	SEQ ID NO: 7051 QSADRTK	SEQ ID NO: 7052 DNSNRIK	SEQ ID NO: 7053 TSGSLSR	SEQ ID NO: 7054 QSGDLTR
	655	SEQ ID NO: 7055 QSANRTK	SEQ ID NO: 7056 DRSNRTT	SEQ ID NO: 7057 QSGDLTR	SEQ ID NO: 7058 HRSSLLN	N/A	N/A
124884		SEQ ID NO: 7059 IDHGRYR	SEQ ID NO: 7060 DRSNLTR	SEQ ID NO: 7061 QSGDLTR	SEQ ID NO: 7062 QSGDLTR	SEQ ID NO: 7063 QRNARTL	N/A
	195	SEQ ID NO: 7064 TSGNLTR	SEQ ID NO: 7065 DRTGLRS	SEQ ID NO: 7066 SQYTLRD	SEQ ID NO: 7067 TSGHLSR	SEQ ID NO: 7068 RSDHLSE	SEQ ID NO: 7069 QSASRKN
124234		SEQ ID NO: 7070 TNQNRIT	SEQ ID NO: 7071 HSNARKT	SEQ ID NO: 7072 QSADRTK	SEQ ID NO: 7073 DNSNRIK	SEQ ID NO: 7074 RSDALTQ	N/A
	424	SEQ ID NO: 7075 TSGNLTR	SEQ ID NO: 7076 QSNQLRQ	SEQ ID NO: 7077 QSGNLAR	SEQ ID NO: 7078 RQEHRVA	SEQ ID NO: 7079 QSGALAR	SEQ ID NO: 7080 QSGHLSR
124257		SEQ ID NO: 7081 QSGSLTR	SEQ ID NO: 7082 WRSCRSA	SEQ ID NO: 7083 QSGNLAR	SEQ ID NO: 7084 WRISLAA	SEQ ID NO: 7085 QKHHLGD	SEQ ID NO: 7086 RSADLSR
	447	SEQ ID NO: 7087 DRSNRTT	SEQ ID NO: 7088 QSANRTK	SEQ ID NO: 7089 QSANRTK	SEQ ID NO: 7090 DRSNRTT	SEQ ID NO: 7091 QSGNLAR	N/A
125316		SEQ ID NO: 7092 QSGNLAR	SEQ ID NO: 7093 TSGNLTR	SEQ ID NO: 7094 DRSNRTT	SEQ ID NO: 7095 QNATRIN	SEQ ID NO: 7096 TSSNRKT	SEQ ID NO: 7097 QSGHLSR
	662	SEQ ID NO: 7098 DSSTRKT	SEQ ID NO: 7099 QSGNLAR	SEQ ID NO: 7100 RSDVLST	SEQ ID NO: 7101 QSGPLTQ	N/A	N/A
124265		SEQ ID NO: 7102 QSGNLAR	SEQ ID NO: 7103 DKSCLPT	SEQ ID NO: 7104 WELNRRT	SEQ ID NO: 7105 TSGNLTR	SEQ ID NO: 7106 DRSNLTR	N/A
	455	SEQ ID NO: 7107 DRSDLSR	SEQ ID NO: 7108 RREHLRA	SEQ ID NO: 7109 RSDNLAR	SEQ ID NO: 7110 QWNYRGS	SEQ ID NO: 7111 RSHSLLR	SEQ ID NO: 7112 RRDTLLD
124273		SEQ ID NO: 7113 QSGDLTR	SEQ ID NO: 7114 QSGNLAR	SEQ ID NO: 7115 HQCCLTS	SEQ ID NO: 7116 RSANLTR	SEQ ID NO: 7117 RSANLAR	SEQ ID NO: 7118 TNQNRIT
	463	SEQ ID NO: 7119 ATKDLAA	SEQ ID NO: 7120 TSGHLSR	SEQ ID NO: 7121 RSDNLSE	SEQ ID NO: 7122 TSSNRKT	SEQ ID NO: 7123 DRSALAR	SEQ ID NO: 7124 RSDYLAK
124888		SEQ ID NO: 7125 rsdnlar	SEQ ID NO: 7126 qsnalnr	SEQ ID NO: 7127 qkgtlge	SEQ ID NO: 7128 qsgsltr	SEQ ID NO: 7129 rsdsllr	SEQ ID NO: 7130 wscclrd
	213	SEQ ID NO: 7131 qsgsltr	SEQ ID NO: 7132 drsyrnt	SEQ ID NO: 7133 dqsnlra	SEQ ID NO: 7134 rhshlts	SEQ ID NO: 7135 qsgnlar	N/A

		SEQ ID NO: 7136 tsgnltr	SEQ ID NO: 7137 lsqdlnr	SEQ ID NO: 7138 rsdslsr	SEQ ID NO: 7139 dssartk	SEQ ID NO: 7140 rsdhlsa	SEQ ID NO: 7141 crrnlrn
124885	215	SEQ ID NO: 7142 seadrsk	SEQ ID NO: 7143 drsnltr	SEQ ID NO: 7144 drsalsr	SEQ ID NO: 7145 tssnrkt	SEQ ID NO: 7146 ergtlar	SEQ ID NO: 7147 drsalar
		SEQ ID NO: 7148 STDYRYP	SEQ ID NO: 7149 QSGNLAR	SEQ ID NO: 7150 RSDNLSV	SEQ ID NO: 7151 TRWWLPE	SEQ ID NO: 7152 RSDHLSQ	SEQ ID NO: 7153 TRSPLTT
124610	480	SEQ ID NO: 7154 TNQSLHW	SEQ ID NO: 7155 QSGNLAR	SEQ ID NO: 7156 RPYTLRL	SEQ ID NO: 7157 QSGSLTR	SEQ ID NO: 7158 RSDVLSE	SEQ ID NO: 7159 TSSNRKT
		SEQ ID NO: 7160 RSDVLST	SEQ ID NO: 7161 RNSYLIS	SEQ ID NO: 7162 RSANLAR	SEQ ID NO: 7163 TNQNRIT	SEQ ID NO: 7164 RSDNLSV	N/A
124614	484	SEQ ID NO: 7165 RSDHLSA	SEQ ID NO: 7166 RSANLTR	SEQ ID NO: 7167 LRHHLTR	SEQ ID NO: 7168 DRSTLRQ	SEQ ID NO: 7169 HNHDLRN	SEQ ID NO: 7170 TSGNLTR
		SEQ ID NO: 7171 QSANRTT	SEQ ID NO: 7172 QNAHRKT	SEQ ID NO: 7173 QSGNLAR	SEQ ID NO: 7174 QRNHRTT	SEQ ID NO: 7175 QSANRTK	N/A
124636	506	SEQ ID NO: 7176 RSDHLSE	SEQ ID NO: 7177 TSGSLTR	SEQ ID NO: 7178 QSGALAR	SEQ ID NO: 7179 QSGHLSR	N/A	N/A
		SEQ ID NO: 7180 YRWLRNS	SEQ ID NO: 7181 TNSNRKR	SEQ ID NO: 7182 QSANRTT	SEQ ID NO: 7183 HRSSLRR	SEQ ID NO: 7184 RSDVLSA	SEQ ID NO: 7185 QNATRIN
124648	518	SEQ ID NO: 7186 RSDSLLR	SEQ ID NO: 7187 QSCARNV	SEQ ID NO: 7188 RPYTLRL	SEQ ID NO: 7189 HRSSLRR	SEQ ID NO: 7190 RSDSLLR	SEQ ID NO: 7191 QSCARNV
		SEQ ID NO: 7192 QSSDLSR	SEQ ID NO: 7193 YHWYLKK	SEQ ID NO: 7194 QSANRTK	SEQ ID NO: 7195 DNSNRIK	SEQ ID NO: 7196 QSGNLAR	SEQ ID NO: 7197 DRTNLNA
121225	233	SEQ ID NO: 7198 RSDNLSE	SEQ ID NO: 7199 TSANLSR	SEQ ID NO: 7200 QSANRTK	SEQ ID NO: 7201 DNSYLPR	SEQ ID NO: 7202 LKQNLDA	SEQ ID NO: 7203 RSHHLKA
		SEQ ID NO: 7204 RSDHLSQ	SEQ ID NO: 7205 TARLLKL	SEQ ID NO: 7206 RSDNLTR	SEQ ID NO: 7207 QSSDLSR	SEQ ID NO: 7208 YHWYLKK	N/A
121227	235	SEQ ID NO: 7209 DRSNLSR	SEQ ID NO: 7210 TSGNLTR	SEQ ID NO: 7211 DRSNRTT	SEQ ID NO: 7212 TNSNRKR	SEQ ID NO: 7213 RSDSLSV	SEQ ID NO: 7214 QNANRKT
		SEQ ID NO: 7215 TSGNLTR	SEQ ID NO: 7216 QRSHLSD	SEQ ID NO: 7217 RSDNLSE	SEQ ID NO: 7218 VRRALSS	SEQ ID NO: 7219 RSDNLSV	N/A
121233	241	SEQ ID NO: 7220 QSSNLAR	SEQ ID NO: 7221 TSGSLTR	SEQ ID NO: 7222 QSGNLAR	SEQ ID NO: 7223 QKVNRAG	SEQ ID NO: 7224 TSGSLSR	SEQ ID NO: 7225 DSSALAK
		SEQ ID NO: 7226 QSGDLTR	SEQ ID NO: 7227 RKDPLKE	SEQ ID NO: 7228 QSGNLAR	SEQ ID NO: 7229 ATCCLAH	SEQ ID NO: 7230 QSSDLSR	SEQ ID NO: 7231 RRDNLHS
121235	243	SEQ ID NO: 7232 QSGNLAR	SEQ ID NO: 7233 HNSSLKD	SEQ ID NO: 7234 QSGALAR	SEQ ID NO: 7235 QSANRTK	SEQ ID NO: 7236 RSDHLST	SEQ ID NO: 7237 RSDHLSR

		SEQ ID NO: 7238 TSGNLTR	SEQ ID NO: 7239 DSTNLRA	SEQ ID NO: 7240 DRSHLAR	SEQ ID NO: 7241 RSDDLTR	SEQ ID NO: 7242 TSSNRKT	N/A
121238	250	SEQ ID NO: 7243 TSGNLTR	SEQ ID NO: 7244 QSGALVI	SEQ ID NO: 7245 QNAHRKT	SEQ ID NO: 7246 LKHHLTD	SEQ ID NO: 7247 RSDNLST	SEQ ID NO: 7248 DRSNRKT
		SEQ ID NO: 7249 DRSALSR	SEQ ID NO: 7250 RSDALTQ	SEQ ID NO: 7251 DRSTRTK	SEQ ID NO: 7252 QSGNLHV	SEQ ID NO: 7253 RSDNLTR	N/A
121246	259	SEQ ID NO: 7254 DRSNLSR	SEQ ID NO: 7255 QSGNLAR	SEQ ID NO: 7256 RSDSLLR	SEQ ID NO: 7257 WLSSLSA	N/A	N/A
		SEQ ID NO: 7258 RSDNLST	SEQ ID NO: 7259 DSSSRIK	SEQ ID NO: 7260 QSGALAR	SEQ ID NO: 7261 QSGNLHV	SEQ ID NO: 7262 RSDVLST	SEQ ID NO: 7263 RYAYLTS
121249	262	SEQ ID NO: 7264 RSDNLSE	SEQ ID NO: 7265 TRSPLRN	SEQ ID NO: 7266 QNAHRKT	SEQ ID NO: 7267 RSDHLSE	SEQ ID NO: 7268 RNDNRKN	N/A
		SEQ ID NO: 7269 QRTNLVE	SEQ ID NO: 7270 ASKTRTN	SEQ ID NO: 7271 RSANLAR	SEQ ID NO: 7272 RSDHLTQ	SEQ ID NO: 7273 RSAHLSR	N/A
125324	670	SEQ ID NO: 7274 RSDNLSV	SEQ ID NO: 7275 QNANRIT	SEQ ID NO: 7276 DQSNLRA	SEQ ID NO: 7277 QNAHRKT	SEQ ID NO: 7278 RSAHLSR	N/A
		SEQ ID NO: 7279 DRSALAR	SEQ ID NO: 7280 RSDYLAK	SEQ ID NO: 7281 RSDDLSR	SEQ ID NO: 7282 RNDNRTK	SEQ ID NO: 7283 RSDHLST	SEQ ID NO: 7284 HSNTRKN
121265	282	SEQ ID NO: 7285 RSDVLSE	SEQ ID NO: 7286 QRSNLKV	SEQ ID NO: 7287 QSSNLAR	SEQ ID NO: 7288 QSGHLSR	N/A	N/A
		SEQ ID NO: 7289 DRSDLSR	SEQ ID NO: 7290 LRFNLRN	SEQ ID NO: 7291 RSDSLSV	SEQ ID NO: 7292 QNANRKT	N/A	N/A
121271	288	SEQ ID NO: 7293 QSGDLTR	SEQ ID NO: 7294 TSGSLTR	SEQ ID NO: 7295 RSDDLTR	SEQ ID NO: 7296 YRWLLRS	SEQ ID NO: 7297 QSGDLTR	N/A
		SEQ ID NO: 7298 RSDNLST	SEQ ID NO: 7299 AACNRNA	SEQ ID NO: 7300 RPYTLRL	SEQ ID NO: 7301 QSGSLTR	SEQ ID NO: 7302 SQYTLRD	SEQ ID NO: 7303 TSGHLSR
124666	538	SEQ ID NO: 7304 QSANRTK	SEQ ID NO: 7305 DRSNRTT	SEQ ID NO: 7306 RSDVLST	SEQ ID NO: 7307 CRRNLRN	N/A	N/A
		SEQ ID NO: 7308 QSGDLTR	SEQ ID NO: 7309 HRSSLLN	SEQ ID NO: 7310 TNQSLHW	SEQ ID NO: 7311 QSGNLAR	SEQ ID NO: 7312 QSGNLAR	N/A
124814	598	SEQ ID NO: 7313 RSCCLHL	SEQ ID NO: 7314 RNASRTR	SEQ ID NO: 7315 QSGNLAR	SEQ ID NO: 7316 RQEHRVA	SEQ ID NO: 7317 RSDNLSE	SEQ ID NO: 7318 TSSNRKT
		SEQ ID NO: 7319 RSDVLSE	SEQ ID NO: 7320 QRSNLKV	SEQ ID NO: 7321 QSGALAR	SEQ ID NO: 7322 YRWLRNS	SEQ ID NO: 7323 QSANRTT	SEQ ID NO: 7324 DRSNRTT
124690	560	SEQ ID NO: 7325 QNAHRKT	SEQ ID NO: 7326 LAHHLVQ	SEQ ID NO: 7327 HAQGLRH	SEQ ID NO: 7328 QSGHLSR	SEQ ID NO: 7329 RSDDLTR	SEQ ID NO: 7330 RRFTLSK

		SEQ ID NO: 7331 RSDNLSE	SEQ ID NO: 7332 KSWSRYK	SEQ ID NO: 7333 RSAHLSR	SEQ ID NO: 7334 RSDDLTR	SEQ ID NO: 7335 YSWTLRD	SEQ ID NO: 7336 TSGNLTR
124815	599	SEQ ID NO: 7337 RSDVLST	SEQ ID NO: 7338 DNSSRTR	SEQ ID NO: 7339 RSDALAR	SEQ ID NO: 7340 RSDSLSA	SEQ ID NO: 7341 DRSDLSR	N/A
		SEQ ID NO: 7342 GTQGLGI	SEQ ID NO: 7343 DRSNLTR	SEQ ID NO: 7344 RNDDRKK	SEQ ID NO: 7345 RSDVLSE	SEQ ID NO: 7346 RSSDRTK	N/A
124816	600	SEQ ID NO: 7347 QSANRTK	SEQ ID NO: 7348 DSSHRTR	SEQ ID NO: 7349 QSANRTK	SEQ ID NO: 7350 SVGNLNQ	SEQ ID NO: 7351 TSGNLTR	N/A
		SEQ ID NO: 7352 TNQNRIT	SEQ ID NO: 7353 HSNARKT	SEQ ID NO: 7354 QSSHLTR	SEQ ID NO: 7355 RLDNRTA	SEQ ID NO: 7356 QSGNLAR	SEQ ID NO: 7357 QGANLIK
124842	631	SEQ ID NO: 7358 RSDNLST	SEQ ID NO: 7359 QKSPLNT	SEQ ID NO: 7360 QSSDLSR	SEQ ID NO: 7361 QSSDLSR	SEQ ID NO: 7362 YHWYLKK	N/A
		SEQ ID NO: 7574 TSSNRKT	SEQ ID NO: 7575 RSDELRG	SEQ ID NO: 7576 RSDTLSA	SEQ ID NO: 7577 DKSTRTK	N/A	N/A
125338	37	SEQ ID NO: 7578 DRSTRTK	SEQ ID NO: 7579 QSGNLHV	SEQ ID NO: 7580 QNAHRKT	SEQ ID NO: 7581 QSANRTK	SEQ ID NO: 7582 TSGSLSR	SEQ ID NO: 7583 FYMQLSR

Table 8. Zinc finger target site of soybean selected genomic loci

Locus ID	Name	pDAB Number	ZFP Number and Binding Sites (5'→3')		
OGL01	soy_ogl_308	124201	391	SEQ ID NO: 7363 TACTATTCCTAAGT TAAA	SEQ ID NO: 7364 TGGTACTAGGGGATAA AG
OGL02	soy_ogl_307	124221	411	SEQ ID NO: 7365 GGAGGAATTTAGAT AC	SEQ ID NO: 7366 TACTTGCTGGTA
OGL03	soy_ogl_2063	125305	651	SEQ ID NO: 7367 ATCATCTGCAAA	SEQ ID NO: 7368 CTTGAATTCCTATGGA
OGL04	soy_ogl_1906	125309	655	SEQ ID NO: 7369 AACTTGTGAGTAAA CTGC	SEQ ID NO: 7370 ATTGCATAATAA
OGL05	soy_ogl_262	124884	195	SEQ ID NO: 7371 GTTGTCTTGCTGCT AT	SEQ ID NO: 7372 ACACAGGGTATCTTCG AT
OGL06	soy_ogl_5227	124234	424	SEQ ID NO: 7373 ATGTACTCATATTC AT	SEQ ID NO: 7374 GGAGTAAGGGAAAAAG AT
OGL07	soy_ogl_4074	124257	447	SEQ ID NO: 7375 GCTCGTCATTGAAT TGTGTA	SEQ ID NO: 7376 GAAAAATAATTAATAC
OGL08	soy_ogl_3481	125316	662	SEQ ID NO: 7377 GGATATATAAACGA TGAA	SEQ ID NO: 7378 ATAATGGAACCC

OGL09	soy_ogl_1016	124265	455	SEQ ID NO: 7379 GACGATCACCTCGAA	SEQ ID NO: 7380 CCGGTGTCAGAGAGGGCC
OGL10	soy_ogl_937	124273	463	SEQ ID NO: 7381 AATGAGAGAGAGAGAAGCA	SEQ ID NO: 7382 CAGATCAATCAGGGTCCC
OGL11	soy_ogl_5109	124888	213	SEQ ID NO: 7383 CTCTACATGGTACCACTCG	SEQ ID NO: 7384 GAAAGGCACCTCGTA
OGL12	soy_ogl_6801	124885	215	SEQ ID NO: 7385 ATCAGCCACGATCCTGCA	SEQ ID NO: 7386 GTCGCCCATGTCTGACTCA
OGL13	soy_ogl_6636	124610	480	SEQ ID NO: 7387 CTATAGTTTTAAGTGAATTA	SEQ ID NO: 7388 TATATGGTATTGGAAATT
OGL14	soy_ogl_4665	124614	484	SEQ ID NO: 7389 CATCGTCTCATGCTT	SEQ ID NO: 7390 GATCCTACAAGTGAGAGG
OGL15	soy_ogl_6189	124636	506	SEQ ID NO: 7391 TTTTCTTTCTCTTTA	SEQ ID NO: 7392 GGAGTAGTTAGG
OGL16	soy_ogl_4222	124648	518	SEQ ID NO: 7393 AACATCTTTAACTCATTGT	SEQ ID NO: 7394 ATAGTGGTTTTGCATAGTG
OGL17	soy_ogl_2543	121225	233	SEQ ID NO: 7395 CACGAAAAACTAAATTTGCT	SEQ ID NO: 7396 AGGTATTTCTAAGATAGG
OGL18	soy_ogl_310	121227	235	SEQ ID NO: 7397 TTTGCTGAGTGAAGG	SEQ ID NO: 7398 CAAATGTGATAACTGATGAC
OGL19	soy_ogl_2353	121233	241	SEQ ID NO: 7399 AAGATGAAGCGAGAT	SEQ ID NO: 7400 ATCGTTCAAGAAGTTGAA
OGL20	soy_ogl_1894	121235	243	SEQ ID NO: 7401 CAGGCTGGCAAAATGGAA	SEQ ID NO: 7402 GGGTGGTAAGTACTTGAA
OGL22	soy_ogl_3218	121238	250	SEQ ID NO: 7403 AATGCGTGGCCACGAT	SEQ ID NO: 7404 AACTAGCGTAGAGTAGAT
OGL24	soy_ogl_3333	121246	259	SEQ ID NO: 7405 GAGAAAGCCATGGTC	SEQ ID NO: 7406 TGTGTGGAAGAC
OGL25	soy_ogl_2546	121249	262	SEQ ID NO: 7407 TGGATGTCAAGTATTCAAG	SEQ ID NO: 7408 TAGGGGAGAATACAG
OGL28	soy_ogl_5957	125324	670	SEQ ID NO: 7409 GGGAGGGAGACCCAA	SEQ ID NO: 7410 GGGAGAAACAAAAAG
OGL30	soy_ogl_3818	121265	282	SEQ ID NO: 7411 GTTTGGTTAGGCGCAGATC	SEQ ID NO: 7412 GGAGAAACAACTG

OGL31	soy_ogl_5551	121271	288	SEQ ID NO: 7413 AAAGTGTCATGCC	SEQ ID NO: 7414 GCAATTGCGGTTGCA
OGL33	optimal_loci_1098	124666	538	SEQ ID NO: 7415 GGTATCGTATTGCATTAG	SEQ ID NO: 7416 CGCACGTAATAA
OGL34	optimal_loci_97772	124814	598	SEQ ID NO: 7417 GAAGAAATTATTGCA	SEQ ID NO: 7418 AATCAGAGGGAAGTGAGA
OGL35	optimal_loci_236662	124690	560	SEQ ID NO: 7419 AACTAACTTGTAACAACTG	SEQ ID NO: 7420 TTGGCGGGAATTAGTAGA
OGL36	optimal_loci_139485	124815	599	SEQ ID NO: 7421 GATCTTGCGGGGTAGCAG	SEQ ID NO: 7422 GACCTGGTGGTCATG
OGL37	optimal_loci_301175	125338	627	SEQ ID NO:7584 ATACGTCAGGGTtantgGTTGTTTAATGAAAAGCC	OGL37
OGL38	optimal_loci_152337	124816	600	SEQ ID NO: 7423 TCTATGTCGGACTTT	SEQ ID NO: 7424 GATCATTTAAGGATAA
OGL39	optimal_loci_202616	124842	631	SEQ ID NO: 7425 ATGAATTCCCTTTTCTTA	SEQ ID NO: 7426 TTTGCTGCTTTATAG

The soybean 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 *Fok*I (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 optimized for soybean 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 soybean genomic polynucleotide target sites *in planta*.

ZFN Construct Assembly

Plasmid vectors containing ZFN gene expression constructs 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) 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 a strong constitutive promoter from the Cassava vein mosaic virus. The expression cassette also includes a 3' UTR from the *Agrobacterium tumefaciens* ORF23. 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 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-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). 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.

Zinc Finger Cloning Via Automated Workflow

A subset of Zinc Finger Nuclease vectors were cloned via an automated DNA construction pipeline. Overall, the automted 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 dicot backbone, pDAB118796 was used in all of the soybean ZFN builds. It contained the Cassava Mosaic Virus promoter and the Opaque2 NLS as well as the FokI domain and the Orf23 3'UTR from *Agrobacterium tumefaciens*. 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 pDAB117443. This vector contains the first monomer Fok1 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, Mannedorf, 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 cylcled (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 soybean 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 contained an 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 was 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 pDAB124280 (SEQ ID NO:7561 and Figure 7). In an additional embodiment, a universal donor polynucleotide sequence is provided as: pDAB124281, SEQ ID NO:7562, Figure 8; pDAB121278, SEQ ID NO:7563, Figure 9; pDAB123812, SEQ ID NO:7564 Figure 10; pDAB121937, SEQ ID NO:7565, Figure 11; pDAB123811, SEQ ID NO:7566, Figure 12; and, pDAB124864 SEQ ID NO:7567, Figure 13. 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 (Table 11).

Table 11: The various universal domain sequences that were transformed into the plant cell protoplasts for donor mediated integration within the genome of soybean are provided. The various elements of the universal domain plasmid system are described and identified by base pair position in the accompanying SEQ ID NO:. "N/A" meas not applicable.

Vector Name	ZFN binding domain	Analytical domain	Plasmid backbone	SEQ ID NO:
pDAB124280	1955-2312bp	2313-2422bp	2423-1954bp	7561
pDAB124281	1955-2256bp	2257-2366bp	2367-1954bp	7562
pDAB121278	1509-1724bp	1725-1834bp	1835-1508bp	7563
pDAB123812	1955-2177bp	2178-2287bp	2288-1954bp	7564
pDAB121937	1955-2127bp	2128-2237bp	2238-1954bp	7565
pDAB123811	1955-2187bp	2288-2297bp	2298-1954bp	7566
pDAB124864	1952-2185	N/A	2186-1951bp	7567

The universal donor polynucleotide sequence was a small 2-3 Kb modular donor system delivered as a plasmid. This was a minimal donor, comprising 1, 2, 3, 4, 5, 6, 7, 8, 9, or more ZFN binding sites, a short 100-150 bp template region referred to as "DNA X" or "UZI Sequence" (SEQ ID NO:7568) that carries restriction sites and DNA sequences for primer design or coding sequences, and a simple plasmid backbone (Fig. 4). 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 were minimized in the donor. Universal donors without the "UZI" sequence but carrying one or more ZFN sites have also been generated

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 (Fig. 5).

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 soybean 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.

Example 4: Soybean Transformation Procedures

Before delivery to *Glycine max* c.v. Maverick 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

Protoplasts were isolated from a Maverick suspension culture derived from callus produced from leaf explants. Suspensions were subcultured every 7 days in fresh LS medium (Linsmaier and Skoog 1965) containing 3% (w/v) sucrose, 0.5 mg/L 2,4-D, and 7 g of bactoagar, pH 5.7 For isolation, thirty milliliters of a Maverick suspension culture 7 days post subculturing was transferred to a 50 ml conical tube and centrifuged at 200 g for 3 minutes, yielding about 10 ml of settled cell volume (SCV) per tube. The supernatant was removed and twenty milliliters of the enzyme solution (0.3% pectolyase (320952; MP Biomedicals), 3%

cellulase ("Onozuka" R10™; Yakult Pharmaceuticals, Japan) in MMG solution (4 mM MES, 0.6 M mannitol, 15 mM $MgCl_2$, pH 6.0) was added for every 4 SCV of suspension cells and the tubes were wrapped with Parafilm™. The tubes were placed on a platform rocker overnight (about 16-18 hr) and an aliquot of the digested cells was viewed microscopically to ensure the digestion of the cell wall was sufficient.

Protoplast Purification

A soybean (*Glycine max* c.v. Maverick) protoplast-based transformation method was developed and used for soybean protoplast transformation. Protoplasts were isolated from a Maverick suspension culture derived from callus produced from leaf explants. The techniques provided below describe the method. Soybean cell suspensions were subcultured every 7 days by a 1:5 dilution in fresh LS medium (Linsmaier and Skoog 1965) containing 3% (w/v) sucrose, 0.5 mg/L 2,4-D, and 7 g of bactoagar, pH 5.7 All experiments were performed starting 7 days post subculture based on the protocol described below.

Protoplast Isolation

Thirty milliliters of a soybean c.v. Maverick suspension culture 7 days post subculturing was transferred to a 50 ml conical centrifuge tube and centrifuged at 200 g for 3 minutes, yielding about 10 ml of settled cell volume (SCV) per tube. The supernatant was removed without disturbing the cell pellet. Twenty milliliters of the enzyme solution (0.3% pectolyase (320952; MP Biomedicals), 3% cellulase ("Onozuka" R10™; Yakult Pharmaceuticals, Japan) in MMG solution (4 mM MES, 0.6 M mannitol, 15 mM $MgCl_2$, pH 6.0) was added for every 4 SCV of suspension cells and the tubes were wrapped with Parafilm™. The tubes were placed on a platform rocker overnight (about 16-18 hr). The next morning, an aliquot of the digested cells was viewed microscopically to ensure the digestion of the cell walls was sufficient.

Protoplast Purification

The cells/enzyme solutions were filtered slowly through a 100 μM cell strainer. The cell strainer was rinsed with 10 ml of W5+ media (1.82 mM MES, 192 mM NaCl, 154 mM $CaCl_2$, 4.7 mM KCl, pH 6.0). The filtering step was repeated using a 70 μM screen. The final volume was brought to 40 ml by adding 10 ml of W5+ media. The cells were mixed by inverting the tube. The protoplasts were slowly layered onto 8 ml of a sucrose cushion solution (500 mM sucrose, 1 mM $CaCl_2$, 5 mM MES-KOH, pH 6.0) by adding the cushion solution to the bottom

of a 50 ml conical centrifuge tube containing the cells. The tubes were centrifuged at 350 x g for 15 minutes in a swinging bucket rotor. A 5 ml pipette tip was used to slowly remove the protoplast band (about 7-8 ml). The protoplasts were then transferred to a 50 ml conical tube and 25 ml of W5+wash was added. The tubes were inverted slowly and the centrifuged for 10 minutes at 200 g. The supernatant was removed, 10 ml of MMG solution was added and the tube was inverted slowly to resuspend the protoplasts. The protoplast density was determined using a haemocytometer or a flow cytometer. Typically, 4 PCV of cells suspension yields about 2 million protoplasts.

Transformation of Protoplasts using PEG

The protoplast concentration was adjusted to 1.6 million/ml with MMG. Protoplast aliquots of 300 µl (about 500,000 protoplasts) were transferred into 2 ml sterile tubes. The protoplast suspension was mixed regularly during the transfer of protoplasts into the tubes. Plasmid DNA was added to the protoplast aliquots according to the experimental design. The rack containing the tubes of protoplasts was slowly inverted 3 times for 1 minute each to mix the DNA and protoplasts. The protoplasts were incubated for 5 minutes at room temperature. Three hundred microliters of a polyethlene glycol (PEG 4000) solution (40% ethylene glycol (81240-Sigma Aldrich), 0.3 M mannitol, 0.4 M $CaCl_2$) was added to the protoplasts and the rack of tubes was mixed for 1 min and incubated for 5 min, with gentle inversion twice during the incubation. One milliliter of W5+ was slowly added to the tubes and the rack of tubes inverted 15-20 times. The tubes were then centrifuged at 350 g for 5 min and the supernatant removed without disturbing the pellet. One milliliter of WI media (4 mM MES 0.6 M mannitol, 20 mM KCl, pH 6.0) was added to each tube and the rack was gently inverted to resuspend the pellets. The rack was covered with aluminum foil and laid on its side to incubate overnight at 23^0C.

Measuring Transformation Frequency and Harvesting the Protoplasts

Quantification of protoplasts and transformation efficiencies were measured using a Quanta Flow Cytometer™ (Beckman-Coulter Inc). Approximately 16-18 hours post transformation, 100 µl from each replicate was sampled, placed in a 96 well plate and diluted 1:1 with WI solution. The replicates were resuspended 3 times and 100 µl was quantified using flow cytometry. Prior to submitting the samples for analysis, the samples were centrifuged at 200 g for 5 min, supernatants were removed and the samples were flash frozen in liquid

nitrogen. The samples were then placed in a -80 °C freezer until processing for molecular analysis.

Transformation of ZFN and Donor

For each of the selected genomic loci of Table 5, the soybean protoplasts were transfected with constructs comprising a *green fluorescent protein* (*gfp*) gene expressing control, ZFN alone, donor alone and a mixture of ZFN and donor DNA at a ratio of 1:10 (by weight). The total amount of DNA for transfection of 0.5 million protoplasts was 80 μg. All treatments were conducted in replicates of three. The *gfp* gene expressing control used was pDAB7221 (Figure 14, SEQ ID NO:7569) containing the Cassava Vein Mosaic Virs promoter – green fluorescent protein coding sequence – Agrobacterium tumefaciens ORF24 3'UTR gene expression cassettes. To provide a consistent amount of total DNA per transfection, either salmon sperm or a plasmid containing a *gfp* gene was used as filler where necessary. In a typical targeting experiment, 4 μg of ZFN alone or with 36 μg of donor plasmids were transfected and an appropriate amount of salmon sperm or pUC19 plasmid DNA was added to bring the overall amount of DNA to the final amount of 80 μg. Inclusion of *gfp* gene expressing plasmid as filler allows assessment of transfection quality across multiple loci and replicate treatments.

Example 5: Cleavage of Genomic Loci in Soybean via Zinc Finger Nuclease

Targeting at select genomic loci was demonstrated by ZFN induced DNA cleavage and donor insertion using the protoplast based Rapid Targeting System (RTA). For each soybean select locus, up to six ZFN designs were generated and transformed into protoplasts either alone or with a universal donor polynucleotide and ZFN mediated clevage and insertion was measured using Next Generation Sequencing (NGS) or junctional (in-out) PCR respectively.

ZFN transfected soybean 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/μL) for PCR amplification to generate

amplicons for sequencing (Illumina, Inc., SanDiego, 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 μM appropriate bar-coded primers, ACCUPRIME PFX SUPERMIX™ (Invitrogen, Carlsbad, CA) and 100 ng of template genomic DNA in a 23.5 μL 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 100 ng of PCR amplicon from the ZFN treated and corresponding untreated controls were pooled together and sequenced using llumina Next Generation Sequencing (NGS).

The cleavage activity of appropriate ZFNs at each soybean optimal 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 was thus a measure of ZFN activity and was 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). Activities were observed for sobyean selected genomic loci targets and were further confirmed by sequence alignments that show a diverse footprint of indels at each ZFN cleavage site. This data suggests that the soybean 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 soybean selected genomic loci targets via non-homologous end joining (NHEJ) meditated donor

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

ZFN Donor Insertion Rapid Targeting Analysis

To determine if a soybean selected genomic loci target can be targeted for donor insertion, a ZFN construct and universal donor polynucleotide construct were co-delivered to soybean 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 soybean selected genomic loci target and in the donor, the linearized donor would then be inserted into the cleaved target site in the soybean genome via the non-homologous end joining (NHEJ) pathway. Confirmation of targeted integration at the soybean 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 soybean selected genomic loci target, would the PCR assay produce an amplification product with the 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

All PCR amplifications were conducted using a TAKARA EX TAQ HS™ kit (Clonetech, Mountain View, CA). The first In-Out PCR was carried out in 25 μL final reaction volume that contains 1X TAKARA EX TAQ HS™ buffer, 0.2 mM dNTPs, 0.2 μM "Out" primer, 0.05 μM "In" primer (designed from the universal donor cassette described above), 0.75 unit of TAKARA EX TAQ HS™ polymerase, and 6 ng extracted soybean protoplast DNA. The reaction was then completed using a PCR program that consists of 94 °C for 3 min, 14 cycles of 98 °C for 12 sec, and 60 °C for 30 sec, and 72 °C for 1 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 25 μL final reaction volume that contained 1X 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 units of TAKARA EX TAQ HS™ polymerase, and 1 μL of the first PCR product. The reaction was then completed using a PCR program that consisted of 94 °C for 3 min, 30 cycles of 98 °C for 12 sec, 60 °C for 30 sec and 72 °C for 45 sec, 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.

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

OGL01	First PCR	5'-end	MAS1057	SEQ ID NO: 7427 CAAACAAGGAGAGAGCGAG
			GM Spec	SEQ ID NO: 7428 GATCGACATTGATCTGGCTA
		3'-end	MAS1059	SEQ ID NO: 7429 GGCAAGGACACAAACGG
			GM Uzi	SEQ ID NO: 7430 ATATGTGTCCTACCGTATCAGG
	Nest PCR	5'-end	MAS1058	SEQ ID NO: 7431 TACCCAAGAAGAAACATTAGACC
			GM Spec Nst	SEQ ID NO: 7432 GTTGCCTTGGTAGGTCC
		3'-end	MAS1060	SEQ ID NO: 7433 ATGTAGTTGTTTCTCTGCTGTG
			GM Uzi Nst	SEQ ID NO: 7434 GAGCCATCAGTCCAACAC
OGL02	First PCR	5'-end	MAS1061	SEQ ID NO: 7435 CACGAGGTTTACGCCAT
		3'-end	MAS1063	SEQ ID NO: 7436 TCTGATAACTTGCTAGTGTGTG
	Nest PCR	5'-end	MAS1062	SEQ ID NO: 7437 GCTGCTCAGTGGATGTC
		3'-end	MAS1064	SEQ ID NO: 7438 TCGTTTATCGGGATTGTCTC
OGL03	First PCR	5'-end	MAS1133	SEQ ID NO: 7439 TTGTTGCTTCTATGCTCCTC
		3'-end	MAS1135	SEQ ID NO: 7440 CGTCGTTGTGGATGAGG
	Nest PCR	5'-end	MAS1134	SEQ ID NO: 7441 CCATTGCTGTTCTGCTTG
		3'-end	MAS1136	SEQ ID NO: 7442 TGTAGGTGACGGGTGTG

OGL04	First PCR	5'-end	MAS1155	SEQ ID NO: 7443 GTGTGTTATTGTCTGTGTTCTC
		3'-end	MAS1139	SEQ ID NO: 7444 GACTCCTATGTGCCTGATTC
	Nest PCR	5'-end	MAS1156	SEQ ID NO: 7445 GAGAACGATGGATAGAAAAGCA
		3'-end	MAS1140	SEQ ID NO: 7446 TTTGTTTCAGTCTTGCTCCT
OGL05	First PCR	5'-end	MAS1121	SEQ ID NO: 7447 CTACCTATAAACTGGACGGAC
		3'-end	MAS1123	SEQ ID NO: 7448 CGTCAAATGCCCATTATTCAT
	Nest PCR	5'-end	MAS1122	SEQ ID NO: 7449 GATTTGGGCTTGGGCATA
		3'-end	MAS1124	SEQ ID NO: 7450 TGAATCCCACTAGCACCAT
OGL06	First PCR	5'-end	MAS1065	SEQ ID NO: 7451 GGAGATAGAGTTAGAAGGTTTTGA
		3'-end	MAS1067	SEQ ID NO: 7452 GAGGTTGTTTTGACGCCA
	Nest PCR	5'-end	MAS1066	SEQ ID NO: 7453 AAGGAAGAAATGTGAAAAAGAAGA C
		3'-end	MAS1068	SEQ ID NO: 7454 AGAGAAGCGAAACCCAAAG
OGL07	First PCR	5'-end	MAS1069	SEQ ID NO: 7455 GACCCATTTATCTATCCCGTAT
		3'-end	MAS1071	SEQ ID NO: 7456 GGCTCGTATCAGTTCCATTTAG
	Nest PCR	5'-end	MAS1070	SEQ ID NO: 7457 AAGTACGAACAAGATTGGTGAG
		3'-end	MAS1072	SEQ ID NO: 7458 TCTATTACATTCCATCCAAAGGC
OGL08	First PCR	5'-end	MAS1141	SEQ ID NO: 7459 GAAACGAGAGAGATGACCAATA
		3'-end	MAS1143	SEQ ID NO: 7460 GGTTCACGGGTTCAGC
	Nest PCR	5'-end	MAS1142	SEQ ID NO: 7461 CCTGACGCAAAAGAAGAAATG
		3'-end	MAS1144	SEQ ID NO: 7462 GTTATACTTACTGTCACCACGAG
OGL09	First PCR	5'-end	MAS1073	SEQ ID NO: 7463 TTATTCCTGCGTCTCTCAC
		3'-end	MAS1075	SEQ ID NO: 7464 TTGTGCGTGATAAATAGGGC
	Nest PCR	5'-end	MAS1074	SEQ ID NO: 7465 GATAGTTGATTGTGTTGTTAGCATA
		3'-end	MAS1076	SEQ ID NO: 7466 CTCACCTGTTGCCCGTA

OGL10	First PCR	5'-end	MAS1077	SEQ ID NO: 7467 GTTTGAGTTGGCAGGTGT
		3'-end	MAS1079	SEQ ID NO: 7468 CCGTGACTTGTGCTAGAG
	Nest PCR	5'-end	MAS1078	SEQ ID NO: 7469 CTGAAGTTGACGCCGC
		3'-end	MAS1080	SEQ ID NO: 7470 AAGCACAGGACGGTTAGA
OGL11	First PCR	5'-end	MAS1125	SEQ ID NO: 7471 CACGGGTCACAAATCTAGTT
		3'-end	MAS1127	SEQ ID NO: 7472 CCATTAAGTCTGTCTCAACTTTC
	Nest PCR	5'-end	MAS1126	SEQ ID NO: 7473 CTGCTTGAGTAGGAAGAAGTG
		3'-end	MAS1128	SEQ ID NO: 7474 ATCACCAAAGCCGAGAAC
OGL12	First PCR	5'-end	MAS1129	SEQ ID NO: 7475 GTAGGCGTGAAGGCTG
		3'-end	MAS1131	SEQ ID NO: 7476 TGAAACCGCACAATCTCG
	Nest PCR	5'-end	MAS1130	SEQ ID NO: 7477 CCCTCCGAAACAATCCG
		3'-end	MAS1132	SEQ ID NO: 7478 ACCCGTTGAATGCGAG
OGL13	First PCR	5'-end	MAS1081	SEQ ID NO: 7479 AAGGTGGATGGGAGGAA
		3'-end	MAS1083	SEQ ID NO: 7480 TGGCACTAATACATTACATAAGACT
	Nest PCR	5'-end	MAS1082	SEQ ID NO: 7481 ATGTTACTTCAATCCCTCGTC
		3'-end	MAS1084	SEQ ID NO: 7482 TGAATAGGGCAAAAACACAC
OGL14	First PCR	5'-end	MAS1085	SEQ ID NO: 7483 CAAGTGAGCAGGGCG
		3'-end	MAS1087	SEQ ID NO: 7484 CTATCATTCGTAAAGTTTGAGGAC
	Nest PCR	5'-end	MAS1086	SEQ ID NO: 7485 AGCCTCACTCACAACAAAG
		3'-end	MAS1088	SEQ ID NO: 7486 TGAAACTGTCTTGTGACTTACC
OGL15	First PCR	5'-end	MAS1089	SEQ ID NO: 7487 GCACTGACATACCAACAATC
		3'-end	MAS1091	SEQ ID NO: 7488 GTTGTCGGGATTTCACTTCAT
	Nest PCR	5'-end	MAS1090	SEQ ID NO: 7489 GATAGGAGAAAGAGCAAGGAC
		3'-end	MAS1092	SEQ ID NO: 7490 TTCTCAACATCAACTCATACACTC

OGL16	First PCR	5'-end	MAS1093	SEQ ID NO: 7491 CTCAAAGCAACATCAACCAT
		3'-end	MAS1095	SEQ ID NO: 7492 AATCCCAAAGCAGCCAAC
	Nest PCR	5'-end	MAS1094	SEQ ID NO: 7493 AAACACAAATCACATCATAGTAAAC
		3'-end	MAS1096	SEQ ID NO: 7494 GCTAGTATGCTTCTGTCAGTTTA
OGL17	First PCR	5'-end	MAS916	SEQ ID NO: 7495 ACTAGTTCTTTCCCGAACATT
		3'-end	MAS918	SEQ ID NO: 7496 CATTTGGTGATTTAACTCATCAGC
	Nest PCR	5'-end	MAS917	SEQ ID NO: 7497 AAATTTACCACGGTTGGTCC
		3'-end	MAS919	SEQ ID NO: 7498 TCTGCATTAACTATATCAGGAGG
OGL18	First PCR	5'-end	MAS920	SEQ ID NO: 7499 ATTCAACATTTACCCTTCACAA
		3'-end	MAS922	SEQ ID NO: 7500 AATTCTTTCTCATACTTGGTTGT
	Nest PCR	5'-end	MAS921	SEQ ID NO: 7501 CCTTGTTTTCCGTACTATCAATT
		3'-end	MAS923	SEQ ID NO: 7502 TATTGGAGTAATGTGGACAAGC
OGL19	First PCR	5'-end	MAS924	SEQ ID NO: 7503 AACAACTTTCCAACCCACAA
		3'-end	MAS1009	SEQ ID NO: 7504 CGTTTTACCTTGACTTGACCT
	Nest PCR	5'-end	MAS925	SEQ ID NO: 7505 CCAGAGAGGAACCAGAAGT
		3'-end	MAS1010	SEQ ID NO: 7506 CCTTAGACAAAACTCGCACTT
OGL20	First PCR	5'-end	MAS1011	SEQ ID NO: 7507 GAAAGAGAAGACGCCACC
		3'-end	MAS930	SEQ ID NO: 7508 TCATTAGAGGGTCAAAAGTGC
	Nest PCR	5'-end	MAS1012	SEQ ID NO: 7509 CCTGAAGAAAAGTGGGAGAA
		3'-end	MAS931	SEQ ID NO: 7510 TTCAATCATAATTAAACTAATAAGA CTGT
OGL22	First PCR	5'-end	MAS960	SEQ ID NO: 7511 ACTGAATGTATTGTCCGACG
		3'-end	MAS962	SEQ ID NO: 7512 GCCCTACATTTTCATTTCATTGG
	Nest PCR	5'-end	MAS961	SEQ ID NO: 7513 GTGAGACCGCCCCTT
		3'-end	MAS963	SEQ ID NO: 7514 CCACTACTTTTTACTCACAGAAGA

OGL24	First PCR	5'-end	MAS968	SEQ ID NO: 7515 GTCAATTCTCATCAGTTCCATCT
		3'-end	MAS970	SEQ ID NO: 7516 CGATGAATAGTATGAGTGCGTAG
	Nest PCR	5'-end	MAS969	SEQ ID NO: 7517 TGCGTCTCTTGCTTCCTA
		3'-end	MAS971	SEQ ID NO: 7518 GCCACGAGAGGATAGAATAAT
OGL25	First PCR	5'-end	MAS972	SEQ ID NO: 7519 TAGTGTACCCTCCTCATCATA
		3'-end	MAS974	SEQ ID NO: 7520 GATAATCAAATGAGTGGACGAATA
	Nest PCR	5'-end	MAS973	SEQ ID NO: 7521 TGTATTTGGATAAGTGTGGGAC
		3'-end	MAS975	SEQ ID NO: 7522 GATTTTAGCGTGATTGATGGAAG
OGL28	First PCR	5'-end	MAS1149	SEQ ID NO: 7523 CTGAAGCAAGTGGTGATGTT
		3'-end	MAS1151	SEQ ID NO: 7524 CTTACCACCACCTGCG
	Nest PCR	5'-end	MAS1150	SEQ ID NO: 7525 GCATAAAGGTCAGCAGAGG
		3'-end	MAS1152	SEQ ID NO: 7526 TACTCTTTAGCCATAGCCAAT
OGL30	First PCR	5'-end	MAS988	SEQ ID NO: 7527 GTTTATTGCCAGAGACGGT
		3'-end	MAS990	SEQ ID NO: 7528 CGTCGTTGCTTGCTTGT
	Nest PCR	5'-end	MAS989	SEQ ID NO: 7529 GGAAAGACATAAAAGTAAATGGAA G
		3'-end	MAS991	SEQ ID NO: 7530 TAACTACCTGATAACCTCCTTTT
OGL31	First PCR	5'-end	MAS992	SEQ ID NO: 7531 GCAAACTTTAAGTAAACTAGAGGC
		3'-end	MAS994	SEQ ID NO: 7532 AGTGTACTCTAGTCAGATTTTGC
	Nest PCR	5'-end	MAS993	SEQ ID NO: 7533 CAACCCAACAAGCAAACAC
		3'-end	MAS995	SEQ ID NO: 7534 CTCGGTTTTGTAGTCATCTATGTA
OGL33	First PCR	5'-end	MAS1101	SEQ ID NO: 7535 GATGAATAACAGTGCGAGGA
		3'-end	MAS942	SEQ ID NO: 7536 CTGTAATCCTCATTTTGCACG
	Nest PCR	5'-end	MAS941	SEQ ID NO: 7537 GGGGTAGTTACACTTCTGC
		3'-end	MAS943	SEQ ID NO: 7538 GGTGTGGTCGGCATATAGA

OGL34	First PCR	5'-end	MAS944	SEQ ID NO: 7539 TTCGCACAAGCCATCC
		3'-end	MAS946	SEQ ID NO: 7540 AACGACTTTTTGAATAGATGCT
	Nest PCR	5'-end	MAS945	SEQ ID NO: 7541 GCATTCCTTCTTGTCTCGT .
		3'-end	MAS947	SEQ ID NO: 7542 AACTTAGAGAAACTCATAACTCATC
OGL35	First PCR	5'-end	MAS948	SEQ ID NO: 7543 TCATAGCTTCAAGGGATTCAC
		3'-end	MAS950	SEQ ID NO: 7544 GTTCATCAAAACACGCAAGA
	Nest PCR	5'-end	MAS949	SEQ ID NO: 7545 CTCATGCCAACAAAAGCC
		3'-end	MAS951	SEQ ID NO: 7546 GTAGTAACAAAAATGGATAACGCA G
OGL36	First PCR	5'-end	MAS936	SEQ ID NO: 7547 TATCTGGCTTGAAGCTGAAT
		3'-end	MAS938	SEQ ID NO: 7548 TTATTTCCTTCGTGGCTTCG
	Nest PCR	5'-end	MAS937	SEQ ID NO: 7549 CTCCACAATTTAGCATCCAAG
		3'-end	MAS939	SEQ ID NO: 7550 CGTCCATGTTTACTTGGCTA
OGL37	First PCR	5'-end	MAS952	SEQ ID NO:7570 GTCATCATAATTGCTGTCCCA
		3'-end	MAS954	SEQ ID NO:7571 GGATGTGTGCCTGAGC
	Nest PCR	5'-end	MAS953	SEQ ID NO:7572 CCTTCCTCGTGCCCTTA
		3'-end	MAS955	SEQ ID NO:7573 CCCCTAATCTCATCGCAAG
OGL38	First PCR	5'-end	MAS932	SEQ ID NO: 7551 TCTGTTGATTCCTAATCGTAGC
		3'-end	MAS934	SEQ ID NO: 7552 GTGATTGACATTTGTCTATAAGCA
	Nest PCR	5'-end	MAS933	SEQ ID NO: 7553 CCTCTTCACTGTGACTGAAC
		3'-end	MAS935	SEQ ID NO: 7554 TTTCGGCTTGACATTTCTTTC
OGL39	First PCR	5'-end	MAS956	SEQ ID NO: 7555 TGGCAAATCACACGGTC
		3'-end	MAS958	SEQ ID NO: 7556 ACTACCTTGCCCCTAAGATC
	Nest PCR	5'-end	MAS957	SEQ ID NO: 7557 TGCCACGACAAGAATTTCAT
		3'-end	MAS959	SEQ ID NO: 7558 TGGTGTGATTCCAACGC

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

First PCR	3'-end	GM_UnDo_3'F	SEQ ID NO: 7559 CAAATTCCCACTAAGCGCT
Nest PCR	3'-end	GM_UnDo_3'_NST	SEQ ID NO: 7560 TAAAGGTGAGCAGAGGCA

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 soybean 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 32 of the optimal nongenic soybean genomic loci. All treatments were conducted in replicates of 3-6 and presence of the anticipated PCR product in multiple replicates ($\geq$ 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 soybean selected genomic loci targets that were tested, targeted integration was demonstrated within the soybean representative genomic loci targets by one or more ZFNs, which confirms that each of these loci were targetable. Furthermore, each of the soybean selected genomic loci targets was suitable for precision gene transformation. The validation of these soybean selected genomic loci targets were repeated multiple times with similar results, thus confirming the reproducibility of the validation process which includes plasmid design and construct, protoplast transformation, sample processing, sample analysis.

Conclusion

The donor plasmid and one ZFN designed to specifically cleave soybean selected genomic loci targets were transfected into soybean 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.

Over 7,018 selected genomic loci were identified by various criteria detailed above. The selected genomic loci were clustered using Principal Component Analysis based on the ten parameters used for defining the selected genomic loci. A representative of the clusters in addition to some other loci of interest were demonstrated to be targetable.

Table 12. Illustrates the results of the integration of a universal donor polynucleotide sequence within the soybean selected genomic loci targets. As indicated by the * below, donor insertion within OGL37 was only confirmed by a PCR reaction of the 5' and 3' junction sequence.

Name	ID	Location	Cluster	ZFN	Donor	Targeta

			Assignment	(pDAB#)	(pDAB#)	ble Locus (Y/N)
OGL01	soy_ogl_308	Gm02:12048001..1209237	1	124201	124280	Y
OGL02	soy_ogl_307	Gm02:11647001..1168400	2	124221	124281	Y
OGL03	soy_ogl_2063	Gm06:43091928..43094600	3	125305	125332	Y
OGL04	soy_ogl_1906	Gm06:11576991..11578665	4	125309	125330	Y
OGL05	soy_ogl_262	Gm01:51061272..51062909	5	124884	124290	Y
OGL06	soy_ogl_5227	Gm16:1298889..1300700	6	124234	123838	Y
OGL07	soy_ogl_4074	Gm12:33610401..33611483	7	124257	123839	Y
OGL08	soy_ogl_3481	Gm10:40763663..40764800	8	125316	125332	Y
OGL09	soy_ogl_1016	Gm03:41506001..41507735	9	124265	123836	Y
OGL10	soy_ogl_937	Gm03:37707001..37708600	10	124273	123837	Y
OGL11	soy_ogl_5109	Gm15:42391349..42393400	11	124888	124290	Y
OGL12	soy_ogl_6801	Gm20:36923690..36924900	12	124885	124291	Y
OGL13	soy_ogl_6636	Gm19:49977101..49978357	13	124610	124294	Y
OGL14	soy_ogl_4665	Gm14:5050547..5051556	14	124614	124845	Y
OGL15	soy_ogl_6189	Gm18:55694401..55695900	15	124636	124293	Y
OGL16	soy_ogl_4222	Gm13:23474923..23476100	16	124648	124292	Y
OGL17	soy_ogl_2543	Gm08:7532001..7534800	17	121225	121277	Y
OGL18	soy_ogl_310	Gm02:12203001..1222300	18	121227	121278	Y
OGL19	soy_ogl_2353	Gm07:17194522..17196553	19	121233	121279	Y
OGL20	soy_ogl_1894	Gm06:10540801..10542300	20	121235	121280	Y
OGL22	soy_ogl_3218	Gm09:40167479..40168800	22	121238	121281	Y
OGL24	soy_ogl_3333	Gm10:2950701..2951800	24	121234	121280	Y
OGL25	soy_ogl_2546	Gm08:7765875..7767500	25	121249	121284	Y

OGL28	soy_ogl_5957	Gm18:6057701..6059100	28	125324	125334	Y
OGL30	soy_ogl_3818	Gm11:10146701..10148200	30	121265	121288	Y
OGL31	soy_ogl_5551	Gm17:6541901..6543200	31	121271	121289	Y
OGL33	soy_OGL_684	Gm02:45903201..45907300	1	124666	123812	Y
OGL34	soy_OGL_682	Gm02:45816543..45818777	9	124814	121937	Y
OGL35	soy_OGL_685	Gm02:45910501..45913200	1	124690	123811	Y
OGL36	soy_OGL_1423	Gm04:45820631..45822916	2	124815	121937	Y
OGL37*	soy_OGL_1434	Gm04:46095801..46097968	1	125338	124871	Y
OGL38	soy_OGL_4625	Gm14:3816738..3820070	1	124816	121937	Y
OGL39	soy_OGL_6362	Gm19:5311001..5315000	1	124842	124864	Y

OGL	Length	RF(cM/MB)	2nd_hit_coverage	Distance to closest gene	GC%	# genes in 20kb neighborhood	Average expression (root + shoot)	Nucleosome Occupancy	Distance to centromere	# OGLs in 1MB neighborhood
soy_OGL_2474	2552	4.7351184	15.125392	10057	30.17	10	4.1413102	0.18099999	0.90326041	22
soy_OGL_2548	2700	3.6582618	14.777778	2852	26.88	12	3.7315607	0.221	0.72770977	22
soy_OGL_2585	2946	1.2899461	10.013577	1042	25.52	12	2.9309559	0.215	0.65109789	14
soy_OGL_3627	2218	3.2073443	13.570785	2001	28.53	10	10.198528	0.23899999	0.91969407	29
soy_OGL_3814	2300	7.074543	19.782608	1590	27.56	8	8.7047796	0.186	0.568618	15
soy_OGL_734	2668	9.5748711	11.844078	2519	31.52	9	10.050238	0.156	0.88482362	12
soy_OGL_3296	2135	5.3721247	13.629976	1001	28.1	9	13.932695	0.178	0.95424259	23
soy_OGL_3720	2387	7.0987005	8.2111435	2001	30.37	11	6.6584253	0.204	0.82388896	27
soy_OGL_3726	1600	7.6693859	22.5625	3273	25.06	9	6.6042786	0.18000001	0.81016737	19
soy_OGL_3828	2200	7.930079	21.5	1111	28.86	10	10.912975	0.248	0.54653221	29
soy_OGL_5487	1721	4.7314305	18.245207	2001	29.34	5	11.680776	0.17900001	0.86275095	33
soy_OGL_5636	2500	9.2479429	16.959999	4619	29.24	13	6.3739691	0.198	0.54605746	17
soy_OGL_6279	2820	6.4955807	16.950356	6360	32.65	9	11.717101	0.18799999	0.93683362	26
soy_OGL_6166	1700	8.9007568	15.647058	1166	25.76	10	5.2071867	0.12	0.80572546	17
soy_OGL_919	1500	6.3260517	15.933333	3895	24.8	9	3.5792489	0.27399999	0.68844461	26
soy_OGL_1778	1652	5.2867265	16.101694	4944	25.78	9	3.0771959	0.248	0.89673209	21
soy_OGL_6811	2400	6.2792668	4.4166665	3354	31.08	9	12.67293	0.18099999	0.79832876	21
soy_OGL_6851	2100	4.1094298	0	1234	29.14	8	3.6721213	0.133	0.82475317	26
soy_OGL_1678	1927	9.1770983	11.157239	2179	27.5	13	1.4518392	0.17299999	0.71464026	16
soy_OGL_2904	1449	13.152136	19.047619	1001	23.94	12	3.8377242	0.28299999	0.9829511	22
soy_OGL_4785	2400	3.5548639	15.583333	1416	26.58	11	28.48035	0.18799999	0.89184189	9
soy_OGL_6518	1500	6.1901021	16.933332	2498	27.26	10	5.8887963	0.19	0.69817567	31
soy_OGL_6916	1100	8.8029718	25.454546	9423	25.18	10	5.6880126	0.211	0.89270854	21
soy_OGL_1134	1393	5.9220409	19.813353	3678	23.47	14	2.5466967	0.19	0.97978538	25
soy_OGL_3558	1200	6.3657079	20	2495	24.41	10	8.3999929	0.18099999	0.82717651	25
soy_OGL_3561	1500	6.3657079	11.333333	1761	29	8	5.7050643	0.15000001	0.83111167	31
soy_OGL_6250	1232	6.0078726	19.48052	6257	26.29	9	7.4068537	0.169	0.90713137	28

soy_OGL_2715	1669	4.0992632	18.034752	1001	25.88	9	3.6603839	0.175	0.44677621	23
soy_OGL_6471	1600	5.050159	15.25	2361	24.37	7	4.7150226	0.15800001	0.61283356	11
soy_OGL_3985	1297	4.8896408	24.055513	4908	24.13	7	19.697422	0.20999999	0.88617796	12
soy_OGL_4335	1500	6.8360319	17.733334	1799	25.33	9	4.4000506	0.12899999	0.45570469	19
soy_OGL_338	2200	9.5033493	5.909091	2470	28.4	7	10.018653	0.197	0.86216217	26
soy_OGL_3557	2301	6.3657079	8.5180359	1001	26.68	11	8.2481689	0.148	0.82706946	26
soy_OGL_3744	2300	7.8206534	3.8695652	3288	28.39	9	6.5889463	0.20100001	0.77727038	26
soy_OGL_4402	3010	8.6964502	1.1960133	1646	28.83	13	9.6980286	0.21699999	0.56416339	23
soy_OGL_4526	1800	7.9699202	9.833333	2051	28.55	5	7.3128204	0.189	0.76210791	33
soy_OGL_6200	2100	6.9670649	11.857142	2319	27.8	6	5.260211	0.18799999	0.86086923	28
soy_OGL_6583	2264	4.8956351	9.2756186	1743	27.38	11	8.0480194	0.20100001	0.78887469	34
soy_OGL_5173	2200	10.05123	10.090909	4833	28.68	6	4.6494236	0.12	0.86561185	18
soy_OGL_236	3276	11.009411	3.6019535	2539	24.66	10	8.8741741	0.14300001	0.84468693	20
soy_OGL_239	3100	10.989239	17.709677	7350	27.32	11	9.0718832	0.149	0.84759241	21
soy_OGL_270	2200	9.600378	16.227272	3100	21.95	11	8.8036737	0.197	0.89068985	18
soy_OGL_308	4437	10.227943	19.855759	3858	28.89	9	5.7789779	0.15000001	0.94552988	13
soy_OGL_421	2382	14.106673	1.4693534	3882	25.23	11	6.0209594	0.17299999	0.69735664	21
soy_OGL_647	2041	6.9747391	22.292994	3240	19.69	7	10.080466	0.17200001	0.75380385	28
soy_OGL_661	2300	5.3564477	20.47826	5455	23.82	12	2.6425765	0.16599999	0.76740551	36
soy_OGL_684	4100	11.121198	16.268293	3834	24.07	8	18.511387	0.162	0.80061787	20
soy_OGL_685	2700	11.121198	3.2222223	1012	27.22	8	18.511387	0.23800001	0.8008709	20
soy_OGL_686	1920	11.121198	10.104167	4998	22.23	11	17.722586	0.15000001	0.80465043	21
soy_OGL_789	2294	6.6936736	3.3565824	1915	24.71	8	8.8841038	0.148	0.88734376	18
soy_OGL_1036	4600	6.3006811	29.673914	4607	25.08	11	26.238087	0.13600001	0.83635819	26
soy_OGL_1046	2437	5.3530307	30.73451	1795	18.58	10	14.279531	0.15000001	0.84846562	28
soy_OGL_1055	2600	4.5279164	0	4596	25.61	8	11.090158	0.107	0.85850567	27
soy_OGL_1056	1800	4.5279164	7.5555553	2989	24.16	8	11.090158	0.153	0.85871905	27
soy_OGL_1168	2000	9.2707253	18.9	5528	26.35	6	9.386816	0.241	0.91372806	25
soy_OGL_1238	2717	8.8961325	1.8770703	3093	23.62	9	19.53434	0.18700001	0.75490791	25
soy_OGL_1257	3000	10.150949	0	2718	23.76	8	10.256938	0.18799999	0.71100438	19
soy_OGL_1468	1600	9.5639515	10	5368	22.56	5	17.178242	0.211	0.9268176	30

soy_OGL_1545	2700	7.6185937	0	4504	24.62	8	9.4041891	0.193	0.86927974	33
soy_OGL_1812	3168	5.8060555	24.337122	2001	25.72	8	4.1260514	0.19	0.78263092	21
soy_OGL_2266	2164	7.0584383	1.8946396	1001	28.83	7	5.9129581	0.167	0.63652915	44
soy_OGL_2562	2800	5.5703273	7.0714288	2203	23	12	6.5078921	0.198	0.70459092	22
soy_OGL_2681	3100	10.232581	23.096775	4844	24.22	11	10.308086	0.134	0.49895805	26
soy_OGL_2682	2590	10.232581	1.8146719	2079	27.68	11	6.1938624	0.15700001	0.49808741	26
soy_OGL_2694	2433	8.1054287	8.0558977	1001	25.19	13	8.257597	0.18099999	0.47756642	20
soy_OGL_2944	2792	10.211808	27.184814	6029	23.85	9	6.9297071	0.14	0.90871489	17
soy_OGL_3211	2129	6.4012876	13.245655	6180	24.94	9	0.17661087	0.14	0.69792336	36
soy_OGL_3219	1833	9.6985064	0	2001	24.11	9	6.8092341	0.197	0.71120119	48
soy_OGL_3240	3949	9.3938437	3.0134211	1377	30.89	8	6.7143378	0.114	0.72976112	36
soy_OGL_3319	2462	16.211069	0	4312	25.71	9	10.899387	0.113	0.89128572	23
soy_OGL_3690	2800	7.5635667	0	2854	26.5	14	13.12662	0.147	0.89913303	17
soy_OGL_3960	2570	8.0179386	19.805447	3626	21.71	11	15.370297	0.205	0.97188574	10
soy_OGL_4473	1952	7.4516363	17.059425	6356	23.82	9	11.739989	0.122	0.70685071	29
soy_OGL_4487	2200	7.7733254	1.2727273	4030	21.59	8	5.2659235	0.155	0.72137427	31
soy_OGL_4619	4982	7.723742	19.991972	1070	32.23	9	7.262331	0.18700001	0.76514381	26
soy_OGL_4625	3333	3.3767221	8.9408941	4312	25.68	7	10.564915	0.168	0.75032222	32
soy_OGL_4862	4100	6.1728721	27.829268	3247	21.53	12	2.9160559	0.029999999	0.94618279	19
soy_OGL_4975	3100	11.117381	4.6129031	4497	26.54	9	13.073186	0.082999997	0.72420627	17
soy_OGL_5184	2800	12.31167	0	5107	25.39	6	45.372944	0.141	0.92358953	19
soy_OGL_5254	2388	11.939192	0	2335	25.92	9	3.398967	0.16	0.85525608	21
soy_OGL_5290	3100	20.713139	0	3072	25.12	6	20.315092	0.20100001	0.73377436	24
soy_OGL_5488	2109	4.7314305	11.095305	1001	24.98	7	13.686507	0.19400001	0.86175829	32
soy_OGL_5514	2000	5.3180718	22.35	2070	20.6	8	5.4827714	0.176	0.81447512	20
soy_OGL_5528	1632	11.696812	22.058823	4055	20.58	7	5.2450814	0.207	0.7888034	24
soy_OGL_5779	2000	14.565392	7.1500001	3232	20.25	6	7.0112343	0.17900001	0.83576077	42
soy_OGL_5788	1900	14.27938	7.6842103	8660	25	5	15.903885	0.18799999	0.85008776	40
soy_OGL_5859	2807	9.3926363	3.4556465	5712	29.39	7	6.4458461	0.15899999	0.93476021	22
soy_OGL_6220	1700	9.6064777	8.9411764	1616	24.05	5	10.918882	0.191	0.87290728	30
soy_OGL_6278	2352	5.9430509	5.6547618	2488	22.27	10	3.899951	0.206	0.93479931	23

soy_OGL_6433	1669	10.893449	17.016178	2614	22.16	7	6.1063437	0.211	0.552836	34
soy_OGL_6502	3742	8.8186426	9.29984	4741	27.2	7	0.4477345	0.079000004	0.68702793	24
soy_OGL_6542	2200	15.158372	1.4090909	5885	22.13	7	7.9943948	0.16	0.74866188	32
soy_OGL_6613	2374	8.5314484	18.744734	2001	22.03	9	8.2163639	0.16599999	0.87919116	17
soy_OGL_6634	3700	7.9076147	23.432432	6408	27.27	9	8.2880936	0.20299999	0.97669977	22
soy_OGL_6785	3900	10.85284	16.358974	2284	25.02	10	15.174826	0.13699999	0.77170449	20
soy_OGL_6937	2731	10.14607	6.0417428	1001	27.16	10	7.5568752	0.193	0.90791065	19
soy_OGL_41	2900	8.7112885	11.068966	10449	28.24	5	13.354621	0.20999999	0.88145453	31
soy_OGL_656	2000	6.5693884	1.5	3551	26.95	6	2.9733	0.146	0.76081783	29
soy_OGL_679	2000	10.176669	7.5	1119	26.2	6	2.5467901	0.146	0.7907415	19
soy_OGL_801	2386	9.380168	1.7183571	2661	23.59	4	2.0566175	0.162	0.8483839	23
soy_OGL_1022	3100	5.5469222	13.67742	8494	30.41	5	3.7565172	0.21699999	0.82373458	28
soy_OGL_1122	2372	2.2730639	3.5413153	4733	24.11	8	13.075909	0.19499999	0.98064148	15
soy_OGL_1228	2548	9.0944204	6.3579278	8305	25.9	8	5.8535628	0.211	0.76910967	20
soy_OGL_1348	2604	9.3001719	16.551458	2439	24.73	7	9.6657457	0.189	0.73832768	14
soy_OGL_1376	2710	5.7269979	14.095941	10182	28.04	5	7.8668766	0.17900001	0.79402196	35
soy_OGL_1429	1666	11.258756	17.346939	7342	21.24	8	20.120493	0.17	0.8771143	22
soy_OGL_1996	2745	6.4805918	5.3916211	2001	27.32	10	25.927839	0.206	0.45056608	19
soy_OGL_2086	3246	1.2675809	10.967344	1760	22.15	8	17.728191	0.161	0.75689882	14
soy_OGL_2180	2400	9.0303373	2.5833333	2305	23.45	5	5.6044245	0.107	0.80283487	26
soy_OGL_2224	1923	6.3921266	10.50442	2840	19.96	10	5.2993641	0.19599999	0.72465032	16
soy_OGL_2404	1942	11.967738	1.6992791	5605	26.72	7	7.1358285	0.118	0.69946527	26
soy_OGL_2418	1964	11.967738	0	2520	19.9	6	4.0673723	0.178	0.71408784	28
soy_OGL_2428	1844	11.372036	6.9956617	4532	25.48	6	8.6511011	0.20200001	0.72509056	26
soy_OGL_3914	2188	9.3006687	0	1001	27.92	4	8.0218563	0.142	0.79138416	23
soy_OGL_4128	2496	10.772899	11.538462	8127	23.99	4	6.7534723	0.102	0.82132208	33
soy_OGL_4319	3894	4.1891932	2.8248587	2001	28.37	9	6.968749	0.111	0.42554167	22
soy_OGL_5266	2148	11.202606	17.039106	7789	24.2	8	3.5827279	0.17399999	0.80597866	19
soy_OGL_5428	2900	6.0296702	12.310345	3065	25.51	5	4.6953516	0.186	0.98236394	11
soy_OGL_5974	2651	10.602359	20.181065	2930	24.44	8	7.8374925	0.161	0.63691068	18
soy_OGL_6304	2378	5.0896368	10.555088	2467	22.75	7	5.991375	0.163	0.98502547	9

soy_OGL_6447	1753	8.9351873	19.224188	3678	23.5	7	11.891234	0.21699999	0.57172096	30
soy_OGL_6764	1500	8.1590166	11.8	9067	24.73	8	2.3516748	0.198	0.74546033	27
soy_OGL_6769	1800	6.4668698	14.611111	3442	19.22	8	7.071579	0.21799999	0.74862766	21
soy_OGL_6864	2066	10.103802	0	5441	27.68	5	16.161953	0.12800001	0.83937597	27
soy_OGL_1098	2200	8.7746096	14.5	1999	25.36	14	23.793364	0.192	0.93384361	19
soy_OGL_1923	2900	12.380065	11.103448	3821	32.55	8	6.3777089	0.17	0.5593279	24
soy_OGL_2469	2132	3.6032016	17.964354	3201	26.21	11	36.975975	0.197	0.90976572	19
soy_OGL_3630	2513	7.9034634	14.484679	2001	27.17	11	5.8406992	0.18099999	0.92203057	30
soy_OGL_825	1800	8.984251	23.166666	1427	25.44	5	10.534933	0.2	0.72409374	23
soy_OGL_211	2459	13.475348	15.819439	6258	30.29	6	2.9730742	0.114	0.82040983	26
soy_OGL_217	2000	12.026331	17.15	2368	25.5	8	8.3443651	0.193	0.82301438	28
soy_OGL_293	2191	11.654119	26.882702	4551	24.96	8	3.448247	0.142	0.91030294	25
soy_OGL_345	3486	6.9483228	27.251865	4374	25.87	9	28.4496	0.20299999	0.85119432	27
soy_OGL_962	2000	12.878034	18.049999	2298	23	9	4.6235776	0.147	0.75113589	28
soy_OGL_1146	2200	5.8387361	1.2727273	4426	27.45	11	19.53536	0.108	0.9654386	28
soy_OGL_1409	1898	14.723554	15.173867	7121	23.76	12	6.1446075	0.191	0.83887756	21
soy_OGL_1434	2168	10.901735	14.391144	2001	23.47	11	25.839436	0.23100001	0.879125	23
soy_OGL_1520	1866	6.1372461	20.73955	2720	24.06	7	4.4258075	0.15000001	0.9082554	34
soy_OGL_1763	2620	17.394621	3.778626	2001	27.74	11	19.989632	0.123	0.95592082	11
soy_OGL_2142	1911	6.6979451	22.135008	2292	24.38	7	6.3605633	0.148	0.86464626	30
soy_OGL_2155	2100	6.6362858	25.476191	3448	25.19	8	15.850225	0.25799999	0.85126603	32
soy_OGL_2192	1745	10.131039	23.610315	7307	24.87	8	4.1819887	0.21699999	0.7859658	28
soy_OGL_2414	2949	11.967738	18.209562	3405	25.43	5	25.648056	0.106	0.7093789	32
soy_OGL_2550	2400	3.931226	25.416666	2627	25.12	10	28.229572	0.162	0.7211678	22
soy_OGL_2916	2212	9.6217709	15.777576	4786	26.35	10	10.522021	0.207	0.96971864	28
soy_OGL_3198	2164	8.3576651	5.4528651	3498	29.75	7	14.392322	0.071000002	0.68987459	32
soy_OGL_3225	3618	7.901536	27.224987	5609	30.09	8	9.0807581	0.163	0.71375972	46
soy_OGL_3578	2339	5.4506187	9.4912357	1192	27.91	7	3.8604512	0.107	0.84207696	41
soy_OGL_3728	2100	8.0193291	16.952381	2294	23.38	12	14.44997	0.169	0.80768239	20
soy_OGL_3765	2200	12.909667	12.454545	2908	26.9	11	10.472178	0.16500001	0.73578113	21
soy_OGL_4138	2400	10.603049	0	4932	29.2	9	24.335798	0.154	0.83807945	27

soy_OGL_4653	1941	6.4945478	19.732098	5177	22.66	8	33.990295	0.171	0.70905226	29
soy_OGL_4690	2400	10.074121	21	3438	28.04	8	4.15446	0.199	0.62565362	39
soy_OGL_4799	2000	13.103085	15.95	1437	25.3	6	4.0823641	0.118	0.9195835	14
soy_OGL_4826	2476	16.127125	17.932148	2189	25.48	10	11.493875	0.2	0.96879971	21
soy_OGL_4950	2124	9.2272205	36.817326	2179	22.36	6	5.8810401	0.175	0.7556991	34
soy_OGL_4986	2200	9.4545498	18.181818	2790	25.77	8	6.9631076	0.12899999	0.70813841	27
soy_OGL_5220	2010	10.696481	16.069653	5169	24.67	8	31.523197	0.192	0.93544155	27
soy_OGL_5237	1922	10.406966	18.05411	1611	25.49	5	8.452527	0.155	0.88810229	25
soy_OGL_5304	1913	24.034395	16.779926	1602	23.47	6	4.1561785	0.18799999	0.70030487	24
soy_OGL_5491	2850	4.7314305	15.368421	3253	26.73	8	32.013023	0.064999998	0.86023754	34
soy_OGL_5520	1880	8.5462761	19.787233	3327	24.14	9	9.9577217	0.13699999	0.80109274	27
soy_OGL_5538	2500	8.6176863	13.64	4582	24.56	7	26.087864	0.067000002	0.78236014	26
soy_OGL_5610	2808	25.029232	8.8675213	2001	27.17	5	6.2008328	0.21600001	0.63164753	27
soy_OGL_5795	1915	14.27938	7.8328981	7062	29.24	6	13.465201	0.184	0.85405886	40
soy_OGL_5800	2079	12.976668	0	5088	27.65	8	16.874744	0.127	0.85881108	37
soy_OGL_5836	2300	13.562174	32.04348	3963	22.21	6	6.9067574	0.15099999	0.96286136	22
soy_OGL_5880	2700	10.300918	11.518518	8563	29.25	11	6.1319299	0.077	0.89808166	35
soy_OGL_5898	2379	10.121329	20.975199	5799	28.75	6	4.4611826	0.12899999	0.87653059	31
soy_OGL_6286	2300	6.7950077	23.304348	7145	24.86	11	8.0094957	0.17200001	0.94097483	29
soy_OGL_6560	2541	11.084569	7.0838251	1128	27.9	11	6.809772	0.17900001	0.76577991	38
soy_OGL_6784	2600	11.164678	19.153847	4087	24.42	10	10.841432	0.123	0.77100062	20
soy_OGL_255	1653	12.798174	34.78524	4408	22.68	5	6.2371178	0.241	0.86754757	19
soy_OGL_2173	2000	8.9299202	19.85	3672	26.7	5	13.323011	0.155	0.81397706	25
soy_OGL_3479	1859	6.0115023	20.27972	2571	25.98	7	21.815693	0.17900001	0.64728469	27
soy_OGL_6417	1700	10.893449	11	3065	24.58	7	19.881029	0.16	0.54186928	32
soy_OGL_4496	2033	7.665381	23.708805	10666	24.34	6	16.984371	0.177	0.73656315	34
soy_OGL_31	2100	10.279623	14.952381	12355	30.47	7	8.898572	0.088	0.89663637	31
soy_OGL_939	2388	12.449766	17.58794	9073	24.87	8	9.2474375	0.085000001	0.70968133	28
soy_OGL_1974	2300	11.715036	19.130434	5621	29	7	10.322206	0.204	0.48638961	26
soy_OGL_2995	1965	9.2852879	31.857506	3915	23.05	6	10.341913	0.126	0.80432314	21
soy_OGL_4173	2523	20.926271	15.973048	1005	25.32	12	5.4792271	0.133	0.1680323	15

soy_OGL_4497	2000	7.665381	29.15	6799	23.25	6	16.984371	0.117	0.73670042	34
soy_OGL_4949	1718	9.4054356	19.906868	5337	23.69	5	10.767612	0.139	0.75622225	35
soy_OGL_5530	1704	11.696812	32.159626	6927	21.36	6	6.7085514	0.17	0.78837913	24
soy_OGL_6319	2100	10.294255	10.476191	6516	27.85	6	11.106761	0.072999999	0.93558723	20
soy_OGL_967	1800	11.99724	3.1111112	2771	22.11	9	14.829833	0.141	0.75862414	42
soy_OGL_3635	1727	7.1081796	16.27099	1001	22.17	7	3.9901657	0.14399999	0.93002641	32
soy_OGL_4134	2000	10.342244	0	2920	26.8	5	5.5997505	0.082999997	0.82999235	32
soy_OGL_5256	1836	11.939192	17.864923	2001	22.22	8	5.493237	0.13500001	0.85100484	19
soy_OGL_5810	2000	12.425729	14.9	2286	20.7	6	9.6553631	0.133	0.88021821	37
soy_OGL_7008	2334	7.8198791	13.4533	2001	23.56	12	10.844602	0.093999997	0.97709817	10
soy_OGL_246	1982	15.037194	5.4994955	6728	23.61	8	18.016417	0.085000001	0.85782057	20
soy_OGL_1289	2489	6.4559865	12.253918	1449	23.18	9	3.4724357	0.061000001	0.65351361	16
soy_OGL_1691	2135	6.2621088	21.358315	2001	20.42	7	21.17968	0.106	0.80464488	21
soy_OGL_3924	1900	8.8987665	19.31579	2951	22.1	6	1.5740427	0.142	0.82245034	19
soy_OGL_351	1568	3.5052428	13.329082	2805	20.66	8	6.7967172	0.175	0.84502548	29
soy_OGL_716	2000	9.6048651	0	2849	24.65	9	3.8705969	0.12	0.85511822	26
soy_OGL_936	1720	12.449766	2.1511629	1499	21.16	9	7.3953042	0.17299999	0.70938921	28
soy_OGL_1681	2101	9.1770983	7.6630177	3744	25.17	11	2.1957674	0.068999998	0.72340864	17
soy_OGL_1769	2046	5.2867265	0	2222	21.94	10	11.733743	0.138	0.90911365	20
soy_OGL_3220	1389	9.6985064	0	6860	20.87	9	7.967824	0.205	0.71141201	48
soy_OGL_3476	1356	7.0972891	13.716814	4728	21.97	10	3.8840365	0.184	0.64103329	30
soy_OGL_83	1411	8.729229	17.71793	3907	22.18	6	6.218513	0.156	0.79727209	29
soy_OGL_272	1744	9.3673096	0	4436	22.99	6	5.7373056	0.15099999	0.89593965	26
soy_OGL_2611	1400	8.0021572	21.785715	1979	21.21	8	2.9736359	0.17900001	0.5985105	21
soy_OGL_6512	1200	7.9388223	16.166666	1998	19.16	6	5.6606731	0.20999999	0.69249296	26
soy_OGL_3634	1600	6.9585147	13	3306	26.81	6	7.2701283	0.111	0.92831689	31
soy_OGL_6991	1649	5.2089171	13.220134	1001	23.71	10	10.86401	0.15700001	0.95283258	27
soy_OGL_1154	2797	5.8387361	17.769039	2001	22.98	8	15.162896	0.016000001	0.95932907	28
soy_OGL_3226	2102	6.8329549	26.97431	2409	22.78	9	5.0474343	0.106	0.71627361	44
soy_OGL_4825	2009	16.127125	12.244898	1985	22.99	8	4.9981112	0.132	0.96793979	22
soy_OGL_5496	2125	4.6145062	27.435293	4687	22.44	9	9.8971109	0.090000004	0.84859282	29

soy_OGL_5804	2000	12.976668	12.4	3441	23.65	8	5.0404358	0.127	0.86174273	39
soy_OGL_6553	1700	13.347547	10.823529	3434	23.11	8	5.138762	0.133	0.75892162	33
soy_OGL_4964	1800	8.548089	11.5	2954	25.94	7	9.1513243	0.122	0.74193734	24
soy_OGL_5789	1593	14.27938	0	8600	27.24	5	15.903885	0.086999997	0.85027719	40
soy_OGL_2985	1456	12.115561	24.931318	10598	22.11	7	2.9843612	0.168	0.82077861	26
soy_OGL_5246	1800	8.8967266	25	3028	21.55	5	4.147193	0.122	0.86860973	22
soy_OGL_3124	1500	6.9868913	19.866667	2302	23.4	9	14.700299	0.147	0.5420993	23
soy_OGL_4708	1500	5.5082192	16.266666	2490	25.86	7	17.006468	0.111	0.59407192	34
soy_OGL_240	1900	10.989239	9.1578951	8925	28.94	9	5.9469886	0.20200001	0.84778827	21
soy_OGL_311	2117	12.280725	1.3226264	1217	25.22	14	7.8003659	0.162	0.94003975	13
soy_OGL_1494	2337	7.2145576	0	1001	26.87	8	4.5038624	0.2	0.97676229	21
soy_OGL_1518	2100	6.1372461	0	3505	29.95	7	4.2856436	0.18700001	0.9088214	34
soy_OGL_1837	2200	7.2193756	5.0454545	3271	28.59	10	12.419601	0.18799999	0.75034738	27
soy_OGL_3692	2200	7.5635667	7.6363635	1525	26.4	11	15.188411	0.183	0.89615881	17
soy_OGL_4505	2044	8.4976664	0	2429	27.78	11	6.9530296	0.17200001	0.74377334	34
soy_OGL_4624	1900	4.2397704	2.2631578	3336	26.73	10	8.0719843	0.186	0.75147712	31
soy_OGL_5568	1727	7.8903503	13.607411	2269	24.14	11	6.7771802	0.21799999	0.7090373	19
soy_OGL_6595	2085	5.3763165	3.2134292	4389	26.28	10	7.6018333	0.17200001	0.80457884	18
soy_OGL_6988	1718	5.3196578	7.2176948	2924	27	8	10.061532	0.192	0.95072281	33
soy_OGL_88	2000	7.4370308	0	1968	30.4	5	6.7680936	0.115	0.77794546	29
soy_OGL_1268	1800	6.6517758	5.6666665	2367	24.77	9	3.7714794	0.171	0.68890792	22
soy_OGL_3976	2517	5.9767532	3.5756853	2310	26.77	8	13.184696	0.222	0.90993398	8
soy_OGL_4413	1400	7.0703177	23.928572	2799	21	10	10.09301	0.29300001	0.58279443	15
soy_OGL_2233	1840	7.2443314	3.4782608	2001	25.48	8	8.1796188	0.138	0.70576608	19
soy_OGL_433	2200	10.683906	1.2727273	2790	24.09	10	18.749006	0.226	0.67552251	20
soy_OGL_952	1800	13.818732	3.7777777	4255	26.72	8	7.0253372	0.191	0.74496537	21
soy_OGL_1230	1800	9.0944204	7.9444447	2944	24.11	10	24.082441	0.208	0.76365787	23
soy_OGL_1231	1900	9.0944204	5.2631578	3898	24.68	9	34.550797	0.192	0.7621491	23
soy_OGL_1399	1800	13.123453	0	1907	23.83	9	5.2277102	0.20299999	0.82409471	30
soy_OGL_1530	1573	7.269011	0	3556	26.7	6	3.7856958	0.18000001	0.88955355	35
soy_OGL_2162	1755	8.4397182	0	2001	23.87	9	17.951363	0.189	0.84325397	30

soy_OGL_2889	1813	8.9753227	8.383894	4155	22.94	10	8.1575403	0.22499999	0.86943179	21
soy_OGL_2943	1845	10.211808	4.0650406	1001	23.9	8	6.8633733	0.175	0.90935743	17
soy_OGL_3732	2074	8.292532	0	2001	25.36	7	4.6587062	0.24600001	0.797921	25
soy_OGL_3741	1600	9.2434053	6.8125	4840	21.62	9	32.929966	0.182	0.78238624	25
soy_OGL_4676	2064	10.891823	0	2441	25.38	6	31.075703	0.23999999	0.64717883	38
soy_OGL_5893	1967	10.038893	1.8301983	2208	25.77	8	20.498253	0.24600001	0.88459355	36
soy_OGL_103	1700	12.394506	13.470589	2607	24.11	7	2.4379919	0.244	0.74197578	20
soy_OGL_733	2000	9.5748711	0	3026	24.05	8	7.3777642	0.146	0.88441813	12
soy_OGL_1467	1654	9.5639515	0	8930	26.66	6	15.43951	0.154	0.92667878	30
soy_OGL_2431	1300	10.836329	19.076923	8909	22.69	10	3.3376844	0.21699999	0.73003125	21
soy_OGL_3462	1961	8.8457031	4.0285568	1001	22.79	9	3.9476848	0.21799999	0.61824048	18
soy_OGL_6578	2000	4.8296428	0	2968	27.55	6	9.4776993	0.17399999	0.78334481	31
soy_OGL_2407	1800	11.967738	2.6666667	2068	31.5	5	5.6370821	0.132	0.70392632	31
soy_OGL_2976	1900	11.959558	8.5263157	1248	29.52	6	7.9338775	0.141	0.83243406	23
soy_OGL_199	1600	11.833065	11	8941	28.62	7	4.6893544	0.171	0.81033242	27
soy_OGL_4663	1771	8.1218634	3.3879163	2543	29.7	7	9.3669758	0.11	0.6754052	28
soy_OGL_1050	1746	5.3472867	9.3928976	1001	25.94	9	29.520901	0.15899999	0.8542254	29
soy_OGL_1755	1653	14.15404	4.7186933	1475	24.19	8	19.939375	0.185	0.9693976	20
soy_OGL_1756	2301	17.394621	0	1001	24.33	10	43.45808	0.16	0.95947725	13
soy_OGL_2941	2039	11.741648	3.9725356	1057	23.49	13	25.120295	0.18700001	0.9166196	20
soy_OGL_3140	1900	12.683842	3.1578948	1147	28.31	10	9.0940962	0.16	0.56490809	29
soy_OGL_4673	2045	10.891823	0	1893	30.56	6	12.59456	0.112	0.64989901	35
soy_OGL_5306	1600	23.026314	2.875	3561	25.62	9	9.9472685	0.175	0.69432926	24
soy_OGL_5865	1700	9.1074429	4.8235292	3935	23.35	7	49.045826	0.176	0.93057144	24
soy_OGL_38	1500	10.190989	9.4666662	3588	28.66	4	19.22706	0.16500001	0.885903	29
soy_OGL_5315	1700	18.329891	11.411765	2381	28.23	3	4.2877789	0.21699999	0.67524999	27
soy_OGL_5590	2000	6.0190163	6.0999999	2431	26.5	9	24.153839	0.108	0.6703065	21
soy_OGL_1261	1200	12.536279	24.833334	2054	23.75	6	10.101346	0.229	0.70959651	21
soy_OGL_1920	1571	13.194177	11.775939	2001	26.92	7	4.3148499	0.163	0.56107265	21
soy_OGL_1373	1363	5.7269979	15.480557	2001	24.72	7	4.5002255	0.193	0.79273224	33
soy_OGL_1513	1500	6.1372461	13.066667	4088	24.06	7	6.2125831	0.182	0.92167264	22

soy_OGL_723	1900	9.0755138	1.6315789	3262	27.73	11	5.2020826	0.118	0.86404163	21
soy_OGL_1838	1782	7.2193756	0	1001	25.86	10	3.8830335	0.147	0.74372137	29
soy_OGL_5499	1762	4.4415636	4.9943247	4856	27.46	8	11.508561	0.111	0.84781373	29
soy_OGL_6628	1300	9.3168287	11.923077	5290	23.84	10	7.9379802	0.19	0.96409327	24
soy_OGL_4808	1700	5.6626678	5.4117646	4842	25.23	8	10.632457	0.13500001	0.94147074	15
soy_OGL_4967	1656	10.245035	13.103865	2001	24.75	8	7.0114961	0.146	0.73609108	16
soy_OGL_6201	1163	6.9670649	12.037833	7556	24.41	7	6.0217009	0.199	0.86099356	26
soy_OGL_295	1260	10.220044	9.3650789	8120	21.66	10	12.692679	0.208	0.91279662	24
soy_OGL_1440	1801	8.1389084	0	2001	19.54	14	17.442259	0.21600001	0.89828491	25
soy_OGL_2156	1700	6.8597155	0	2123	25.88	7	13.869737	0.127	0.8506881	32
soy_OGL_4656	1653	7.6261792	5.5656381	1001	21.29	9	14.67893	0.156	0.68531615	24
soy_OGL_4706	1527	9.078599	6.0248852	2126	24.29	11	2.5662351	0.153	0.60136598	32
soy_OGL_4934	1378	9.3127365	3.2656024	8880	23.58	11	18.761217	0.162	0.76324075	40
soy_OGL_5486	1600	4.7314305	0	2040	24.5	6	14.019121	0.162	0.86336017	33
soy_OGL_196	1796	10.74993	0	6449	24.44	8	6.3244686	0.13500001	0.8040728	22
soy_OGL_316	1780	12.282213	1.8539326	4972	21.4	9	4.0902534	0.156	0.92767209	14
soy_OGL_428	1684	12.23607	0	2762	25.35	7	6.0587306	0.13600001	0.68440163	22
soy_OGL_991	1400	9.5245228	5.8571429	2644	24.5	4	2.0967381	0.16500001	0.77290571	30
soy_OGL_1415	1657	11.014842	7.1816535	5183	23.71	9	3.6490135	0.13600001	0.85397673	16
soy_OGL_2645	1331	7.4653587	14.876033	3664	20.51	9	8.59657	0.183	0.545443	26
soy_OGL_4675	1520	10.891823	0	5118	21.11	6	31.075703	0.17	0.64735377	36
soy_OGL_6350	1983	5.8339896	0	1236	26.12	6	2.6293054	0.114	0.88745105	23
soy_OGL_6756	1454	9.5540066	0	3234	23.38	5	4.1094713	0.156	0.73882061	31
soy_OGL_1034	1897	6.3006811	5.3241959	2001	27.14	10	10.701594	0.127	0.83564883	26
soy_OGL_681	1263	10.540062	19.081553	2486	24.54	8	12.144063	0.19	0.7972647	23
soy_OGL_1171	1358	8.592926	11.045655	3450	25.11	8	11.654327	0.153	0.9104799	27
soy_OGL_1380	1100	5.7269979	16	4828	24.27	8	11.415756	0.19400001	0.79680997	35
soy_OGL_1131	1213	5.8739777	24.072548	1001	19.04	11	32.151379	0.226	0.9888252	16
soy_OGL_4701	1282	9.078599	13.26053	2566	24.8	10	11.920033	0.20299999	0.61070585	39
soy_OGL_4915	1405	17.460024	12.669039	3983	23.62	8	16.693867	0.16500001	0.7804594	22
soy_OGL_5793	1200	14.27938	7.3333335	1349	24.33	6	11.499333	0.207	0.85328239	40

soy_OGL_2417	1370	11.967738	13.065694	1001	25.47	5	5.4993415	0.156	0.71307361	28
soy_OGL_3825	1500	7.7698202	14.933333	3127	25.8	8	15.441713	0.12899999	0.55381972	27
soy_OGL_1009	1998	5.2490602	16.266266	2339	24.57	11	9.0358582	0.176	0.80811375	20
soy_OGL_1095	2442	8.2058859	12.776413	1001	26	12	5.3322392	0.18799999	0.931651	17
soy_OGL_2867	2355	5.7699661	19.915073	5224	24.58	12	8.187376	0.13600001	0.79344147	18
soy_OGL_6967	1538	4.4204926	25.097528	3102	22.62	7	3.7845838	0.226	0.93962443	32
soy_OGL_610	2140	7.0958691	15.233644	1001	24.71	9	2.0661132	0.121	0.68405229	17
soy_OGL_736	2100	9.5748711	19.619047	6978	26.57	9	7.4709315	0.15099999	0.88845879	10
soy_OGL_989	2100	9.5245228	18.047619	6744	30.76	4	2.0967381	0.226	0.77276731	31
soy_OGL_2572	2400	6.9173665	11.333333	2523	26.95	9	5.66365	0.197	0.68406993	16
soy_OGL_2713	2069	4.0992632	28.081198	3908	24.31	10	4.3808403	0.191	0.4473787	23
soy_OGL_2725	3070	6.6581216	24.592834	3550	27.62	9	5.9576149	0.20100001	0.42973426	17
soy_OGL_4341	3567	5.8494349	5.2705355	1045	30.92	10	2.6560655	0.17200001	0.46536359	15
soy_OGL_4399	2800	8.2008438	13.357142	6275	32.03	7	2.2511752	0.169	0.56037229	25
soy_OGL_5142	3200	4.3852158	29.8125	6245	28.21	7	8.1066923	0.18700001	0.74005955	21
soy_OGL_5761	2200	9.3894997	26.818182	3508	26.13	7	3.7393308	0.23800001	0.77670193	14
soy_OGL_6158	2913	5.245831	22.142122	5169	29	6	5.5651112	0.148	0.79457057	18
soy_OGL_669	2798	4.2763386	12.902073	3850	28.05	10	3.8762839	0.12800001	0.77518195	31
soy_OGL_317	1783	12.282213	21.536736	2322	26.92	6	7.4557204	0.17399999	0.92686033	14
soy_OGL_412	2538	11.200636	27.659575	2215	27.34	10	6.6451292	0.20999999	0.72619647	16
soy_OGL_697	1712	11.121198	20.502337	1902	25.64	8	5.81318	0.167	0.81601238	18
soy_OGL_772	2200	10.280827	22.045454	3217	26.4	10	9.2871389	0.226	0.95328122	17
soy_OGL_1096	2000	8.3014231	20.1	1613	23.9	11	3.5724134	0.17399999	0.93224621	17
soy_OGL_1185	2400	4.3006682	18.25	7015	29.58	10	15.216886	0.20100001	0.89490348	28
soy_OGL_2217	2900	6.146626	29.793104	2959	27.27	8	4.5546699	0.17	0.75035322	25
soy_OGL_3589	2749	5.1424751	31.247726	2001	27.5	6	5.7113924	0.16599999	0.85348511	32
soy_OGL_3625	1766	3.9820173	23.839184	4059	23.44	12	7.0094223	0.176	0.91653258	25
soy_OGL_3746	2198	7.8206534	14.149226	2403	27.52	12	5.8663383	0.114	0.77684981	26
soy_OGL_4094	2500	12.218921	16.959999	2560	30.32	7	7.4986134	0.18700001	0.66347319	19
soy_OGL_4107	2055	12.218921	9.051095	1715	29.92	8	2.6119208	0.090999998	0.69881886	19
soy_OGL_5212	1700	7.9554181	23.411764	7817	27.41	7	6.3373933	0.138	0.95407319	26

soy_OGL_5249	1509	9.2979841	25.9112	1001	23.65	7	4.5305872	0.243	0.86467075	21
soy_OGL_5255	3108	11.939192	13.642214	1538	30.98	9	4.3969364	0.20200001	0.85347563	21
soy_OGL_5637	2735	9.2479429	23.107861	1001	26.54	12	6.4862795	0.126	0.54588282	17
soy_OGL_5853	2300	8.4169607	5.4347825	2833	26.52	15	6.1049166	0.131	0.94951022	16
soy_OGL_6246	2770	5.8414173	16.498196	1164	25.99	13	3.1639693	0.093999997	0.90208763	20
soy_OGL_6821	2637	6.4448819	23.170269	4912	30.18	6	9.7099628	0.164	0.8077755	33
soy_OGL_6923	1765	8.8029718	14.957507	1685	28.04	4	8.976058	0.21799999	0.89673173	26
soy_OGL_6949	1945	10.483934	24.884319	1198	25.24	8	9.6910143	0.204	0.92379749	22
soy_OGL_4281	2309	5.0444984	24.512775	2001	25.03	11	6.4427238	0.148	0.37003669	22
soy_OGL_3645	2353	5.1482658	25.58436	2001	26.22	6	10.90022	0.139	0.93672913	29
soy_OGL_2695	1800	8.1054287	30.333334	1460	24.61	10	7.0172319	0.191	0.47592309	21
soy_OGL_2249	2300	3.1746132	35.391304	4750	26.6	7	13.574811	0.215	0.65801376	27
soy_OGL_3189	1761	9.911809	22.544008	1724	26.12	6	8.9500923	0.15099999	0.66896093	24
soy_OGL_4445	2300	6.1747808	24.608696	2010	28.13	7	15.452724	0.147	0.63963956	17
soy_OGL_4534	1996	7.1095409	34.919838	9449	24.79	8	2.6231968	0.17200001	0.77642733	30
soy_OGL_4291	2272	4.9876347	30.017605	1379	22.4	9	4.8266916	0.108	0.38516104	25
soy_OGL_357	1297	4.0336118	30.7633	6418	21.74	7	1.0748448	0.182	0.83666217	29
soy_OGL_1704	1500	6.6742897	21.933332	2105	23.13	9	2.2142594	0.18000001	0.81470692	29
soy_OGL_1808	1300	5.8060555	32.153847	2408	21.92	8	6.3081136	0.204	0.78341556	21
soy_OGL_2251	1579	4.5184188	39.075363	2001	20.45	11	7.4144316	0.183	0.65510446	25
soy_OGL_2253	1348	4.5184188	35.237389	5002	21.06	10	6.9639869	0.20100001	0.65384406	26
soy_OGL_2295	1627	9.7439394	19.791027	2001	25.56	9	2.6099527	0.14300001	0.60603774	28
soy_OGL_2934	1400	10.117199	29.071428	5831	23.07	8	4.4632311	0.176	0.9326936	17
soy_OGL_3542	1600	8.9636507	17.75	4672	26	9	2.9686823	0.14399999	0.79967874	24
soy_OGL_4581	1637	5.9374781	30.238241	1200	21.74	8	5.7000861	0.13699999	0.83575362	19
soy_OGL_5261	1500	10.745309	25.866667	2960	24.4	9	3.1348195	0.17200001	0.81610364	15
soy_OGL_6977	1600	4.486526	20.625	3762	24.81	8	9.0974751	0.132	0.94339371	33
soy_OGL_6990	1700	5.2089171	20.17647	2750	25.47	10	10.86401	0.147	0.95279348	27
soy_OGL_1474	1875	9.0376148	6.6666665	1843	28.26	11	3.6160002	0.109	0.93958235	27
soy_OGL_2124	1309	8.9817944	27.11994	3130	22.3	8	3.2018571	0.178	0.90222043	19
soy_OGL_2160	1377	8.3984585	18.228031	2001	25.12	8	7.0188665	0.15899999	0.84549648	30

soy_OGL_6199	1400	7.8401752	21.142857	2703	25.35	6	5.260211	0.147	0.86062223	28
soy_OGL_6205	1292	6.0506825	22.755419	2256	25.85	6	5.6331906	0.163	0.86637127	31
soy_OGL_6622	1700	9.2474756	30.17647	5029	24.29	6	6.0738239	0.13	0.95193809	15
soy_OGL_5239	1624	9.6026649	12.068966	4540	27.83	5	3.9811876	0.103	0.88298023	25
soy_OGL_5481	1490	4.7314305	18.993288	5587	26.3	6	14.212135	0.113	0.86412644	33
soy_OGL_6901	1800	7.0806479	18.611111	5909	25.38	7	5.4564981	0.085000001	0.8718214	24
soy_OGL_676	1417	3.8562949	17.501764	3118	23.85	8	6.1691256	0.2	0.78103495	25
soy_OGL_1445	1705	10.643933	8.6217012	3610	28.91	9	6.5441084	0.169	0.90603346	27
soy_OGL_3757	1800	7.166008	12.444445	2106	28.77	6	16.883402	0.184	0.75122744	22
soy_OGL_5251	1533	9.3134089	18.264841	4057	28.11	5	11.389889	0.189	0.86065853	22
soy_OGL_6575	1200	4.8296428	16.083334	3103	24.75	5	6.8550858	0.20100001	0.78203601	30
soy_OGL_1428	1273	11.258756	18.931658	2054	24.35	8	4.2034006	0.19400001	0.87688363	22
soy_OGL_6834	1600	4.1189404	5.125	2229	28.06	8	4.441812	0.12899999	0.81214923	35
soy_OGL_6871	1300	8.3950586	17.153847	4250	24.92	9	6.5127029	0.19599999	0.8434788	27
soy_OGL_98	1300	10.343252	15.230769	1767	25.53	7	6.575788	0.18000001	0.76221818	22
soy_OGL_100	2100	11.020363	1.7619047	10167	28	5	8.093523	0.193	0.75394547	24
soy_OGL_321	2300	6.0939898	18.869566	5181	22.39	6	4.7707028	0.22400001	0.90000451	14
soy_OGL_472	3100	6.0821934	1.3870968	2029	26.83	4	1.1585951	0.221	0.53551352	25
soy_OGL_497	3545	5.067452	2.9055007	6941	23.44	6	20.439039	0.17200001	0.47603852	24
soy_OGL_831	2376	8.4033613	20.03367	6129	21.04	6	11.642982	0.17	0.71822065	23
soy_OGL_858	2200	7.8775821	5.181818	2781	22.95	6	0.82502174	0.211	0.5868125	14
soy_OGL_1217	2000	6.7576227	1.65	7118	22.95	7	11.496306	0.126	0.81332892	23
soy_OGL_1977	2600	8.880722	0	2474	27.46	4	14.890047	0.21699999	0.48098052	27
soy_OGL_2276	1255	13.583581	14.422311	11152	23.02	5	11.276885	0.227	0.6270358	42
soy_OGL_2379	2900	7.888226	4.2413793	3810	27.03	8	5.2150187	0.121	0.59221417	12
soy_OGL_2540	2559	4.4041967	1.172333	5001	27.62	7	4.7407203	0.126	0.74230272	19
soy_OGL_2636	3143	7.9126515	22.271715	7665	22.81	6	6.4081903	0.193	0.5582782	22
soy_OGL_2662	2400	6.8734031	2.1666667	9747	27.58	8	0.31857952	0.18799999	0.52677619	25
soy_OGL_3029	2104	6.2575397	14.211026	2768	22.14	6	15.037894	0.17	0.74368495	19
soy_OGL_4210	4684	3.5955544	7.4508967	5891	23.12	10	26.026056	0.17900001	0.24140322	13
soy_OGL_4339	2900	5.0690784	8.5172415	6500	24.75	8	16.733919	0.154	0.46198791	19

soy_OGL_4352	2564	3.4308596	6.5132604	1508	25.54	7	9.6073008	0.192	0.48610762	17
soy_OGL_4355	3400	4.5183697	19.705883	3728	25.26	7	8.7101288	0.149	0.49001426	17
soy_OGL_4378	2900	6.6361041	9.034483	6691	26.51	5	9.7372732	0.206	0.52832258	27
soy_OGL_4429	1900	8.8796873	15.263158	2305	24.31	6	21.11968	0.198	0.61539018	23
soy_OGL_4485	2100	7.7733254	18.380953	10230	23.61	7	5.8588023	0.162	0.72115958	30
soy_OGL_5041	1940	7.1623974	13.814433	3296	20	5	10.342859	0.192	0.65014249	21
soy_OGL_5163	1568	6.6491861	11.79847	1496	20.91	3	6.0104885	0.19599999	0.82316512	15
soy_OGL_5601	2000	4.509737	3.95	3525	19	7	8.9869328	0.18700001	0.64968199	21
soy_OGL_5672	2192	6.3148546	10.720803	3149	22.81	6	13.487383	0.199	0.48682407	22
soy_OGL_5953	2490	8.7246323	3.9759035	5537	25.3	7	17.545338	0.108	0.69564337	20
soy_OGL_6215	2300	6.9321399	0	10833	24.86	5	12.188808	0.204	0.86955637	30
soy_OGL_6397	3600	6.8150654	15.166667	8470	29.66	10	14.35309	0.184	0.46793768	12
soy_OGL_6485	2349	8.5538664	6.3431249	3344	25.58	7	5.2517185	0.11	0.64860338	19
soy_OGL_6679	5713	8.8698769	34.430248	8251	32.06	7	0.064067081	0.22499999	0.016893907	28
soy_OGL_6724	2200	8.8704958	17.5	2688	19.04	7	7.8579874	0.171	0.70653409	8
soy_OGL_6740	1940	9.4566698	0	11812	21.7	6	6.9555354	0.186	0.72915387	28
soy_OGL_5158	2480	4.2149191	0	1794	23.99	1	10.243546	0.15700001	0.78354853	19
soy_OGL_93	2000	10.351217	31.299999	12068	25.6	5	7.370636	0.26100001	0.76853335	23
soy_OGL_381	2589	8.0134726	17.921978	11732	26.68	7	1.7226105	0.13	0.78774232	20
soy_OGL_467	1757	5.5066857	17.188389	5053	22.48	7	4.7066665	0.17299999	0.54864609	22
soy_OGL_533	2200	10.494274	15.681818	5586	24.81	8	3.2233608	0.18099999	0.377491	21
soy_OGL_613	1900	3.8726745	17.789474	4033	23.68	7	7.4752541	0.14	0.69285786	21
soy_OGL_997	2000	8.6706457	16.200001	1003	24.4	5	6.4818726	0.126	0.78823107	16
soy_OGL_2181	2164	9.0303373	31.608133	8763	22.04	5	7.6967459	0.182	0.80188984	26
soy_OGL_2268	2400	9.1252251	3.375	12193	26.45	6	3.9890997	0.043000001	0.63564223	43
soy_OGL_3130	1608	8.0850887	16.231344	1824	24.37	5	17.139071	0.162	0.55230165	25
soy_OGL_3257	1647	5.2893763	22.465088	6528	22.95	7	14.836263	0.193	0.82994741	17
soy_OGL_5051	3742	6.5904026	28.166756	2181	26	6	7.7608023	0.142	0.61251324	12
soy_OGL_5746	1760	13.020522	11.988636	5874	23.75	7	7.7043829	0.15800001	0.70817673	15
soy_OGL_6182	2400	6.9349771	1.5416666	6760	28.45	6	4.0068455	0.066	0.82842177	12
soy_OGL_6420	2529	10.893449	17.121391	5737	26.37	4	26.060837	0.206	0.542925	33

soy_OGL_1350	1493	11.76944	12.793035	2251	21.96	1	1.6019849	0.18000001	0.74645257	18
soy_OGL_2836	2086	5.5548873	0	3198	23.44	3	3.2647965	0.131	0.66565418	23
soy_OGL_4773	2339	6.7980485	8.5934162	7768	25.18	3	20.501026	0.229	0.84077072	9
soy_OGL_5648	3400	8.7322464	0	9564	30.2	5	19.165895	0.132	0.53314173	18
soy_OGL_5753	2600	6.5565777	12.576923	9926	27.11	3	4.0766273	0.214	0.75898427	15
soy_OGL_6105	2622	0.46364269	12.128146	1001	20.9	4	3.7327101	0.14399999	0.67263907	12
soy_OGL_6135	2500	3.5176268	5.8000002	8395	24.08	3	21.362064	0.19	0.76276702	15
soy_OGL_6209	2500	5.0835438	0	20844	28.56	3	0.89782125	0.207	0.86877269	29
soy_OGL_6339	1700	5.6879897	15.882353	15429	27.11	4	9.270257	0.204	0.9006936	28
soy_OGL_6362	4000	1.2353655	0	15107	27.67	4	7.4683485	0.152	0.77382976	5
soy_OGL_6477	2004	8.4090519	18.063871	6947	23.3	6	5.8847322	0.16599999	0.63581556	17
soy_OGL_1958	1962	17.340572	19.77574	6913	30.47	6	6.4762211	0.257	0.50349152	22
soy_OGL_2320	2440	11.954895	26.721312	3263	26.47	7	10.145254	0.15099999	0.53030795	17
soy_OGL_6443	1200	9.47616	19.166666	3085	24.83	3	14.663908	0.208	0.5608204	35
soy_OGL_81	1900	8.729229	7.2105265	2668	22.42	4	11.630946	0.122	0.79938179	26
soy_OGL_667	2089	3.7500732	2.7285783	2410	20.77	5	8.5458269	0.094999999	0.77183783	31
soy_OGL_832	2150	8.6910162	5.2558141	4316	21.06	7	8.5962257	0.104	0.71450782	22
soy_OGL_2483	1510	6.4331512	14.238411	9082	22.98	8	5.0985284	0.16599999	0.88733184	22
soy_OGL_3910	2000	9.3006687	10.5	3726	21.75	6	5.2159028	0.107	0.78449982	22
soy_OGL_5484	1400	4.7314305	14.714286	9740	23.71	6	14.019121	0.161	0.86365515	33
soy_OGL_922	1510	11.336674	7.5496688	5431	23.04	6	5.7879272	0.15700001	0.69631636	28
soy_OGL_2085	1847	1.2675809	13.643746	1142	17.16	9	16.820671	0.17299999	0.75613505	14
soy_OGL_5942	1700	9.668354	14.411765	2997	22.11	5	3.3608844	0.146	0.72408676	23
soy_OGL_4365	1587	7.2716579	19.281664	2001	23.06	8	5.2458792	0.123	0.5126937	20
soy_OGL_4612	2012	6.7095437	7.2067595	6243	23.35	8	3.0957539	0.093000002	0.83255553	8
soy_OGL_4713	1235	5.6724916	11.497975	11585	20.8	7	8.433548	0.193	0.58384871	33
soy_OGL_5668	1665	7.7953877	11.171171	4647	19.51	6	6.583478	0.145	0.49533939	20
soy_OGL_3010	2161	6.7379055	0	1474	28.45	4	8.8494091	0.19499999	0.77555317	21
soy_OGL_3152	2530	9.2073507	2.964427	3711	30.94	6	14.045343	0.20100001	0.58348882	19
soy_OGL_6500	1732	8.8186426	8.5450344	10986	27.82	8	2.7572544	0.219	0.68530846	26
soy_OGL_1673	1900	9.1770983	10.947369	5762	25.47	9	18.361645	0.191	0.7053867	15

soy_OGL_2411	1676	11.967738	2.4463007	8898	30.48	5	5.3432283	0.18700001	0.70652366	32
soy_OGL_4947	1075	9.4054356	10.325582	9941	23.72	5	9.1168709	0.25600001	0.75668734	36
soy_OGL_5159	1943	4.2149191	2.9850745	2001	23.05	2	24.922091	0.198	0.78425783	19
soy_OGL_4720	1700	5.4238782	5.4705882	2709	24.17	8	9.0150032	0.15700001	0.57624835	23
soy_OGL_6207	1578	5.0835438	0	8319	24.01	5	1.0745676	0.169	0.8684752	29
soy_OGL_1980	1708	9.5797806	13.348947	4658	27.34	6	7.6422009	0.17900001	0.47706434	26
soy_OGL_4712	1156	5.6724916	13.581315	10205	27.16	7	8.433548	0.177	0.58394402	33
soy_OGL_6154	2085	5.245831	3.5491607	7764	29.44	2	9.8333807	0.204	0.78884023	17
soy_OGL_69	1400	11.427641	8.3571424	14934	27	4	4.8996096	0.234	0.82008487	32
soy_OGL_212	1550	13.095701	2	11342	27.61	4	10.106998	0.183	0.82123142	26
soy_OGL_2416	1644	11.967738	0	8859	27.43	5	25.695505	0.13	0.71115345	30
soy_OGL_5631	1620	24.815081	4.9382715	9078	22.53	9	8.9720602	0.163	0.60237473	13
soy_OGL_5747	1741	15.796243	2.9867892	2872	25.78	3	4.3049641	0.147	0.71982247	14
soy_OGL_5924	1311	8.3593283	17.467583	5071	22.42	6	16.722326	0.2	0.83017349	15
soy_OGL_5040	1766	7.1623974	0	5273	24.06	5	10.342859	0.155	0.65019411	21
soy_OGL_6185	1800	6.60361	0	8232	25.22	5	1.7016568	0.138	0.83841509	15
soy_OGL_4303	1861	4.4824991	15.959162	2423	27.18	7	21.680733	0.17200001	0.39808556	25
soy_OGL_1665	1671	8.7383938	11.011371	1993	23.15	9	2.9340968	0.145	0.62717837	10
soy_OGL_4343	2034	8.1137762	0	2951	22.71	10	5.8134742	0.119	0.46735594	18
soy_OGL_4381	1700	6.6147962	1.6470588	2664	23.58	7	5.9475994	0.156	0.53130758	25
soy_OGL_5768	1251	20.915419	0	12018	24.38	6	3.0320652	0.184	0.81166029	23
soy_OGL_471	1913	6.0821934	0	4688	26.86	7	5.0158277	0.093999997	0.53613454	25
soy_OGL_3013	1700	12.431061	0	10276	27.58	6	9.0727768	0.1	0.7695362	25
soy_OGL_4073	1500	5.8943801	9.333333	3242	22.8	6	5.6086822	0.175	0.52567106	19
soy_OGL_5382	1648	9.3595705	4.186893	5890	20.99	6	7.34658	0.156	0.68703741	14
soy_OGL_809	1643	7.4636521	20.937309	1525	23.73	5	1.4406714	0.207	0.81670314	14
soy_OGL_3699	2266	7.5635667	26.610767	5185	27	5	7.8273826	0.229	0.87791991	12
soy_OGL_4453	2448	3.088691	18.586601	4254	25.73	9	15.32869	0.18000001	0.66401917	10
soy_OGL_614	1800	3.8726745	13.444445	6133	26.11	6	8.1308317	0.177	0.69293064	21
soy_OGL_2532	2434	7.7228384	1.3557929	5209	30.07	7	4.7893958	0.032000002	0.75836366	13
soy_OGL_3394	2732	5.6634336	22.144949	8888	28.14	5	3.1401823	0.212	0.69702762	18

soy_OGL_5981	1789	7.1452026	24.650642	4329	23.7	6	3.3525434	0.18700001	0.61847448	16
soy_OGL_1637	2169	3.861047	9.9585066	7215	24.98	9	3.6471522	0.124	0.56493968	9
soy_OGL_990	1101	9.5245228	24.159855	5391	25.52	4	2.0967381	0.221	0.77283508	30
soy_OGL_4630	1800	3.3767221	29.5	8529	27.61	5	10.339046	0.208	0.74788237	33
soy_OGL_2541	1997	4.1527185	18.077116	4706	26.03	8	8.8115702	0.079000004	0.73781466	18
soy_OGL_3729	1425	6.7785597	21.052631	4497	24.35	6	3.371511	0.16599999	0.80122209	22
soy_OGL_6348	1703	5.6157908	8.3382263	7363	29.71	3	10.773394	0.156	0.893085	23
soy_OGL_184	1400	5.00559	14.571428	3217	23.57	6	2.9806948	0.164	0.7786656	15
soy_OGL_6482	1300	8.3500423	21.23077	6763	23.15	9	6.2699986	0.16	0.6443423	16
soy_OGL_454	1700	3.3159945	9.3529415	2410	23.11	8	4.8089857	0.133	0.57919818	12
soy_OGL_3567	1400	5.4506187	0	3757	24.57	5	7.5929127	0.154	0.83526081	34
soy_OGL_5229	1700	10.238331	5.1176472	3260	26.17	12	12.134748	0.122	0.91863412	21
soy_OGL_1826	1638	9.0145245	0	7651	27.83	8	9.0366697	0.090000004	0.76443505	24
soy_OGL_768	2000	11.362736	23.35	3239	26.95	12	11.601129	0.206	0.97335154	12
soy_OGL_942	1699	12.449766	18.246027	1001	29.54	7	6.2780204	0.156	0.71129572	25
soy_OGL_961	2337	12.878034	16.730852	2414	32.56	9	4.5433908	0.191	0.75064492	28
soy_OGL_2183	1196	9.9214792	30.351171	2001	25	7	7.9453473	0.226	0.79772037	27
soy_OGL_4143	2201	11.063471	19.127668	4030	33.12	6	14.314804	0.189	0.85446519	29
soy_OGL_4442	2000	8.3014889	14.65	2745	28.9	11	12.568135	0.115	0.63501424	20
soy_OGL_6853	1700	8.1319342	23.058823	3850	26.58	10	8.6614132	0.16	0.82872206	24
soy_OGL_6978	1700	4.486526	22.235294	5962	27.52	9	8.3509026	0.16	0.94344151	33
soy_OGL_963	1297	12.433824	27.987663	2780	27.21	8	4.3812647	0.199	0.75394434	30
soy_OGL_5945	1537	10.436343	25.8946	2011	28.43	8	16.51646	0.17399999	0.71676058	25
soy_OGL_244	1600	15.037194	25.5	7524	31.62	7	15.098627	0.163	0.85760373	20
soy_OGL_4514	1483	8.8380184	14.430209	2367	29.19	8	0.9945097	0.139	0.74891138	36
soy_OGL_4645	1300	4.3523932	26.076923	3054	24.38	10	9.1603413	0.19	0.72213727	33
soy_OGL_1079	1617	7.9827704	24.860853	3801	25.47	12	17.474819	0.131	0.89246321	15
soy_OGL_3489	1600	5.426621	19.6875	3524	26.81	10	18.325756	0.15899999	0.65239	21
soy_OGL_426	1625	13.017153	22.092308	2591	29.96	10	13.580084	0.154	0.68897295	24
soy_OGL_966	1100	11.99724	26.363636	2388	29.63	10	14.719779	0.24600001	0.75833291	39
soy_OGL_1101	1796	8.7746096	19.54343	3575	29.51	13	30.508171	0.12899999	0.935395	18

soy_OGL_1220	1500	6.7576227	32.533333	1472	25	13	37.990582	0.244	0.80702633	21
soy_OGL_4383	1680	6.3989863	19.940475	2098	27.5	10	26.531061	0.175	0.53652424	21
soy_OGL_1448	2190	10.671152	12.420092	6514	31.82	9	22.412865	0.21699999	0.9084335	32
soy_OGL_3693	2100	7.5635667	26	2085	23.28	14	22.348526	0.17900001	0.8928026	17
soy_OGL_6944	1435	10.781964	29.89547	5281	24.8	8	20.972143	0.24600001	0.92171949	21
soy_OGL_1251	2496	14.230903	21.033653	2001	27.52	10	14.015292	0.156	0.72587734	18
soy_OGL_2265	1943	9.2565804	20.020586	3965	28.66	6	6.5033641	0.122	0.63666517	44
soy_OGL_2286	2392	12.293853	28.762543	4437	24.45	9	12.359873	0.171	0.62194532	40
soy_OGL_2406	2420	11.967738	36.776859	1125	24.95	5	4.0882888	0.168	0.70270926	30
soy_OGL_2614	2900	8.5876789	27.655172	3624	23.06	12	45.445011	0.079000004	0.59155244	23
soy_OGL_3214	2100	8.5918398	25.666666	8357	25.57	9	13.597588	0.147	0.70408684	42
soy_OGL_3311	1881	14.175031	28.017012	2483	22.64	10	6.1557183	0.15099999	0.90903229	19
soy_OGL_4424	3705	9.7329044	33.711201	5271	30.41	11	24.442911	0.23	0.61441493	24
soy_OGL_4700	1174	8.5891142	23.424191	5715	24.27	9	14.301408	0.214	0.6130017	37
soy_OGL_5215	3316	9.6746111	37.786491	1071	25.18	7	4.4966764	0.064999998	0.95128661	28
soy_OGL_5522	2930	8.5462761	9.5563145	2908	29.21	11	35.497887	0.15700001	0.797912	26
soy_OGL_5766	1600	20.915419	23.9375	3843	24.81	7	2.6367111	0.155	0.8107065	22
soy_OGL_5772	1200	19.448713	18.5	7124	26.5	6	7.1170144	0.19499999	0.8199442	30
soy_OGL_6522	2512	21.291258	23.009554	2214	23.92	10	11.069589	0.156	0.70864177	21
soy_OGL_6747	1958	25.512024	3.6772215	3775	27.47	8	11.37267	0.132	0.73402822	26
soy_OGL_1726	1559	27.230612	22.322001	1001	29.89	11	7.4522734	0.164	0.84480655	24
soy_OGL_2270	1900	10.181895	32.684212	2140	24.52	10	11.429723	0.205	0.63278443	42
soy_OGL_3501	1823	47.600048	39.056499	1967	21	5	8.1240253	0.2	0.71733308	21
soy_OGL_3511	1656	47.600048	29.045895	2427	29.28	6	5.0673656	0.178	0.72791547	23
soy_OGL_3740	1724	9.2434053	21.055685	6640	26.56	11	27.149883	0.132	0.78246349	25
soy_OGL_4508	1783	8.8380184	21.592821	2488	28.88	9	34.511875	0.219	0.74633116	37
soy_OGL_4631	1768	21.698753	23.246607	5178	28.05	7	12.163902	0.14300001	0.7450788	36
soy_OGL_4680	1531	10.891823	26.453299	2001	26.91	8	17.022524	0.163	0.64442283	39
soy_OGL_5219	2219	10.696481	32.131592	2001	26.72	8	31.523197	0.141	0.93562198	27
soy_OGL_5234	1700	28.324619	24.647058	3546	31.7	7	36.420975	0.175	0.90520734	27
soy_OGL_5300	1700	23.178028	14	2611	27.23	9	7.364819	0.16	0.71236587	27

soy_OGL_5607	1291	24.945646	25.484121	4214	27.73	10	3.5488322	0.189	0.6339429	28
soy_OGL_5786	1859	14.27938	35.180206	2001	24.58	4	19.414236	0.167	0.84965271	40
soy_OGL_5796	1400	14.27938	25	6763	27.07	6	8.0969248	0.155	0.85439301	40
soy_OGL_6521	2000	21.291258	26.9	3588	24.5	9	5.8238935	0.113	0.70841658	21
soy_OGL_953	1920	13.818732	27.395834	1707	26.92	5	10.377754	0.17399999	0.74614412	21
soy_OGL_1574	2598	9.8763494	22.517321	5223	26.94	5	43.074696	0.116	0.79642272	28
soy_OGL_4475	1700	7.9795275	21.411764	8786	26.41	10	34.609226	0.149	0.7094872	28
soy_OGL_1952	1757	21.06424	24.871941	2068	24.07	8	11.886632	0.213	0.5153715	15
soy_OGL_3197	1648	8.3576651	31.432039	5556	24.27	7	14.377604	0.142	0.68810278	30
soy_OGL_5767	1131	20.915419	26.436781	7412	27.4	7	2.6367111	0.182	0.81093967	23
soy_OGL_554	2148	21.11812	16.759777	3105	31.56	9	5.3065062	0.167	0.32866451	18
soy_OGL_307	3700	10.227943	9.4324322	1217	25.62	8	240.25928	0.191	0.9473694	13
soy_OGL_1935	2102	18.734249	32.44529	2398	25.73	9	9.7736921	0.152	0.54510707	26
soy_OGL_3217	1400	8.3544016	36.42857	6832	24.64	6	27.235998	0.208	0.7064389	42
soy_OGL_3346	2800	10.06963	20.571428	2615	30.1	10	151.46315	0.171	0.85046083	22
soy_OGL_3499	1635	47.600048	29.051989	3427	24.64	5	5.8800721	0.139	0.71650201	18
soy_OGL_3507	1414	47.600048	33.87553	1381	29.7	7	4.6008244	0.16500001	0.72355372	22
soy_OGL_4146	1518	13.177082	33.135704	3294	27.47	7	33.810951	0.139	0.86302632	30
soy_OGL_4507	1800	8.4976664	24.277779	5487	27.33	8	38.817326	0.13699999	0.74593693	37
soy_OGL_5301	1400	24.034395	31.857143	5920	28.21	9	23.516148	0.13600001	0.70665246	27
soy_OGL_5338	1300	46.125168	22.538462	4971	25.92	9	5.1150856	0.176	0.54373783	11
soy_OGL_5624	1200	36.55751	35.916668	1622	25.66	5	4.44767	0.206	0.61684293	29
soy_OGL_5845	2162	12.328249	24.884367	2001	31.08	7	48.899033	0.13	0.97416353	20
soy_OGL_6540	2574	16.022715	30.03108	3903	29.48	7	17.233465	0.097000003	0.74594653	31
soy_OGL_6750	1723	26.599495	29.889727	2001	29.01	7	7.1662169	0.126	0.73562831	28
soy_OGL_6893	1583	7.0806479	35.249527	2236	21.35	6	46.349056	0.16	0.86713564	26
soy_OGL_1576	2014	8.3843002	5.4121151	2432	30.48	5	43.074696	0.052999999	0.79601109	28
soy_OGL_3213	1427	8.5918398	19.901892	6699	26.06	8	9.6544733	0.15700001	0.70390892	42
soy_OGL_3330	2000	11.347876	32.400002	2552	22.3	9	14.164609	0.115	0.87435025	30
soy_OGL_4137	1700	10.873235	36.882355	3169	21.11	12	6.1128616	0.164	0.83400309	29
soy_OGL_4824	1570	16.127125	22.356688	4015	24.2	9	4.7448487	0.17299999	0.96789318	22

soy_OGL_5781	1367	14.565392	8.2662764	5263	26.84	7	7.5810962	0.167	0.83682567	42
soy_OGL_5908	1765	7.9141469	28.441927	1765	22.54	9	16.557247	0.154	0.86143547	32
soy_OGL_6786	1740	10.647929	19.482759	1734	24.65	10	12.953485	0.148	0.77459282	22
soy_OGL_1725	1747	27.230612	3.777905	1176	23.46	12	10.561194	0.146	0.84449905	23
soy_OGL_5783	1419	14.565392	8.1747713	2001	22.48	8	31.744009	0.184	0.84283847	41
soy_OGL_2940	1657	10.08299	24.984913	2001	25.58	10	37.80241	0.115	0.92434901	17
soy_OGL_3500	1511	47.600048	0	6927	24.28	6	5.209465	0.164	0.71662283	18
soy_OGL_4643	1266	17.461983	35.545025	1001	25.75	8	14.195957	0.16	0.72720236	33
soy_OGL_4923	1264	14.560184	24.683544	2361	25.71	8	7.8557801	0.193	0.77292168	32
soy_OGL_5236	1252	32.623028	28.674122	1717	21.8	5	1.45372	0.21699999	0.89545733	23
soy_OGL_3581	1189	6.0902267	23.5492	5699	24.13	10	29.548262	0.16500001	0.84583777	38
soy_OGL_5634	1748	24.815081	21.624714	3653	21.96	9	17.938488	0.122	0.60066897	13
soy_OGL_2667	1700	6.8734031	22.588236	2781	25	9	16.412588	0.086999997	0.51946855	29
soy_OGL_1761	1178	17.394621	35.908318	3663	22.66	7	22.315786	0.183	0.95789284	12
soy_OGL_3354	1579	12.108066	23.622545	2001	24.88	8	32.483772	0.115	0.82612538	16
soy_OGL_3506	1178	47.600048	21.392191	3553	33.44	7	6.9910493	0.125	0.72322702	22
soy_OGL_4632	2000	21.698753	26.700001	5760	26.8	8	10.885808	0.054000001	0.74492157	36
soy_OGL_4678	1196	10.891823	31.354515	1730	25	6	23.104298	0.15099999	0.64599371	40
soy_OGL_6875	1800	8.3950586	13.777778	2704	25.38	7	50.970997	0.104	0.8455056	25
soy_OGL_64	1200	11.49644	18.75	3667	25.58	8	17.917261	0.223	0.8320303	29
soy_OGL_934	1000	12.449766	25.1	4918	24.2	9	8.5663166	0.273	0.70905817	28
soy_OGL_1232	1769	9.0944204	18.937252	5997	27.86	9	36.685863	0.206	0.76196188	23
soy_OGL_3216	1240	8.5244722	15.967742	3467	27.17	5	18.444984	0.22499999	0.70556229	42
soy_OGL_1717	1023	33.748749	16.226784	2374	25.7	9	6.1362877	0.23999999	0.83484447	26
soy_OGL_3503	1200	47.600048	7.9166665	6016	30.41	6	6.608542	0.175	0.71777231	21
soy_OGL_3509	1595	47.600048	7.2727275	5730	30.9	7	10.304008	0.182	0.72745502	23
soy_OGL_5925	2000	36.541531	19.799999	4615	30.05	10	8.8003216	0.26300001	0.77391326	5
soy_OGL_3231	1600	8.2360296	12.4375	7019	31	7	19.943205	0.138	0.72272962	37
soy_OGL_6912	1314	8.8029718	25.266363	5524	24.73	7	28.266319	0.186	0.89048189	17
soy_OGL_4425	1247	9.7329044	27.906977	3887	23.97	9	26.948387	0.20900001	0.61491328	24
soy_OGL_2621	1764	8.8686056	18.537415	2610	27.21	9	34.005161	0.15099999	0.58372027	23

soy_OGL_4405	1643	8.6647367	19.111382	6807	24.52	10	52.018208	0.176	0.57125974	24
soy_OGL_1949	1200	24.208584	25.916666	3343	27.58	7	3.2484913	0.23199999	0.52193832	16
soy_OGL_3540	1925	8.9636507	14.12987	1858	23.37	9	114.39545	0.15700001	0.7978701	24
soy_OGL_5285	1645	17.399168	25.957447	1001	29.96	9	56.305309	0.169	0.7408753	23
soy_OGL_5302	1061	24.034395	24.128181	5318	29.12	9	21.633783	0.175	0.70611823	26
soy_OGL_5623	1500	36.55751	0	4473	31.06	5	6.557972	0.116	0.61790419	28
soy_OGL_958	1400	13.85167	16.142857	3828	26.42	8	8.6872473	0.168	0.74750853	21
soy_OGL_374	1276	8.1091738	25.235109	3835	23.58	11	25.442657	0.168	0.80449212	22
soy_OGL_5231	1400	9.6439486	17.357143	1373	25.21	9	19.261192	0.15899999	0.91337806	21
soy_OGL_6226	1400	11.29869	17.142857	2015	24.28	11	10.320093	0.17900001	0.87921244	27
soy_OGL_3253	1786	8.2854548	15.117581	2166	25.92	10	29.595303	0.113	0.74995238	16
soy_OGL_4638	1400	19.257402	0	5167	25.57	9	16.426542	0.16599999	0.7344771	37
soy_OGL_1102	1574	8.7746096	21.664549	1001	24.33	12	32.941418	0.148	0.93547565	18
soy_OGL_5474	1380	4.9895315	19.42029	2001	26.08	8	33.051857	0.131	0.86970884	28
soy_OGL_5613	1152	27.376841	18.663195	2044	23.69	13	11.49055	0.229	0.62964171	25
soy_OGL_6948	1200	10.483934	17	8967	27.33	7	22.889725	0.15000001	0.92332995	22
soy_OGL_4476	1330	7.9795275	22.781956	4156	26.39	10	33.945286	0.156	0.70966321	28
soy_OGL_4931	1255	9.3127365	28.525896	2001	26.93	13	87.926178	0.105	0.76498288	33
soy_OGL_27	1600	10.054278	22.125	3426	26.87	10	6.4305115	0.15899999	0.90348482	31
soy_OGL_1141	1900	5.5214667	33.473682	8367	24.84	10	16.855062	0.169	0.97584212	26
soy_OGL_1150	1414	5.8387361	25.530411	3695	25.74	9	26.886911	0.21600001	0.96014512	28
soy_OGL_1411	1838	16.339678	21.490751	2499	27.52	11	4.9253087	0.207	0.84084576	22
soy_OGL_1423	2286	11.385625	23.009624	2001	29.09	8	10.548765	0.186	0.86855936	23
soy_OGL_1472	1855	9.2116108	18.867924	3343	29	9	19.226234	0.19400001	0.93667966	26
soy_OGL_1531	1900	7.5794353	30.947369	2836	27.1	5	3.8705611	0.13500001	0.8863095	38
soy_OGL_2145	1945	7.0482421	27.55784	2001	26.22	9	4.6601334	0.15099999	0.8575536	30
soy_OGL_2193	1300	10.131039	37.384617	3895	23.38	10	4.008575	0.20900001	0.7852844	28
soy_OGL_2671	1947	6.8734031	33.590137	1001	24.29	12	12.816778	0.21600001	0.50812238	23
soy_OGL_3191	1774	9.9972277	22.266066	1445	27.39	8	3.6436827	0.189	0.67312402	29
soy_OGL_3199	1900	8.5168486	21.68421	6062	28.31	10	5.7195139	0.154	0.69173205	34
soy_OGL_3241	2138	9.3938437	11.693172	6445	32.03	8	9.3002024	0.12899999	0.72998106	36

soy_OGL_3784	1647	13.260455	32.604736	1001	24.52	9	10.863132	0.21600001	0.69624078	17
soy_OGL_4488	1829	7.7733254	39.803169	2001	23.94	8	5.2659235	0.15099999	0.72145873	31
soy_OGL_4489	1866	8.5875254	14.308681	3305	27.75	12	4.990612	0.163	0.72284567	30
soy_OGL_4823	1800	16.127125	19.444445	6385	28.38	9	4.7448487	0.178	0.96781695	22
soy_OGL_5031	2800	10.882226	25.892857	3561	31.67	7	1.7936987	0.147	0.6602689	30
soy_OGL_5035	2000	9.4548454	31.9	1001	25.35	11	6.3005185	0.22400001	0.65612793	27
soy_OGL_5264	2370	11.202606	20	2365	27.72	10	9.3787441	0.125	0.80706888	19
soy_OGL_5325	2500	11.453777	20.76	1135	29.76	9	16.15383	0.163	0.66049999	25
soy_OGL_5815	1895	13.055554	15.672823	4572	29.65	7	5.884871	0.113	0.89582598	23
soy_OGL_5905	2400	7.8267756	28.5	2909	27.41	9	2.8602943	0.121	0.86727554	34
soy_OGL_6216	1658	7.7151871	24.909529	2001	27.02	6	11.589777	0.17200001	0.86978137	30
soy_OGL_6606	1787	8.5314484	28.091774	1820	24.84	12	21.335638	0.17	0.8696084	16
soy_OGL_6994	2109	5.2089171	24.940731	1001	25.41	9	12.35889	0.13600001	0.9536863	27
soy_OGL_719	2000	9.6048651	31.5	1325	23.85	9	6.1124072	0.161	0.8562029	26
soy_OGL_1532	1877	7.5794353	36.760788	5559	25.67	5	3.8705611	0.18799999	0.88614881	38
soy_OGL_2203	2500	7.6249928	31.280001	2358	25.8	8	9.8363342	0.123	0.76687157	29
soy_OGL_2429	2299	11.372036	32.274902	2001	25.61	7	6.1821861	0.152	0.72554356	25
soy_OGL_5477	1372	4.9895315	38.046646	7089	22.37	10	25.076777	0.19599999	0.86778635	29
soy_OGL_5873	1861	10.500387	36.915638	5789	23.8	10	3.3439326	0.18700001	0.91037756	34
soy_OGL_6251	2700	5.5960298	23.814816	3664	27.77	10	14.009269	0.057999998	0.91328186	23
soy_OGL_223	1960	11.092773	25.510204	4027	30.15	10	22.820234	0.164	0.8312844	24
soy_OGL_1489	1800	7.653698	28.333334	3884	26.77	11	30.461931	0.16599999	0.96766794	24
soy_OGL_1562	1535	10.973433	31.400652	2001	26.51	8	10.441794	0.161	0.82549793	25
soy_OGL_1903	1602	23.127859	34.893883	2001	26.21	12	13.055576	0.233	0.6269123	12
soy_OGL_2921	2285	9.3318186	26.870897	3826	28.57	12	11.694722	0.116	0.9629702	29
soy_OGL_3221	1800	7.6237597	30.611111	3280	31.44	6	14.688925	0.20100001	0.71281803	49
soy_OGL_4689	1606	10.074121	25.716064	2120	27.77	11	8.315979	0.141	0.62915647	38
soy_OGL_4926	2200	14.560184	33.454544	7349	30.72	9	7.1262965	0.178	0.76940209	37
soy_OGL_5837	2600	13.562174	29.076923	1650	31.19	4	8.2565889	0.138	0.96346891	22
soy_OGL_6528	1822	21.291258	24.807903	1467	28.21	10	8.0783768	0.132	0.71722835	17
soy_OGL_6547	1653	13.347547	24.803389	2127	27.76	10	8.1166039	0.14399999	0.75295109	30

soy_OGL_6554	1492	13.347547	36.930294	4579	25.87	9	5.4410682	0.177	0.75901592	33
soy_OGL_6744	1857	9.6085119	29.133011	2001	25.25	12	8.18857	0.13699999	0.73132753	29
soy_OGL_68	2700	12.397855	30.555555	4442	31.03	8	5.316905	0.139	0.82475758	35
soy_OGL_296	2974	8.0453501	34.498993	3398	28.07	10	14.452727	0.112	0.91478461	25
soy_OGL_2294	2000	9.6573048	36.700001	4356	25.6	11	15.089855	0.193	0.60835779	31
soy_OGL_4517	2201	8.9862776	28.668787	2469	27.12	8	7.8060603	0.098999999	0.75331491	35
soy_OGL_1833	1400	8.3344145	36	4789	24.5	9	12.965135	0.19499999	0.75635064	26
soy_OGL_3021	1802	10.401243	23.751387	2476	26.3	7	10.581325	0.118	0.75289363	21
soy_OGL_4433	2000	8.4435787	30.799999	2332	25.4	9	8.6412735	0.126	0.62116295	25
soy_OGL_5014	2242	8.0536013	29.438002	2249	28.54	7	16.801319	0.14399999	0.67438793	22
soy_OGL_688	1630	11.121198	22.883436	8707	28.34	8	8.9658375	0.147	0.80853981	21
soy_OGL_1389	1531	6.9438424	21.032005	10716	29.58	6	10.681188	0.154	0.80868995	34
soy_OGL_1404	1167	14.126931	33.247643	8151	24.59	8	4.2285218	0.211	0.82983249	20
soy_OGL_2269	1126	9.1252251	31.705151	12334	27.26	7	4.8073325	0.23999999	0.63552177	43
soy_OGL_6440	1137	10.461443	28.232189	5131	26.82	6	3.2480991	0.193	0.55712956	36
soy_OGL_6515	1500	7.4994183	28.799999	5779	27.86	6	13.651072	0.183	0.69432831	29
soy_OGL_6894	2191	7.0806479	27.88681	6567	29.43	6	13.049986	0.101	0.86754841	26
soy_OGL_3350	2126	10.722426	32.126057	3076	27.56	5	10.524307	0.142	0.84588939	25
soy_OGL_4531	2500	6.7637272	36.400002	8935	27.52	8	16.166748	0.18099999	0.77136904	28
soy_OGL_6437	2134	10.461443	26.2418	3311	29.28	5	7.5097895	0.17900001	0.55621582	36
soy_OGL_6956	2300	5.7448678	29.782608	12593	28.95	6	18.696987	0.14300001	0.92957544	30
soy_OGL_342	1174	9.9017172	31.175468	6941	25.97	8	16.186171	0.19	0.85715884	29
soy_OGL_373	1475	7.0452614	33.694916	2139	25.96	10	29.828594	0.156	0.80582994	22
soy_OGL_2120	1582	9.8124828	31.099874	2001	26.35	8	21.716604	0.147	0.91686779	18
soy_OGL_2932	2186	9.9275036	28.042086	6122	29.23	7	22.389673	0.12800001	0.93375319	18
soy_OGL_2939	2275	9.9764471	26.681318	2054	30.98	9	41.630013	0.106	0.92473632	17
soy_OGL_4481	2104	7.5810852	29.705322	6932	30.08	10	24.04722	0.117	0.7119264	30
soy_OGL_6426	2069	10.893449	18.318027	4740	31.31	8	10.520811	0.090000004	0.54680353	34
soy_OGL_6870	1800	8.3950586	25.888889	3646	29.22	7	33.777191	0.132	0.84256208	27
soy_OGL_1754	1886	14.60705	24.125132	5927	28.89	9	18.041075	0.083999999	0.96996105	20
soy_OGL_3236	1663	9.8079872	35.417919	4285	26.39	8	9.5296211	0.125	0.72699976	38

soy_OGL_3318	2200	16.336683	35.454544	2532	28.45	9	9.1389809	0.068999998	0.89383411	25
soy_OGL_4914	1300	17.460024	33.384617	2483	26.38	7	17.170074	0.167	0.78050131	22
soy_OGL_347	1881	6.2913775	27.48538	5852	25.57	9	5.1741939	0.104	0.8479808	30
soy_OGL_692	1404	11.121198	25.569801	1441	23.86	11	5.3050137	0.184	0.81228578	21
soy_OGL_3344	1700	10.744705	22.294117	2901	25.58	8	1.1472249	0.13	0.85258526	24
soy_OGL_4545	1667	5.6849523	29.694061	2762	23.27	11	4.6827121	0.145	0.7879976	32
soy_OGL_5030	1479	10.882226	20.622042	1667	27.31	7	2.692034	0.146	0.66078401	30
soy_OGL_5835	1500	13.562174	19.666666	7677	28.8	8	5.9149113	0.131	0.96116275	22
soy_OGL_3246	1354	8.3858376	20.605614	2397	25.48	11	10.874005	0.164	0.73364365	33
soy_OGL_5872	1668	10.500387	32.853718	3108	23.92	9	2.9763439	0.14399999	0.91052419	34
soy_OGL_979	1619	13.02616	26.374306	2066	28.16	9	3.8975697	0.115	0.76735747	33
soy_OGL_1527	2200	7.269011	18.681818	1726	28.68	9	5.7204299	0.046	0.89212501	37
soy_OGL_3554	1405	6.3657079	33.523132	1001	22.56	11	14.619552	0.168	0.82557756	27
soy_OGL_3943	1205	24.96867	38.672199	3523	28.13	10	6.2774024	0.15099999	0.87572414	28
soy_OGL_4644	1890	4.3523932	21.481482	3558	27.14	11	16.568645	0.07	0.72373205	33
soy_OGL_5780	1478	14.565392	15.493911	2001	31.79	6	7.0112343	0.117	0.83589792	42
soy_OGL_5846	1444	9.6763773	36.703602	1278	23.26	9	15.171915	0.17399999	0.97752589	20
soy_OGL_6963	1400	16.297258	28.071428	3368	28.78	9	6.2086382	0.12899999	0.93485206	32
soy_OGL_4927	1328	14.560184	31.927711	3772	26.65	10	6.8778472	0.14399999	0.76930869	39
soy_OGL_201	1200	11.833065	31.166666	4641	24.83	7	5.5969653	0.169	0.81045198	27
soy_OGL_329	1500	10.351954	36.666668	3394	23.53	7	4.7436218	0.139	0.87806755	22
soy_OGL_2400	1730	11.483459	24.393064	1459	26.41	9	11.02244	0.126	0.68688208	16
soy_OGL_5283	1400	16.257269	27.285715	2535	25.78	6	2.327045	0.15700001	0.7466768	22
soy_OGL_2594	1770	5.1120324	28.418079	2120	22.88	11	21.129028	0.124	0.63154012	17
soy_OGL_3773	1724	12.101471	13.921114	3048	28.94	7	9.7000217	0.093000002	0.71687019	20
soy_OGL_4511	1152	8.8380184	37.934029	12911	23.09	9	3.2167299	0.18000001	0.74820554	37
soy_OGL_5275	1800	8.3274832	30.333334	4248	23.16	10	5.4208322	0.114	0.77700001	20
soy_OGL_5024	1379	12.416456	23.277737	1330	28.71	6	8.5845413	0.12800001	0.66555148	28
soy_OGL_29	1959	10.279623	31.6488	1001	26.49	6	4.5594029	0.059999999	0.89775401	31
soy_OGL_804	1876	9.4385977	36.247334	3632	24.25	8	13.643888	0.097999997	0.84260803	21
soy_OGL_4557	1970	8.4823227	24.162437	2001	26.44	8	17.821413	0.064999998	0.80290943	24

soy_OGL_5819	1600	13.314646	9.375	2713	29.43	7	4.201088	0.13699999	0.90405077	23
soy_OGL_1928	1500	15.733195	15.333333	2215	30.6	7	7.1148205	0.12800001	0.55287337	26
soy_OGL_5587	1232	5.8065071	29.058441	2001	22.56	12	27.347927	0.18000001	0.67864627	19
soy_OGL_3309	1100	14.902535	27.545454	4609	24.9	9	8.5589418	0.19599999	0.9131797	19
soy_OGL_5223	1071	11.680604	25.770308	3206	25.58	8	20.011751	0.18799999	0.9329713	25
soy_OGL_920	1651	11.336674	7.389461	5962	32.34	6	5.7879272	0.085000001	0.69622552	28
soy_OGL_3539	1600	8.9636507	13.375	4063	29.25	7	9.73353	0.116	0.79377252	24
soy_OGL_2063	2673	1.7882655	8.567153	7900	28.88	5	0.26076359	0.17900001	0.58802748	9
soy_OGL_157	1936	4.1056633	11.466942	4771	28.66	3	2.893321	0.113	0.69683546	12
soy_OGL_1611	1600	1.1756582	20.9375	10792	24	2	1.6799207	0.233	0.33335352	4
soy_OGL_2019	1768	2.1072574	16.063349	5653	25.33	2	3.0507793	0.15000001	0.35471296	5
soy_OGL_2800	1158	0.8990916	27.89292	13023	25.38	2	12.59503	0.16500001	0.32177672	10
soy_OGL_3898	1000	1.5956808	23.700001	37944	28.7	1	0.19858819	0.242	0.66117364	4
soy_OGL_4035	1200	1.2838418	23.333334	30280	27.5	1	0.068498544	0.235	0.54039228	3
soy_OGL_5415	1523	4.7039185	20.223244	10088	25.8	4	13.873959	0.17200001	0.8309111	4
soy_OGL_5694	1400	1.387786	33.57143	22790	30.07	2	25.497341	0.257	0.4030115	13
soy_OGL_6012	1735	1.5527503	15.043227	3577	25.24	3	4.9021716	0.139	0.49522781	7
soy_OGL_1604	1100	5.281703	26.363636	16768	29.81	2	18.957331	0.16	0.68427384	14
soy_OGL_2341	2000	11.14712	18.65	6444	30.95	5	15.280161	0.19599999	0.31158257	12
soy_OGL_5365	1996	9.3292475	9.4689379	2803	31.41	4	4.8025694	0.088	0.6183759	15
soy_OGL_5426	1903	12.267535	26.274303	5221	25.53	5	7.8355508	0.12800001	0.98172909	11
soy_OGL_2745	2047	5.5443225	19.882755	3024	26.23	7	19.901682	0.185	0.39241958	21
soy_OGL_876	2684	2.4722638	13.52459	4039	25.59	3	7.9523935	0.185	0.62296516	8
soy_OGL_60	2000	11.010665	16.35	13643	24.5	4	3.9521847	0.078000002	0.83914548	28
soy_OGL_900	1547	6.5197372	19.84486	13378	24.36	7	13.296107	0.14	0.67062378	31
soy_OGL_1957	2000	19.348343	11.05	4136	22.4	5	1.4680911	0.121	0.50869483	19
soy_OGL_4984	1400	9.9015322	20.214285	4858	25.85	2	2.6295288	0.16599999	0.71046478	26
soy_OGL_4998	1215	8.6126404	26.090534	7275	21.06	4	21.437262	0.20200001	0.70146698	25
soy_OGL_461	2600	4.9836407	14.346154	4875	26.69	6	6.6225529	0.057999998	0.55248201	19
soy_OGL_499	1700	4.4821186	12.941176	5526	22.05	4	2.8332477	0.17399999	0.47367117	25
soy_OGL_811	2200	7.571846	16.545454	16656	26.63	4	3.2197626	0.206	0.81392968	12

soy_OGL_2412	1400	11.967738	9.4285717	15921	28.78	5	5.3432283	0.153	0.70683885	32
soy_OGL_2427	1652	11.967738	1.6949153	14846	24.63	3	7.4612837	0.138	0.72274816	26
soy_OGL_2596	1991	3.7431359	22.953289	7958	24.1	6	27.161163	0.178	0.62953526	15
soy_OGL_3131	2850	8.0850887	19.473684	10203	29.64	3	20.754673	0.213	0.55461466	24
soy_OGL_3138	2043	8.3777838	6.9995103	14140	26.97	4	7.6506586	0.17399999	0.55954438	27
soy_OGL_4215	2297	4.4291444	3.744014	7277	23.68	5	23.191057	0.193	0.25221032	23
soy_OGL_5679	1200	9.2884445	33.416668	2814	18.66	6	7.8512616	0.235	0.46775478	15
soy_OGL_6092	3467	0.69722927	11.883472	13643	24.68	2	5.961226	0.213	0.55883098	6
soy_OGL_6138	2199	3.3948011	6.7303319	12270	24.19	4	2.246058	0.156	0.76855689	14
soy_OGL_6337	1200	5.6879897	20.416666	13062	23.08	3	10.131947	0.221	0.90268934	28
soy_OGL_2425	1463	11.967738	21.941217	8652	28.5	4	5.954741	0.192	0.722049	27
soy_OGL_59	2458	11.04541	1.179821	12319	24.61	3	84.129501	0.12	0.84121209	28
soy_OGL_418	2100	12.999779	25.190475	7738	25.47	6	5.1838717	0.118	0.70735133	17
soy_OGL_886	2200	8.0451517	27.454546	2671	24.31	4	46.203808	0.18799999	0.65395319	14
soy_OGL_1823	2811	8.2052183	26.289577	11849	27.07	7	13.834001	0.107	0.76614612	25
soy_OGL_3370	1800	14.596085	19.611111	9106	26.77	7	5.506062	0.13	0.77547002	15
soy_OGL_3383	1714	5.5155735	25.204201	3043	20.24	5	43.65847	0.167	0.71830809	17
soy_OGL_4220	1600	4.8260355	19.5625	4208	25.75	8	26.005314	0.142	0.26003057	32
soy_OGL_5241	1900	8.6306667	25.789474	9133	26.63	4	11.693774	0.112	0.8807317	24
soy_OGL_5618	2359	28.530188	8.9020767	15721	29.84	5	4.8432841	0.16	0.62620306	22
soy_OGL_5948	1500	11.686487	32.933334	7267	22.8	5	6.3404379	0.16599999	0.712699	28
soy_OGL_5959	2035	9.0571718	24.864864	4713	24.96	5	12.765559	0.115	0.69034183	17
soy_OGL_1324	1351	0.24154867	22.057735	35836	28.34	1	4.4111633	0.226	0.62326807	14
soy_OGL_6353	1900	5.2286477	5.8421054	13103	29.05	2	0.65211523	0.127	0.87871915	18
soy_OGL_133	1503	9.5898628	19.627411	38445	29.67	2	0.60615385	0.126	0.60012823	7
soy_OGL_185	2535	5.00559	6.9033532	24644	29.62	3	2.9207804	0.16500001	0.78187549	12
soy_OGL_488	2300	5.2689199	21.826086	9598	24.78	6	5.4455647	0.15000001	0.50045496	13
soy_OGL_500	1707	4.4821186	2.6362038	14848	23.6	4	3.6943085	0.149	0.47246748	25
soy_OGL_545	2101	10.749329	22.989054	23708	31.6	3	3.5368268	0.12800001	0.358518	18
soy_OGL_547	1400	10.749329	13.428572	27009	26	3	3.5368268	0.175	0.35840091	18
soy_OGL_588	1200	1.0339187	31.5	26650	22.83	2	5.3180141	0.21600001	0.60859674	8

soy_OGL_1306	2000	1.7763864	3.75	31839	25	1	3.3109093	0.046999998	0.57931912	14
soy_OGL_1310	3810	2.0239863	4.4881887	17390	31.23	3	2.9055865	0.105	0.59180552	13
soy_OGL_1342	1407	7.1417031	23.312012	23250	25.01	2	18.978786	0.153	0.72855771	13
soy_OGL_1593	1400	5.281703	2.1428571	35049	27.92	1	0.56343722	0.138	0.70949405	18
soy_OGL_1600	1547	5.281703	12.023271	26505	23.98	1	4.0281377	0.15899999	0.68936032	15
soy_OGL_1616	1462	1.131759	39.261288	35829	27.7	1	20.237679	0.184	0.39877507	8
soy_OGL_1620	1541	1.1600796	35.885788	32880	22.9	2	1.6462885	0.153	0.4066824	7
soy_OGL_1645	1400	7.0483088	25.071428	7393	24.64	4	13.197753	0.183	0.59004706	21
soy_OGL_1647	2300	7.0483088	23.086956	12618	27.95	3	11.689715	0.072999999	0.59111834	21
soy_OGL_1900	1600	9.4963474	18.0625	11802	24.68	7	11.073497	0.16	0.64954221	11
soy_OGL_1976	1859	11.715036	10.328134	14723	21.78	4	3.4388063	0.134	0.48464611	27
soy_OGL_1988	2035	8.9979553	25.257986	9744	23.53	5	3.2884071	0.101	0.46221104	19
soy_OGL_1989	1226	7.5878448	21.288744	10614	21.85	5	9.4129648	0.184	0.46083179	19
soy_OGL_2008	2700	3.0006773	30.444445	17294	27.96	3	29.05121	0.081	0.39735389	8
soy_OGL_2324	2571	11.537634	22.559315	2471	25.86	4	5.5001063	0.071999997	0.5203231	15
soy_OGL_2325	2482	11.537634	27.07494	6665	26.83	4	5.5001063	0.18000001	0.52013481	15
soy_OGL_2355	1900	2.8688939	9.9473686	23662	24.84	1	0.20772424	0.149	0.2053578	13
soy_OGL_2656	2672	6.8734031	14.97006	21893	24.7	2	27.018221	0.17900001	0.53234017	25
soy_OGL_2674	2333	8.56392	24.774967	20237	28.88	3	7.6726513	0.15000001	0.50403494	23
soy_OGL_3052	1900	32.517826	13.368421	18117	26.31	2	0.11267935	0.134	0.59670639	4
soy_OGL_3059	1500	12.11379	19.266666	11124	21.66	3	10.63656	0.178	0.49110213	3
soy_OGL_3076	1900	0.69136071	13.789474	27832	28.21	2	0.36628908	0.207	0.22742397	10
soy_OGL_3087	1494	1.0152045	26.171352	30088	25.7	2	6.4479017	0.088	0.28270575	6
soy_OGL_3418	1458	0.4680596	37.791496	27061	23.73	1	19.78817	0.141	0.53427845	6
soy_OGL_3854	1795	10.560259	11.142061	8811	23.23	7	10.487982	0.117	0.27942491	18
soy_OGL_3887	2400	0.027143367	23.416666	13764	24.25	2	4.510829	0.024	0.4058868	8
soy_OGL_3917	1700	9.3006687	2.8823528	25281	26.64	2	0.77467537	0.082999997	0.79295337	22
soy_OGL_4216	1865	4.4291444	13.941019	7324	25.84	5	5.3800344	0.134	0.25234637	23
soy_OGL_4734	1300	1.3662759	14.692307	39419	25.92	1	14.708558	0.141	0.15037909	9
soy_OGL_4735	1400	1.3662759	34.57143	36919	22.78	1	14.708558	0.090000004	0.15021569	9
soy_OGL_5054	2036	6.5904026	29.715128	8099	19.94	5	10.750006	0.134	0.60770613	13

soy_OGL_5078	2805	0.32877564	4.7771835	28105	20.96	1	0.01417708	0.183	0.4146761	4
soy_OGL_5107	1600	6.700357	12.6875	24814	25.06	6	0.54625005	0.094999999	0.29100868	8
soy_OGL_5133	1700	3.908869	22.941177	21389	26.76	2	22.635124	0.20200001	0.67266607	9
soy_OGL_5156	2700	3.9693906	8.8888893	24322	25.11	1	3.5326583	0.171	0.77826643	19
soy_OGL_5157	1254	6.310122	28.30941	28980	27.35	1	10.243546	0.13	0.78140998	21
soy_OGL_5198	2111	13.332328	12.174325	17881	26.81	3	18.667997	0.131	0.9655757	14
soy_OGL_5646	2400	9.0987301	17.625	14466	27.5	5	8.9574986	0.18700001	0.53670114	17
soy_OGL_5727	2300	4.5680037	15.217391	22936	25.43	2	33.222359	0.18700001	0.57281184	5
soy_OGL_5735	1173	4.9724145	28.729753	16455	21.73	1	0.72414768	0.23199999	0.6599105	8
soy_OGL_6053	1400	1.8251891	12.5	30016	24.28	2	12.860574	0.094999999	0.1549949	6
soy_OGL_6093	1904	0.69722927	11.817227	6039	21.21	2	0.36923388	0.133	0.56068259	6
soy_OGL_6214	1900	6.6037278	0	29333	24.94	3	10.153718	0.154	0.8691265	29
soy_OGL_6354	1600	5.6697817	36.9375	39385	28.06	1	0.34473887	0.061000001	0.87572765	17
soy_OGL_6673	2640	9.9655132	24.128788	12589	27.27	2	3.3256476	0.12800001	0.012364759	27
soy_OGL_6683	2300	7.6147938	12.217391	2169	24.13	5	33.679317	0.145	0.021964621	20
soy_OGL_6703	2575	0.14302784	0	33566	28.11	1	0.000596684	0.125	0.49377275	6
soy_OGL_6717	1700	2.7221162	32.823528	35863	19.29	1	0.22283298	0.125	0.65717185	8
soy_OGL_828	1642	9.6582899	26.613886	12505	28.07	3	20.684807	0.169	0.72134829	23
soy_OGL_853	2300	4.8822522	26.173914	5262	26.78	4	37.614822	0.089000002	0.59606248	14
soy_OGL_1822	1365	8.2052183	22.271063	16149	25.56	6	16.013433	0.147	0.76628572	25
soy_OGL_2282	1700	13.338867	25.529411	16671	21.05	3	34.384678	0.15700001	0.62522477	41
soy_OGL_3143	2200	10.669563	24.045454	14729	27.18	5	5.1604772	0.071000002	0.56868351	28
soy_OGL_3378	1400	10.989937	28	7974	25.92	4	22.895531	0.199	0.75291246	13
soy_OGL_4982	1300	12.662311	38.46154	12758	23.15	2	2.6295288	0.177	0.71067101	26
soy_OGL_5342	2281	7.1243448	28.803156	4077	24.41	6	25.428053	0.086000003	0.52097064	9
soy_OGL_2185	1538	9.8723383	26.267879	11235	22.69	6	4.2633967	0.138	0.79509461	30
soy_OGL_5964	1300	7.5982332	28.307692	9550	21.23	8	5.4668884	0.19499999	0.66733164	20
soy_OGL_1368	2300	5.1550312	6.9130435	11509	25.86	5	18.130026	0.008	0.78959525	29
soy_OGL_2500	1514	7.4874678	19.881109	9099	24.04	5	11.658975	0.132	0.83998865	18
soy_OGL_2537	1167	4.4041967	32.047985	8786	19.1	6	8.770051	0.20999999	0.74310142	19
soy_OGL_2829	1754	5.5548873	1.9384265	12364	18.47	4	8.0427065	0.138	0.66163093	22

soy_OGL_4240	1181	4.9720435	32.260796	5842	18.79	8	2.8756092	0.18000001	0.2757481	31
soy_OGL_5180	1709	14.850507	3.978935	13331	25.39	5	3.5217779	0.097000003	0.90364504	17
soy_OGL_473	1366	6.0821934	17.0571	5705	23.64	6	4.8223391	0.162	0.53430182	25
soy_OGL_1455	1200	9.5686789	4.1666665	17052	25.75	5	8.1625299	0.12800001	0.91609341	31
soy_OGL_3687	1300	7.5635667	18.538462	11470	23.38	6	8.6794538	0.15099999	0.902309	15
soy_OGL_4376	2000	6.6361041	3.6500001	4349	27.2	5	21.347528	0.044	0.5279389	26
soy_OGL_1908	1713	14.749738	31.58202	2466	22.65	6	5.0572171	0.127	0.61745411	13
soy_OGL_3775	1277	13.809534	25.606892	8970	21.45	7	9.0123625	0.18000001	0.7156266	21
soy_OGL_166	1100	1.9087936	16.454546	30407	27.09	1	6.6193571	0.089000002	0.72573495	8
soy_OGL_167	1100	1.9087936	31.90909	26007	20.9	1	6.6193571	0.106	0.72584683	8
soy_OGL_458	1878	4.091258	18.423855	10061	23.69	5	4.3419032	0.050999999	0.5650866	16
soy_OGL_854	1000	5.0977836	30.4	20626	25.6	3	18.69911	0.12899999	0.59444529	14
soy_OGL_1994	1462	6.3444653	24.965799	29351	18.67	3	2.160917	0.093999997	0.45259506	19
soy_OGL_3065	1569	13.119327	26.386232	2952	22.81	3	4.0886559	0.092	0.13988085	5
soy_OGL_3421	1501	0.84260994	21.185877	25424	22.51	2	1.8516887	0.048999999	0.40824127	5
soy_OGL_4017	1636	7.0667925	23.16626	20784	22.67	1	2.1888874	0.072999999	0.69937426	16
soy_OGL_5082	1247	20.251705	23.576584	16300	24.69	2	0.37830243	0.106	0.39989173	4
soy_OGL_5130	1476	6.3039489	30.149052	8380	20.18	3	5.8196912	0.15800001	0.65360379	8
soy_OGL_1969	1548	8.2513695	12.015504	1939	26.42	3	4.0702653	0.11	0.49155205	25
soy_OGL_2768	1744	4.4690285	2.4082568	20712	23.1	4	19.453714	0.057	0.32731467	12
soy_OGL_3398	1573	2.8635902	22.059759	9125	23.58	7	23.058424	0.092	0.69537866	18
soy_OGL_6716	1076	2.7221162	0	37663	20.81	1	0.22283298	0.111	0.65714628	8
soy_OGL_400	1400	8.1793365	19.714285	16585	27.28	4	10.513146	0.078000002	0.75886935	26
soy_OGL_1285	1091	7.132494	27.864346	17473	26.21	3	18.673264	0.116	0.65838969	18
soy_OGL_3859	1774	10.036083	11.837655	6210	27.5	4	30.004681	0.057999998	0.27071244	24
soy_OGL_4181	1380	16.214922	39.347828	2001	18.91	5	7.5692778	0.13699999	0.17856677	15
soy_OGL_496	1400	5.067452	21.928572	4441	23.07	5	23.518349	0.12899999	0.47624776	24
soy_OGL_4686	1141	10.870666	4.4697633	24189	34.09	3	2.3279402	0.045000002	0.63808495	40
soy_OGL_3866	1600	9.8148384	18.875	3018	25.25	7	11.543681	0.182	0.25557083	19
soy_OGL_1340	1900	1.9391037	0	14483	24.78	8	1.7481443	0.12800001	0.71225262	12
soy_OGL_3435	2227	7.3611813	0	11857	25.46	8	50.337318	0.142	0.54380393	13

soy_OGL_3470	1500	8.2846069	2.7333333	13497	26.86	5	2.8540747	0.133	0.63255203	25
soy_OGL_4299	1693	4.1622143	4.0165386	12443	26.52	6	6.7995744	0.149	0.39639318	28
soy_OGL_5354	1900	2.9911871	1.4736842	8415	22.78	4	9.9945936	0.15800001	0.49296105	14
soy_OGL_5748	1591	13.586713	0	13308	23.82	3	5.3990297	0.171	0.72106701	14
soy_OGL_6211	1511	6.6037278	4.1694241	26944	29.18	3	9.7808542	0.24600001	0.86891752	29
soy_OGL_6321	1662	9.4922562	0	18879	28.09	4	4.8501863	0.163	0.93124419	18
soy_OGL_1984	1600	9.6599522	14	2032	28.06	4	13.06749	0.16500001	0.47103572	21
soy_OGL_155	1200	5.5040874	20.916666	15728	23.66	5	2.3009439	0.23800001	0.69191122	11
soy_OGL_3422	1785	0.84260994	8.6274509	23340	28.23	2	1.8516887	0.17399999	0.40830341	5
soy_OGL_1601	1268	5.281703	0	27574	20.89	1	18.616068	0.156	0.68842262	14
soy_OGL_1999	1298	7.0577431	11.55624	11722	21.8	4	2.5105858	0.22400001	0.44319487	15
soy_OGL_2331	1700	6.0952759	9.6470585	7298	22.94	6	5.9548397	0.15099999	0.49474311	4
soy_OGL_3102	1300	1.1479118	13.384615	29225	27.15	2	0.01692898	0.108	0.4129363	7
soy_OGL_4034	1400	1.2838418	14.142858	21205	24.5	1	6.4727707	0.17	0.54184228	3
soy_OGL_4685	1034	10.870666	0	31367	29.4	3	2.3279402	0.15000001	0.6385541	40
soy_OGL_4736	1375	1.3662759	17.890909	24744	23.27	2	9.5198784	0.205	0.14941993	9
soy_OGL_4741	1939	1.3662759	8.8189793	34040	30.17	1	11.856342	0.17	0.1041915	3
soy_OGL_4777	1200	6.5453987	17.416666	13015	22.08	3	9.6603918	0.2	0.8567332	4
soy_OGL_5709	1830	6.578464	15.628415	8094	22.73	2	7.356411	0.183	0.096362837	3
soy_OGL_5940	1200	29.346493	0	22143	28	3	2.8638413	0.21799999	0.72558165	23
soy_OGL_6023	1484	1.8269773	8.5579519	20159	23.38	3	10.079192	0.13600001	0.38913858	14
soy_OGL_6423	1100	10.893449	11.909091	18544	25.72	3	6.7327886	0.20999999	0.54409945	33
soy_OGL_6680	1721	9.4066839	14.468332	3622	27.77	2	2.7664933	0.176	0.0195859	25
soy_OGL_6688	1551	6.1426415	22.243713	8076	23.85	6	23.569967	0.167	0.024979837	18
soy_OGL_6687	1100	6.1426415	31.09091	13548	25.72	6	23.569967	0.204	0.024870763	18
soy_OGL_1304	1810	1.5215753	20.883978	2438	22.87	2	72.71769	0.211	0.57693851	12
soy_OGL_3375	1249	10.989937	26.741394	11284	24.57	5	36.175362	0.205	0.75465602	13
soy_OGL_6659	1087	15.682825	31.922724	2546	20.79	10	6.8296838	0.226	0	17
soy_OGL_4019	1900	7.0667925	0	6890	27.57	4	2.5948939	0.054000001	0.69596922	16
soy_OGL_5361	1500	9.3808632	16.866667	7198	21.8	8	9.5277758	0.156	0.59821469	9
soy_OGL_1948	1500	24.208584	7.4666667	7043	25.8	6	3.7146583	0.132	0.52205843	16

soy_OGL_5065	1482	5.2891674	15.384615	4135	21.86	5	1.9739037	0.139	0.56510228	6
soy_OGL_2368	1141	3.9981964	19.719543	12278	20.85	2	6.2265954	0.12899999	0.1077917	10
soy_OGL_2377	1500	0.77929288	11.466666	6706	17.46	2	10.15065	0.14399999	0.55777109	2
soy_OGL_2831	1386	5.5548873	4.9062047	19607	28.78	5	7.9335485	0.074000001	0.66211998	22
soy_OGL_5720	1300	3.9622605	9.2307692	13916	21.84	3	0.28470495	0.14300001	0.47595927	7
soy_OGL_6048	1212	2.1657593	8.2508249	18315	22.19	2	5.0487928	0.108	0.19643368	9
soy_OGL_6370	1086	1.8393538	10.77348	32697	23.48	2	0.5956226	0.119	0.63079208	6
soy_OGL_884	2495	8.6892815	27.935871	2001	25.21	6	10.633586	0.167	0.64652568	8
soy_OGL_2314	2100	7.6951575	24.666666	2709	25.85	5	9.0762024	0.14300001	0.55283946	17
soy_OGL_2716	1907	4.0992632	11.798636	3051	26.84	7	4.4625683	0.102	0.44662213	23
soy_OGL_4364	2200	7.8500838	20.59091	10688	28.86	8	2.5786703	0.193	0.51236635	20
soy_OGL_6145	2792	7.3366766	33.524357	2340	26.86	3	0.1855005	0.14300001	0.77568394	17
soy_OGL_3135	1400	8.0353642	30.785715	7535	25.64	3	8.1860914	0.26699999	0.55779552	26
soy_OGL_6113	3127	1.5760107	3.4218102	2001	28.23	5	12.577241	0.056000002	0.71180075	3
soy_OGL_474	2021	6.0821934	16.724394	7065	28.35	8	8.7325516	0.12	0.53176129	26
soy_OGL_2637	1200	7.9126515	33.083332	4452	24.08	6	7.1486039	0.189	0.55804896	21
soy_OGL_2692	1869	9.7915058	20.0107	8092	27.6	8	5.9151459	0.15099999	0.48456752	22
soy_OGL_2736	1900	6.8346286	31.789474	3598	24.57	8	3.700469	0.177	0.40786713	18
soy_OGL_3043	2000	12.289925	27.549999	3235	25.9	7	1.2276733	0.103	0.6740213	11
soy_OGL_3133	1722	8.0850887	27.46806	2001	26.3	4	6.0131369	0.15099999	0.5550195	24
soy_OGL_3860	1468	9.8148384	24.931881	1001	25.74	6	0.69444478	0.18000001	0.2668812	23
soy_OGL_4992	1380	8.6126404	26.884058	6361	26.37	6	5.2647204	0.169	0.70491385	26
soy_OGL_5936	1634	7.4355073	30.293758	8084	25.33	7	7.819572	0.17200001	0.73681122	22
soy_OGL_6336	1304	5.6879897	39.493866	9358	24.61	3	10.131947	0.212	0.90284258	28
soy_OGL_5738	1410	13.263012	28.085106	2075	23.54	3	0.32171398	0.18000001	0.68725723	14
soy_OGL_168	1500	1.9087936	32.133335	20107	26	1	6.6193571	0.184	0.72598678	8
soy_OGL_504	2153	4.4821186	27.217836	8317	27.91	5	3.7695317	0.146	0.46615022	23
soy_OGL_509	2213	4.4821186	14.053321	4660	29.91	5	9.4460554	0.088	0.45832431	22
soy_OGL_527	2163	2.3637695	9.0614891	16275	30.28	3	0.72030658	0.134	0.41020271	12
soy_OGL_839	1789	5.4804659	31.470095	6418	23.42	6	7.6754203	0.153	0.65231735	15
soy_OGL_1301	2358	1.5215753	5.5131469	31538	33.79	2	0.084305748	0.133	0.56809735	8

soy_OGL_1617	1527	1.131759	20.759659	6166	24.42	1	1.7349792	0.132	0.40130979	8
soy_OGL_2370	1400	4.1625123	29.071428	28602	28.21	2	0.028759431	0.075999998	0.099165142	6
soy_OGL_3034	1582	7.153666	36.662453	5386	23	1	0.19352168	0.229	0.71206808	6
soy_OGL_4040	2313	0.4582673	24.297449	2259	25.03	4	8.349618	0.086999997	0.42546874	10
soy_OGL_4067	1345	5.8943801	30.929369	7993	24.83	4	2.8227994	0.167	0.51614004	18
soy_OGL_4204	1937	3.197732	20.753742	14179	28.08	5	6.9959784	0.2	0.22108382	19
soy_OGL_4251	2200	9.7208376	11.909091	3010	28.36	6	1.8767226	0.106	0.30456579	14
soy_OGL_4739	1186	1.3662759	32.040474	9729	22.51	1	11.054619	0.146	0.13158262	11
soy_OGL_5099	1801	8.406477	26.762909	2315	24.93	3	2.1648073	0.15700001	0.088507026	5
soy_OGL_5119	1900	4.8253789	29.947369	13298	25.89	3	1.610454	0.18000001	0.38078424	13
soy_OGL_5127	1540	1.3629088	22.727272	23360	26.29	2	9.5343218	0.105	0.58767337	2
soy_OGL_5733	1985	0.27211389	19.345089	21495	28.41	4	9.8207941	0.063000001	0.6451925	8
soy_OGL_6059	3004	2.0422838	24.467377	21973	32.29	2	5.6778278	0.23800001	0.055889644	12
soy_OGL_6087	1200	0.40784842	31.75	19089	23.33	3	3.6954246	0.18700001	0.41798571	3
soy_OGL_6715	1349	2.7221162	36.026688	32143	27.42	1	2.604495	0.19400001	0.65691662	8
soy_OGL_2796	1395	3.1879244	31.541218	26275	24.87	1	2.7024755	0.094999999	0.17261888	4
soy_OGL_4119	1049	7.7928329	35.843662	15786	24.02	3	0.005968305	0.23999999	0.79822719	26
soy_OGL_4198	2781	3.1617231	27.220425	5893	25.99	6	1.3112268	0.046	0.21309888	19
soy_OGL_4400	2600	8.125845	22.423077	10573	30.19	5	3.9247718	0.104	0.56113619	25
soy_OGL_4760	2780	0.84740651	32.158272	38931	32.23	1	0.9351781	0.163	0.74142903	5
soy_OGL_5120	1797	4.134584	32.943794	2001	20.64	2	0.37288746	0.161	0.38172337	13
soy_OGL_6403	1600	6.8150654	34.125	5447	22.12	5	4.5854707	0.18799999	0.47604614	16
soy_OGL_2243	1864	7.3392978	39.75322	2114	22.9	5	9.7354145	0.15899999	0.6810413	14
soy_OGL_917	2236	6.3260517	26.654741	17633	30.76	6	4.8302326	0.132	0.68485665	28
soy_OGL_918	1500	6.3260517	29.533333	14497	28.33	6	4.8302326	0.169	0.68506819	26
soy_OGL_1343	1139	7.2529912	30.992098	18990	28.44	2	18.978786	0.12800001	0.72913414	13
soy_OGL_4190	2127	5.3633652	11.800658	4668	29.38	7	7.6569033	0.039999999	0.20359322	21
soy_OGL_4332	1465	6.1024008	33.378841	7288	24.02	8	4.2601452	0.146	0.44648927	19
soy_OGL_4763	1600	5.1086917	37.9375	18832	28.12	2	30.54439	0.17900001	0.80818021	7
soy_OGL_5742	1300	13.020522	27.923077	9557	27.15	5	4.9610882	0.17900001	0.6993767	16
soy_OGL_5967	1900	7.5982332	29.736841	6840	25.73	6	10.515461	0.104	0.66213775	15

soy_OGL_399	1300	8.1701508	28.692308	10685	25.69	5	9.2546844	0.161	0.75913966	25
soy_OGL_3134	1700	8.0353642	39.235294	8899	24.35	4	6.3981376	0.197	0.55735725	26
soy_OGL_2788	1700	4.2498212	27.647058	4278	22	6	1.3534534	0.083999999	0.21804196	11
soy_OGL_5129	1400	6.3039489	31.785715	10456	23.5	3	5.8196912	0.13	0.65343904	8
soy_OGL_5695	1357	1.387786	28.887251	6533	23.87	1	14.639076	0.113	0.40238863	13
soy_OGL_6155	1092	5.245831	18.131868	18917	27.1	3	7.2431712	0.096000001	0.78926492	17
soy_OGL_486	1403	4.9804826	38.845333	16967	24.37	3	1.3756965	0.090000004	0.50920254	17
soy_OGL_1308	1869	1.7763864	26.056715	5857	22.95	2	4.3583798	0.066	0.59049761	13
soy_OGL_1319	1101	0.24154867	25.703905	17840	22.52	1	0.078865454	0.131	0.61958575	14
soy_OGL_3080	1600	0.83059096	32.375	2451	21	2	7.8205018	0.093000002	0.24502492	10
soy_OGL_5639	1100	9.2479429	28.272728	20619	25.63	6	2.503937	0.125	0.54049808	17
soy_OGL_6022	1689	1.8269773	22.972174	21743	26.99	4	7.9570532	0	0.38921937	14
soy_OGL_6387	1809	1.8953118	25.428413	10220	24.32	2	8.1805372	0.048	0.3579087	7
soy_OGL_2327	1572	8.2941523	27.671755	2326	24.61	4	2.3475461	0.124	0.51797897	14
soy_OGL_3119	1867	5.7961874	30.905195	1001	24.69	5	8.4402161	0.081	0.52382684	15
soy_OGL_4764	1500	5.1086917	30.066668	1334	24	3	20.754265	0.12800001	0.80891609	6
soy_OGL_6395	1400	6.8150654	33.07143	4996	22.5	8	16.027893	0.14399999	0.46563977	12
soy_OGL_5666	1400	7.7668753	20.928572	5838	26.21	6	7.3109965	0.105	0.4969157	20
soy_OGL_890	1400	8.0451517	38.5	5811	22.07	4	6.9300776	0.123	0.66043514	21
soy_OGL_5650	1219	7.6806297	32.977852	13465	23.37	7	11.239203	0.114	0.52977705	18
soy_OGL_5681	1300	9.2884445	37.307693	2418	20.61	5	3.9527252	0.171	0.46439081	14
soy_OGL_1589	1753	5.281703	16.77125	1001	24.87	5	19.030468	0.142	0.73010117	9
soy_OGL_4196	2088	3.415179	10.105364	2425	27.01	6	0.82826394	0.17299999	0.21136285	19
soy_OGL_1292	1900	6.4559865	14.578947	4288	28.68	6	24.135088	0.13	0.64475441	15
soy_OGL_147	1712	7.3133149	7.2429905	8112	28.09	3	0.95013291	0.13600001	0.67677695	11
soy_OGL_3099	2010	1.1479118	2.9353235	14746	28.9	3	5.4739289	0.077	0.39957476	5
soy_OGL_5098	1841	7.4159703	13.959805	13077	30.52	5	2.8900735	0.030999999	0.085949935	5
soy_OGL_5754	1200	6.5565777	21	13026	25.66	3	4.0766273	0.178	0.7591868	15
soy_OGL_6061	1241	2.0422838	20.225624	26888	28.84	2	5.6778278	0.083999999	0.055728827	12
soy_OGL_6385	1000	1.0395986	28	35129	26.2	2	1.8399013	0.20900001	0.34145138	3
soy_OGL_2764	1707	3.2010031	11.540714	4851	27.35	5	11.306363	0.078000002	0.32929021	12

soy_OGL_3058	1010	12.11379	24.257425	12625	25.84	2	5.9110146	0.12	0.49249744	3
soy_OGL_6020	1500	2.3629057	22.066668	4576	25.46	5	19.742716	0.094999999	0.39517856	12
soy_OGL_6720	1091	2.7221162	24.106325	13168	25.38	1	6.7336202	0.114	0.66609585	10
soy_OGL_2808	1100	1.0325171	34.81818	12459	25.27	1	32.970032	0.109	0.35497707	5
soy_OGL_855	1358	5.0977836	16.126657	18968	31.73	3	18.69911	0.024	0.59431577	14
soy_OGL_6414	1200	10.411439	14.916667	11405	30	5	2.5536406	0.083999999	0.53695381	26
soy_OGL_153	1512	4.8982654	0	5566	21.62	2	4.5510955	0.134	0.68452197	13
soy_OGL_447	1074	5.6306467	0	25483	21.22	2	0.61232048	0.132	0.60457551	12
soy_OGL_1307	1047	1.7763864	2.6743076	23392	23.01	1	3.3109093	0.119	0.57968003	14
soy_OGL_1906	1675	23.127859	26.985075	2876	33.13	9	20.408596	0.12899999	0.62406933	13
soy_OGL_3178	1413	13.249586	31.847134	7428	24.55	7	2.4444396	0.183	0.65277576	24
soy_OGL_5595	2800	4.3595667	32.107143	2240	24.17	9	40.722958	0.057999998	0.65579695	18
soy_OGL_6525	2201	21.291258	33.530212	5279	27.94	4	5.1097422	0.19	0.71314776	16
soy_OGL_3502	1696	47.600048	26.297171	4494	31.42	6	7.7834482	0.093999997	0.71742034	21
soy_OGL_3510	1400	47.600048	29.714285	3330	31.28	6	0.96450597	0.123	0.72754461	23
soy_OGL_5311	1900	18.329891	36.894737	8511	26.42	7	6.0563107	0.14300001	0.68186587	27
soy_OGL_6753	2600	10.217542	32	7143	29.26	5	29.763126	0.123	0.73768336	32
soy_OGL_6807	2600	6.2792668	8.6923075	2926	26.03	8	140.38675	0.075000003	0.79624546	22
soy_OGL_561	2200	21.124374	17.318182	1879	31.09	8	6.647234	0.111	0.32300901	18
soy_OGL_3038	1632	48.141987	16.727942	9856	27.63	3	34.836491	0.234	0.68535608	12
soy_OGL_4361	2153	5.1394582	34.463539	4179	28.37	8	53.39669	0.197	0.50126773	21
soy_OGL_1718	2317	34.72348	17.263702	4425	19.2	8	262.78976	0.048999999	0.83706993	25
soy_OGL_3042	1719	43.052528	35.3694	7613	31.41	5	29.241043	0.15800001	0.67905104	12
soy_OGL_3496	1344	47.600048	24.702381	13037	25.59	5	34.229294	0.177	0.7109617	17
soy_OGL_4170	1690	61.380577	21.952663	4052	29.23	8	21.560427	0.14	0.15586664	7
soy_OGL_6309	2499	10.926672	22.609043	2566	32.05	6	98.548691	0.082999997	0.96942127	14
soy_OGL_3041	1321	43.052528	24.299772	12361	25.35	5	29.241043	0.19400001	0.6792531	12
soy_OGL_3172	1900	12.822569	24.421053	6292	33.26	7	48.784161	0.096000001	0.64465207	21
soy_OGL_6527	1382	21.291258	30.535456	2341	21.92	5	6.1934299	0.178	0.7149626	16
soy_OGL_1901	1281	11.551387	32.084309	2001	21.23	9	18.22419	0.177	0.64630193	10
soy_OGL_2415	1315	11.967738	31.939163	2001	24.33	5	25.778419	0.12800001	0.71084571	30

soy_OGL_5310	1300	18.329891	38.23077	5381	23.61	7	6.0563107	0.177	0.68210363	27
soy_OGL_5764	1564	16.606831	26.726343	3179	27.42	6	15.051555	0.112	0.78961128	20
soy_OGL_6751	1200	27.203409	32.916668	2181	29.75	5	7.5691195	0.11	0.73584336	28
soy_OGL_2684	1404	10.232581	35.82621	4127	22.36	10	20.762367	0.15800001	0.49218678	25
soy_OGL_5289	1290	20.713139	30.697674	3966	23.33	5	23.785765	0.131	0.73397624	23
soy_OGL_3495	1100	47.600048	17.818182	10300	29.18	5	31.906487	0.117	0.71080291	17
soy_OGL_213	1616	13.095701	26.361385	4977	27.16	3	13.475997	0.075000003	0.82146794	27
soy_OGL_1950	1638	24.549034	24.358974	3319	28.87	7	4.2583532	0.093000002	0.52088189	16
soy_OGL_2280	1800	13.338867	27.555555	5242	30.16	3	33.880493	0	0.62586695	42
soy_OGL_5619	1500	29.539919	20.200001	7421	31.33	5	4.1865201	0.071000002	0.62588507	22
soy_OGL_3834	1974	7.7801862	22.644377	4144	31.66	9	52.357777	0.167	0.54112017	25
soy_OGL_1025	1341	5.5469222	32.736763	2799	26.84	10	85.885765	0.145	0.82589883	29
soy_OGL_711	1400	8.4636536	24.071428	9128	26.85	8	48.681385	0.178	0.84746665	23
soy_OGL_3049	1100	56.688179	20.454546	6278	26.72	3	1.5717312	0.244	0.63126808	2
soy_OGL_4360	2000	5.509479	25.4	2086	28.3	9	65.369675	0.17200001	0.49988085	21
soy_OGL_5941	1300	29.346493	8	10143	31.46	5	3.5833595	0.145	0.72496939	23
soy_OGL_985	1227	9.9324665	38.30481	2323	21.84	9	194.09158	0.176	0.77136374	32
soy_OGL_1721	1949	34.72348	24.679323	5034	26.88	9	232.86699	0.117	0.83819854	25
soy_OGL_3541	2163	8.9636507	34.997688	3042	32.4	7	147.04712	0.17299999	0.79822332	24
soy_OGL_6419	1200	10.893449	17.5	2291	27	6	20.151438	0.139	0.54217768	33
soy_OGL_5759	1800	14.102677	30.444445	2722	26.61	6	9.6564541	0.127	0.77048528	13
soy_OGL_6761	2173	10.113653	23.653934	3742	29.26	5	5.4942174	0.067000002	0.74222535	31
soy_OGL_938	1500	12.449766	37.733334	7819	27.53	8	9.2474375	0.153	0.70957142	28
soy_OGL_1575	1600	9.8763494	29.1875	5146	31.56	5	43.074696	0.15000001	0.79617262	28
soy_OGL_2296	1377	9.7439394	39.651417	4257	26.36	8	19.807732	0.161	0.60429925	28
soy_OGL_4684	1751	10.870666	38.834953	6912	29.18	4	3.006197	0.17399999	0.64076471	40
soy_OGL_5627	1842	24.815081	31.813246	2066	31.7	10	8.756032	0.117	0.60539466	16
soy_OGL_6754	1985	10.217542	34.760704	8219	33.14	5	29.763126	0.15700001	0.73775756	33
soy_OGL_77	1700	9.6598225	18.411764	3102	30.94	5	15.03484	0.088	0.80050302	26
soy_OGL_1736	1564	17.655291	25.511509	7076	29.09	7	15.562757	0.106	0.86823654	13
soy_OGL_1927	2414	14.905339	26.636288	4698	31.89	5	5.4319773	0.12899999	0.55343461	26

soy_OGL_2625	2002	8.794776	33.916084	6434	27.52	9	17.676622	0.146	0.58034611	24
soy_OGL_4410	2021	8.6647367	33.349827	5164	29.39	8	41.276947	0.186	0.57776046	17
soy_OGL_5313	1374	18.329891	35.880642	6924	26.49	7	4.2586498	0.15800001	0.68057722	28
soy_OGL_5897	3163	10.121329	38.096745	10720	28.45	8	5.6085744	0	0.87685364	31
soy_OGL_5928	1707	28.940582	38.37141	3047	29.05	6	2.7672679	0.177	0.75228572	15
soy_OGL_4559	2100	8.4823227	28.857143	4432	27.52	6	23.265608	0.056000002	0.8036828	24
soy_OGL_5309	1800	18.329891	24.388889	2717	32.33	4	8.5175724	0.056000002	0.68601829	30
soy_OGL_1390	1311	6.9438424	30.816172	6240	26.62	6	7.5768118	0.123	0.80899709	33
soy_OGL_2267	1100	9.1252251	16.90909	9993	30.72	6	3.9890997	0.111	0.63580275	43
soy_OGL_1549	1400	8.9413004	32.142857	6933	27.78	7	14.763446	0.115	0.85927975	30
soy_OGL_3141	1800	12.683842	24.611111	2946	30.16	9	9.9564734	0.066	0.56503397	29
soy_OGL_4916	1191	17.460024	32.913517	5895	28.71	8	16.693867	0.14300001	0.78041506	22
soy_OGL_4667	1566	8.714469	25.287355	6333	27.84	8	14.779904	0.079999998	0.6662876	35
soy_OGL_5628	2000	24.815081	27	2632	30.65	11	11.155895	0.037	0.60427201	15
soy_OGL_3367	1800	11.584485	31.111111	1064	27.88	7	30.5828	0.048999999	0.78156221	10
soy_OGL_1466	1800	9.5639515	33.388889	9468	28.11	6	15.43951	0.048999999	0.92659491	30
soy_OGL_3045	1100	32.207867	39.727272	3024	28.9	4	1.1916893	0.118	0.66997445	10
soy_OGL_3233	1398	8.2360296	37.911301	5357	26.1	4	18.384989	0.1	0.72373641	38
soy_OGL_2613	1500	8.5876789	31.333334	1379	30.86	9	62.818638	0.125	0.59198952	23
soy_OGL_2672	1580	6.8734031	31.772152	3570	29.05	8	48.160072	0.15099999	0.50570351	23
soy_OGL_5857	1100	8.370719	38.363636	9930	29.45	8	60.290184	0.2	0.94570917	18
soy_OGL_557	2282	20.895227	22.217354	4895	27.38	8	15.432343	0.15899999	0.32503605	18
soy_OGL_2619	1541	8.8686056	23.815704	3690	25.89	7	30.399998	0.139	0.5841189	23
soy_OGL_6258	1775	4.9920311	15.549295	5143	25.52	3	54.334961	0.112	0.91607052	25
soy_OGL_70	1900	11.427641	17.947369	11134	30.42	4	4.8996096	0.061000001	0.81985456	31
soy_OGL_2665	1972	6.8734031	37.170387	8162	22.87	9	29.879412	0.12800001	0.52342057	23
soy_OGL_3048	1500	32.134468	21.333334	3396	26.46	2	5.1259222	0.176	0.63738298	2
soy_OGL_552	1332	18.677822	28.528528	9619	24.62	7	9.4437199	0.17200001	0.33489639	17
soy_OGL_648	1375	6.2027626	24.072727	19571	29.89	4	24.76837	0.104	0.75542653	29
soy_OGL_1305	1763	1.5215753	30.743052	1001	24.78	2	72.71769	0.162	0.57723874	12
soy_OGL_2685	1200	10.232581	31.916666	3127	25.16	6	23.647154	0.17200001	0.49063987	25

soy_OGL_3018	1300	10.088968	33.076923	6316	26.84	4	30.753052	0.12800001	0.75688934	22
soy_OGL_3037	1472	32.088409	27.581522	10980	28.66	5	12.912634	0.117	0.69475687	11
soy_OGL_518	2200	2.3637695	39.81818	16218	21.9	4	137.0737	0.131	0.42714864	14
soy_OGL_551	1703	18.677822	33.294186	8706	27.18	7	9.4437199	0.16500001	0.33500451	17
soy_OGL_875	1981	2.4722638	33.467945	4684	25.99	4	76.086998	0.030999999	0.62010819	8
soy_OGL_3067	1700	43.383347	39.64706	15019	27.17	1	5.2538152	0.17	0.1294468	6
soy_OGL_5138	2207	3.8446505	32.351608	13836	30.72	5	70.407242	0.012	0.71563351	12
soy_OGL_5340	1000	24.855507	33.099998	21926	30.3	3	21.225418	0.115	0.53338414	10
soy_OGL_6666	2100	12.019849	38.476189	15980	30.57	6	29.363962	0.14	0.007926915	22
soy_OGL_3142	1299	10.669563	39.030022	8041	23.17	5	5.1604772	0.155	0.56839329	28
soy_OGL_6436	1686	11.181879	21.055754	7710	28.46	5	7.7375259	0.048999999	0.55542779	38
soy_OGL_492	1300	5.023427	28	10399	25.69	4	37.329941	0.082000002	0.48409459	19
soy_OGL_5196	1356	13.332328	32.079647	16159	25.58	3	18.667997	0.113	0.9650293	14
soy_OGL_6424	1044	10.893449	26.819923	18765	27.87	4	6.3985171	0.092	0.54461098	33
soy_OGL_3352	1400	12.108066	37.642857	8379	25.5	6	41.25135	0.092	0.82897699	17
soy_OGL_6526	1389	21.291258	32.757378	7633	25.19	4	3.9353161	0.127	0.71364462	16
soy_OGL_3255	1601	5.2893763	37.226734	4124	27.73	3	87.866577	0	0.82664037	14
soy_OGL_5089	1303	23.446672	34.458942	2753	24.55	3	6.1058717	0.131	0.22572847	2
soy_OGL_6259	1100	4.8718433	28.727272	8033	26.81	4	42.123158	0.219	0.91685838	24
soy_OGL_1925	1600	12.936749	19.8125	10937	29.87	8	23.261513	0.175	0.55738312	24
soy_OGL_564	1100	21.491308	28.09091	5438	25.9	8	9.4132662	0.207	0.31496397	23
soy_OGL_3051	1800	32.517826	1.8333334	17761	33.44	3	0.076934606	0.061000001	0.59740001	4
soy_OGL_3376	1500	10.989937	13.866667	13573	29.2	4	45.104172	0.097999997	0.75441015	13
soy_OGL_3868	1900	9.8148384	14.052631	2611	27.21	7	32.070759	0.112	0.25483692	19
soy_OGL_558	1300	20.895227	26	6547	29.61	8	15.432343	0.175	0.32491443	18
soy_OGL_4660	1100	8.5887651	30.636364	9588	25	6	116.62761	0.12	0.67767972	26
soy_OGL_71	1139	10.400795	13.696225	9809	27.48	5	19.568296	0.123	0.81612492	31
soy_OGL_6421	1065	10.893449	14.741784	4207	22.34	2	52.109798	0.146	0.54356027	33
soy_OGL_4022	1100	7.0667925	36.363636	2066	27.36	6	64.452332	0.133	0.6936	16
soy_OGL_3254	1296	5.2893763	24.382715	4388	22.83	2	128.35632	0.057	0.82600296	14
soy_OGL_297	1800	8.1388817	35.333332	9885	25.16	7	16.604488	0.121	0.91970634	17

soy_OGL_3484	1900	5.426621	29.631578	7452	27.05	7	21.541693	0.121	0.64939725	27
soy_OGL_4230	1716	4.3900228	23.310024	6927	29.31	9	20.532913	0.12899999	0.26965782	30
soy_OGL_910	1438	5.9492388	33.03199	8980	28.37	3	21.986818	0.19400001	0.6776365	27
soy_OGL_195	1926	10.74993	39.51194	13643	26.89	6	11.848988	0.079000004	0.80353546	22
soy_OGL_929	1701	11.994018	36.625515	4901	24.86	4	3.8874454	0.139	0.70332021	24
soy_OGL_4127	1457	10.237288	29.169527	14627	29.71	3	9.0029306	0.085000001	0.82092386	32
soy_OGL_5197	2157	13.332328	34.306908	20015	31.33	3	18.667997	0.141	0.96534693	14
soy_OGL_6213	1900	6.6037278	32.578949	31933	33.21	3	10.153718	0.004	0.86906475	29
soy_OGL_549	1600	17.431976	26.3125	3138	29.06	7	7.0138831	0.121	0.33770269	21
soy_OGL_2565	1456	6.5413885	31.25	11612	31.66	4	46.581635	0.093000002	0.69273424	19
soy_OGL_3852	1600	9.9024754	37	7310	27.75	10	26.979399	0.107	0.28701288	14
soy_OGL_829	1800	9.6582899	38.333332	5808	27.55	5	19.251059	0.093999997	0.72066408	23
soy_OGL_3853	1675	9.9024754	32.597015	5210	25.55	9	22.39007	0.102	0.28692275	14
soy_OGL_3380	1100	10.989937	35.636364	4672	24	6	16.953121	0.171	0.75214744	12
soy_OGL_1962	1360	7.7554264	26.102942	6991	27.64	5	8.5045691	0.108	0.49375325	24
soy_OGL_2640	1400	7.9126515	32.42857	7425	26.78	4	10.050557	0.097999997	0.55558044	22
soy_OGL_1929	1300	15.320704	27.76923	7502	30.76	6	8.1030178	0.104	0.55257469	25
soy_OGL_6658	1238	13.947652	37.399033	1001	25.44	7	9.7676115	0.147	0.12373525	20
soy_OGL_6669	1600	9.9655132	29.5625	2074	26.93	7	13.592624	0.090000004	0.010651038	22
soy_OGL_4375	1095	6.6361041	31.780823	3079	25.84	6	24.868338	0.19599999	0.52756947	25
soy_OGL_5404	1500	9.4738331	21.533333	5868	28.2	7	20.233892	0.088	0.74133366	14
soy_OGL_5139	1200	3.8446505	35.666668	7032	30.75	5	70.407242	0.039999999	0.716277	12
soy_OGL_1112	1993	5.1327338	4.2147517	1001	25.63	12	13.070252	0.079000004	0.95473993	10
soy_OGL_3981	1788	5.9596634	4.8657718	2676	26.11	11	6.4915757	0.092	0.89268124	14
soy_OGL_6293	1345	6.0841422	13.903346	1001	23.27	10	4.7985878	0.175	0.94773161	22
soy_OGL_6268	1347	6.782124	12.175204	3033	26.2	11	6.7974467	0.15800001	0.92589939	30
soy_OGL_6572	1200	4.8296428	16.25	3459	26.91	6	2.5219452	0.12	0.78099805	31
soy_OGL_4114	1100	8.1381798	18.818182	2035	23.9	10	3.3870571	0.124	0.79086196	17
soy_OGL_678	1234	3.8562949	13.857374	1001	24.87	8	7.4855475	0.108	0.78165364	25
soy_OGL_5557	1122	6.151978	18.716578	4158	23.26	9	3.045614	0.113	0.73209876	16
soy_OGL_5497	1767	4.6145062	13.299377	3811	24.16	8	7.2766161	0.088	0.84847522	28

soy_OGL_5797	1600	12.976668	4.9375	2025	19.18	6	24.479622	0.15700001	0.85539258	40
soy_OGL_783	1700	10.960977	11.823529	7010	18.64	8	3.1558492	0.113	0.92783594	18
soy_OGL_1566	1394	10.710433	14.060258	1505	22.16	5	12.924914	0.156	0.81734526	27
soy_OGL_3602	2010	4.9321332	0	2001	24.67	8	5.6593542	0.089000002	0.87405652	22
soy_OGL_3994	1500	11.197123	17.533333	1445	19.8	8	5.4949589	0.16	0.82703459	14
soy_OGL_4618	1397	7.723742	15.891195	3938	21.97	8	7.8806539	0.14399999	0.76549762	24
soy_OGL_5947	1500	10.436343	7.1333332	6855	20.46	9	14.809605	0.15000001	0.7165153	24
soy_OGL_803	1822	9.4385977	20.691547	1698	22	8	13.643888	0.086999997	0.84276336	21
soy_OGL_4150	1545	10.959122	17.475729	2207	20.45	8	18.994202	0.126	0.87669402	24
soy_OGL_5809	1300	12.425729	19.615385	9386	23.3	7	8.2762794	0.142	0.87980008	37
soy_OGL_5868	1415	7.2906718	27.844522	1001	20.14	10	6.4651794	0.162	0.92083597	28
soy_OGL_6905	1900	7.0806479	17	3211	23	9	4.4128528	0.067000002	0.87285113	23
soy_OGL_4641	1653	17.461983	15.003025	11450	20.87	7	1.250223	0.083999999	0.72862089	34
soy_OGL_1572	1384	9.8763494	26.228323	3903	20.08	7	17.513138	0.148	0.80084378	26
soy_OGL_75	1306	9.8974447	25.421133	5460	20.36	8	20.390003	0.13600001	0.80523032	25
soy_OGL_4407	1647	8.6647367	13.418336	4366	22.58	11	32.045147	0.106	0.57367444	24
soy_OGL_3637	2000	7.1081796	11.5	6961	24.95	6	1.7031627	0	0.93138903	32
soy_OGL_5027	2000	7.1732235	14.05	1604	21.7	6	9.8929319	0.018999999	0.66264492	29
soy_OGL_3584	1600	4.1718922	22.5625	4650	22.75	6	8.9060173	0.075000003	0.84840214	40
soy_OGL_2409	1145	11.967738	12.751092	2365	23.4	5	2.3872302	0.176	0.70490152	31
soy_OGL_51	1284	9.9992008	11.604362	2001	25.93	5	12.427788	0.139	0.85624945	30
soy_OGL_786	1917	7.6410537	18.727179	3003	25.97	9	8.8759899	0.074000001	0.89633459	19
soy_OGL_1694	1500	5.6909261	34.400002	3468	21	10	3.768259	0.13699999	0.81020749	26
soy_OGL_6989	1266	6.052465	20.221169	2515	22.82	11	4.4108562	0.19599999	0.95189053	28
soy_OGL_6331	1241	6.7954488	32.151489	1176	23.6	4	2.8311105	0.15899999	0.91517699	27
soy_OGL_2501	1473	7.4874678	17.651052	1001	25.86	6	11.289385	0.118	0.83944756	18
soy_OGL_4579	1205	5.9374781	20	5378	20.24	7	4.5965381	0.192	0.8328954	21
soy_OGL_5949	1900	11.551946	0	3660	23.68	5	1.8585685	0.086000003	0.71080613	23
soy_OGL_1810	1169	5.8060555	20.188194	5045	20.87	7	5.7046494	0.18000001	0.78318828	21
soy_OGL_4227	2493	4.0722065	8.7444849	1041	20.57	10	9.0884924	0	0.26637387	30
soy_OGL_905	1254	6.4160132	26.794258	4281	20.25	6	13.02787	0.149	0.67494982	29

soy_OGL_3483	1400	5.426621	12.928572	5552	23.92	7	21.541693	0.113	0.64933163	27
soy_OGL_3128	1000	6.2185674	28.799999	2224	21.1	7	5.786746	0.197	0.55055279	26
soy_OGL_346	1600	6.2913775	5.5	2692	24.75	7	5.822391	0.094999999	0.84857661	28
soy_OGL_1544	1633	8.1076202	3.8579302	2001	20.75	10	14.060459	0.152	0.87083328	33
soy_OGL_3646	1944	4.3527098	0	3881	22.63	8	15.476603	0.075000003	0.9376784	26
soy_OGL_2949	1915	11.29328	1.8276763	2001	25.22	7	10.617508	0.068999998	0.89651066	17
soy_OGL_4959	1364	12.134647	0	10955	19.5	8	9.381278	0.16599999	0.75082505	33
soy_OGL_5749	1217	13.586713	20.706656	2001	18.98	8	2.5093875	0.17	0.72262675	14
soy_OGL_16	1169	11.006102	21.300257	3744	21.38	10	6.7505126	0.178	0.92348069	24
soy_OGL_3771	1625	12.101471	12.861539	2143	23.2	12	5.5059962	0.112	0.71891308	16
soy_OGL_4538	1476	7.1064296	14.295393	2001	22.42	11	6.7893567	0.14300001	0.77850765	34
soy_OGL_3703	1353	8.5720577	19.364376	2961	22.76	7	8.5251007	0.124	0.84376395	19
soy_OGL_219	1700	11.379414	3.2941177	3787	18.88	11	11.393044	0.108	0.82669234	24
soy_OGL_1164	2260	9.6878195	0	1001	21.81	10	14.858408	0	0.92884827	19
soy_OGL_5472	2000	4.9895315	2.4000001	3027	21.15	13	14.221847	0.064000003	0.87303829	26
soy_OGL_5770	1600	20.915419	5.1875	1369	21.25	5	3.5731845	0.093999997	0.81233323	23
soy_OGL_9	1693	8.163537	9.2734795	1395	23.44	7	11.031654	0.067000002	0.95723677	15
soy_OGL_3154	2005	10.71382	0	2981	23.49	10	13.666006	0.041999999	0.59108853	19
soy_OGL_4954	1567	12.134647	3.5098915	5714	22.08	6	9.1550274	0.082000002	0.75142568	33
soy_OGL_6880	1800	4.5204587	3.6111112	2919	23.11	9	5.8563099	0.071000002	0.85128838	19
soy_OGL_67	1500	12.433825	0	1782	22.73	8	6.6063929	0.078000002	0.82628483	34
soy_OGL_969	1038	13.568718	7.2254333	3192	18.78	7	3.3867972	0.044	0.76307327	36
soy_OGL_1529	1263	7.269011	3.3254156	3912	24.3	6	3.7856958	0.088	0.88978386	35
soy_OGL_1547	1038	7.6185937	5.9730248	5896	18.68	9	11.519375	0.11	0.86792034	33
soy_OGL_2908	1600	10.078434	5.5625	3785	19.93	11	4.877398	0.086000003	0.97812343	25
soy_OGL_2946	1886	10.631252	3.8176033	1842	21.95	9	1.5969754	0	0.90596861	17
soy_OGL_3243	1115	9.3938437	0	3320	17.66	8	7.0554242	0.112	0.73030919	36
soy_OGL_4951	1539	6.3694191	0	2001	21.96	11	6.5128989	0.103	0.7545076	36
soy_OGL_5886	1443	10.300918	0	3552	20.3	10	10.350056	0.071999997	0.89108455	35
soy_OGL_6951	1600	8.566577	9.125	2052	20.12	10	11.322671	0.093000002	0.92744869	25
soy_OGL_260	1500	9.1737165	4.3333335	3340	22.6	7	9.1721563	0.090999998	0.8752507	22

soy_OGL_663	1477	6.8420768	0	3042	21.66	6	4.8541975	0.090999998	0.76945716	33
soy_OGL_4525	1100	7.9699202	0	5300	17.54	8	5.9389243	0.119	0.7615658	33
soy_OGL_4674	1092	10.891823	10.714286	2887	15.29	6	12.771862	0.13	0.64852339	35
soy_OGL_5319	1438	11.453777	6.4673157	2317	18.35	8	6.7177696	0.12	0.66671342	26
soy_OGL_5489	1600	4.7314305	0	3418	22.43	7	11.32381	0.046	0.86085439	33
soy_OGL_6757	1492	9.5540066	0	1620	22.65	6	2.2784572	0.102	0.73901516	30
soy_OGL_6830	1200	6.5125389	10.25	2734	22.16	6	3.218195	0.098999999	0.81075025	34
soy_OGL_291	1200	11.654119	15.583333	2183	23.08	8	6.8078423	0.146	0.90957546	26
soy_OGL_1553	1680	9.3490543	11.666667	2001	22.32	10	9.6182747	0.059999999	0.84867859	26
soy_OGL_1693	1574	6.9235315	18.170267	2440	22.49	13	11.902357	0.114	0.80751109	25
soy_OGL_3340	1900	10.878196	0	5022	26.68	8	9.768507	0	0.85712445	26
soy_OGL_3517	1200	38.161209	0	4653	19.41	5	7.2827311	0.153	0.74217367	20
soy_OGL_3631	2100	7.9034634	6.0952382	2618	24.14	11	5.8406992	0	0.92214143	30
soy_OGL_4524	1900	7.9699202	1.7894737	5995	28.47	9	5.8025231	0	0.76141095	34
soy_OGL_4930	2074	14.560184	2.1697204	1589	21.84	9	13.4665	0.039999999	0.7670033	35
soy_OGL_6275	1983	6.1533623	14.473021	2001	22.39	9	8.7067032	0	0.93141121	26
soy_OGL_6788	1200	9.1081762	18.916666	4955	22.83	10	3.8858609	0.12	0.77730262	25
soy_OGL_19	1274	10.21663	12.480377	2470	24.41	6	6.1726484	0.097000003	0.91875756	26
soy_OGL_36	1298	9.8391256	12.01849	2538	23.11	10	11.044274	0.114	0.89276373	31
soy_OGL_1441	1400	8.1389084	0	5102	20.5	13	18.047152	0	0.898404	24
soy_OGL_3725	1300	7.6693859	7.4615383	2323	24.23	10	4.7556353	0	0.81124032	25
soy_OGL_4696	1174	8.5891142	0	6235	20.78	11	13.639303	0	0.61440694	39
soy_OGL_4699	1200	8.5891142	11.166667	6989	21.66	10	13.5937	0.079999998	0.61308497	37
soy_OGL_5900	1000	10.121329	13.7	2199	22.2	6	4.4611826	0.13500001	0.87634695	31
soy_OGL_6818	1012	6.8960595	13.043478	2001	20.45	8	11.428139	0.106	0.80498701	33
soy_OGL_6970	1000	4.3050809	23.299999	4687	20.2	9	3.2637677	0.146	0.94015694	33
soy_OGL_200	1100	11.833065	17.454546	6541	19.18	7	4.6893544	0.106	0.81040615	27
soy_OGL_690	1900	11.121198	0	3192	23.89	7	10.079429	0	0.80888981	21
soy_OGL_2199	1300	8.5738249	0	4231	23.61	7	7.2241607	0	0.77250457	34
soy_OGL_4642	1247	17.461983	0	10448	19	8	10.271504	0.050999999	0.72838253	34
soy_OGL_6960	1245	6.068716	6.5863452	5069	20.64	7	13.79142	0	0.93147922	33

soy_OGL_1556	1500	9.3490543	21.933332	5698	21.46	9	6.7765508	0.072999999	0.84213692	25
soy_OGL_892	1279	7.4788356	22.204847	3983	22.43	8	3.6492405	0.101	0.66312301	25
soy_OGL_5022	1700	12.549186	0	1093	26.23	5	6.4659705	0.037	0.66625851	28
soy_OGL_5609	1108	25.029232	11.01083	4973	22.02	5	4.610301	0.125	0.63283139	27
soy_OGL_4444	1300	8.6510143	18.76923	2244	21.15	10	14.821145	0.106	0.63653839	19
soy_OGL_5307	1455	18.329891	0	6692	24.74	7	4.1684542	0	0.69073725	29
soy_OGL_6897	1100	7.0806479	28.363636	1672	19.09	6	11.252283	0.103	0.86830223	27
soy_OGL_4803	1795	5.6626678	4.1782732	2667	21.22	16	3.2377098	0.149	0.93438232	14
soy_OGL_271	1486	9.3673096	0	3602	22.94	7	6.730937	0.14	0.89553016	26
soy_OGL_362	1685	7.2958274	0	2846	24.39	8	4.9784341	0.113	0.82669437	29
soy_OGL_436	1656	10.683906	2.2342994	1633	22.22	11	13.631361	0.114	0.67411178	19
soy_OGL_1140	1600	5.5214667	0	4131	22.31	11	15.486933	0.13600001	0.97605264	26
soy_OGL_1172	1545	8.4058905	3.1715209	2154	19.61	9	10.213177	0.18099999	0.90932894	26
soy_OGL_1554	1523	9.3490543	0	3409	22.78	10	9.6182747	0.155	0.84858197	26
soy_OGL_5478	1182	3.8617556	9.5600681	2066	18.35	9	27.794392	0.214	0.86759388	30
soy_OGL_6749	1162	26.298864	0	4195	20.56	7	7.7935801	0.19400001	0.73528373	28
soy_OGL_396	1735	9.5874052	0	2603	25.76	8	6.2937293	0.093999997	0.76318818	24
soy_OGL_3644	1438	5.1482658	0	4122	20.79	6	10.90022	0.156	0.93658763	28
soy_OGL_5025	1567	7.1732235	0	2508	24.56	8	9.4246492	0.11	0.66335481	28
soy_OGL_6957	1300	5.1221623	0	3461	17.38	5	24.504807	0.193	0.93007505	29
soy_OGL_242	1320	12.079522	14.090909	1001	23.78	10	3.9513865	0.14399999	0.84903204	20
soy_OGL_1174	1204	8.3456259	14.700996	5127	23.75	8	9.534934	0.142	0.90821469	26
soy_OGL_2911	1430	10.078434	8.2517481	2001	24.82	7	10.097049	0.125	0.97360426	26
soy_OGL_3224	1027	7.901536	5.1606622	9500	28.33	7	10.248329	0.142	0.71370333	47
soy_OGL_5291	1383	21.185158	4.0491686	4172	22.41	7	17.332621	0.139	0.73294663	24
soy_OGL_5787	1100	14.27938	4.5454545	5060	25.27	5	15.903885	0.14399999	0.84985256	40
soy_OGL_5813	1200	12.729729	14.5	2727	22.5	8	4.3907647	0.177	0.89310789	25
soy_OGL_6964	1132	16.297258	3.5335689	6822	23.93	7	13.337164	0.17200001	0.93534517	33
soy_OGL_3939	1243	8.8798027	7.964602	7116	23.25	7	29.008036	0.118	0.86613989	27
soy_OGL_2123	1117	8.9625301	15.398389	4247	22.11	8	2.5877657	0.121	0.90331572	17
soy_OGL_2955	1200	9.1648493	12.583333	2360	23.08	8	4.6936259	0.127	0.87991065	18

soy_OGL_250	1280	13.280943	11.40625	2001	21.32	9	2.7782507	0.153	0.86638051	19
soy_OGL_4482	1290	7.5810852	9.3798447	2346	21.86	9	11.645471	0.142	0.71407574	31
soy_OGL_4503	1500	8.7601175	4.8666668	2186	22	12	5.3049798	0.139	0.74261755	31
soy_OGL_15	1312	10.159842	4.7256098	5879	23.62	10	4.5899482	0.072999999	0.92858785	21
soy_OGL_206	1271	11.890499	0	2545	21.08	7	8.1446753	0.146	0.81253076	28
soy_OGL_208	1300	14.722309	0	2639	19.53	7	5.3420558	0.167	0.81572467	25
soy_OGL_1210	1400	6.7576227	3	3363	23.28	10	18.11375	0.096000001	0.82282454	27
soy_OGL_1436	1421	10.565134	0	2043	20.68	10	14.674491	0.13699999	0.8869462	24
soy_OGL_1534	1070	7.5677972	0	5441	19.53	7	9.7090359	0.126	0.88504231	38
soy_OGL_1543	1069	8.1677341	2.8063612	1362	18.61	10	11.658602	0.126	0.87325782	31
soy_OGL_3298	1017	7.0984483	5.1130776	5927	22.12	10	3.8931081	0.028999999	0.94998997	24
soy_OGL_3568	1000	5.4506187	5	3382	21.3	8	9.9279194	0.145	0.8358925	35
soy_OGL_4523	1083	7.9699202	0	4212	18.46	9	5.8025231	0.121	0.76134819	34
soy_OGL_4691	1100	10.074121	0	3110	21.27	8	4.15446	0.098999999	0.62548363	39
soy_OGL_5495	1543	4.5870309	0	2001	23.59	9	22.48159	0.079000004	0.85119176	31
soy_OGL_5884	1041	10.300918	0	2001	18.53	11	3.7303109	0.085000001	0.89373696	35
soy_OGL_6233	1469	8.3000326	0	4446	21.78	10	4.2948804	0.13	0.89454645	20
soy_OGL_6292	1488	6.0841422	2.4865592	1624	22.44	9	5.238739	0.093999997	0.94769567	22
soy_OGL_6829	1141	6.5125389	0	1719	21.2	8	3.5250289	0.124	0.81056774	34
soy_OGL_6955	1276	5.9321976	4.5454545	2242	19.74	7	24.113876	0.126	0.92898726	27
soy_OGL_6972	1034	4.3050809	0	2001	16.53	9	3.2637677	0.124	0.94021451	33
soy_OGL_6984	1100	4.6887946	0	1258	18.72	10	6.3182101	0.103	0.94742996	33
soy_OGL_398	1502	8.8643551	0	1760	22.5	8	6.614748	0.107	0.76059002	25
soy_OGL_1371	1100	5.6842537	0	1562	20.18	6	13.730577	0.122	0.7909506	33
soy_OGL_1857	1116	5.4487619	8.6021509	4388	23.02	6	11.641839	0.131	0.72757465	37
soy_OGL_2187	1100	10.96957	0	2213	20.9	5	12.632515	0.123	0.79328901	30
soy_OGL_2405	1418	11.967738	0	2140	23.27	7	7.1358285	0.097999997	0.69964427	27
soy_OGL_3122	1000	8.1608553	7.5999999	5416	16.7	13	9.2269335	0.1	0.53986877	24
soy_OGL_4861	1110	5.903389	11.351352	3297	21.17	8	5.8093905	0.103	0.94806504	17
soy_OGL_4909	1238	14.910236	0	7528	20.19	11	11.803347	0.086000003	0.78350389	18
soy_OGL_4948	1100	9.4054356	2.909091	2666	21.27	5	10.767612	0.122	0.75630808	35

soy_OGL_4955	1035	12.134647	0	3847	20.28	6	9.1550274	0.108	0.75136983	33
soy_OGL_6204	1028	6.3214092	10.408561	2001	20.33	7	5.5806918	0.13699999	0.86182499	28
soy_OGL_6792	1100	8.9071083	5.818182	2994	21.27	9	1.4747676	0.094999999	0.77947277	24
soy_OGL_6981	1100	4.8485398	0	4832	22.9	5	10.968753	0.106	0.94421488	33
soy_OGL_1517	1156	6.1372461	3.8062284	5397	25.17	10	2.5476129	0.066	0.91006213	34
soy_OGL_965	1500	12.385811	0	1228	23.6	10	13.638389	0.118	0.75754285	37
soy_OGL_978	1029	13.02616	0	3406	23.32	9	3.8975697	0	0.76719654	33
soy_OGL_1209	1415	6.7576227	8.4805651	2470	23.53	11	16.866644	0.088	0.82298619	27
soy_OGL_1241	1505	8.69104	1.9269103	3061	23.38	10	19.154371	0.078000002	0.7539342	25
soy_OGL_2143	1100	6.9987392	14	2115	22.9	7	6.5582757	0.122	0.86144495	30
soy_OGL_2292	1217	11.585636	9.03862	3570	23	12	11.487501	0.119	0.61182112	31
soy_OGL_2293	1270	9.6573048	0	1635	23.07	11	13.999751	0	0.60886699	30
soy_OGL_3202	1188	8.2018318	0	2195	23.06	10	5.8514123	0	0.69281697	36
soy_OGL_3244	1173	9.3938437	0	2001	23.95	8	7.0554242	0.071000002	0.73036391	36
soy_OGL_3823	1081	7.8729119	9.7132282	2001	20.9	12	9.8159037	0.048	0.55615371	26
soy_OGL_4509	1218	8.8380184	6.5681443	3805	25.69	8	4.8388886	0.082999997	0.7477597	37
soy_OGL_4938	1074	9.3127365	6.0521417	1022	22.25	9	6.7256265	0.097000003	0.76114428	37
soy_OGL_5801	1024	12.976668	0	3993	22.16	8	16.874744	0.075000003	0.85895151	37
soy_OGL_6953	1000	8.566577	4.6999998	5047	21.2	11	9.6075592	0.068999998	0.92811561	25
soy_OGL_970	1000	13.568718	0	5492	23.2	7	3.3867972	0.050999999	0.76313955	36
soy_OGL_2513	1549	7.4874678	0	4391	26.53	9	0.55344528	0.006	0.82377625	25
soy_OGL_14	1211	10.159842	4.4591246	4192	24.52	7	1.1481969	0.043000001	0.92991513	20
soy_OGL_1424	1000	11.385625	0	5071	20.6	8	10.548765	0.035999998	0.8686772	23
soy_OGL_5405	1625	9.4738331	0	1425	22.76	10	10.024912	0	0.74543029	14
soy_OGL_2194	1092	8.5738249	11.080586	4002	25.82	6	6.9483781	0.123	0.78125268	29
soy_OGL_243	1336	13.848411	6.8862276	6312	23.27	8	13.324379	0.085000001	0.85219592	18
soy_OGL_658	1149	5.4899426	0	4995	26.37	8	8.6120062	0.002	0.76434904	36
soy_OGL_1276	1125	7.387959	6.1333332	1661	24.44	9	7.0391445	0	0.68032879	24
soy_OGL_1372	1100	5.6842537	6.909091	6256	23.81	8	12.99356	0.057999998	0.7916187	33
soy_OGL_1464	1065	9.5639515	9.3896713	7352	23.66	6	15.966932	0.11	0.92580914	31
soy_OGL_3179	1066	12.608178	19.136961	2651	23.07	7	7.08781	0.125	0.65487754	22

soy_OGL_4158	1471	8.5009871	9.7212782	1001	24.47	6	20.284187	0.078000002	0.89530408	17
soy_OGL_5816	1100	13.055554	2.5454545	3561	21.81	8	5.3142133	0	0.9006536	23
soy_OGL_6938	1146	10.270785	2.4432809	2001	23.29	9	6.2053542	0	0.90809864	19
soy_OGL_3621	1400	3.8661525	15.142858	8198	22.14	12	5.9635634	0.097999997	0.91473716	22
soy_OGL_1698	1400	6.9589791	14	2390	24.78	9	2.822082	0.101	0.81199837	27
soy_OGL_6630	1320	8.3712139	18.939394	2933	22.8	10	4.5709047	0.126	0.96906894	24
soy_OGL_1136	1000	5.6738558	23.9	2856	20.6	13	3.7506435	0.146	0.97791231	25
soy_OGL_1701	1319	6.9589791	13.419257	2001	25.54	8	2.8418443	0.057	0.81253231	28
soy_OGL_4567	1189	4.667098	14.213625	1001	21.44	10	3.047852	0.074000001	0.82182181	24
soy_OGL_2557	1334	5.4913468	24.662668	2001	21.58	10	9.6273718	0.108	0.71082401	17
soy_OGL_5544	1138	7.2413769	23.11072	3830	21.79	9	7.4447684	0.121	0.76690423	17
soy_OGL_5932	1500	7.3944454	11.6	4643	26.6	9	5.8285913	0.034000002	0.7379694	22
soy_OGL_3640	1448	5.7721701	22.513813	2875	23.68	6	4.9603882	0.092	0.93377268	27
soy_OGL_4870	1741	5.4112797	23.147615	2001	22.22	8	5.8048105	0.050999999	0.939686	21
soy_OGL_6261	1300	5.350945	14.923077	5694	24.92	9	3.681603	0.142	0.91844952	24
soy_OGL_262	1638	10.963178	9.4017096	1623	28.14	7	2.4826207	0.083999999	0.87652934	21
soy_OGL_361	1700	7.2958274	0	2644	28.7	9	5.1810784	0.085000001	0.82679278	29
soy_OGL_3577	1200	5.4506187	9.083333	4557	27.83	7	5.1038799	0.111	0.84178144	41
soy_OGL_3702	1400	8.5720577	12.642858	2734	26	7	11.547366	0.111	0.84453219	19
soy_OGL_6334	1400	5.6879897	8.5714283	3511	28.5	5	3.5650322	0.082000002	0.90727818	29
soy_OGL_4882	1354	3.9014754	11.004432	2232	20.31	13	2.3942809	0.079999998	0.92349726	19
soy_OGL_641	1241	8.1319628	14.343271	1001	22.4	12	3.4782391	0.083999999	0.74488592	21
soy_OGL_4552	1600	3.8827412	5.5625	3424	26.06	12	7.3621979	0.057	0.7943266	28
soy_OGL_7015	1595	7.3307347	7.2100315	2298	23.51	12	11.146887	0.075999998	0.9900741	9
soy_OGL_1363	1100	5.3546586	12.818182	3945	23.9	9	7.8975601	0.106	0.78521782	24
soy_OGL_4843	1300	6.4237089	11.230769	4049	23.92	10	8.8825769	0.052999999	0.97757179	14
soy_OGL_6498	1200	8.8186426	13.166667	2968	24.58	9	2.5611458	0.121	0.68333519	26
soy_OGL_1697	1000	6.8353257	18.799999	5342	24.7	8	2.2346623	0.104	0.81089473	26
soy_OGL_3563	1068	6.3657079	11.048689	5233	25.46	7	5.2021227	0.081	0.83156842	31
soy_OGL_6323	1430	6.7954488	2.3076923	3176	26.01	9	4.0916629	0	0.92480725	19
soy_OGL_6855	1056	8.4172974	10.795455	3625	24.05	8	1.7651855	0.057	0.83190548	23

soy_OGL_4472	1500	7.3361325	0	7591	19.86	9	11.739989	0.127	0.70672047	29
soy_OGL_5195	1636	13.332328	0	2700	18.7	4	4.9722757	0.15899999	0.96029872	16
soy_OGL_6237	1701	6.1202364	0	3750	20.92	4	0.83648753	0.134	0.89941043	19
soy_OGL_1364	1583	5.1467152	0	2001	18.95	6	6.9486394	0.117	0.78853995	26
soy_OGL_1381	1313	8.1746645	0	2001	20.79	3	4.5882316	0.089000002	0.80135179	35
soy_OGL_2255	1105	6.0701208	0	3236	16.65	7	4.0762787	0.112	0.648633	35
soy_OGL_3813	1527	7.3470869	14.407334	6814	22.26	11	9.2487001	0.090000004	0.57112873	16
soy_OGL_666	1123	3.7500732	9.8842382	5877	21.1	5	8.5458269	0.107	0.77175111	31
soy_OGL_1203	1800	6.7576227	0	2362	22.61	6	0.93558508	0	0.82813156	25
soy_OGL_1873	1100	5.0498676	18.09091	4998	20.81	8	10.197219	0.107	0.71247077	24
soy_OGL_3482	1400	5.426621	2.0714285	2452	18.28	6	25.125208	0.097999997	0.64922464	27
soy_OGL_3550	1400	8.9636507	4.0714288	9882	19.64	7	2.0246992	0.088	0.80666536	22
soy_OGL_3730	1035	8.292532	13.140097	4644	20.86	6	5.4254708	0.090000004	0.79833478	25
soy_OGL_4985	1076	9.4545498	11.710037	5688	20.63	5	2.1896992	0.119	0.70892948	27
soy_OGL_6886	1200	6.5062184	15	6213	21.41	8	12.369576	0.118	0.85986698	21
soy_OGL_3549	1387	8.9636507	0	11595	20.62	7	2.0246992	0.097000003	0.80660665	22
soy_OGL_1426	1014	11.258756	20.611441	4556	21.49	6	2.4276395	0.132	0.8758651	20
soy_OGL_6625	1200	9.2474756	14.916667	4594	23.41	6	13.821016	0.079000004	0.95823377	19
soy_OGL_983	1600	5.8942852	0	5951	25.12	6	14.617379	0.098999999	0.76932734	32
soy_OGL_6238	1600	6.1202364	0	4408	26.18	4	0.83648753	0.089000002	0.89967167	19
soy_OGL_2275	1058	13.583581	0	9987	26.08	5	11.276885	0.127	0.62709826	42
soy_OGL_2632	1600	7.9126515	0	5498	25.5	9	3.4251685	0.075999998	0.56594408	22
soy_OGL_6448	1600	8.9351873	1.8125	9113	26.37	8	10.53612	0.07	0.57194138	29
soy_OGL_431	1300	12.23607	0	6082	21.23	4	12.067479	0.147	0.68254507	21
soy_OGL_1659	1354	8.7383938	12.555391	2452	21.19	9	28.669725	0.15000001	0.61130089	19
soy_OGL_2463	1520	5.2698236	2.3026316	4852	25.32	8	4.5364461	0.056000002	0.92481118	17
soy_OGL_91	1300	10.535975	0	4522	23.15	6	4.1598477	0.119	0.77223033	28
soy_OGL_775	1572	8.7638731	0	3968	23.53	5	2.9653993	0.089000002	0.94420528	17
soy_OGL_792	1100	8.9440403	0	1819	19.27	5	5.8073549	0.113	0.87466407	22
soy_OGL_1365	1098	5.1467152	0	4786	17.85	6	6.9486394	0.098999999	0.78864688	26
soy_OGL_1370	1146	5.1550312	0	2001	19.89	4	18.134071	0.127	0.79028612	32

soy_OGL_1818	1100	0.91241473	0	4720	19.63	7	3.8595233	0.104	0.768987	31
soy_OGL_4097	1235	12.218921	4.3724694	2309	18.54	7	8.429307	0.146	0.67390847	23
soy_OGL_4629	1114	3.3767221	0	6639	20.73	6	8.770978	0.126	0.74853575	33
soy_OGL_6796	1300	4.8344703	0	5655	18.38	9	2.9671144	0.074000001	0.7850883	21
soy_OGL_6958	1004	6.068716	0	7994	20.71	7	12.812439	0.072999999	0.93136752	32
soy_OGL_1816	1127	0.91241473	0	6659	21.11	5	3.6398239	0.12800001	0.76993507	32
soy_OGL_629	1197	4.6759496	11.86299	4084	22.3	9	4.8174324	0.106	0.71600676	19
soy_OGL_6191	1532	6.5324054	4.3733683	1404	24.67	8	9.4103556	0.02	0.84832054	15
soy_OGL_6434	1000	10.893449	6.5999999	8614	23.4	6	6.1605306	0.13500001	0.55306166	35
soy_OGL_1581	1353	7.7159863	0	1356	21.13	5	8.6603107	0.075000003	0.78820109	23
soy_OGL_2846	1171	5.5548873	0	6774	21.43	8	7.0856414	0.044	0.67839229	26
soy_OGL_4344	1717	7.6070819	0	3052	23.52	11	8.5605154	0.014	0.46834093	18
soy_OGL_4811	1364	5.9010963	0	2367	21.7	7	26.570757	0	0.94348514	14
soy_OGL_5529	1095	11.696812	5.844749	7155	20.45	6	6.0977349	0.125	0.78870517	24
soy_OGL_5751	1385	12.480519	7.2202168	2824	23.75	7	2.4657011	0.081	0.73126453	16
soy_OGL_5914	1176	8.4431925	0	8487	23.38	7	3.1001492	0.061000001	0.84539551	22
soy_OGL_5933	1205	7.3944454	5.5601659	6743	22.4	9	5.8285913	0.027000001	0.73787731	22
soy_OGL_6460	1062	5.8666077	7.3446326	4886	19.67	9	2.2027783	0.115	0.58708036	22
soy_OGL_6738	1400	8.8684349	2.4285715	7078	24.85	7	4.9774494	0.041000001	0.72791648	25
soy_OGL_6763	1063	8.1590166	0	7543	21.26	7	2.5553894	0.081	0.74541259	27
soy_OGL_674	1400	3.8562949	0	8834	24.78	6	7.0850282	0.088	0.78041118	25
soy_OGL_5170	1400	8.0355263	0	6948	21.5	6	4.7568765	0.090000004	0.84976232	18
soy_OGL_5574	1035	8.3779068	0	6606	19.13	7	10.178035	0.075000003	0.69902664	22
soy_OGL_6333	1000	5.6879897	2.9000001	10698	21.5	5	6.4900389	0.12899999	0.90882552	28
soy_OGL_1773	1400	5.2867265	2.8571429	5531	27.07	7	13.050597	0.035999998	0.90107143	24
soy_OGL_5652	1090	8.7949114	19.449541	1001	22.66	9	8.2436256	0.127	0.52760863	21
soy_OGL_4438	1136	10.04345	5.6338029	5470	23.94	9	6.7497249	0.052999999	0.62393546	26
soy_OGL_4662	1030	8.1218634	11.84466	2001	23.3	6	9.1652136	0.112	0.67618102	28
soy_OGL_6920	1000	8.8029718	15.1	8932	24.2	7	7.809248	0.119	0.89442468	24
soy_OGL_3574	1126	5.4506187	25.932505	4026	23.62	13	4.3946495	0.183	0.83811551	37
soy_OGL_1043	1566	5.3530307	14.750957	1001	26.69	12	15.185414	0.119	0.84784091	27

soy_OGL_5909	1200	7.9141469	18	3890	27.25	10	15.018958	0.147	0.86097962	31
soy_OGL_1497	1559	8.5456972	12.764593	2001	26.74	10	6.3328009	0.097000003	0.98240417	20
soy_OGL_3537	1192	8.9636507	18.120806	1001	26.67	7	8.2012806	0.113	0.79350013	24
soy_OGL_1044	1400	5.3530307	13.785714	3247	27.07	11	15.810555	0.093000002	0.84792066	27
soy_OGL_3611	1337	5.2449269	23.485415	2001	24.68	11	22.204567	0.106	0.89043593	17
soy_OGL_5218	1100	11.000355	16.727272	4540	28.45	10	15.081091	0.109	0.94570732	28
soy_OGL_2906	1231	13.152136	18.440292	3274	25.34	16	3.1103382	0.133	0.98087233	24
soy_OGL_5227	1812	11.269387	1.6004415	1001	30.4	12	7.9804759	0.012	0.92068905	22
soy_OGL_3968	1300	8.0769224	19.23077	2208	24.3	10	14.30653	0.101	0.94606155	10
soy_OGL_644	1008	7.5262041	17.261906	2212	26.48	7	8.4534349	0.098999999	0.75067461	26
soy_OGL_21	1244	10.798586	13.102894	4329	29.34	7	6.4189687	0.07	0.91707093	26
soy_OGL_302	1700	10.392898	20.117647	4230	23.7	12	34.222988	0.093000002	0.92812538	8
soy_OGL_1451	1700	9.5029097	8.0588236	3496	26.82	10	8.2948456	0.096000001	0.91187745	33
soy_OGL_5784	1600	14.565392	0	6399	25.68	8	32.120434	0.082000002	0.8435939	40
soy_OGL_6823	1300	6.5125389	21.461538	4257	24	7	12.505066	0.12800001	0.80863655	37
soy_OGL_2918	1842	9.6113396	37.296417	2001	21.76	11	19.157797	0.088	0.96847481	28
soy_OGL_4636	1200	19.448103	31	3166	21.58	9	7.117136	0.182	0.7383464	39
soy_OGL_1730	1114	30.668314	34.201077	2001	24.32	12	13.231986	0.148	0.85633832	22
soy_OGL_4831	1166	17.834297	33.533447	1138	21.78	10	13.301957	0.169	0.97894526	15
soy_OGL_5807	1320	12.425729	25.30303	12786	24.62	7	8.2762794	0.101	0.87957662	37
soy_OGL_1933	1181	17.808937	23.624048	3081	21.42	9	5.8219919	0.162	0.54744446	26
soy_OGL_6446	1387	9.0478334	21.557318	1001	24.44	7	13.615551	0.119	0.57004637	29
soy_OGL_5305	1100	24.034395	23.727272	2193	25.09	6	4.1561785	0.131	0.69997561	24
soy_OGL_6429	1600	10.893449	13.1875	1013	29.06	7	10.525334	0.050999999	0.54739404	34
soy_OGL_5883	1186	10.300918	32.883644	2162	18.04	14	6.0565968	0.192	0.89506412	36
soy_OGL_220	1669	11.247388	25.883762	2163	23.36	10	13.169693	0.068999998	0.82923156	23
soy_OGL_4703	1818	9.078599	24.69747	2379	23.59	12	15.135615	0.017000001	0.60971242	38
soy_OGL_3649	1600	1.8333012	27.5625	4082	22.18	9	32.674976	0.066	0.94538993	24
soy_OGL_5808	1082	12.425729	23.844732	11386	23.56	7	8.2762794	0.121	0.87968367	37
soy_OGL_4933	1300	9.3127365	31.76923	6754	24.46	11	18.761217	0.078000002	0.76338381	40
soy_OGL_3222	1000	9.7705011	15.9	2415	28.3	6	10.698803	0.146	0.71338218	49

soy_OGL_3948	1133	28.647972	26.566637	2001	28.5	11	12.682665	0.13	0.88786626	20
soy_OGL_5187	1500	12.553019	12.6	4770	26.53	8	26.710304	0.104	0.94050175	19
soy_OGL_1457	1300	9.9040642	19.23077	4125	27.46	7	11.14095	0.12899999	0.9173221	32
soy_OGL_3210	1400	6.4012876	25.785715	2409	24.78	9	0.28704575	0.112	0.69775975	36
soy_OGL_4513	1292	8.8380184	16.33127	3276	26.62	8	0.9945097	0.14	0.74885154	36
soy_OGL_4615	1581	8.1715069	29.791271	2631	23.71	12	7.6783247	0.124	0.76998037	22
soy_OGL_6836	2000	3.9573007	20.299999	3917	26.8	10	1.4578713	0.022	0.81476474	36
soy_OGL_6274	1600	6.1533623	27.4375	5177	23.37	9	8.7067032	0.085000001	0.93134487	26
soy_OGL_4820	1500	19.378592	31.066668	1628	25.8	9	3.6977479	0.121	0.96351922	16
soy_OGL_2964	1500	12.075033	22.533333	2861	26.2	12	17.462011	0.112	0.86011487	19
soy_OGL_4516	1300	8.9862776	22.923077	1069	26.23	9	7.2282329	0.115	0.75326562	35
soy_OGL_4635	1042	19.448103	35.3167	5138	28.69	12	9.0968246	0.116	0.74025065	39
soy_OGL_6961	1300	15.710792	34.615383	2731	26.38	9	13.355711	0.125	0.93237561	33
soy_OGL_5235	1133	32.623028	38.570168	2001	29.39	12	16.018623	0.11	0.90012807	21
soy_OGL_893	1665	7.0541968	31.05105	1957	23.54	8	3.078414	0.11	0.66379577	27
soy_OGL_259	1395	9.1737165	23.297491	4615	24.3	8	9.224411	0.115	0.87504971	21
soy_OGL_2260	1027	6.9284716	19.279455	4713	27.36	7	7.3165908	0.138	0.6391468	44
soy_OGL_3629	1848	3.2073443	29.870131	6364	23.43	10	10.198528	0.050000001	0.91995293	29
soy_OGL_2213	1566	6.4445391	28.416348	3617	26.5	9	23.684866	0.086000003	0.75277418	27
soy_OGL_6555	1600	13.347547	29.75	2379	27.68	9	5.4410682	0.067000002	0.7590946	33
soy_OGL_1041	1145	8.4023438	30.131004	1001	25.24	7	16.111345	0.127	0.84107602	26
soy_OGL_5812	1298	12.687993	15.40832	7043	30.35	7	3.4897976	0.096000001	0.8839159	33
soy_OGL_6867	1176	8.3950586	35.119049	2725	24.4	9	19.727076	0.117	0.84010136	26
soy_OGL_6946	1405	10.009709	27.900356	2001	26.47	7	25.567991	0.094999999	0.92242408	22
soy_OGL_977	1000	13.02616	38.099998	2552	23.5	7	6.0367126	0.145	0.76661122	32
soy_OGL_3571	1700	5.4506187	18.470589	2925	26.35	9	8.9033861	0.050000001	0.8365553	37
soy_OGL_6224	1440	11.301011	32.5	1361	23.33	11	6.2967348	0.116	0.87490118	27
soy_OGL_1702	1800	6.9589791	22.222221	1417	25.33	8	2.6006143	0.045000002	0.81378114	28
soy_OGL_2983	1400	11.277602	28.928572	1635	25.28	7	5.8389182	0.086999997	0.82609361	23
soy_OGL_3228	1600	7.5872769	22.125	5271	28.18	8	5.833662	0.035999998	0.71816009	39
soy_OGL_1435	1300	10.901735	24.846153	2735	26.15	10	28.725206	0.133	0.87942064	23

soy_OGL_4520	1500	8.9862776	15.733334	3785	26.4	11	17.07654	0.090000004	0.7557261	32
soy_OGL_4913	1529	14.602632	15.042511	1001	25.83	9	13.963644	0.097000003	0.78152096	21
soy_OGL_5894	1249	10.038893	16.573259	2064	25.62	7	18.895208	0.124	0.88431263	36
soy_OGL_5597	1458	4.4148474	22.908092	2274	22.42	10	37.224129	0.111	0.65544444	18
soy_OGL_1037	1351	6.3006811	18.72687	3679	22.2	9	26.791906	0.093999997	0.83773935	28
soy_OGL_1841	1464	7.2193756	14.54918	6730	25.27	12	17.115499	0.066	0.74232519	29
soy_OGL_2262	1527	7.6927543	12.639162	1001	26.58	7	7.3205218	0.066	0.63797706	44
soy_OGL_2273	1278	12.386147	13.14554	2944	24.64	9	10.253579	0.097000003	0.6306743	41
soy_OGL_2460	1598	6.0447655	30.100124	2229	19.21	11	23.884113	0.093000002	0.9291032	16
soy_OGL_3300	1781	7.8766026	13.082538	1168	25.09	9	15.222729	0.059999999	0.94154376	19
soy_OGL_4702	1700	9.078599	10.823529	3948	25.64	10	11.920033	0.055	0.61058825	38
soy_OGL_335	1000	11.110282	24.1	1469	20.4	11	13.533195	0.106	0.86909461	23
soy_OGL_343	1589	9.9017172	7.3631215	1001	25.17	10	20.059605	0.066	0.8552798	27
soy_OGL_721	1357	9.4288235	15.254237	1001	20.85	12	18.132006	0.035	0.86316431	21
soy_OGL_1187	1230	4.3006682	11.626017	3185	23.41	10	16.928492	0.041000001	0.89473552	28
soy_OGL_1400	1104	13.123453	7.427536	4421	24.45	9	5.8353238	0.034000002	0.82456082	30
soy_OGL_1401	1200	13.710943	15.666667	1246	23.25	9	2.8514457	0.125	0.82693994	27
soy_OGL_1526	1146	7.3093705	18.673647	1688	22.33	12	3.8379085	0.12800001	0.89582497	39
soy_OGL_3579	1528	6.0902267	10.536649	2001	22.44	11	19.031517	0.006	0.84521854	37
soy_OGL_4939	1056	9.3127365	15.530303	2001	23.48	8	16.333809	0.132	0.75945848	37
soy_OGL_5803	1600	12.976668	0	1682	27.62	7	17.596092	0.016000001	0.85948229	37
soy_OGL_6565	1254	5.9188476	14.513556	2001	22.32	11	28.466328	0.090999998	0.77585018	35
soy_OGL_1450	1100	9.5029097	25.09091	1097	23.09	10	16.49165	0.123	0.91145122	33
soy_OGL_3585	1200	4.1718922	33.166668	2895	21.33	10	22.957668	0.093999997	0.84961724	37
soy_OGL_4634	1233	19.448103	30.251419	3391	25.95	11	9.3156013	0.071999997	0.74035233	39
soy_OGL_5608	1100	25.029232	16.272728	2169	23.36	8	5.7983479	0.132	0.63338697	28
soy_OGL_5614	1500	27.376841	10.666667	2001	21.6	12	12.991765	0.123	0.62897974	25
soy_OGL_5798	1400	12.976668	11.428572	2007	26.92	9	16.622011	0.083999999	0.85846967	37
soy_OGL_5811	1293	12.687993	21.732405	1443	25.59	7	5.8189139	0.075999998	0.88355005	33
soy_OGL_968	1300	11.99724	13.769231	1763	22.61	9	20.015448	0.023	0.75907683	42
soy_OGL_1715	1036	31.132702	3.4749036	2001	21.04	9	4.6660585	0.064999998	0.83142567	31

soy_OGL_3508	1058	47.600048	0	3567	16.35	8	9.8970928	0.07	0.72679806	23
soy_OGL_3949	1300	29.424124	0	2669	22.38	11	8.4719944	0	0.88906401	20
soy_OGL_4637	1300	19.448103	0	3800	27.76	9	8.1162882	0	0.73660785	38
soy_OGL_4822	1021	16.127125	20.959843	2023	22.82	9	3.6273549	0.057	0.96716553	20
soy_OGL_5523	1577	8.5462761	14.331008	1001	24.66	12	34.246269	0	0.79763967	26
soy_OGL_5895	1100	10.420918	9.636364	2989	24.63	9	18.291897	0	0.88217854	35
soy_OGL_6227	1642	11.29869	14.311815	3515	26.43	10	10.906671	0.005	0.87924808	27
soy_OGL_6965	1137	16.297258	16.446791	3114	26.56	9	11.050739	0.009	0.93584269	33
soy_OGL_198	1046	11.833065	19.502869	3447	23.99	8	4.5355496	0.121	0.81014419	25
soy_OGL_232	1200	7.944356	19.25	4983	22.58	9	27.600569	0.112	0.84124887	24
soy_OGL_2965	1100	11.266098	30	2059	19.9	8	10.75528	0.132	0.85655743	17
soy_OGL_5828	1600	14.406287	15.25	6885	24.5	9	6.9213305	0.026000001	0.9256621	20
soy_OGL_1456	1000	9.5686789	22.6	5413	23.4	5	7.5325999	0.108	0.91672313	32
soy_OGL_6450	1673	8.9351873	11.8948	2640	26.18	8	10.736296	0.045000002	0.57218206	29
soy_OGL_46	1000	10.664074	21.4	1200	19.6	8	5.662674	0.017999999	0.86887878	33
soy_OGL_4151	1237	10.608291	18.108326	4288	22.71	9	18.195381	0.061000001	0.88657039	23
soy_OGL_1352	1100	11.526744	24.272728	2529	21.09	9	13.541037	0.104	0.75281495	15
soy_OGL_1387	1000	6.9438424	18.6	1816	24.5	5	12.198069	0.081	0.80834818	35
soy_OGL_2688	1647	10.232581	4.5537338	3011	23.01	10	39.525494	0.037999999	0.48887947	27
soy_OGL_4692	1200	8.8883963	16.166666	8384	26.66	11	11.499081	0.082999997	0.61918956	40
soy_OGL_4932	1600	9.3127365	28.3125	4354	24.75	11	18.761217	0	0.76343864	40
soy_OGL_6548	1792	13.347547	23.27009	1001	26.22	8	10.082113	0	0.75339311	30
soy_OGL_1747	1233	13.638608	15.977291	2316	23.19	9	27.950378	0.037999999	0.98089826	16
soy_OGL_3504	1400	47.600048	0	6318	22.57	7	6.3404999	0.032000002	0.72230119	21
soy_OGL_4929	1600	14.560184	7.375	2645	28.12	8	11.375995	0	0.76721931	35
soy_OGL_5612	1536	27.376841	7.03125	2001	21.28	8	9.4883537	0	0.63044047	25
soy_OGL_5771	1100	19.448713	10.636364	2001	22.9	7	6.1516075	0	0.81876177	29
soy_OGL_6557	1720	13.347547	1.6279069	3328	25.69	10	75.808235	0	0.76207626	35
soy_OGL_4681	1310	10.891823	7.3282442	2147	27.55	8	18.186325	0.11	0.64345032	40
soy_OGL_5926	1519	36.541531	0	5230	24.09	8	2.4717078	0.13600001	0.77165306	5
soy_OGL_4000	1647	11.197123	2.003643	4634	23.01	8	52.069458	0.061000001	0.81944615	20

soy_OGL_4172	1300	62.196968	0	2190	20.61	9	10.986813	0.154	0.15955879	8
soy_OGL_17	1337	10.816959	8.8257294	2001	26.02	10	7.4655728	0.081	0.92295796	26
soy_OGL_1156	1465	8.7633495	1.9112628	2001	25.05	14	12.327825	0	0.95141923	21
soy_OGL_2153	1073	6.6362858	12.488351	6615	26.18	9	17.822592	0.092	0.8516376	32
soy_OGL_5225	1500	11.796818	0	3990	27.66	10	3.3742697	0.029999999	0.93054879	25
soy_OGL_6828	1500	6.5125389	2.6666667	1238	28	9	10.042812	0.052000001	0.81053299	34
soy_OGL_3331	1200	13.000942	12.833333	3389	26.75	7	5.7824192	0.105	0.86418897	30
soy_OGL_339	1028	9.9017172	18.482491	4959	23.73	8	7.8726072	0.124	0.86143118	26
soy_OGL_976	1315	13.12372	6.9201522	4375	25.85	9	6.8087044	0.093000002	0.76582068	32
soy_OGL_1724	1086	27.230612	0	1151	18.32	14	23.166264	0.113	0.84353501	24
soy_OGL_2174	1200	8.9299202	14.666667	2133	25.16	8	17.203102	0.105	0.81153667	27
soy_OGL_2290	1000	10.320536	0	1344	24.8	9	7.8868036	0	0.61658716	39
soy_OGL_4835	1339	17.834297	0	4252	23	13	8.9488058	0	0.98213363	14
soy_OGL_4941	1098	9.3127365	12.386157	2302	24.86	10	17.086134	0.119	0.75837535	38
soy_OGL_5773	1267	19.448713	0	1001	23.59	9	6.3970661	0.097999997	0.82336318	33
soy_OGL_2973	1100	10.460068	21.363636	1171	23.81	10	21.158092	0.127	0.83766383	23
soy_OGL_5224	1073	11.680604	14.72507	2077	25.81	8	20.011751	0.111	0.93290246	25
soy_OGL_6932	1058	8.8029718	23.62949	1001	23.72	13	32.903225	0.13500001	0.90365589	24
soy_OGL_4639	1300	19.479895	0	3521	27.84	9	15.937278	0	0.7325294	35
soy_OGL_4935	1100	9.3127365	10.272727	2058	24.63	10	20.364605	0.055	0.76306266	39
soy_OGL_6566	1000	5.9188476	14.8	4680	24.1	11	28.466328	0.097000003	0.77595091	35
soy_OGL_108	1358	15.30664	11.340206	2356	25.11	9	3.9552579	0.064999998	0.73307526	14
soy_OGL_2683	1367	10.232581	14.923189	2673	24.94	11	19.014194	0.072999999	0.49230722	25
soy_OGL_2879	1006	7.0442643	16.10338	4205	22.26	11	21.738546	0.037999999	0.84363723	18
soy_OGL_3020	1115	9.2658463	19.372198	2001	22.78	8	17.690765	0.116	0.75402129	21
soy_OGL_4144	1048	11.497028	12.59542	2308	25.57	5	16.880182	0.113	0.85467488	29
soy_OGL_3779	1200	16.902504	19.583334	3771	26	12	14.654942	0.068000004	0.70697427	17
soy_OGL_1607	1006	79.304001	11.630219	2350	25.94	11	4.8013263	0.134	0.47049999	2
soy_OGL_2209	1115	6.3052983	23.318386	3720	25.65	14	48.631416	0.023	0.7555275	26
soy_OGL_20	1500	10.798586	12.933333	1961	27.46	8	5.796381	0.082000002	0.91786063	26
soy_OGL_3281	1304	2.9175985	22.009203	3765	23.08	10	23.093187	0.133	0.96979725	26

soy_OGL_4502	1400	8.7601175	18	3451	25.42	11	6.2841787	0.119	0.74213535	32
soy_OGL_6926	1419	8.8029718	20.084566	1256	25.58	9	3.1722405	0.115	0.89923167	30
soy_OGL_1686	1321	9.1770983	28.841787	2203	23.08	11	20.967457	0.12	0.73705649	10
soy_OGL_383	1668	7.1420999	23.021584	4109	23.5	15	4.3599367	0.090999998	0.77792597	26
soy_OGL_1514	1135	6.1372461	19.030836	1001	22.55	11	4.7172575	0	0.9134773	29
soy_OGL_4548	1207	5.7242432	28.748964	4453	23.03	11	7.0814981	0.081	0.79158449	32
soy_OGL_3555	1011	6.3657079	36.300694	5667	19.09	11	6.6388178	0.14399999	0.82648957	26
soy_OGL_1492	1541	7.3526444	20.960415	1901	23.55	9	7.912149	0.037999999	0.97480589	22
soy_OGL_4484	1100	7.6094356	27.272728	2204	23.63	11	7.3689189	0.122	0.71857232	28
soy_OGL_1706	1431	7.9271779	17.190775	2693	25.43	12	5.5562263	0	0.8181985	33
soy_OGL_6544	1004	15.158372	30.179283	1001	25	11	8.7486515	0.071000002	0.74995172	32
soy_OGL_292	1082	11.654119	31.238447	1001	22.45	8	6.8078423	0.117	0.90960854	26
soy_OGL_2880	1494	7.0442643	22.289156	2317	24.23	10	22.301723	0.064000003	0.84371501	18
soy_OGL_3351	1293	11.780388	27.842228	2001	22.89	9	4.8231325	0.102	0.83358228	19
soy_OGL_3544	1446	8.9636507	18.603043	1001	26.41	7	5.8104205	0.059	0.80181384	24
soy_OGL_6758	1025	9.6724033	25.560976	3432	25.65	7	1.3512336	0.119	0.73954505	32
soy_OGL_2892	1207	8.9753227	25.517813	2386	23.03	7	9.3781614	0.108	0.87078136	21
soy_OGL_6913	1164	8.8029718	27.663231	1723	21.9	9	6.2361555	0.111	0.89254129	19
soy_OGL_4162	1008	9.3938532	31.349207	2001	20.53	8	10.334458	0.112	0.90271091	15
soy_OGL_727	1313	9.6941814	12.947449	1001	23.68	9	3.7183442	0	0.86920464	20
soy_OGL_2207	1240	6.2900872	23.064516	5278	22.58	9	6.1407647	0.050000001	0.76176786	28
soy_OGL_6921	1013	8.8029718	28.035538	4254	22.8	7	11.338894	0.106	0.89503294	24
soy_OGL_935	1047	12.449766	28.366762	3271	24.83	9	8.5663166	0.113	0.7091043	28
soy_OGL_2990	1769	9.8460093	15.545506	1001	28.26	10	8.9436502	0.005	0.80950344	23
soy_OGL_3738	1098	9.2037325	30.965391	2799	24.49	11	17.253544	0.111	0.78288418	24
soy_OGL_1521	1021	6.1372461	23.016651	2061	24.09	8	4.3645778	0.044	0.90723217	34
soy_OGL_2150	1200	7.3043337	19.583334	2359	27.83	11	26.712982	0	0.85332108	32
soy_OGL_6602	1023	8.5314484	25.317694	4632	21.7	12	16.581352	0.046	0.8657639	15
soy_OGL_987	1055	9.5245228	31.184834	1385	23.03	6	8.1101475	0.121	0.77238953	31
soy_OGL_1723	1168	39.200481	30.821918	1394	35.53	13	25.793118	0	0.84241623	24
soy_OGL_422	1500	14.106673	16.866667	3712	26.26	10	6.3914127	0.035999998	0.69722974	21

soy_OGL_769	1271	11.362736	20.377655	1001	22.97	12	14.388053	0.15899999	0.97105694	14
soy_OGL_1458	1300	9.1846943	16.153847	4087	24.84	13	9.7109232	0.138	0.92041689	31
soy_OGL_6538	1143	11.936101	16.360455	2001	27.47	8	9.8061781	0.145	0.74497086	31
soy_OGL_2663	1134	6.8734031	22.751324	3685	25.3	12	20.711994	0.12	0.5256387	26
soy_OGL_4110	1355	12.218921	22.066422	2047	25.31	10	12.553756	0.106	0.7078281	15
soy_OGL_48	1314	10.004758	11.111111	2001	27.85	8	9.1196051	0.096000001	0.86032122	28
soy_OGL_372	1419	7.7600741	14.02396	2001	25.58	11	8.6775455	0.103	0.81143695	22
soy_OGL_1169	1000	8.8010788	17.299999	3916	26	7	7.2338176	0.13500001	0.91220176	27
soy_OGL_1374	1100	5.7269979	13.818182	1539	25.81	7	4.5368786	0.103	0.79343492	36
soy_OGL_2505	1229	7.4874678	14.48332	2001	24.32	11	4.7028208	0.086000003	0.83529967	21
soy_OGL_3282	1034	2.9916637	15.473887	2001	23.69	8	18.584831	0.082000002	0.9689585	26
soy_OGL_5277	1100	8.2168961	23.272728	2461	22.45	11	15.129727	0.132	0.77465856	17
soy_OGL_2917	1200	9.6217709	12.666667	1162	26.33	11	9.5255842	0.079999998	0.96918297	28
soy_OGL_6895	1074	7.0806479	20.391062	4131	25.79	7	10.98561	0.11	0.86791611	27
soy_OGL_369	1339	8.2798424	3.8088126	4295	26.58	10	7.3061643	0	0.81650001	24
soy_OGL_392	1531	8.4611053	0	2001	29.58	8	5.7443228	0	0.76556188	27
soy_OGL_2494	1383	7.548306	15.256688	2299	24.43	11	24.883781	0.029999999	0.86665022	8
soy_OGL_3301	1100	9.4088583	8.454545	2621	24.81	8	7.5113416	0	0.93574196	18
soy_OGL_3325	1100	10.829322	9.636364	3734	26.81	7	3.1949787	0.046999998	0.88000923	26
soy_OGL_2989	1110	9.8460093	10.540541	4570	26.03	9	9.9349003	0.015	0.80965531	25
soy_OGL_3782	1151	13.260455	19.895742	2001	25.1	11	9.3722401	0.112	0.69687033	18
soy_OGL_6451	1243	9.1464834	10.619469	1590	27.03	11	12.579126	0	0.5741474	28
soy_OGL_2581	1000	5.237216	23.6	4219	23.3	8	10.500379	0.103	0.66318882	15
soy_OGL_3473	2300	8.2846069	18.73913	1197	23.95	4	1.9134001	0	0.63294899	25
soy_OGL_4363	1960	7.8500838	17.857143	7532	22.39	8	2.5786703	0.057999998	0.51220936	21
soy_OGL_6141	1568	4.9215565	20.025511	1001	21.55	4	5.2626381	0.097000003	0.7702561	16
soy_OGL_816	1400	11.647924	12.571428	14717	23.78	7	2.2195246	0.098999999	0.75173438	23
soy_OGL_6489	1376	9.3729401	19.331396	3064	23.32	4	5.3833508	0.124	0.65526479	19
soy_OGL_5938	2200	6.6873031	14.409091	1144	26.04	5	10.519156	0.023	0.73508674	24
soy_OGL_548	2180	10.749329	3.119266	2927	28.3	9	3.8075345	0.015	0.3563883	20
soy_OGL_895	1500	7.0074801	21.799999	6317	24.26	7	2.1635842	0.082000002	0.66737843	29

soy_OGL_1290	1923	6.4559865	13.26053	5025	26.41	8	19.324512	0.043000001	0.64861143	16
soy_OGL_1383	1142	8.1746645	23.992994	5414	22.67	2	5.7991509	0.146	0.80148286	35
soy_OGL_3001	1296	8.7826014	21.296297	10548	24.07	8	8.7775726	0.107	0.79239577	25
soy_OGL_4946	1022	9.4054356	22.015656	11594	22.89	5	9.1168709	0.124	0.7567305	36
soy_OGL_5482	1000	4.7314305	29.200001	12377	22.7	7	12.18399	0.13699999	0.86388505	33
soy_OGL_6473	1631	7.2875495	22.133661	6657	22.74	10	8.7570047	0.081	0.6211347	14
soy_OGL_6817	1400	6.6239986	20.428572	4924	25.71	3	6.2747641	0.094999999	0.80407679	32
soy_OGL_125	1129	7.7176685	22.409212	15258	20.9	2	10.823194	0.117	0.58601433	8
soy_OGL_126	1400	5.3318148	16.142857	33701	24.35	1	0.33166361	0	0.58729112	8
soy_OGL_859	1707	5.045455	0	9748	21.26	4	0.77783704	0.103	0.5841822	13
soy_OGL_1369	1721	5.1550312	2.614759	14220	27.25	5	14.926658	0.015	0.78979486	30
soy_OGL_2832	1000	5.5548873	27.1	17793	22.2	5	7.9335485	0.12	0.66224223	22
soy_OGL_2834	1900	5.5548873	17.31579	3017	24.68	4	9.2260847	0.017000001	0.66507626	23
soy_OGL_6024	1787	1.8328881	15.668718	2001	22.21	4	3.2254357	0.07	0.38677618	14
soy_OGL_6073	1877	1.4229615	5.9669685	16298	23.38	5	7.5268512	0	0	3
soy_OGL_6210	1100	5.0835438	12.636364	24444	26.27	2	0.58338207	0.064999998	0.86885816	29
soy_OGL_1579	1419	8.3843002	23.608175	7004	20.57	5	3.2208574	0.093999997	0.79086792	24
soy_OGL_6338	1100	5.6879897	22.818182	9729	22.36	3	10.758282	0.117	0.9009617	28
soy_OGL_1893	1469	9.4963474	11.708645	8835	23.82	8	10.022001	0.118	0.65887362	16
soy_OGL_5750	1400	12.480519	15.214286	6925	24.35	8	7.89258	0.118	0.72844225	15
soy_OGL_3047	1025	32.947975	4.390244	18154	22.04	3	40.721748	0.122	0.66471487	10
soy_OGL_2997	1400	10.117564	18.928572	4294	26.07	6	1.5416789	0.096000001	0.80330211	21
soy_OGL_3003	1135	6.4039621	22.026432	5448	25.63	4	8.3077583	0.126	0.787	23
soy_OGL_3030	1500	9.2140102	20.666666	2175	25.06	5	1.5475408	0.094999999	0.73435748	15
soy_OGL_5168	1800	8.5415621	10.555555	2901	28.66	5	0.25877887	0.054000001	0.84149158	16
soy_OGL_4063	1137	0.41162741	33.597187	8768	20.49	4	10.361552	0.122	0.061588462	3
soy_OGL_5660	1378	7.3934207	32.510887	2335	20.82	7	2.2608349	0.104	0.5039885	20
soy_OGL_5985	1363	6.6010385	23.477623	2001	23.11	8	7.7244382	0.14	0.61017537	15
soy_OGL_1963	1000	7.7554264	26.4	4591	25.2	4	8.3350639	0.145	0.49367532	25
soy_OGL_1983	1564	9.3477869	22.506393	1480	20.71	9	14.358272	0.089000002	0.47332585	23
soy_OGL_3232	1456	8.2360296	8.4478025	3601	26.51	4	18.384989	0.052000001	0.72366023	38

soy_OGL_3347	1083	11.12724	22.345337	2327	20.77	5	5.6993585	0.078000002	0.8474803	25
soy_OGL_1190	1415	4.0395017	25.017668	5393	22.82	9	8.0431252	0.034000002	0.88424933	20
soy_OGL_2998	1346	10.117564	14.784547	6854	25.26	6	0.36834088	0.108	0.80229717	21
soy_OGL_1227	1445	9.0944204	6.2283735	10422	23.59	7	6.3736272	0.093000002	0.76927871	20
soy_OGL_2432	2119	0.78866917	1.8404908	6903	21.94	7	2.6701577	0.048	0.74964249	8
soy_OGL_932	1100	12.449766	18.272728	10490	23.54	8	7.9510646	0.124	0.70781833	27
soy_OGL_5293	1429	21.185158	0	11756	25.75	6	19.147211	0.063000001	0.73244947	24
soy_OGL_169	1400	1.9087936	16.571428	7442	21.85	2	3.8741975	0.097000003	0.72681594	8
soy_OGL_502	1029	4.4821186	26.044704	8158	21.86	5	3.0133138	0.13	0.46686035	24
soy_OGL_1993	1490	6.3444653	13.087248	2956	23.75	6	12.749681	0.077	0.45463344	20
soy_OGL_2426	1036	11.967738	9.8455601	17886	24.71	3	7.4612837	0.105	0.72246337	26
soy_OGL_2659	1137	6.8734031	22.955145	1001	22.16	2	2.2202265	0.12800001	0.53160965	25
soy_OGL_5058	1064	6.5904026	12.218045	21673	21.61	2	10.649961	0.090999998	0.60025418	9
soy_OGL_6713	1500	2.7221162	0	24309	21.26	4	1.3426611	0.071999997	0.6554057	8
soy_OGL_80	1568	8.729229	14.92347	5100	21.74	4	11.22646	0.048	0.79952919	26
soy_OGL_3731	1871	8.292532	8.4446821	7342	24.53	7	4.6587062	0	0.79815024	25
soy_OGL_6415	1261	10.411439	19.349722	2805	21.01	5	3.4534619	0.089000002	0.53727496	26
soy_OGL_3921	1276	9.3006687	11.912226	3174	20.76	7	5.3629456	0.001	0.80496311	18
soy_OGL_4132	1100	10.342244	0	11720	23.54	7	8.310441	0.023	0.82941622	32
soy_OGL_4426	1263	9.7329044	9.6595411	6734	20.26	8	30.273026	0.096000001	0.61501354	24
soy_OGL_5037	1685	10.512985	0	2416	20.89	5	21.123562	0	0.65375495	24
soy_OGL_6861	1100	10.103802	0	5139	22.27	5	11.294002	0	0.83826733	28
soy_OGL_6919	1400	8.8029718	0	10032	23.42	7	7.809248	0.001	0.89439207	24
soy_OGL_3280	1004	1.0940363	13.346614	7285	18.32	5	4.6100678	0.011	0.97778523	22
soy_OGL_5162	1429	6.6482263	0	2841	20.78	4	5.5673146	0	0.8204993	16
soy_OGL_5409	1800	9.4738331	0	3072	25.55	5	5.5766711	0	0.74836338	14
soy_OGL_4958	1013	12.134647	15.893386	12542	22.3	8	9.381278	0.11	0.75086647	33
soy_OGL_824	1328	8.9841375	14.533133	4003	25.6	6	9.2659378	0.057999998	0.72531813	23
soy_OGL_921	1100	11.336674	14.272727	7241	23.45	6	5.7879272	0.093999997	0.69627601	28
soy_OGL_2410	1003	11.967738	14.955134	4532	24.42	5	2.3872302	0.105	0.70547009	32
soy_OGL_4152	1400	9.8956871	18.071428	7272	23.14	7	11.020811	0.027000001	0.89048904	21

soy_OGL_5023	1644	12.549186	0	4089	26.09	6	8.5845413	0	0.66562349	28
soy_OGL_5335	1130	24.160017	17.699116	2001	18.76	8	2.4848127	0.12	0.56202143	9
soy_OGL_87	1071	7.4370308	18.394024	9102	21.75	4	8.342742	0.090999998	0.77885628	30
soy_OGL_164	1183	1.6461914	30.346577	3904	16.82	3	0.4642663	0.12800001	0.71828753	12
soy_OGL_319	1300	10.951384	17.076923	13573	22.69	5	8.1754532	0.086000003	0.91154957	14
soy_OGL_846	1095	5.9970145	31.780823	7725	18.9	5	3.9663272	0.104	0.64000213	15
soy_OGL_863	1491	7.9338479	19.382965	2001	22.4	6	8.3454552	0.072999999	0.56843829	14
soy_OGL_899	1257	6.5197372	14.797136	12146	23.38	6	10.092576	0.064000003	0.67054564	30
soy_OGL_1956	1665	19.348343	0	12290	25.46	5	2.0861754	0	0.50941235	20
soy_OGL_3840	1064	7.3592849	35.902256	3964	15.78	4	5.192966	0.13600001	0.52646548	17
soy_OGL_4068	1255	5.8943801	15.219124	12593	23.9	4	2.8227994	0.050000001	0.5164755	18
soy_OGL_6128	1801	1.5205039	3.4980567	15290	16.99	3	1.2916712	0.052999999	0.74539936	7
soy_OGL_150	1025	4.8982654	24.390244	3135	19.12	4	5.3307257	0.029999999	0.68354493	11
soy_OGL_254	1200	12.798174	0	8508	22.25	4	6.9227238	0.002	0.86745477	19
soy_OGL_503	1500	4.4821186	0	15182	21.13	4	3.758431	0	0.46645945	23
soy_OGL_794	1100	9.3835421	0	18108	23.27	4	7.5178504	0	0.87163281	22
soy_OGL_2002	1185	7.3541341	16.202532	2001	20	3	2.8522375	0.117	0.44228458	15
soy_OGL_2045	1199	2.5895314	13.261051	11968	19.59	6	9.4705801	0.057999998	0.47612083	11
soy_OGL_2234	1233	7.2443314	16.301702	5508	18.73	7	7.2036252	0.022	0.70563304	19
soy_OGL_2395	1100	7.888226	17.90909	1609	14.36	6	12.728395	0.094999999	0.63114941	8
soy_OGL_2618	1569	8.8686056	0	5890	23.07	6	17.240135	0.002	0.58419579	22
soy_OGL_2802	1299	0.8990916	18.78368	4903	21.63	2	13.129824	0	0.32329148	10
soy_OGL_4045	1386	0.43234766	0	11620	20.27	2	2.2522616	0	0.40875053	15
soy_OGL_4224	1300	4.0722065	4.6923075	15262	21.15	10	23.349226	0.011	0.2643989	30
soy_OGL_5155	1700	7.3907619	3.8823528	2122	20.64	1	3.5326583	0	0.77643764	19
soy_OGL_5651	1263	7.6806297	10.213777	14802	25.17	6	12.449982	0	0.52972412	19
soy_OGL_5741	1000	13.020522	11.8	13357	20.8	5	4.9610882	0.074000001	0.69914806	16
soy_OGL_6040	1511	1.4509761	0	23781	20.64	3	1.6381968	0	0.2230573	7
soy_OGL_6208	1300	5.0835438	0	17944	25.84	4	1.3429811	0.035	0.86870378	29
soy_OGL_6327	1200	6.7954488	5.8333335	15339	20.66	7	5.0981779	0	0.91853619	23
soy_OGL_5248	1728	8.8967266	28.125	3997	22.56	4	3.9502525	0	0.86744684	22

soy_OGL_110	1086	14.638623	24.309393	6548	23.66	5	4.2828245	0.098999999	0.72718269	12
soy_OGL_544	1000	10.749329	29.299999	11609	23.1	4	2.2191281	0.081	0.35911262	18
soy_OGL_194	1249	8.3450031	11.529223	10121	24.09	8	6.7889934	0	0.8017354	20
soy_OGL_3480	1154	6.0115023	13.171577	3395	22.01	6	13.355197	0	0.6476264	27
soy_OGL_1293	1000	6.4559865	25.799999	6288	18	6	24.135088	0.057	0.64470613	15
soy_OGL_3144	1101	9.2910147	18.891916	11626	24.52	5	5.8927259	0	0.56922597	27
soy_OGL_4774	1062	6.7980485	29.472692	4626	20.62	3	15.661089	0	0.84201354	9
soy_OGL_5683	1058	9.2884445	32.514179	1001	18.43	6	2.0456254	0.102	0.46195945	14
soy_OGL_805	1039	9.2155247	13.570741	10358	23.86	7	15.245289	0.13	0.84214795	21
soy_OGL_4714	1344	5.6724916	0	13011	28.57	7	8.433548	0.063000001	0.58366293	33
soy_OGL_2693	1900	9.7915058	0	1261	21.05	7	66.853783	0.059	0.48392308	22
soy_OGL_1605	1000	5.281703	19.9	6268	21.7	2	14.782898	0.139	0.68364882	14
soy_OGL_2654	1000	6.8734031	0	20336	21.8	2	27.018221	0.121	0.5327028	25
soy_OGL_2655	1300	6.8734031	0	23236	31.53	2	27.018221	0	0.53259093	25
soy_OGL_5068	1000	4.6671739	20.799999	15574	21.8	4	0.89910638	0.141	0.55673891	7
soy_OGL_6041	1400	0.69832134	7.3571429	11958	20.21	3	3.4689326	0.090999998	0.22245409	8
soy_OGL_3379	1400	10.989937	13.928572	4674	25.85	4	22.895531	0.086000003	0.75276035	13
soy_OGL_1366	1200	5.1467152	6.5833335	7714	27	5	7.5851874	0.075000003	0.78877354	26
soy_OGL_2228	1418	6.4599118	2.0451341	8041	26.16	8	2.9117713	0	0.72102463	17
soy_OGL_3467	1100	8.5749073	16.727272	6599	22.9	7	5.420599	0.126	0.62752604	19
soy_OGL_732	1800	9.5748711	1.7777778	3032	26.33	6	9.4642086	0.011	0.88399887	12
soy_OGL_2205	1045	6.9489923	7.3684211	7123	26.22	4	8.3576164	0.093999997	0.76473188	30
soy_OGL_4011	1500	7.0667925	2.8	2839	23.6	7	5.0208158	0.034000002	0.70561922	15
soy_OGL_6239	1589	6.1478391	0	2001	26.68	4	5.0436692	0	0.89972907	19
soy_OGL_6910	1000	7.0806479	8.5	7972	22.6	8	4.0681224	0.012	0.8786853	16
soy_OGL_815	1000	11.647924	6.3000002	13819	22.8	7	2.2195246	0.13699999	0.75194532	23
soy_OGL_1258	1442	10.150949	0	11676	26.07	7	7.6366978	0.044	0.71067983	20
soy_OGL_3387	1360	5.6634336	7.4264708	3255	22.35	4	6.4024534	0.107	0.7097885	17
soy_OGL_4013	1278	7.0667925	0	6787	15.02	3	7.8815346	0.15000001	0.7037701	15
soy_OGL_5029	1100	7.1732235	0	9937	22.72	5	9.6955204	0.122	0.66222453	30
soy_OGL_6168	1054	10.100551	14.041746	6048	24.66	6	8.0569124	0.082000002	0.8088091	15

soy_OGL_955	1300	14.275198	5.4615383	4112	25.53	6	9.0945778	0.061999999	0.74666661	21
soy_OGL_1735	1000	17.655291	11.7	9176	22.5	7	15.562757	0.117	0.86817443	13
soy_OGL_2256	1400	6.0701208	0	6541	27.64	7	4.0762787	0.001	0.6484679	36
soy_OGL_3754	1100	7.7082705	11.909091	5471	22.9	9	19.928658	0.035999998	0.7584163	22
soy_OGL_3913	1316	9.3006687	8.7386017	5553	26.13	5	8.1068077	0.068999998	0.7881608	22
soy_OGL_5036	1297	10.184509	0	4609	25.44	7	16.151352	0	0.65426856	24
soy_OGL_5190	1385	13.332328	3.3212996	7613	26.2	6	24.174467	0.028999999	0.95394582	16
soy_OGL_5193	1200	13.332328	0	3270	24.66	4	9.0773964	0	0.95710915	16
soy_OGL_6332	1200	6.7954488	2.3333333	6676	27.16	5	2.2802701	0	0.91494471	28
soy_OGL_6442	1074	9.47616	3.9106145	1024	23.46	2	21.210407	0.093000002	0.56035125	36
soy_OGL_6523	1500	21.291258	2.5333333	2479	26.73	4	5.1097422	0.054000001	0.7130425	16
soy_OGL_6888	1244	7.0806479	0	4451	22.74	7	41.933655	0	0.86605382	24
soy_OGL_4203	1200	3.0646741	17.5	5861	22.08	8	5.9338946	0.089000002	0.21890624	18
soy_OGL_5146	1300	4.3001404	4.7692308	4965	25.76	2	1.0066352	0.082999997	0.76306772	21
soy_OGL_61	1000	11.010665	2.9000001	11443	26	4	3.9521847	0	0.83901215	28
soy_OGL_1346	1300	8.1570683	5.3846154	4060	23.23	5	5.7389903	0.034000002	0.73396212	12
soy_OGL_1586	1400	6.6485653	3.7857144	6792	24.35	6	17.787373	0	0.7734524	17
soy_OGL_2050	1279	3.2522252	0	11926	22.83	3	5.894237	0	0.49286348	11
soy_OGL_2057	1715	3.071409	0	2001	25.88	3	11.486713	0.002	0.56536669	11
soy_OGL_2782	1200	2.5931845	11	4833	21.33	6	7.8973269	0	0.23408741	10
soy_OGL_2786	1100	3.1128991	13	4596	18.36	4	1.8985044	0.103	0.22495455	11
soy_OGL_2820	1174	2.0155141	11.925042	20224	25.55	2	14.573421	0	0.53605676	6
soy_OGL_3036	1500	9.6306324	5.4666667	8499	25.93	5	8.6926556	0	0.70032763	10
soy_OGL_3427	1329	2.8198702	10.910459	16752	23.62	6	8.1394033	0	0.50897437	6
soy_OGL_4069	1000	5.8943801	7	18393	25.5	6	1.887027	0	0.51689845	18
soy_OGL_4223	1100	4.0722065	3.1818182	9162	20.36	8	27.928349	0	0.26418418	30
soy_OGL_4278	1256	5.4117041	4.77707	2001	20.06	6	7.7247005	0	0.36349437	19
soy_OGL_4769	1400	6.7980485	8.9285717	3508	20.78	7	28.525553	0	0.83900297	9
soy_OGL_5655	1100	5.120719	8	12359	20.81	5	5.090477	0.111	0.51028353	20
soy_OGL_5686	1154	9.2884445	9.2720966	5404	23.31	5	7.1541667	0	0.44900176	8
soy_OGL_6146	1600	7.0188165	0	1361	25.37	3	23.776741	0	0.77684742	18

soy_OGL_6412	1389	10.411439	3.9596832	8801	22.89	7	20.236904	0.071000002	0.5321064	22
soy_OGL_6506	1484	7.9388223	0	8271	26.54	6	9.4914494	0	0.6886462	23
soy_OGL_3381	1100	10.989937	24	4583	22.9	6	16.953121	0.116	0.7520507	12
soy_OGL_1973	1300	11.715036	2.5384614	3582	26.07	7	10.322206	0	0.48657143	26
soy_OGL_2675	1100	10.232581	7.7272725	8837	25.72	4	6.7602062	0	0.50363636	23
soy_OGL_3841	1300	7.3592849	22.615385	8574	24.3	5	4.3533444	0.081	0.52625751	17
soy_OGL_5393	1220	9.4848547	19.918034	7518	27.62	4	1.8130116	0.077	0.71241558	20
soy_OGL_3791	1200	4.9141068	22.916666	3251	20.16	10	6.685071	0.074000001	0.65741199	10
soy_OGL_2605	1588	7.2494159	21.095718	2734	21.03	9	1.9276595	0.056000002	0.60447681	14
soy_OGL_808	1100	6.8196387	39.272728	1134	19	6	4.7054672	0.12899999	0.82462502	14
soy_OGL_1807	1119	4.1940126	22.341375	2001	22.34	6	5.9037504	0.11	0.78493148	20
soy_OGL_2250	1100	3.1746132	22.545454	4316	23.63	9	12.284534	0.097000003	0.65705961	25
soy_OGL_191	1498	8.3450031	14.485981	3622	24.63	6	3.5907898	0.009	0.80030334	20
soy_OGL_1872	1366	5.0498676	14.494876	2001	23.27	7	5.167706	0	0.71265006	24
soy_OGL_2819	1171	2.0155141	28.437233	15647	22.54	3	0.74709105	0.055	0.53422874	6
soy_OGL_6139	1289	3.3948011	12.567883	1001	22.88	5	3.4324322	0	0.76966995	15
soy_OGL_2067	1516	3.4504049	23.08707	8218	23.48	3	3.316045	0.045000002	0.6410147	12
soy_OGL_523	1569	2.3637695	17.590822	5103	22.3	8	9.9958744	0	0.4170104	12
soy_OGL_2013	1000	2.7130883	25.200001	16103	23.9	4	10.420037	0	0.38354871	10
soy_OGL_3410	1170	2.4898665	38.205128	9944	16.75	3	1.271538	0	0.61098617	5
soy_OGL_5154	1200	4.0681992	23.75	6159	23.16	2	2.7854269	0.050999999	0.77553976	19
soy_OGL_1889	1200	9.4963474	28.75	5478	23.91	6	5.0912738	0.097000003	0.66732794	13
soy_OGL_5971	1000	8.3158064	24.299999	3298	22.7	7	3.4196832	0.079999998	0.65628064	15
soy_OGL_4282	1300	5.4775915	31.23077	4359	20.46	10	7.1021528	0.097000003	0.37067521	22
soy_OGL_505	1000	4.4821186	36.799999	1382	20.4	3	1.9512852	0.015	0.46583784	24
soy_OGL_1679	1147	9.1770983	22.406277	6276	24.06	9	5.5635357	0.12800001	0.71796328	19
soy_OGL_526	1118	2.3637695	19.677996	13850	22.62	4	1.1774486	0.112	0.41122973	12
soy_OGL_887	1200	8.0451517	15.666667	16194	28.66	4	2.4471958	0.052000001	0.6553055	13
soy_OGL_6881	1483	4.5204587	4.8550234	7550	26.7	7	7.3944702	0.034000002	0.85187495	19
soy_OGL_2088	1200	1.7034707	16.333334	7133	21.66	8	3.0138075	0.090000004	0.75879377	15
soy_OGL_774	1006	10.280827	12.127236	9336	26.73	7	4.9399786	0.052000001	0.94611675	17

soy_OGL_3800	1257	6.9383955	19.093079	2232	23.07	10	6.8810859	0.074000001	0.63179487	14
soy_OGL_5555	1408	6.151978	14.417614	4583	25.14	10	11.661985	0.035999998	0.73495758	17
soy_OGL_524	1027	2.3637695	13.145082	25508	28.62	6	4.7874279	0	0.4138096	12
soy_OGL_1327	1448	0.24154867	4.7651935	7826	25.41	4	3.2512007	0.013	0.63517106	13
soy_OGL_2811	1024	0.41487023	19.824219	6352	18.75	4	0.063233674	0.138	0.39101377	6
soy_OGL_5059	1200	6.5904026	14.583333	3993	24.16	2	0.51741338	0	0.59773105	8
soy_OGL_5063	1110	5.2891674	24.414415	4021	21.26	6	1.4199408	0.104	0.56623471	6
soy_OGL_5347	1086	2.9911871	22.191528	3611	19.88	6	2.7736998	0.13	0.47469914	12
soy_OGL_6045	1000	1.461244	21.299999	1233	21.9	1	9.2988129	0.024	0.20097449	10
soy_OGL_5644	1000	9.2479429	25.200001	1979	23.2	6	5.0126324	0.13	0.53831416	17
soy_OGL_4074	1083	5.8943801	11.819021	4660	26.4	6	5.6086822	0	0.52580231	19
soy_OGL_6342	1108	5.6157908	8.3032494	6800	27.43	4	8.5079031	0	0.89553189	24
soy_OGL_3481	1138	6.0115023	21.528997	2013	27.24	7	16.211184	0.124	0.64770103	27
soy_OGL_3166	1557	10.875026	10.019268	1001	28.77	10	8.3528242	0	0.61766338	16
soy_OGL_2967	1800	10.693128	29	3007	22.11	5	16.259047	0.082000002	0.85343832	19
soy_OGL_1938	1705	18.633888	20.117302	2599	21.93	8	14.048999	0.079999998	0.5435487	23
soy_OGL_2278	1100	13.583581	36.272728	4319	23.09	4	14.089167	0.15099999	0.62663764	42
soy_OGL_3512	1400	45.245277	19.928572	6273	28.71	8	17.305138	0.079000004	0.73003685	19
soy_OGL_6174	1093	9.9950914	36.322048	2001	22.5	9	38.534607	0.132	0.81710821	17
soy_OGL_2566	1520	7.0306044	23.026316	2001	24.27	9	33.786243	0.102	0.69136012	20
soy_OGL_1943	1600	22.922543	33.625	2895	26.81	8	9.3831291	0.068999998	0.53329545	19
soy_OGL_5616	1372	27.974483	33.236153	7578	24.56	7	14.489635	0.103	0.62744445	24
soy_OGL_6427	1000	10.893449	36.599998	7640	23.7	7	10.394678	0.132	0.54691261	34
soy_OGL_2285	1100	12.293853	37.545456	2395	23.9	8	24.463951	0.1	0.62272936	40
soy_OGL_3946	1800	26.245321	38.5	2007	24.16	8	3.9812493	0.003	0.87902057	25
soy_OGL_4467	1705	7.5555859	36.129032	2001	24.51	11	50.401505	0	0.70177817	24
soy_OGL_4494	1100	7.665381	25.90909	8577	26.63	8	8.0918341	0.117	0.7351833	31
soy_OGL_4994	1067	8.6126404	33.364574	3146	23.61	6	6.4871373	0.127	0.70410007	25
soy_OGL_6739	1137	8.8684349	30.694811	5818	25.24	7	4.9774494	0.12	0.72794956	26
soy_OGL_5028	1697	7.1732235	31.82086	2840	24.86	6	8.4402084	0.079000004	0.66239429	30
soy_OGL_714	1049	8.8120899	37.368923	2183	26.59	10	55.709488	0.103	0.84988892	25

soy_OGL_960	1049	14.874959	32.507149	6460	27.16	8	6.040082	0.133	0.7497288	27
soy_OGL_1848	1100	5.552063	33.909092	8630	25.81	11	28.752882	0.123	0.73620456	26
soy_OGL_2271	1000	12.386147	22.799999	8605	29.9	8	11.531806	0.115	0.63101834	42
soy_OGL_5297	1500	23.178028	33.400002	2447	28.06	9	11.172051	0.071999997	0.71312803	25
soy_OGL_4147	1065	12.634075	33.051643	2654	25.35	5	9.097065	0.118	0.86475462	30
soy_OGL_5308	1000	18.329891	29.299999	2001	26.1	6	4.809092	0.126	0.6904512	29
soy_OGL_4474	1115	7.9795275	35.246635	2001	27.17	7	31.545551	0.104	0.70828336	29
soy_OGL_4687	1000	10.870666	29.5	8989	28	5	2.6000493	0.12	0.63709152	40
soy_OGL_5279	2008	8.2288141	32.818726	5460	26.19	8	17.484406	0.008	0.76929039	20
soy_OGL_5532	1700	11.696812	31.705883	8581	26.11	7	5.5069585	0.046999998	0.78747123	24
soy_OGL_6439	1400	10.461443	38.57143	6431	23.78	6	3.2480991	0.101	0.55707079	36
soy_OGL_3332	1008	13.000942	30.853174	7081	25.59	7	5.7824192	0.116	0.86402768	30
soy_OGL_2689	1900	10.209874	35.105263	1414	26.89	14	30.237734	0	0.48713985	25
soy_OGL_2931	1378	9.9275036	33.962265	1362	23.36	7	22.489958	0.086000003	0.93399233	18
soy_OGL_5186	1200	13.212205	37.166668	4582	22.83	7	16.435446	0.088	0.93411744	20
soy_OGL_6945	1221	10.009709	30.876331	7625	27.68	7	25.567991	0.057999998	0.922252	22
soy_OGL_1367	1608	5.1467152	28.544777	1001	25.68	5	20.799328	0.039999999	0.78919172	27
soy_OGL_5326	1500	11.747804	37.599998	2761	22.8	8	2.604275	0.054000001	0.65776831	23
soy_OGL_2551	1100	3.931226	31.272728	5427	24.63	10	28.229572	0.132	0.72111541	22
soy_OGL_4156	1700	9.8956871	13.705882	3411	27.05	5	23.62254	0.059	0.89328927	18
soy_OGL_3377	1319	10.989937	19.711903	6661	25.24	3	30.21183	0.096000001	0.75300097	13
soy_OGL_2281	1193	13.338867	24.811399	12388	23.97	2	50.819614	0.085000001	0.62556702	42
soy_OGL_5617	1000	28.530188	33.900002	26750	30.8	5	19.926899	0	0.62672412	22
soy_OGL_4495	1098	7.665381	37.52277	9794	21.49	5	20.381203	0.089000002	0.73631674	34
soy_OGL_4179	1000	18.090168	26.1	8478	22.9	6	11.709677	0.14300001	0.17835215	15
soy_OGL_6889	1300	7.0806479	18.846153	7551	28.46	6	48.317772	0.064999998	0.86612117	25
soy_OGL_608	1856	7.0958691	20.528017	1050	26.34	7	11.678254	0.024	0.68296224	16
soy_OGL_5424	1156	12.267535	32.00692	5059	23.09	5	8.4590149	0.124	0.98007518	12
soy_OGL_4991	1100	8.6126404	29.727272	5041	23.18	6	5.2647204	0.126	0.70495564	26
soy_OGL_4284	1100	5.3592715	31.363636	6554	24.63	10	16.591681	0.125	0.37350881	25
soy_OGL_4396	1200	8.2008438	36.333332	5289	23.5	5	2.9729493	0.118	0.55990416	22

soy_OGL_904	1700	6.4160132	26.941177	8821	26.11	7	12.832253	0.044	0.67480606	30
soy_OGL_988	1891	9.5245228	22.633528	8944	29.5	5	1.8149728	0.013	0.77270991	31
soy_OGL_5562	1500	7.7774553	39.866665	7567	22.26	7	8.332057	0.074000001	0.71921456	20
soy_OGL_6504	1421	7.9388223	33.638283	6999	24.98	6	9.4914494	0.088	0.68837774	23
soy_OGL_3136	1144	8.3777838	36.363636	2735	23.42	3	8.1860914	0.125	0.55801493	26
soy_OGL_4245	1400	9.9370441	33.92857	3196	21.14	10	4.3158221	0.126	0.28908476	20
soy_OGL_6438	1070	10.461443	32.616821	9331	25.7	6	3.2480991	0.114	0.55697411	36
soy_OGL_1946	1467	24.109264	29.584185	4143	32.58	4	10.771916	0.024	0.52529651	18
soy_OGL_430	1010	12.23607	28.910891	4799	26.23	5	7.6492915	0.122	0.68339479	22
soy_OGL_5930	1100	5.8363252	33.18182	6171	24.72	8	28.247995	0.111	0.74251533	18
soy_OGL_6671	1035	9.9655132	38.647343	1001	23.67	6	13.875745	0.111	0.010875876	22
soy_OGL_536	1500	10.071255	39.400002	1196	23.6	6	5.1524892	0.074000001	0.37513965	21
soy_OGL_2424	1173	11.967738	29.582268	5449	26.42	4	5.9498463	0.111	0.72190523	28
soy_OGL_4428	1900	8.8796873	21.68421	5105	28.52	7	18.496197	0.001	0.6152916	23
soy_OGL_5240	1000	9.6026649	37.400002	14440	24.2	4	4.1412082	0.071000002	0.88241464	24
soy_OGL_92	1500	10.535975	34.533333	8068	24.33	5	7.370636	0	0.76880604	23
soy_OGL_2999	1041	8.7826014	23.439001	2316	26.99	4	17.510834	0.139	0.7937302	24
soy_OGL_535	1147	10.494274	25.632084	1001	24.84	5	5.5812659	0.125	0.37682432	21
soy_OGL_4924	1100	14.560184	24	8291	21.27	6	10.636489	0.103	0.77077025	35
soy_OGL_5946	1807	10.436343	11.455451	3602	27.61	8	16.51646	0	0.71666563	24
soy_OGL_30	1041	10.279623	20.557158	7214	23.72	6	4.9050479	0.079000004	0.89701211	31
soy_OGL_5000	1210	8.9428253	20	1730	22.97	6	12.333051	0.061999999	0.70040965	26
soy_OGL_2274	1394	13.583581	18.436155	2030	29.69	6	9.6541538	0	0.62812388	41
soy_OGL_3516	1022	38.161209	19.863014	6563	24.46	6	10.899384	0.079999998	0.73997593	22
soy_OGL_5259	1100	11.175008	34.18182	3924	23	10	30.856979	0.122	0.82970124	16
soy_OGL_5625	1400	36.55751	18.071428	3716	29.21	9	9.2684908	0	0.6150766	29
soy_OGL_6873	1003	8.3950586	34.297108	2001	22.43	8	46.517944	0.082999997	0.84444761	27
soy_OGL_713	1008	8.4636536	27.876984	3305	23.71	8	48.710068	0.086999997	0.84803003	25
soy_OGL_1716	1107	31.132702	33.87534	2001	26.1	8	3.4388704	0	0.8326841	30
soy_OGL_3314	1220	16.56156	23.032787	4906	23.93	8	9.6485319	0	0.90317971	20
soy_OGL_3505	1100	47.600048	11.545455	3419	27.18	7	5.1035805	0	0.7224772	21

soy_OGL_3742	1300	9.2434053	14	3440	25.84	10	31.219353	0	0.78232616	25
soy_OGL_5536	1158	8.6176863	21.588947	1001	23.31	7	18.947451	0.050999999	0.7828905	26
soy_OGL_566	1032	21.491308	21.22093	1519	21.8	10	2.6781733	0.104	0.30944595	21
soy_OGL_4500	1099	8.7435341	18.198362	2478	23.93	6	22.891724	0	0.73810846	36
soy_OGL_2991	1205	9.2852879	34.937759	4431	20.99	6	17.602253	0.079999998	0.80759555	24
soy_OGL_3498	1100	47.600048	19.363636	4882	29	4	39.279327	0	0.71214223	17
soy_OGL_5630	1399	24.815081	21.729807	2596	27.8	8	7.8393497	0.057999998	0.60297322	14
soy_OGL_5794	1000	14.27938	37.799999	3377	22.4	6	13.465201	0	0.85381812	40
soy_OGL_56	1100	11.04541	21.363636	5107	27.27	5	51.287495	0	0.84487879	28
soy_OGL_3778	1000	16.902504	26.299999	8800	23.8	12	12.075264	0	0.70730901	17
soy_OGL_4791	1137	13.341439	20.404573	4370	24.53	6	30.036924	0.122	0.91245389	14
soy_OGL_5633	1125	24.815081	25.866667	2361	25.86	9	17.938488	0.112	0.60074234	13
soy_OGL_5987	1322	45.929386	7.1104388	1722	32.14	5	6.8589234	0.059999999	0.60041213	14
soy_OGL_1737	1102	17.655291	19.600725	5174	25.86	7	15.562757	0.122	0.86833215	13
soy_OGL_3180	1100	12.608178	19.90909	2313	24.45	7	7.08781	0.094999999	0.65492815	22
soy_OGL_5821	1300	13.314646	9.1538458	3359	28.61	5	8.3399916	0.017999999	0.90595192	23
soy_OGL_4677	1045	10.891823	3.5406699	3426	28.7	6	23.108593	0	0.64660132	39
soy_OGL_6783	1100	11.164678	25.636364	6787	25.18	9	12.037078	0.115	0.77097458	20
soy_OGL_4575	1100	5.9374781	18	2010	23.9	9	17.419079	0	0.82844257	21
soy_OGL_6202	1100	6.3214092	11.727273	4591	25.72	8	3.2832642	0	0.86166477	26
soy_OGL_3832	1690	7.7801862	22.307692	4692	24.97	10	6.0559936	0	0.54331803	27
soy_OGL_3551	1000	8.9636507	33.900002	1527	19.4	7	2.8391688	0.046999998	0.80754906	21
soy_OGL_1385	1466	6.9438424	11.050477	5366	32.4	6	15.37778	0.009	0.80697608	37
soy_OGL_2289	1032	10.571202	30.038759	1212	26.93	6	5.9921865	0.055	0.61786699	40
soy_OGL_972	1258	13.568718	19.236883	10754	30.36	7	0.82375985	0.039999999	0.76340604	36
soy_OGL_4154	1251	9.8956871	30.855316	5927	24.22	8	9.7893705	0.086000003	0.89091927	20
soy_OGL_2517	1200	7.4874678	24.416666	1843	24.58	11	20.636683	0	0.82058394	21
soy_OGL_3326	1300	9.9528103	22	4701	27.15	9	10.634618	0	0.87685251	28
soy_OGL_3643	1238	5.6271753	21.082392	1001	25.76	6	12.438443	0.022	0.93565953	26
soy_OGL_215	1414	12.907678	29.20792	1297	27.72	6	13.993959	0.008	0.82242996	29
soy_OGL_3950	1500	23.570066	31.200001	2498	28.4	9	5.5293403	0	0.89227611	20

soy_OGL_5217	1156	11.000355	39.359863	5940	24.22	10	15.081091	0.055	0.94579268	28
soy_OGL_5299	1027	23.178028	28.919182	1001	28.72	8	12.565261	0.066	0.71292853	25
soy_OGL_964	1500	12.443513	15.6	2018	28.06	6	4.1339521	0	0.75554466	34
soy_OGL_1132	1360	5.8739777	39.485294	2001	20.8	10	34.840954	0.035	0.9885658	16
soy_OGL_3317	1249	16.411713	31.865492	4654	26.74	8	9.6982422	0.012	0.89437199	25
soy_OGL_3533	1111	8.9636507	26.372637	3272	24.21	10	21.439034	0.044	0.79193574	23
soy_OGL_6743	1185	9.6085119	25.654009	2859	23.62	9	9.6132221	0.033	0.7307058	29
soy_OGL_6824	1200	6.5125389	19.083334	5657	27.41	7	12.505066	0	0.80866694	36
soy_OGL_6874	1301	8.3950586	32.89777	3603	29.51	8	46.517944	0	0.84448242	27
soy_OGL_1924	1482	12.936749	17.071526	2133	29.68	7	13.087845	0.018999999	0.55777919	24
soy_OGL_42	1000	8.7112885	26.700001	6865	27.6	6	11.802042	0.013	0.88105452	32
soy_OGL_1254	1000	11.432598	24.299999	2703	25.5	8	7.9112363	0.026000001	0.72134209	19
soy_OGL_1421	1200	11.385625	18.25	2739	28.25	5	7.5647316	0.025	0.86751378	22
soy_OGL_3215	1200	8.5244722	33.416668	4958	26.75	5	18.444984	0	0.70541042	43
soy_OGL_3359	1119	13.178452	36.371761	5104	22.87	8	11.239169	0.111	0.81167281	15
soy_OGL_207	1000	15.172221	31.9	1155	25.5	5	4.8290596	0	0.81518292	25
soy_OGL_2261	1000	7.6927543	36.700001	2413	23.7	7	7.3165908	0	0.6390413	44
soy_OGL_5840	1100	14.047599	28.636364	3128	24.81	7	11.096366	0	0.96668971	21
soy_OGL_715	1100	9.6048651	32.81818	12158	24.9	10	6.2166438	0	0.85295236	25
soy_OGL_926	1000	11.929564	25.700001	4373	23.3	8	3.4833732	0	0.69985145	24
soy_OGL_1427	1413	11.258756	26.893135	5035	25.4	7	2.746418	0	0.87597263	20
soy_OGL_1954	1207	21.449512	30.903065	2652	26.59	10	4.6602082	0.002	0.51281148	15
soy_OGL_3358	1145	13.178452	24.716158	2284	24.54	7	12.810069	0	0.81180155	15
soy_OGL_1565	1000	10.29399	31.299999	2297	28.5	9	51.865131	0.088	0.82041073	27
soy_OGL_5182	1000	13.715208	25.200001	5215	26	6	8.5989075	0.124	0.9119907	16
soy_OGL_415	1458	13.282036	9.6021948	1001	26.68	8	4.1540623	0.027000001	0.70906878	17
soy_OGL_1675	1081	9.1770983	34.597595	2484	24.88	12	37.194218	0.102	0.70754141	16
soy_OGL_3175	1041	11.522595	21.902018	4072	25.84	10	4.4895511	0.048999999	0.64837974	22
soy_OGL_5586	1300	5.8065071	14.076923	1457	26.38	10	30.075253	0	0.67897701	19
soy_OGL_1732	1100	20.814644	24.545454	2125	28.18	13	32.735954	0	0.86075628	17
soy_OGL_1582	1107	7.7159863	29.810299	1870	27.73	7	44.191189	0.057999998	0.78661311	21

soy_OGL_4657	1139	8.7303162	24.934153	1001	28.35	10	50.50164	0	0.68424433	25
soy_OGL_5188	1000	12.553019	24.9	2698	28.1	8	26.710304	0	0.94127607	19
soy_OGL_925	1035	11.929564	21.73913	4830	22.22	6	15.610137	0.112	0.69930834	26
soy_OGL_5611	1000	25.029232	3.2	6209	22.3	6	6.0486059	0.048	0.63155556	27
soy_OGL_1955	1113	19.095425	22.012579	2429	20.84	5	13.459276	0.125	0.50990909	18
soy_OGL_469	1384	5.8994384	20.736994	3196	24.06	7	26.64043	0	0.5421899	23
soy_OGL_1953	1100	21.449512	12.363636	5300	21.9	10	4.6602082	0	0.51290262	15
soy_OGL_3789	1000	13.802341	27.299999	3490	20.1	8	17.301466	0.054000001	0.6840601	10
soy_OGL_5950	1044	11.551946	28.735632	9160	22.89	5	1.8585685	0.050999999	0.7105692	22
soy_OGL_3437	1100	7.3611813	35.18182	1284	18.45	9	43.401207	0.108	0.54420781	12
soy_OGL_4279	1300	5.5609851	35.923077	1033	25.46	9	96.342125	0	0.36612734	19
soy_OGL_562	1000	21.491308	31.700001	3754	20.4	8	9.4132662	0.061999999	0.31529731	24
soy_OGL_1279	1205	7.1300635	23.153526	4273	24.64	5	23.644365	0	0.66881138	24
soy_OGL_4294	1184	3.9414778	39.695946	6554	18.15	11	32.686649	0	0.39032573	23
soy_OGL_4659	1270	8.59167	25.51181	5018	27.71	6	116.62761	0	0.67796731	26
soy_OGL_6406	1000	6.8150654	34.700001	2956	27.1	5	58.585674	0.078000002	0.47973934	16
soy_OGL_203	1011	11.890499	7.7151337	6034	27.1	6	6.6497402	0	0.81119186	28
soy_OGL_3356	1300	11.131104	14.615385	3268	25.15	7	20.024742	0.074000001	0.82251149	14
soy_OGL_6235	1000	6.1202364	18.6	7007	24.9	5	29.531097	0.063000001	0.89909935	19
soy_OGL_1947	1422	24.109264	0	6243	28.69	4	10.771916	0	0.52522981	18
soy_OGL_1991	1200	6.3401136	13.75	8250	25.41	9	25.638062	0.046	0.45783767	20
soy_OGL_5337	1099	32.314224	11.282985	4967	27.02	5	3.6590505	0.039000001	0.54922569	11
soy_OGL_6890	1200	7.0806479	12.583333	7391	29.41	5	57.758587	0	0.86617112	25
soy_OGL_560	1100	21.124374	15.545455	7179	27.09	7	7.5583582	0	0.32324776	18
soy_OGL_5004	1040	4.348846	30.865385	3972	22.88	6	18.012817	0.138	0.69220364	20
soy_OGL_3167	1450	11.683348	19.103449	5133	26.27	9	2.7914271	0.067000002	0.62364203	15
soy_OGL_3786	1000	14.175368	25.5	3737	22.2	9	5.9147005	0.081	0.68887985	12
soy_OGL_6850	1279	4.0300374	16.810007	5364	24	8	16.279037	0	0.82384777	24
soy_OGL_795	1000	9.3835421	24	4408	26.7	4	8.7542324	0.103	0.87056249	22
soy_OGL_4718	1283	5.318872	30.007793	3557	23.38	7	7.5893664	0.086000003	0.57852942	27
soy_OGL_6487	1600	8.5538664	22.375	3348	25.18	7	5.2517185	0.048999999	0.64917505	20

soy_OGL_5400	1120	9.4738331	19.196428	3312	25.89	6	7.9064126	0	0.73532683	20
soy_OGL_4191	1000	5.3633652	31.1	7995	23.4	7	7.6569033	0.028000001	0.20371033	21
soy_OGL_394	1200	9.5874052	15.416667	5142	26.75	6	6.4867473	0	0.76410359	24
soy_OGL_2612	1244	8.0021572	22.990355	2001	23.15	8	6.0297899	0	0.59597749	23
soy_OGL_2845	1200	5.5548873	32.25	3709	20.41	8	3.3282802	0	0.67571777	24
soy_OGL_5935	1400	7.4355073	17.5	6518	24.78	8	10.077048	0	0.73690307	22
soy_OGL_1353	1195	11.526744	26.025105	2001	25.18	6	20.698202	0.089000002	0.75391692	14
soy_OGL_1910	1500	15.216813	18.333334	4526	29.13	6	6.8650885	0	0.61582142	13
soy_OGL_826	1000	10.746717	36.700001	2288	22	5	10.534933	0.103	0.72356248	23
soy_OGL_901	1200	6.5197372	28	10078	25.66	8	12.647342	0.030999999	0.67072892	31
soy_OGL_2971	1007	11.978155	36.842106	10536	23.13	7	4.8957019	0.054000001	0.84989756	21
soy_OGL_3190	1400	10.529183	32.714287	3264	25	5	4.7417526	0	0.67169625	28
soy_OGL_5425	1267	12.267535	33.701656	10992	25.96	5	8.4590149	0	0.98036045	12
soy_OGL_2624	1200	8.794776	32.666668	4254	22.08	9	4.4608855	0.023	0.58054543	24
soy_OGL_6445	1100	9.0478334	32.545456	2297	24.09	6	11.61035	0	0.567496	29
soy_OGL_6524	1100	21.291258	25.363636	4079	28.36	4	5.1097422	0	0.71310264	16
soy_OGL_3523	1000	1.9912556	36.299999	5882	23.8	7	44.820503	0.01	0.75102091	17
soy_OGL_6887	1200	6.5062184	19.166666	6711	28.33	6	25.491898	0.086000003	0.86114001	24
soy_OGL_3906	1223	9.3006687	20.850368	4936	27.55	6	22.389164	0.071999997	0.76607245	20
soy_OGL_6236	1700	6.1202364	7.5294118	3707	30.52	5	24.552103	0	0.8991611	19
soy_OGL_468	1000	5.5066857	18.299999	4048	23.8	9	6.4829116	0.033	0.54701352	24
soy_OGL_706	1421	9.20959	11.681914	4282	29.27	6	14.093465	0.018999999	0.84138483	19
soy_OGL_1249	1400	11.287494	13.714286	3836	29.07	7	5.402895	0.014	0.73023248	19
soy_OGL_4206	1200	3.6495144	28.75	2260	22.08	13	22.752178	0.046	0.22943813	16
soy_OGL_6651	1100	13.28592	12.363636	5447	25.9	8	3.053539	0	0.71798563	12
soy_OGL_4273	1000	4.9097567	23.799999	3013	23.6	6	14.624303	0.046	0.35655642	21
soy_OGL_615	1100	3.8726745	19	1079	26.72	5	34.027176	0	0.69433415	22
soy_OGL_4111	1081	12.218921	15.263645	5042	26.08	8	15.367756	0.002	0.70827103	15
soy_OGL_1016	1735	6.0355277	1.6714697	1001	27.66	9	9.627018	0.222	0.81906343	24
soy_OGL_5564	1800	7.787199	0	2883	27.61	10	8.9710941	0.21600001	0.71813029	21
soy_OGL_5561	1800	7.7752442	2.6666667	4645	28.66	8	7.6616893	0.22400001	0.71934098	20

soy_OGL_438	1683	6.5997066	7.1301246	2001	23.11	13	4.1688166	0.206	0.66513926	14
soy_OGL_3783	1413	13.260455	14.649681	1342	25.26	11	9.2098055	0.264	0.6965279	18
soy_OGL_3970	1668	11.100904	0	2001	27.81	9	9.6342793	0.161	0.94206536	10
soy_OGL_5505	1204	5.7864904	3.4883721	2001	26.91	9	21.531029	0.23899999	0.83195156	20
soy_OGL_427	1517	13.017153	2.5708635	4535	30.85	9	13.079314	0.219	0.68865764	24
soy_OGL_6892	1069	7.0806479	0	4570	31.15	5	50.526379	0.396	0.86652088	25
soy_OGL_2680	1097	10.232581	6.4721971	2447	26.25	11	10.308086	0.222	0.49911189	26
soy_OGL_3195	1100	8.1154594	6.909091	3030	27.18	11	19.127066	0.23800001	0.68446332	32
soy_OGL_3709	1100	7.0062461	2.5454545	3244	27.63	9	21.530809	0.22400001	0.83500856	23
soy_OGL_5323	1100	11.453777	0	1370	27.9	9	16.140268	0.252	0.66165245	25
soy_OGL_6806	1168	6.2792668	2.7397261	5129	28.51	10	24.752777	0.228	0.79340476	23
soy_OGL_913	1300	6.1910648	6.2307692	2526	28.46	8	22.870914	0.2	0.68140048	26
soy_OGL_993	1200	8.2221594	6	5278	29.25	7	15.960431	0.19499999	0.7739985	29
soy_OGL_6249	1809	6.0078726	0	5163	29.35	9	2.1832757	0.28400001	0.90707797	28
soy_OGL_2870	1400	5.5274458	11.142858	3372	25.57	9	4.2722106	0.23899999	0.79814261	18
soy_OGL_1113	2200	4.4006457	1.4545455	3116	26.4	12	13.853506	0.139	0.96060461	8
soy_OGL_2484	1500	6.4331512	12.533334	4891	27.4	9	6.2209368	0.208	0.88708043	22
soy_OGL_2521	1800	7.5373769	5.4444447	1535	27.55	12	11.799488	0.228	0.81642658	18
soy_OGL_5449	1968	5.0694704	2.0325203	1959	27.74	11	6.9900832	0.161	0.93618619	18
soy_OGL_5919	1503	9.5798969	6.4537592	2109	28.07	8	4.7703791	0.19499999	0.83893353	18
soy_OGL_5202	1577	6.245574	11.477489	5394	29.04	6	6.3846922	0.185	0.97282928	20
soy_OGL_5913	1500	8.4431925	10.8	5409	28.2	6	3.5827973	0.205	0.84570408	22
soy_OGL_6999	1600	5.7162013	8.125	7770	28.62	7	6.6815772	0.20299999	0.95974499	21
soy_OGL_7000	1302	5.8714023	15.745008	4581	24.96	8	6.4077549	0.20900001	0.95982075	21
soy_OGL_3491	1339	5.426621	15.683346	2797	25.09	9	8.4679823	0.199	0.65357959	21
soy_OGL_2556	1707	4.8110962	12.009373	4988	28.88	9	10.576658	0.176	0.71519208	20
soy_OGL_659	1400	6.4094901	4	3045	30.07	9	5.7310119	0.19599999	0.76620996	36
soy_OGL_682	2235	10.540062	0	3174	32.61	9	11.1258	0.175	0.79761487	23
soy_OGL_3177	1767	13.249586	16.468592	4861	30.84	7	2.4444396	0.278	0.65266436	24
soy_OGL_3614	1956	5.2820034	8.3844585	2289	27.86	11	15.399803	0.16500001	0.89578253	13
soy_OGL_6986	1900	4.9338017	0	1488	30.84	10	7.4841352	0.162	0.95001721	35

soy_OGL_4904	1600	9.0506868	14.75	7152	26.18	11	9.4658213	0.18099999	0.88859528	11
soy_OGL_3194	1838	8.1144657	0	1956	30.95	10	1.5879364	0.119	0.68373424	31
soy_OGL_4512	1175	8.8380184	14.553191	2001	26.97	8	0.9945097	0.20900001	0.74880666	36
soy_OGL_5533	1324	11.696812	9.8187313	3557	28.24	8	6.1653848	0.186	0.78681612	25
soy_OGL_4540	1500	5.1131511	2.8	1846	26.53	11	6.9039898	0.17900001	0.78198892	27
soy_OGL_6833	1411	4.1189404	3.9688165	2001	28.63	7	5.1620641	0.15700001	0.81157672	35
soy_OGL_2849	1531	5.5548873	0	3238	27.75	9	5.9082513	0.152	0.68036723	26
soy_OGL_3975	1638	5.0162044	6.0439563	4454	26.06	10	12.899006	0.156	0.9115926	8
soy_OGL_1213	1176	6.7576227	16.581633	1001	24.65	12	8.8276911	0.219	0.81893182	24
soy_OGL_1555	1023	9.3490543	19.550343	2582	24.63	8	6.8261609	0.20999999	0.84252977	25
soy_OGL_1768	1500	5.2867265	12.933333	2107	25.73	12	12.020113	0.16599999	0.91045779	20
soy_OGL_2515	1200	7.4874678	13.25	3449	25.33	11	13.361275	0.215	0.82095456	21
soy_OGL_2925	1300	8.5070477	13.769231	2045	26.3	10	6.0728183	0.199	0.95415318	25
soy_OGL_3245	1561	8.3858376	0	1530	30.04	10	7.2060614	0.149	0.7315433	36
soy_OGL_4471	1500	7.4102635	5.7333331	2338	28.2	12	9.7450514	0.145	0.70453101	28
soy_OGL_6950	1738	8.7501049	0	4706	30.03	10	8.5434961	0.097999997	0.9271872	25
soy_OGL_7003	1287	6.3244863	18.414919	4935	24.7	12	19.990871	0.185	0.96414399	15
soy_OGL_1672	1706	9.1770983	0	1454	28.31	13	11.422449	0.22400001	0.70461172	14
soy_OGL_1850	1900	4.8108158	5.4210525	3443	30.42	9	6.7204213	0.32600001	0.73134089	27
soy_OGL_5177	1410	10.392078	0	3152	29.36	9	11.984594	0.26300001	0.88698816	16
soy_OGL_6762	1000	10.113653	2.8	5106	30	7	4.1271238	0.271	0.74248642	30
soy_OGL_782	1200	10.960977	0	3048	29.25	7	3.1313317	0.235	0.92820311	18
soy_OGL_3562	1000	6.3657079	8.1000004	2301	28.2	7	5.2021227	0.26499999	0.83146721	31
soy_OGL_4589	1500	4.07375	0	1481	27.06	12	25.914267	0.25299999	0.97039866	12
soy_OGL_6294	1380	6.0601311	0	2001	26.88	10	9.1623478	0.208	0.94897139	21
soy_OGL_3641	1200	5.6271753	0	4850	29.58	6	12.814153	0.18700001	0.93530005	27
soy_OGL_4628	1100	3.3767221	6.6363635	3213	27.63	6	7.8805008	0.20999999	0.74952942	33
soy_OGL_1836	1805	8.3344145	0	2001	30.8	11	5.6839094	0.198	0.75436687	28
soy_OGL_2201	1221	8.5738249	0	3058	33	6	7.8922873	0.29699999	0.77215594	35
soy_OGL_6579	1380	5.0139508	0	3694	32.02	5	10.45339	0.182	0.78351104	31
soy_OGL_252	1300	13.280943	2.5384614	1082	29.76	8	3.0115771	0.185	0.866445	19

soy_OGL_645	1264	7.5262041	6.25	2001	29.66	8	7.3969212	0.208	0.75115973	26
soy_OGL_2170	1200	8.2492304	0	2388	29.25	10	13.402763	0.23899999	0.82110548	20
soy_OGL_6742	1100	9.2634287	0	1680	31	7	6.1017532	0.249	0.72983682	28
soy_OGL_2408	1000	11.967738	0	2276	31.9	5	2.3872302	0.221	0.70479697	31
soy_OGL_4530	1122	6.7637272	0	4335	32.7	7	18.475098	0.20100001	0.77120715	28
soy_OGL_5579	1500	5.9725876	3.5999999	5747	30.13	12	11.842384	0.168	0.68724906	20
soy_OGL_3182	1755	10.90356	1.8803419	1426	31.73	8	12.150808	0.15800001	0.65654069	22
soy_OGL_2628	1500	7.9126515	0	3390	30.2	11	9.6578856	0.18099999	0.56797904	27
soy_OGL_3651	1600	1.8333012	0	6440	30.75	9	33.467297	0.13	0.94578689	23
soy_OGL_6240	1602	5.9223814	0	1978	27.59	4	5.0436692	0.164	0.90000409	19
soy_OGL_1351	2640	11.76944	1.439394	11204	37.5	3	22.037344	0.248	0.74710763	18
soy_OGL_812	1500	8.8038511	0	2479	25.73	7	2.4788299	0.248	0.7734375	12
soy_OGL_4786	1600	3.5548639	5.5625	4958	27.56	8	35.429214	0.175	0.8956852	9
soy_OGL_2705	1405	3.2460434	0	3122	25.48	10	4.568222	0.19400001	0.45631909	24
soy_OGL_3145	1057	9.2910147	0	2394	28.76	4	7.3289666	0.24600001	0.56962854	28
soy_OGL_6899	1100	7.0806479	2.8181818	6823	28.27	6	9.3049116	0.219	0.86895394	27
soy_OGL_2609	1077	8.0021572	0	8598	28.13	7	4.1500378	0.25400001	0.59915292	21
soy_OGL_3397	1000	2.8635902	0	7301	26.9	7	23.058424	0.24699999	0.69554842	18
soy_OGL_5060	1200	3.1510634	0	5412	25.16	4	9.9553947	0.292	0.58365273	3
soy_OGL_4021	1200	7.0667925	4.5833335	15357	28.41	3	4.245554	0.33899999	0.69518077	16
soy_OGL_6002	1780	3.4906964	3.0898876	2240	28.08	5	15.25239	0.192	0.54100615	14
soy_OGL_476	1125	5.5857544	0	2740	28.08	4	6.6709051	0.236	0.52773875	23
soy_OGL_1023	1000	5.5469222	0	17094	29.8	6	2.9553194	0.19400001	0.82398254	29
soy_OGL_1336	1149	2.2828174	3.3072236	8641	24.1	8	7.1391459	0.234	0.70397425	10
soy_OGL_5661	1278	7.3934207	4.6948357	3236	27.38	5	8.3864012	0.193	0.50253254	20
soy_OGL_4221	1697	4.8260355	0	7384	34.35	9	27.647419	0.197	0.26030171	32
soy_OGL_4244	1581	9.1999483	0	5216	30.67	10	13.460354	0.171	0.28532892	21
soy_OGL_2100	2118	9.64013	10.292729	1001	27.52	7	3.4058859	0.211	0.80251724	5
soy_OGL_4320	1919	3.5637994	0	3983	27.98	12	6.9818273	0.16599999	0.42812887	20
soy_OGL_6136	1574	3.3948011	13.977128	7078	25.22	7	5.0989347	0.242	0.76529938	15
soy_OGL_6187	1938	4.7146115	3.1991744	1589	27.81	7	3.2256651	0.13699999	0.84219968	12

soy_OGL_6457	1597	5.9874048	4.1327491	4675	27.61	8	4.369297	0.2	0.5800423	20
soy_OGL_5659	1939	7.3934207	4.8478599	1974	28.88	8	1.8669453	0.127	0.50464368	20
soy_OGL_181	1848	4.2186117	3.3008659	1001	29	4	9.7487288	0.122	0.77545059	14
soy_OGL_3033	1786	2.1420259	10.078387	2697	23.96	7	3.7315834	0.16	0.72150636	7
soy_OGL_3162	1700	8.1492577	14.529411	6670	27.82	6	7.7065454	0.214	0.60926288	15
soy_OGL_2076	1671	1.0828819	10.532616	1001	24.53	7	3.2372901	0.15899999	0.68104798	11
soy_OGL_3396	1354	2.8635902	13.66322	4701	27.03	7	23.058424	0.164	0.69565189	18
soy_OGL_6591	1192	5.3763165	14.848993	5731	27.01	7	13.000634	0.20200001	0.80261177	20
soy_OGL_2073	1181	3.5357072	14.902625	1001	23.28	5	0.27462721	0.20999999	0.65464115	12
soy_OGL_2092	1669	1.3710024	7.9089274	1210	26.24	4	3.2468398	0.13600001	0.76257998	15
soy_OGL_4064	1168	0.90285671	14.041096	1001	20.89	6	3.4573336	0.229	0.50347549	15
soy_OGL_906	1000	5.9492388	9.8999996	3872	28.7	6	5.1469183	0.242	0.67600268	29
soy_OGL_3348	1002	11.28932	0	4463	31.33	4	3.7417524	0.26699999	0.84703225	25
soy_OGL_6303	1700	3.5560801	0	4004	27.64	7	7.6688504	0.23100001	0.98660427	9
soy_OGL_6772	1600	7.8559184	8.375	3413	28.25	7	5.3768115	0.23800001	0.75225329	15
soy_OGL_1580	1200	7.7159863	3.8333333	2363	29.58	5	8.6603107	0.219	0.78867859	23
soy_OGL_3438	1065	7.5834217	0	3301	27.6	9	15.867051	0.249	0.5515703	11
soy_OGL_6737	1200	8.8684349	0	9778	31.83	8	4.7401357	0.19	0.72786218	25
soy_OGL_2602	1700	6.5441737	0	3259	28.58	8	5.498385	0.17900001	0.61441958	18
soy_OGL_4620	1417	7.723742	0	7040	30.91	6	4.8376198	0.222	0.76326799	26
soy_OGL_6774	1677	7.6195984	0	5653	29.99	7	12.206922	0.16599999	0.75302446	16
soy_OGL_6330	1200	6.7954488	5.9166665	4839	28	5	3.0799832	0.215	0.91808939	23
soy_OGL_2075	1525	3.6825252	4.52459	2194	25.37	7	7.953577	0.177	0.6618917	13
soy_OGL_6896	1100	7.0806479	6	8705	31.63	6	10.926623	0.20999999	0.86801547	27
soy_OGL_5018	1190	8.8939037	2.3529413	7316	30.67	8	14.040364	0.182	0.6690107	26
soy_OGL_6004	1700	3.4906964	4.647059	2956	29.23	5	15.325985	0.198	0.5395357	14
soy_OGL_6364	1658	1.2353655	0	3316	27.68	4	18.001196	0.213	0.76936775	5
soy_OGL_2299	1237	7.6596303	0	2289	27.8	4	0.11322137	0.227	0.59325516	14
soy_OGL_3155	1000	8.7529049	0	7101	31.8	5	7.1640654	0.23199999	0.59849638	21
soy_OGL_6455	1100	5.9874048	0	11272	29.72	8	4.3669896	0.2	0.57981288	20
soy_OGL_882	1670	2.4722638	0	8372	27.42	5	1.9007876	0.21699999	0.62820804	9

soy_OGL_2310	1500	7.6112018	0	2327	28.93	6	1.8739754	0.153	0.56102753	17
soy_OGL_1869	1224	5.0498676	10.04902	5696	30.47	6	13.168991	0.206	0.71333116	26
soy_OGL_2730	1500	8.2150984	0	5860	31.26	10	7.9833422	0.167	0.4206818	20
soy_OGL_3303	1286	9.4088583	0	10207	32.11	6	9.6430969	0.141	0.93500984	18
soy_OGL_5140	1704	4.0574603	0	2001	29.51	9	12.998578	0.12	0.72634619	14
soy_OGL_238	1110	10.989239	11.441442	3350	25.49	10	9.9135027	0.211	0.84749067	21
soy_OGL_1206	1151	6.7576227	0	2628	26.06	7	1.2309921	0.227	0.82688123	28
soy_OGL_248	1000	12.860178	0	2627	28	9	25.31386	0.237	0.86273146	18
soy_OGL_2937	1200	10.919902	0	2058	26.75	9	5.984725	0.206	0.92710215	19
soy_OGL_6777	1149	10.114168	10.443864	2001	23.15	11	10.296715	0.21799999	0.76417077	12
soy_OGL_6975	1000	4.5740175	0	4715	26.5	10	5.748785	0.248	0.94220328	34
soy_OGL_2862	1311	5.7699661	0	1001	22.95	10	6.1850662	0.205	0.78026533	14
soy_OGL_3559	1000	6.3657079	0	5462	27.2	8	5.3850923	0.20200001	0.83077681	30
soy_OGL_1879	1451	4.2531829	6.8228807	2081	26.05	13	25.985241	0.149	0.70034415	21
soy_OGL_4109	1300	12.218921	0	3863	29	9	13.927808	0.146	0.70468187	16
soy_OGL_5386	1000	9.3595705	0	2940	27.2	11	11.483829	0.199	0.69451046	20
soy_OGL_4587	1054	4.07375	0	4105	27.7	12	28.505186	0.25799999	0.97319907	12
soy_OGL_1127	1000	3.0311241	0	2737	27.4	8	12.004765	0.255	0.98547697	15
soy_OGL_2490	1544	6.9427032	0	2025	29.59	12	16.199041	0.162	0.88360685	17
soy_OGL_3452	1000	10.085547	0	3748	28.6	13	20.604944	0.23100001	0.59130538	12
soy_OGL_4857	1318	6.8892426	0	1001	26.17	12	5.0714235	0.205	0.95898128	14
soy_OGL_6266	1200	6.5872955	0	1250	27	12	5.8424788	0.223	0.92280972	27
soy_OGL_6569	1171	4.8296428	0	1001	29.12	7	2.6465969	0.191	0.77879184	32
soy_OGL_285	1100	7.6405764	0	3129	29.27	6	6.0913997	0.193	0.90452152	26
soy_OGL_2873	1109	6.2971745	10.550045	2001	25.33	9	8.6543274	0.214	0.80549783	17
soy_OGL_3657	1303	1.9542303	0	4020	24.78	11	9.1898546	0.20200001	0.95539349	10
soy_OGL_1199	1203	6.7576227	3.3250208	1909	26.84	11	7.7169404	0.178	0.84114021	17
soy_OGL_3966	1283	8.0769224	9.5869055	2353	23.46	12	14.496478	0.191	0.94744617	10
soy_OGL_2847	1200	5.5548873	0	5307	27.66	9	6.9243832	0.17900001	0.67886299	26
soy_OGL_1408	1000	14.723554	0	3151	28.3	11	4.6703668	0.23	0.83352113	18
soy_OGL_2516	1278	7.4874678	0	2326	30.28	10	14.66328	0.147	0.82088065	21

soy_OGL_2119	1233	7.0475831	0	2001	28.14	12	9.8153009	0.171	0.92410553	15
soy_OGL_2191	1000	10.96957	0	2060	28.8	7	1.6697304	0.211	0.79033488	29
soy_OGL_3292	1153	5.0341988	0	7122	29.22	10	16.314804	0.17900001	0.9561404	26
soy_OGL_6308	1500	6.8833284	0	1475	26.6	12	20.507517	0.164	0.97756171	12
soy_OGL_6580	1100	5.2729778	3	3418	28.81	9	16.620815	0.20100001	0.78563899	33
soy_OGL_5232	1361	9.6439486	0	1217	30.34	5	8.5155277	0.12800001	0.91159755	22
soy_OGL_2616	1200	8.5876789	0	1519	27.16	8	15.774424	0.20999999	0.58604199	21
soy_OGL_6149	1100	4.9855185	0	3054	24.63	8	15.90489	0.233	0.78441608	16
soy_OGL_4219	1064	4.8260355	0	2058	29.13	7	12.091471	0.19599999	0.25931376	32
soy_OGL_4249	1000	9.7208376	0	2409	25.6	9	11.940843	0.23999999	0.29463232	14
soy_OGL_3977	1000	5.9767532	0	3054	23.7	9	16.045	0.25099999	0.90981537	8
soy_OGL_5330	1400	6.8539505	0	1713	24.5	10	2.5293972	0.19599999	0.63820732	13
soy_OGL_1335	1269	2.3491204	0	3662	22.69	10	3.1418793	0.197	0.70210123	11
soy_OGL_5135	1020	0.82107258	0	2001	22.45	6	5.0720057	0.212	0.68862104	12
soy_OGL_3810	1200	8.2365665	7.25	2893	24.58	9	11.152919	0.183	0.60813731	12
soy_OGL_4315	1406	2.1374688	0	3839	27.09	12	24.782219	0.127	0.4184418	17
soy_OGL_6329	1200	6.7954488	3.25	7739	28.66	6	5.829483	0.15700001	0.91821277	23
soy_OGL_6164	1067	6.0447426	0	2463	27.74	4	5.7592225	0.221	0.80176425	16
soy_OGL_5166	1100	8.5415621	0	6014	31	4	1.5505449	0.17	0.83777636	17
soy_OGL_512	1300	3.8568666	0	3402	26.84	8	7.8383617	0.182	0.45509461	21
soy_OGL_2382	1000	7.888226	0	3230	28.8	9	4.6613426	0.211	0.59838921	13
soy_OGL_1765	1400	5.2867265	0	2030	26	8	9.3718052	0.175	0.91541237	10
soy_OGL_5917	1228	8.4431925	0	7345	28.74	7	4.1640239	0.13699999	0.84399348	21
soy_OGL_3269	1144	5.2893763	0	2606	28.84	7	21.567369	0.17200001	0.85043263	16
soy_OGL_84	1604	8.729229	3.3665836	2001	27.68	7	5.3574696	0.169	0.79651308	28
soy_OGL_214	2209	13.095701	3.1235852	2593	31.82	4	13.373614	0.292	0.82151347	27
soy_OGL_253	1806	13.280943	2.3809524	2001	26.63	7	3.2467754	0.211	0.86661017	19
soy_OGL_2893	1708	8.9753227	2.4590163	3338	25.05	8	9.8445396	0.28799999	0.87309968	19
soy_OGL_4142	1800	11.063471	4.7777777	7531	28.66	7	14.370344	0.35600001	0.85423917	28
soy_OGL_5185	1506	13.212205	2.7888446	4107	27.02	7	12.997959	0.20999999	0.93270004	20
soy_OGL_5465	1800	6.4554529	8.666667	4652	24.38	13	12.444818	0.208	0.89833719	13

soy_OGL_6982	2100	4.6027212	0	4419	29.66	9	11.518851	0.25099999	0.94608092	35
soy_OGL_817	1428	11.647924	7.352941	1493	27.1	5	4.5648298	0.184	0.74932814	23
soy_OGL_2890	1600	8.9753227	2.625	4263	28.12	7	9.3781614	0.163	0.870305	21
soy_OGL_4649	1449	5.2841516	10.282954	4888	23.46	9	4.888607	0.25999999	0.71348363	27
soy_OGL_6341	1800	5.6157908	0	2471	26.83	4	1.9889303	0.214	0.89729363	27
soy_OGL_6516	1556	6.1901021	1.8637532	2001	27.76	7	12.124317	0.184	0.69506919	30
soy_OGL_6822	1518	6.4448819	2.0421607	8431	29.24	6	9.7099628	0.19	0.80785191	33
soy_OGL_11	1500	9.4707623	5.5333333	4251	25.93	10	14.001542	0.182	0.95172119	17
soy_OGL_652	1600	6.4309473	0	3063	26.87	8	2.429085	0.17299999	0.76030147	29
soy_OGL_1021	1657	5.5469222	0	2118	25.16	7	4.970129	0.177	0.82288468	27
soy_OGL_4463	1900	7.5555859	0	2268	27.94	11	6.3879871	0.13500001	0.69791692	25
soy_OGL_416	1519	13.092012	2.3041475	1462	25.41	7	4.9928098	0.205	0.70848197	17
soy_OGL_4435	1273	8.4435787	8.0125685	1879	23.95	8	6.2117472	0.22	0.62236685	26
soy_OGL_6206	1070	5.0835438	6.3551402	4474	24.39	6	12.680996	0.23999999	0.86838388	30
soy_OGL_946	1986	11.357085	1.510574	1001	26.33	9	13.484636	0.156	0.72098851	16
soy_OGL_2272	1431	12.386147	0	5113	25.85	9	10.253579	0.197	0.63077378	41
soy_OGL_5638	2000	9.2479429	0	1093	22.75	12	5.5799437	0.18799999	0.54553258	17
soy_OGL_956	1900	13.85167	0	5612	27.94	6	9.0945778	0.206	0.74670982	21
soy_OGL_655	1452	6.4309473	0	1700	22.52	6	2.9733	0.215	0.76075363	29
soy_OGL_4906	1700	9.0506868	0	7329	25	11	29.670212	0.148	0.88400781	9
soy_OGL_5543	1500	7.2413769	0	2941	22.2	9	7.4447684	0.222	0.76700002	17
soy_OGL_1149	1772	5.8387361	0	1899	28.89	10	26.27586	0.169	0.96020818	28
soy_OGL_2987	1822	12.134035	0	1001	30.46	7	4.9108949	0.169	0.81907791	26
soy_OGL_3324	1900	10.829322	0	1258	28.52	11	5.5002465	0.19599999	0.88138711	25
soy_OGL_5817	1300	12.84843	13.538462	4645	26.92	7	5.8378019	0.20200001	0.90278339	23
soy_OGL_40	1000	10.190989	16.6	5715	26.2	4	14.20615	0.26300001	0.88486665	29
soy_OGL_1931	1400	16.356848	14	6276	28.64	6	12.939448	0.28299999	0.55000001	26
soy_OGL_82	1432	8.729229	5.2374301	1001	29.39	5	11.795938	0.15800001	0.79870301	29
soy_OGL_299	1700	8.1388817	8.5294113	2508	26.88	8	15.568912	0.14300001	0.92008018	17
soy_OGL_3201	1276	8.3908644	7.8369908	3724	26.88	10	5.7195139	0.219	0.69198483	35
soy_OGL_5527	1319	11.696812	4.0940108	5312	26.3	9	12.411586	0.20200001	0.79223371	25

soy_OGL_6856	1427	8.4172974	5.1857042	1240	26.62	8	14.770067	0.185	0.83278	24
soy_OGL_5776	1543	14.783132	0	6303	29.22	11	5.8784475	0.20200001	0.83067805	41
soy_OGL_5294	1300	21.787222	0	8885	27.3	6	19.147211	0.20299999	0.73227441	24
soy_OGL_1186	1400	4.3006682	6.8571429	4515	25	10	15.216886	0.17399999	0.89479387	28
soy_OGL_1216	1525	6.7576227	2.3606558	2147	25.77	8	7.4939833	0.169	0.81401318	24
soy_OGL_2470	1746	4.5953841	0	2266	23.82	10	10.864722	0.161	0.90755594	20
soy_OGL_3295	1580	5.0341988	0	1001	26.2	8	14.481934	0.16599999	0.95464975	23
soy_OGL_1193	1600	4.0395017	0	5215	24.12	9	7.4830456	0.16	0.88280702	20
soy_OGL_4391	1700	9.4882059	0	4276	27.94	10	5.8044138	0.117	0.55370188	23
soy_OGL_222	1600	11.444668	0	2611	24.87	11	16.083366	0.169	0.83015913	24
soy_OGL_1378	1400	5.7269979	0	2291	25.64	7	9.1735535	0.176	0.79614574	35
soy_OGL_1459	1400	9.1846943	0	6012	24.21	10	9.5500946	0.193	0.92378813	30
soy_OGL_1473	1600	9.0376148	0	3357	24.75	10	18.634615	0.176	0.93824452	27
soy_OGL_3636	1310	7.1081796	0	2393	22.29	6	4.4873595	0.221	0.93074667	32
soy_OGL_4908	1254	14.910236	7.7352471	7871	22.56	12	12.496555	0.21600001	0.7835443	18
soy_OGL_4936	1400	9.3127365	0	6833	25.71	11	6.0647588	0.19	0.7620914	39
soy_OGL_5493	1522	5.1794319	0	2001	25.16	9	22.583601	0.17	0.85806131	32
soy_OGL_1223	1754	6.7576227	0	2559	19.95	9	49.374729	0.139	0.8052237	18
soy_OGL_4103	1498	12.218921	0	2001	23.49	8	6.8514585	0.186	0.69082654	20
soy_OGL_5011	1518	11.712706	4.5454545	1507	22.13	8	5.7659636	0.182	0.67687422	19
soy_OGL_1749	1700	13.638608	0	3814	28.11	10	4.0671563	0.15000001	0.97675323	16
soy_OGL_3014	1463	12.769964	2.8708134	2070	27.27	7	3.1969121	0.161	0.76422554	25
soy_OGL_3831	1299	7.7801862	14.626636	1375	24.32	11	7.7966967	0.19499999	0.54497015	28
soy_OGL_5791	1200	14.27938	4	2131	27.58	5	10.879172	0.19499999	0.85267484	41
soy_OGL_3838	1739	7.1014504	4.4278321	1340	27.77	9	23.524755	0.096000001	0.53477943	22
soy_OGL_1469	1300	9.5639515	0	3105	27.38	6	13.481956	0.20900001	0.92849171	29
soy_OGL_1834	1188	8.3344145	5.5555553	2001	25.92	8	10.222577	0.22400001	0.75626016	26
soy_OGL_6640	1300	6.8812695	0	1908	25	7	11.968531	0.219	0.98172808	20
soy_OGL_97	1200	10.343252	0	3367	27	7	6.575788	0.23800001	0.76231515	22
soy_OGL_4501	1143	8.7435341	0	9392	23.88	8	39.918571	0.25	0.73904324	34
soy_OGL_6435	1200	11.181879	0	2006	30	6	7.3432846	0.229	0.55387026	38

soy_OGL_933	1300	12.449766	2.6923077	3752	28.84	9	8.5663166	0.17900001	0.70899189	28
soy_OGL_1840	1379	7.2193756	0	5310	27.91	12	17.115499	0.193	0.74237406	29
soy_OGL_6311	1200	21.00876	4.5	6020	26.75	9	2.9941256	0.215	0.95765531	11
soy_OGL_2102	1568	4.9611359	0	1001	27.48	9	50.83025	0.162	0.97730732	7
soy_OGL_3186	1100	10.885145	0	2157	28.63	8	27.571529	0.236	0.66300845	24
soy_OGL_4096	1400	12.218921	2.3571429	2771	28.21	7	12.024877	0.16599999	0.66838092	21
soy_OGL_1449	1092	10.671152	0	1001	25.64	10	26.192881	0.25099999	0.9099195	33
soy_OGL_3938	1200	8.8798027	4.25	2760	26.25	5	32.472439	0.213	0.86465341	26
soy_OGL_897	1202	6.5197372	16.139767	1001	25.87	5	11.625068	0.20299999	0.67022425	29
soy_OGL_1891	1900	9.4963474	0	4330	27.63	6	4.0851679	0.20999999	0.66540259	15
soy_OGL_2309	1457	9.1589794	11.050103	5154	25.18	9	4.4801707	0.193	0.56254482	17
soy_OGL_2969	1300	10.693128	6.3076925	6661	27.38	5	15.245432	0.212	0.85286808	19
soy_OGL_5192	1700	13.332328	2.8823528	9318	28.64	5	7.7614179	0.228	0.95614535	16
soy_OGL_807	1600	7.4665518	0	2718	25.06	7	3.5585182	0.176	0.83027345	16
soy_OGL_1229	1400	9.0944204	3.2857144	6705	26.14	8	5.8535628	0.185	0.76903945	20
soy_OGL_2254	1195	5.5494199	5.9414225	6727	26.19	7	7.438005	0.20299999	0.65123415	28
soy_OGL_2398	1600	7.888226	5.125	2042	22.87	8	11.53441	0.17900001	0.63276494	8
soy_OGL_4389	1225	7.8134475	13.795918	5134	24.89	9	5.502368	0.199	0.5459218	24
soy_OGL_1568	1400	10.710433	0	10671	26.28	7	9.4952345	0.19	0.81468451	29
soy_OGL_2389	1700	7.888226	3.6470587	1996	23.47	8	10.984213	0.20200001	0.60639524	16
soy_OGL_3478	1148	6.0115023	12.543554	3924	24.3	6	21.881742	0.237	0.64653218	27
soy_OGL_5403	1800	9.4738331	4.0555553	7468	25.55	6	23.605164	0.22400001	0.74124229	14
soy_OGL_646	1600	6.6890612	0	8782	28.56	8	13.676594	0.13600001	0.75335336	29
soy_OGL_2413	1100	11.967738	6.818182	7079	27.18	5	4.8664331	0.199	0.70737737	32
soy_OGL_3465	1695	7.6505504	0	2001	22.83	6	21.826475	0.161	0.62451929	19
soy_OGL_3477	1324	6.0115023	10.574018	2093	25.3	6	21.881742	0.192	0.64641482	27
soy_OGL_5943	1644	9.668354	0	1001	24.45	5	3.3608844	0.168	0.72373074	23
soy_OGL_617	1600	3.2326741	0	3856	24.5	4	11.993151	0.17200001	0.69731438	23
soy_OGL_1287	1243	7.3108006	0	1846	20.35	3	12.023419	0.23199999	0.65707707	17
soy_OGL_6479	1546	9.90658	0	6944	21.86	7	12.281408	0.184	0.63825673	17
soy_OGL_810	1400	7.4636521	5.8571429	11504	26.28	6	2.4293113	0.183	0.81534374	13

soy_OGL_5757	1617	14.102677	7.544836	5374	26.4	4	7.9315591	0.18799999	0.76550341	13
soy_OGL_856	1778	7.1209521	3.9370079	1001	25.3	3	14.587191	0.183	0.59207219	15
soy_OGL_6816	1044	6.6239986	4.2145596	11680	25.86	4	5.139185	0.222	0.80393773	31
soy_OGL_1259	1200	10.150949	0	11702	24.08	6	8.8642483	0.204	0.71046054	20
soy_OGL_4225	1563	4.0722065	0	6125	23.22	9	25.866713	0.178	0.26471925	30
soy_OGL_6411	1200	10.411439	0	10198	23	6	22.232815	0.20299999	0.53197062	22
soy_OGL_5939	1054	29.346493	0	11020	25.99	3	9.7068291	0.223	0.72781634	25
soy_OGL_2277	1171	13.583581	0	9919	28.6	5	11.276885	0.167	0.62689447	42
soy_OGL_4237	1247	4.8173609	10.344828	1887	22.13	10	5.8866372	0.197	0.27516663	30
soy_OGL_5984	1500	6.6010385	3.5999999	2225	24.2	7	1.6019124	0.175	0.61301023	16
soy_OGL_1926	1455	12.936749	0	2001	23.98	7	23.861385	0.163	0.55659741	24
soy_OGL_4133	1200	10.342244	0	9720	25.66	6	4.6677389	0.19400001	0.8295548	32
soy_OGL_4711	1200	5.6724916	5.5	5305	22.91	7	5.0120363	0.20900001	0.58426142	33
soy_OGL_4723	1079	5.8001513	6.858202	2001	20.94	6	3.4519484	0.25099999	0.56475818	23
soy_OGL_5573	1255	8.6886683	10.916335	7504	25.65	7	7.0177703	0.146	0.70087737	22
soy_OGL_6257	1455	4.9920311	0	3418	23.02	3	54.334961	0.149	0.91602957	25
soy_OGL_1966	1400	8.2513695	0	3057	25.07	4	8.4801741	0.161	0.49247402	26
soy_OGL_2396	1700	7.888226	0	3262	22.7	7	12.171898	0.16	0.63163853	8
soy_OGL_4997	1150	8.6126404	0	8445	25.47	4	21.437262	0.175	0.70150781	25
soy_OGL_5671	1521	9.3411837	0	4468	25.9	5	2.409338	0.139	0.49166968	22
soy_OGL_6729	1357	7.3430734	5.6742816	7886	22.32	6	4.4309382	0.186	0.71465743	14
soy_OGL_3039	1404	24.358362	0	2435	28.13	4	9.4897022	0.14	0.68255317	12
soy_OGL_5649	1400	8.7322464	4	2864	27.64	6	17.070826	0.25400001	0.53255939	18
soy_OGL_6857	1022	8.4172974	7.436399	9205	25.53	6	17.724142	0.28	0.83427894	25
soy_OGL_689	1068	11.121198	5.4307117	7892	24.71	8	8.952796	0.233	0.80875576	21
soy_OGL_2690	1381	9.7915058	0	1634	25.99	8	5.4785938	0.18700001	0.4848986	21
soy_OGL_2755	1738	8.2878428	0	2587	23.87	12	20.797125	0.17	0.35998818	7
soy_OGL_4971	1496	10.245035	0	1895	27.47	5	4.5232167	0.178	0.73273623	16
soy_OGL_5032	1076	9.2836533	0	7350	28.34	6	3.105042	0.198	0.65925413	28
soy_OGL_4293	1549	3.9414778	4.64816	1001	23.95	10	37.817619	0.23	0.38988701	23
soy_OGL_683	1073	11.121198	0	4533	24.32	5	24.133003	0.23199999	0.79987979	20

soy_OGL_5758	1300	14.102677	0	4214	23.69	6	9.6564541	0.20999999	0.77022117	13
soy_OGL_2127	1134	9.2421608	0	13041	23.54	6	15.875431	0.226	0.8980397	17
soy_OGL_3118	1683	5.7961874	0	6509	27.15	7	6.0428939	0.20299999	0.52310932	15
soy_OGL_5410	1000	9.4738331	2.8	9998	25.3	4	6.5322752	0.264	0.74932504	14
soy_OGL_2308	1200	9.1589794	0	6977	26.83	8	4.9698634	0.197	0.56262845	17
soy_OGL_2617	1167	8.8686056	0	6388	27.84	6	17.240135	0.198	0.58431447	21
soy_OGL_4797	1300	13.341439	0	9214	29.61	5	2.1043279	0.155	0.91873628	13
soy_OGL_6665	1800	12.137495	0	6518	26.88	11	18.259581	0.20999999	0.006640886	25
soy_OGL_3870	1593	9.8148384	0	1496	24.79	9	31.50157	0.154	0.25208613	18
soy_OGL_4393	1400	8.2660208	0	1025	22.71	7	56.595776	0.17399999	0.55728877	21
soy_OGL_2312	1700	7.6951575	12.882353	2658	27	6	8.7960396	0.18799999	0.55369264	16
soy_OGL_1179	1228	4.3006682	9.5276871	8291	24.59	11	19.366291	0.175	0.90270722	29
soy_OGL_2519	1978	7.5373769	0	3349	26.03	15	10.490211	0.105	0.81674141	18
soy_OGL_3290	1217	3.2396839	0	2709	21.61	8	4.4979563	0.222	0.96122122	23
soy_OGL_3908	1539	9.3006687	2.7940221	2765	26.7	10	3.8139637	0.133	0.77437234	21
soy_OGL_6517	1302	6.1901021	0	2420	25.88	9	11.529434	0.171	0.69646817	31
soy_OGL_6906	1303	7.0806479	10.053722	2866	24.55	8	5.2735229	0.177	0.87494308	23
soy_OGL_1061	1500	4.5279164	0	5705	27	9	12.166699	0.13500001	0.86326623	24
soy_OGL_5571	1400	8.0406218	0	2705	24.07	9	5.7516785	0.186	0.70429885	22
soy_OGL_2157	1160	7.9192505	0	3367	21.63	7	16.173702	0.22	0.85018075	32
soy_OGL_3315	1220	16.56156	0	1906	23.03	9	9.6968203	0.211	0.90304148	21
soy_OGL_4698	1232	8.5891142	0	6153	21.02	10	13.5937	0.206	0.61331278	38
soy_OGL_5245	1300	8.810091	0	5460	24.07	9	8.039465	0.186	0.87631708	24
soy_OGL_6568	1283	5.9188476	0	2147	22.99	8	31.326372	0.20200001	0.77739948	35
soy_OGL_703	1300	10.043607	0	4190	22.3	8	3.6093464	0.207	0.839517	20
soy_OGL_6285	1220	6.7950077	10.819673	4326	24.01	11	8.1141291	0.192	0.940763	29
soy_OGL_1661	1227	8.7383938	0	1001	25.59	9	15.59867	0.226	0.61929423	17
soy_OGL_944	1100	12.186299	0	2209	22.27	11	46.609482	0.24699999	0.71859652	17
soy_OGL_22	1148	10.798586	0	5353	25.78	8	6.6288238	0.19	0.91686183	26
soy_OGL_404	1086	7.8474822	0	2001	23.11	11	4.5947714	0.23199999	0.74890542	24
soy_OGL_726	1208	9.7375937	0	1613	22.59	10	4.663909	0.23899999	0.86840457	20

soy_OGL_1215	1108	6.7576227	7.3104692	2424	23.73	10	8.9141979	0.226	0.81732857	24
soy_OGL_1443	1216	8.1389084	0	5310	24.75	13	9.776639	0.197	0.8987413	22
soy_OGL_2524	1655	13.994713	0	1001	26.16	10	7.1116385	0.13699999	0.80023211	8
soy_OGL_3753	1354	8.2278624	0	1001	24.66	11	9.3519583	0.182	0.76114452	25
soy_OGL_4159	1302	9.3938532	0	2611	23.88	9	7.7105131	0.199	0.90018761	16
soy_OGL_628	1230	4.6759496	2.6016259	2001	22.84	9	3.6059692	0.228	0.7145201	20
soy_OGL_708	1295	9.20959	0	1001	24.55	7	12.110048	0.191	0.8417111	19
soy_OGL_2670	1300	6.8734031	0	1514	24.46	11	5.2391539	0.20100001	0.51012588	21
soy_OGL_2864	1468	5.7699661	2.520436	2758	25.06	10	28.640602	0.141	0.78492999	14
soy_OGL_3026	1379	11.296754	0	2264	25.96	7	10.63604	0.16599999	0.74915743	19
soy_OGL_425	1299	14.106673	0	4106	24.78	11	5.8134623	0.2	0.69144601	24
soy_OGL_2291	1133	11.585636	0	2001	22.41	12	11.487501	0.23999999	0.61189693	31
soy_OGL_4912	1109	14.602632	0	3616	22.45	12	18.128496	0.22	0.78218204	21
soy_OGL_6254	1205	5.2737613	0	3254	23.31	7	22.261189	0.206	0.91444069	24
soy_OGL_6413	1273	10.411439	0	1001	23.33	8	7.0011039	0.213	0.53533709	25
soy_OGL_6900	1108	7.0806479	0	4915	23.91	6	9.3049116	0.21699999	0.86899519	27
soy_OGL_1405	1360	14.723554	0	3306	28.52	8	5.667027	0.154	0.83105373	20
soy_OGL_2615	1330	8.5876789	0	2996	25.78	13	16.209997	0.18099999	0.58926576	23
soy_OGL_6660	1235	17.215902	2.3481781	1813	26.07	16	4.2303538	0.19599999	0.002666903	22
soy_OGL_5843	1181	12.328249	0	5501	25.82	8	36.722652	0.184	0.97315091	20
soy_OGL_5863	1300	9.285593	0	3306	24.92	8	41.887978	0.17399999	0.93233162	23
soy_OGL_1932	1148	17.325855	0	1334	24.82	7	8.1240606	0.18000001	0.54847401	25
soy_OGL_3836	1372	7.0545988	2.3323615	2001	22.3	12	42.119957	0.17	0.5358541	22
soy_OGL_268	1400	6.2561297	0	3695	25.28	5	10.540352	0.14300001	0.88677537	18
soy_OGL_6650	1501	13.28592	0	3734	25.84	8	2.8012803	0.15899999	0.72992665	12
soy_OGL_731	1227	9.9175148	5.6234717	4782	21.18	7	9.1223621	0.19499999	0.88281369	12
soy_OGL_770	1400	11.245727	0	5342	25.78	6	8.1027832	0.15700001	0.96266407	16
soy_OGL_891	1249	7.4788356	5.6845474	2001	22.49	7	4.157496	0.20200001	0.66306585	25
soy_OGL_954	1190	14.275198	0	4839	21.26	5	10.377754	0.19599999	0.74629205	21
soy_OGL_4092	1255	12.218921	2.4701195	2203	21.19	8	5.1435637	0.22400001	0.66042835	17
soy_OGL_5402	1233	9.4738331	0	3510	20.03	8	12.955996	0.221	0.73651093	19

soy_OGL_6760	1300	9.6407576	0	3872	25.61	5	7.1461368	0.167	0.74136984	30
soy_OGL_6898	1151	7.0806479	0	7594	22.41	6	9.3049116	0.211	0.86892676	27
soy_OGL_4368	1500	7.6906767	4.1999998	1382	27.2	9	10.28589	0.134	0.51578784	22
soy_OGL_1941	1300	15.018729	0	5066	24.3	7	18.81238	0.16	0.53944802	21
soy_OGL_465	1200	5.5066857	0	6531	19.66	5	6.1500635	0.20999999	0.55005854	20
soy_OGL_2318	1202	8.2685928	0	4148	23.21	4	4.280601	0.169	0.53889823	20
soy_OGL_3357	1500	11.131104	0	9568	23.26	7	20.024742	0.13699999	0.82221198	14
soy_OGL_3463	1500	7.6505504	0	3755	25.33	6	19.756832	0.13	0.62401205	19
soy_OGL_5931	1339	5.5747819	0	9932	24.42	8	28.247995	0.134	0.74231124	19
soy_OGL_2236	1300	8.8189211	8.9230766	2325	26.53	7	12.257002	0.139	0.69955504	19
soy_OGL_539	1112	10.749329	0	1001	24.91	8	12.453653	0.23	0.36184362	18
soy_OGL_6458	1188	5.8666077	0	2001	23.4	9	3.6394033	0.243	0.58490509	21
soy_OGL_3158	1200	11.004972	0	3273	24.41	9	40.78677	0.204	0.60185957	19
soy_OGL_6454	1042	5.9874048	0	12472	25.14	8	4.3669896	0.211	0.57976997	20
soy_OGL_3851	1174	9.9024754	0	4583	24.78	10	26.979399	0.19499999	0.28717643	14
soy_OGL_776	1241	8.9971619	0	7333	26.18	7	2.3860292	0.189	0.94263279	17
soy_OGL_2699	1294	3.3123655	0	4203	24.11	10	8.1143932	0.207	0.46781489	20
soy_OGL_2865	1341	5.7699661	8.6502609	4151	24.68	9	29.292818	0.169	0.78534502	14
soy_OGL_3494	1242	4.7162509	0	3920	24.23	10	9.9185019	0.19	0.66133243	18
soy_OGL_174	1222	2.1532793	0	6331	21.11	8	3.5154796	0.226	0.76762164	12
soy_OGL_4782	1000	3.5324056	0	5279	21.5	5	10.622014	0.228	0.88703412	8
soy_OGL_3127	1211	6.2185674	0	3713	22.79	7	5.786746	0.21699999	0.55039656	26
soy_OGL_4430	1204	8.8796873	0	1001	23.17	5	24.603594	0.205	0.61546057	23
soy_OGL_4966	1200	10.245035	0	2287	23	7	7.0597391	0.215	0.73615664	16
soy_OGL_4189	1199	5.2657661	0	2001	20.76	9	6.6340551	0.227	0.20068316	20
soy_OGL_5408	1200	9.4738331	0	3596	21.33	5	5.5766711	0.208	0.74830085	14
soy_OGL_3251	1200	9.1212559	0	5946	29	9	23.694427	0.146	0.74554712	20
soy_OGL_328	1200	9.5832195	0	9374	27.83	6	8.8795881	0.16	0.88270271	21
soy_OGL_5968	1435	7.5982332	0	2001	27.03	6	10.82803	0.133	0.66071427	15
soy_OGL_540	1268	10.749329	0	2773	26.02	8	12.453653	0.171	0.36175677	18
soy_OGL_2719	1220	5.8336949	0	2001	23.6	7	28.104492	0.177	0.44329301	25

soy_OGL_5369	1213	7.7868629	0	4157	23.16	5	6.8458424	0.197	0.62398654	14
soy_OGL_2583	1100	4.336894	0	1159	25.36	9	47.462925	0.17299999	0.65750349	14
soy_OGL_3366	1246	11.584485	0	3364	26	6	34.86425	0.149	0.78166819	10
soy_OGL_621	1263	2.9936664	14.885194	2545	23.19	7	5.3584714	0.17399999	0.70257962	21
soy_OGL_937	1600	12.449766	4.625	6119	31.43	9	8.8706217	0.16500001	0.70952243	28
soy_OGL_1844	1700	5.552063	7.2941175	2837	30.35	11	40.222153	0.204	0.73767209	25
soy_OGL_3187	1407	10.885145	0	2609	31.62	9	24.406136	0.20299999	0.66367674	24
soy_OGL_216	1368	12.907678	0	4668	31.5	7	7.8842735	0.153	0.822972	28
soy_OGL_1106	1100	6.4156709	0	8651	31.36	10	57.908276	0.20900001	0.94480926	18
soy_OGL_2622	1110	8.794776	0	4063	30.45	9	34.222958	0.235	0.58293706	27
soy_OGL_5281	1200	10.296659	0	2158	30.25	6	24.973972	0.177	0.75287193	23
soy_OGL_4431	1200	8.4435787	5.3333335	4720	33.58	11	47.837044	0.234	0.61830473	25
soy_OGL_5855	1029	8.370719	22.837706	1001	27.3	9	50.299286	0.26800001	0.94616836	18
soy_OGL_72	1315	10.445262	0	1001	35.43	9	50.04269	0.126	0.81300002	28
soy_OGL_5799	1200	12.976668	0	5307	33.41	8	16.874744	0.19	0.85868526	37
soy_OGL_5336	1600	32.314224	7.25	3002	37.93	9	27.790663	0.19	0.55490851	10
soy_OGL_3157	1100	11.004972	19.09091	2073	30.27	8	45.327625	0.241	0.60180748	19
soy_OGL_44	2067	10.198316	2.322206	2587	35.26	6	4.7227583	0.156	0.87522018	32
soy_OGL_301	1800	10.392898	19.666666	2669	27.88	12	20.919281	0.191	0.9267773	9
soy_OGL_2146	1200	7.0482421	14.916667	2678	27.5	10	13.979856	0.234	0.85609633	28
soy_OGL_3763	2000	10.661443	11.85	4828	32.6	11	16.785376	0.237	0.74256653	19
soy_OGL_7001	1276	6.3244863	18.730408	6850	26.56	12	19.719011	0.21699999	0.96398813	15
soy_OGL_5960	1810	8.7810621	9.6685085	2210	31.49	8	17.499907	0.153	0.68224436	19
soy_OGL_205	1091	11.890499	15.307057	2576	29.42	5	6.9146829	0.199	0.81225026	28
soy_OGL_5316	1325	12.163104	14.18868	5488	28.52	9	4.2835188	0.192	0.67298168	27
soy_OGL_3826	1200	7.7698202	18.916666	4001	27.25	9	15.207882	0.22499999	0.55207294	27
soy_OGL_1139	1639	5.5214667	8.1147041	1892	28.98	11	15.486933	0.154	0.97614914	26
soy_OGL_4960	1251	9.81145	9.9920063	1734	28.77	10	8.1921511	0.19599999	0.74728984	30
soy_OGL_1727	1300	28.425341	15.538462	2449	36.61	10	11.559277	0.149	0.84906507	24
soy_OGL_5537	1481	8.6176863	16.610399	2482	31.33	8	23.986822	0.212	0.78247964	26
soy_OGL_2152	1325	6.5589557	14.113208	5188	30.41	9	17.822592	0.16	0.85169148	32

soy_OGL_5419	1700	10.443309	19.294117	2572	27.35	13	26.948494	0.18099999	0.95728868	10
soy_OGL_5492	1571	5.1794319	10.884787	1844	31.38	8	32.447323	0.164	0.85977507	34
soy_OGL_5778	1250	14.783132	13.2	2001	32.48	8	6.8770123	0.189	0.83475465	42
soy_OGL_6930	1711	8.8029718	4.266511	1001	31.15	13	32.54488	0.134	0.90344405	27
soy_OGL_3805	1569	8.2365665	20.267687	3198	26.64	11	17.248466	0.18000001	0.61470091	12
soy_OGL_3601	1409	4.7934084	19.517387	3159	31.22	9	45.704678	0.148	0.86788118	23
soy_OGL_49	1150	10.004758	11.565217	2001	29.3	8	9.1196051	0.18700001	0.85947573	28
soy_OGL_34	1658	9.8391256	0	2001	30.75	10	10.288862	0.111	0.89352119	32
soy_OGL_360	1348	7.2958274	9.3471813	4349	28.11	11	15.298789	0.15899999	0.82928586	28
soy_OGL_1073	1400	7.9827704	17.071428	2218	25.78	10	23.961641	0.141	0.8834011	13
soy_OGL_1157	1500	8.7633495	11.133333	1025	25.73	13	12.225442	0.18000001	0.9506579	22
soy_OGL_4937	1300	9.3127365	5.4615383	2202	29.38	9	7.0648017	0.176	0.76133418	37
soy_OGL_5825	1200	16.034658	14.833333	2129	27.58	8	3.3637316	0.193	0.91771138	18
soy_OGL_2154	1200	6.6362858	6	8648	31.83	8	15.850225	0.12800001	0.85150456	32
soy_OGL_3580	1500	6.0902267	7.5999999	3629	31.13	12	25.908348	0.13600001	0.84527475	37
soy_OGL_4432	1445	8.4435787	19.16955	1001	30.72	10	30.995899	0.088	0.62058508	26
soy_OGL_1752	1700	13.638608	0	2216	32	13	13.292564	0.28999999	0.97405845	22
soy_OGL_4439	1124	8.9722738	0	2400	32.74	8	18.83721	0.25299999	0.62871343	26
soy_OGL_1094	1180	8.3440781	11.271187	1001	27.54	10	20.543207	0.20900001	0.92727911	16
soy_OGL_5010	1200	11.712706	8.666667	2849	29.75	10	9.6263027	0.20200001	0.67774153	20
soy_OGL_5230	1235	10.238331	10.769231	2611	28.66	10	18.374521	0.2	0.91396743	20
soy_OGL_5524	1569	11.696812	0	1001	32.31	11	9.8548536	0.14300001	0.79331034	25
soy_OGL_6563	1287	5.9188476	0	1479	32.09	12	17.382736	0.205	0.77223939	38
soy_OGL_3360	1305	13.791044	5.0574713	9304	31.87	10	4.8050876	0.17	0.80802178	14
soy_OGL_1439	1500	8.1389084	0	3842	34.53	10	34.019161	0.16599999	0.8959735	26
soy_OGL_6545	1581	15.158372	4.5540795	1862	34.85	12	11.727743	0.20999999	0.75098234	31
soy_OGL_4980	1253	13.183422	0	1001	33.28	8	26.685205	0.2	0.71487886	22
soy_OGL_3925	1500	8.1360826	8.6000004	1859	32.53	6	27.611574	0.155	0.84374577	21
soy_OGL_2403	1034	11.483459	21.470018	3472	26.49	6	13.173924	0.23	0.68963766	18
soy_OGL_3903	1410	9.3006687	0	3204	32.76	7	20.078566	0.15899999	0.76407689	18
soy_OGL_1539	1200	7.7790313	6.75	5156	28.75	12	11.322295	0.17	0.88109523	37

soy_OGL_2899	1085	8.9753227	0	2924	34	10	40.372707	0.18099999	0.89301062	13
soy_OGL_4470	1150	7.0369272	0	2885	30.52	11	17.703436	0.161	0.70278156	24
soy_OGL_3991	1235	11.197123	0	1632	28.17	15	11.906651	0.178	0.83553845	12
soy_OGL_4902	1223	9.0506868	0	2158	30.08	12	20.990297	0.169	0.89206266	12
soy_OGL_247	1038	16.376354	0	8541	32.65	9	8.0692682	0.154	0.86018187	22
soy_OGL_4477	1203	7.9795275	0	2001	33.99	8	22.023218	0.118	0.71051502	29
soy_OGL_76	1000	9.6598225	0	1168	32.9	6	18.723602	0.13500001	0.802297	28
soy_OGL_3334	1000	12.770006	0	11491	35.2	7	3.9050553	0.12800001	0.86353916	29
soy_OGL_6432	1000	10.893449	0	3036	32.4	6	4.2135592	0.134	0.55017334	35
soy_OGL_6815	1000	6.6239986	0	2143	34.5	7	40.231842	0.13	0.80344462	29
soy_OGL_6234	1100	6.2574277	0	5519	31.63	6	28.58453	0.12800001	0.89782405	19
soy_OGL_2165	1235	8.802146	14.65587	1421	25.99	6	24.490053	0.223	0.83209014	30
soy_OGL_4829	1700	17.834297	8.2352943	2994	29.41	7	16.096285	0.213	0.97760552	17
soy_OGL_5476	2078	4.9895315	12.030799	1003	30.51	7	36.062157	0.25299999	0.86877412	28
soy_OGL_1444	1215	10.803866	16.872429	8384	26.58	9	37.053978	0.192	0.9028607	23
soy_OGL_5295	1500	23.831551	0	5736	29.46	6	10.752457	0.211	0.72823781	26
soy_OGL_5635	1240	24.815081	19.112904	4435	23.38	10	13.352768	0.21699999	0.59821838	12
soy_OGL_5842	1800	13.472019	3.4444444	3727	29.61	8	38.247566	0.197	0.97158295	21
soy_OGL_3944	1182	26.245321	11.167513	1001	30.54	7	4.525774	0.20999999	0.87856287	25
soy_OGL_1583	1174	7.7159863	23.253834	1308	23.76	8	50.463409	0.241	0.78493607	21
soy_OGL_6558	1817	11.084569	0	7648	28.17	10	75.808235	0.116	0.76223868	36
soy_OGL_6559	1200	11.084569	24.833334	1037	28.25	9	82.140694	0.198	0.76281786	37
soy_OGL_4560	1450	8.4823227	11.172414	4652	28.48	7	22.48382	0.148	0.80415624	24
soy_OGL_2283	1200	12.293853	10.583333	7844	28.91	4	28.818199	0.208	0.62481987	40
soy_OGL_4145	1400	12.646983	6.1428571	10241	28.92	6	36.28157	0.16599999	0.85781968	29
soy_OGL_1145	1272	5.8387361	31.839622	2030	29.4	7	76.224312	0.21799999	0.97035962	28
soy_OGL_3252	1175	8.2854548	20.510639	2001	22.63	13	24.970791	0.208	0.74876106	18
soy_OGL_1243	1205	10.032667	9.6265564	2001	25.14	10	28.797318	0.205	0.74807531	26
soy_OGL_5539	1400	8.6397324	5.7142859	1889	24.85	8	46.8521	0.161	0.78138316	24
soy_OGL_5622	1258	29.539919	0	4722	25.11	8	9.5303583	0.17	0.62194091	25
soy_OGL_6748	1283	26.298864	0	6412	27.2	8	7.0091677	0.149	0.73523295	28

soy_OGL_1753	1769	14.60705	1.5828152	6121	32.78	10	18.770798	0.071000002	0.97070879	22
soy_OGL_3947	1400	28.647972	9.0714283	1233	27.85	11	13.788262	0.175	0.88605875	21
soy_OGL_6746	1069	25.512024	9.5416279	3513	27.4	8	16.638861	0.17900001	0.73383063	26
soy_OGL_2279	1400	13.583581	0	1842	30.5	3	33.880493	0.104	0.62604129	42
soy_OGL_3940	1494	8.8798027	0	3978	29.71	9	24.416506	0.156	0.86917102	27
soy_OGL_1758	1533	17.394621	3.3268101	2001	26.28	9	47.20163	0.183	0.95834631	12
soy_OGL_5785	1315	14.565392	8.4410648	3879	32.39	7	34.171482	0.27599999	0.84641516	36
soy_OGL_5844	1539	12.328249	2.9889538	5397	31.77	8	36.722652	0.17399999	0.97326195	20
soy_OGL_5436	1209	5.0888424	21.670803	2256	27.95	13	90.463257	0.17399999	0.95932567	17
soy_OGL_5831	1500	13.992782	2	5023	34.26	9	38.183407	0.105	0.9514938	24
soy_OGL_4919	1200	16.032492	4.1666665	2893	28.66	9	30.512001	0.18000001	0.77848303	24
soy_OGL_5286	1312	17.88682	0	2001	30.79	11	46.828823	0.17200001	0.73903656	22
soy_OGL_5858	1203	8.5508003	14.713217	2596	27.51	8	60.360092	0.19	0.94532144	19
soy_OGL_5274	1200	7.2467418	28.916666	3282	29.08	11	81.809593	0.213	0.78115243	18
soy_OGL_6802	1300	4.8344703	5.5384617	11501	35.76	10	116.29536	0.264	0.78607023	23
soy_OGL_1944	1300	23.406984	6.4615383	2197	25.76	8	82.207191	0.183	0.53126621	20
soy_OGL_3321	1692	10.753889	3.250591	1001	31.5	10	107.22443	0.096000001	0.88707376	22
soy_OGL_4863	2078	5.5955515	11.260828	2482	26.32	14	177.73097	0.103	0.94414884	17
soy_OGL_6798	1478	4.8344703	0	2790	32.88	9	125.64165	0.227	0.78560317	21
soy_OGL_984	1400	5.7834659	0	1724	23.35	10	182.72876	0.156	0.77047783	32
soy_OGL_1608	1015	83.521873	0	1001	40.68	10	24.02816	0.14399999	0.46135715	2
soy_OGL_4865	1117	5.5955515	16.56222	1569	25.78	14	178.18713	0.153	0.94383287	18
soy_OGL_6541	1000	16.022715	4.6999998	1360	28.9	7	10.903463	0.206	0.7467739	31
soy_OGL_1222	1800	6.7576227	0	6359	31.61	10	44.534256	0.068000004	0.80539036	18
soy_OGL_1487	1446	7.653698	19.571232	4036	28.35	9	32.989323	0.191	0.96530658	25
soy_OGL_6752	1042	10.014749	22.648752	1001	29.07	5	29.763126	0.17200001	0.7375499	31
soy_OGL_2974	1500	11.380832	8.9333334	1812	26.86	11	9.6719522	0.146	0.83513194	22
soy_OGL_4987	1179	11.451385	15.267176	3138	26.12	9	7.1093616	0.191	0.70707887	26
soy_OGL_2626	1655	8.794776	1.8126888	2158	32.2	7	29.07687	0.104	0.57887065	24
soy_OGL_4390	1162	9.0853081	9.552496	2520	26.07	7	39.593479	0.197	0.54873776	25
soy_OGL_4956	1426	12.134647	2.6647966	1001	28.96	7	9.5070124	0.12800001	0.75129551	33

soy_OGL_6567	1300	5.9188476	7.7692308	3690	26.92	12	26.427982	0.15899999	0.77599227	35
soy_OGL_4640	1163	19.479895	3.783319	2001	23.64	8	17.870893	0.198	0.73242396	35
soy_OGL_1488	1240	7.653698	2.983871	2001	27.25	9	32.563332	0.154	0.96628416	24
soy_OGL_1745	1500	13.638608	0	1401	28.13	10	26.047308	0.156	0.98175651	16
soy_OGL_1904	1000	23.127859	0	3007	27.3	11	10.46974	0.229	0.62502271	13
soy_OGL_5629	1154	24.815081	0	4732	26.6	10	12.266418	0.198	0.60422397	15
soy_OGL_1584	1153	7.7159863	0	3538	30.78	10	50.972351	0.127	0.7827152	20
soy_OGL_3320	1000	14.816146	0	1264	35.4	13	90.615463	0.096000001	0.88917512	21
soy_OGL_1144	1300	5.8387361	0	2138	28.53	8	67.162964	0.13500001	0.97058332	28
soy_OGL_306	1134	9.9048204	0	1059	31.48	17	118.50684	0.121	0.95051646	11
soy_OGL_6556	1000	13.347547	9.3000002	2102	31.2	9	83.50206	0.12800001	0.76120448	35
soy_OGL_1221	1100	6.7576227	2.5454545	6069	27.63	9	48.032593	0.147	0.80547369	18
soy_OGL_2687	1362	10.232581	0	4001	26.57	9	43.916771	0.138	0.48897204	27
soy_OGL_6684	1000	7.6147938	0	3760	31.6	5	33.679317	0.39899999	0.022044996	20
soy_OGL_6366	1428	1.3764535	0	4002	25.7	2	11.206637	0.25600001	0.65140307	6
soy_OGL_508	1154	4.4821186	0	9572	28.76	5	9.064846	0.19400001	0.45920476	23
soy_OGL_2058	1556	3.071409	0	2591	26.86	3	11.486713	0.147	0.56546468	11
soy_OGL_3844	1036	6.4413486	13.706564	4254	24.22	5	7.939734	0.227	0.52423882	16
soy_OGL_3072	1200	2.1047292	0	17331	30.83	1	10.89752	0.182	0.21079473	8
soy_OGL_5692	1434	1.4749078	4.3235703	11276	27.96	3	12.127497	0.292	0.40471646	14
soy_OGL_2799	1100	0.8990916	0	10581	27.81	2	12.59503	0.215	0.321641	10
soy_OGL_2803	1314	0.8990916	0	5838	26.1	4	16.465038	0.162	0.32545862	10
soy_OGL_5111	1100	13.015882	0	8991	29.63	5	5.3147578	0.213	0.32987463	11
soy_OGL_6005	1233	3.4906964	10.705596	2091	25.54	4	20.387768	0.185	0.53657484	13
soy_OGL_6372	1197	1.5219625	0	12485	25.22	3	8.0259056	0.212	0.48225969	2
soy_OGL_4088	1600	7.4914689	17.75	4986	27.25	5	10.883198	0.19400001	0.5775556	10
soy_OGL_6691	1782	8.4025631	8.4736252	3855	28.78	11	4.4153371	0.146	0.029998349	17
soy_OGL_529	1893	11.005226	14.315901	3818	29.31	9	7.9638166	0.17399999	0.38518468	11
soy_OGL_632	1700	5.6276793	8.4117651	1888	30.05	5	12.342882	0.123	0.72085482	16
soy_OGL_4386	1200	5.5947452	21.833334	5759	26	8	15.917703	0.20200001	0.53932261	21
soy_OGL_4395	1500	8.5982914	14.733334	8191	30.2	8	12.647203	0.153	0.55850673	22

soy_OGL_4048	1902	0.37265155	2.3659306	8391	31.49	3	6.6009517	0.119	0.40586537	14
soy_OGL_4057	1586	0.30725217	15.636822	34713	32.72	1	0.00422008	0.329	0.35691592	3
soy_OGL_1629	1394	3.0774791	11.836442	16803	28.19	3	2.8619728	0.17399999	0.49110419	9
soy_OGL_2051	1468	3.2522252	6.3351498	12476	27.72	4	4.5665679	0.14300001	0.49432173	10
soy_OGL_2792	1700	4.0242782	11.705882	2924	27.47	5	11.023542	0.16	0.1984091	6
soy_OGL_3400	1465	2.8159552	8.6689425	8467	28.12	3	5.0092673	0.167	0.67519975	14
soy_OGL_4759	1464	0.84740651	3.0737705	37266	35.1	1	0.9351781	0.13600001	0.74138021	5
soy_OGL_5109	2052	8.5575886	0	5107	32.06	4	10.101892	0.107	0.29584822	8
soy_OGL_5118	1176	4.8253789	16.156462	18978	28.23	3	4.3623548	0.221	0.38037598	13
soy_OGL_5755	1604	6.5565777	4.3017454	12696	31.54	3	4.0766273	0.103	0.76008183	15
soy_OGL_6029	1724	2.8787286	5.6844549	15786	32.07	3	3.2936881	0.125	0.38144389	15
soy_OGL_6066	2639	1.6618187	0	11016	36.15	3	24.153093	0.103	0.043490358	12
soy_OGL_6704	1411	0.14302784	0	31432	32.45	1	0.000596684	0.090999998	0.49384439	6
soy_OGL_109	1200	14.638623	12.416667	11534	30.91	4	5.3531904	0.186	0.72748482	12
soy_OGL_6006	1000	3.6136997	23.5	16162	29	5	22.333427	0.12800001	0.53308672	14
soy_OGL_4717	1377	5.4552517	2.5417573	9680	30.42	7	8.5509129	0.117	0.5789296	27
soy_OGL_4317	1300	2.6951132	18.384615	2082	26	9	23.151396	0.164	0.42399639	22
soy_OGL_5343	1214	3.0400639	20.510708	2837	22.24	6	6.8308029	0.18799999	0.5146516	8
soy_OGL_5730	1172	1.4187498	16.12628	4754	22.69	3	3.9451611	0.19499999	0.6242941	5
soy_OGL_5734	1100	4.9724145	10.181818	14155	29	1	0.72414768	0.122	0.65976024	8
soy_OGL_880	1400	2.4722638	2	7528	27.28	4	2.5074496	0.242	0.62676257	9
soy_OGL_1313	1300	2.0239863	9	10702	26.15	5	1.9771914	0.28600001	0.59677047	10
soy_OGL_3139	1133	8.3777838	5.2956753	12750	33.18	4	7.6506586	0.27700001	0.55964422	27
soy_OGL_2726	1224	6.5523348	14.787581	1690	26.63	6	5.4361005	0.185	0.42843196	14
soy_OGL_2727	1119	6.5671282	0	6515	29.75	6	5.1866846	0.23100001	0.42724779	13
soy_OGL_3401	1000	2.4752502	0	9349	27.5	5	10.338584	0.22499999	0.67169124	7
soy_OGL_4260	1400	2.2741857	3.9285715	1052	26.92	7	6.3465176	0.192	0.33033934	13
soy_OGL_5670	1100	9.3411837	0	4862	31.36	4	0.93493617	0.21600001	0.49256706	20
soy_OGL_3117	1334	5.7961874	2.0989506	2001	27.66	5	6.1374922	0.177	0.52198392	14
soy_OGL_4300	1864	4.1622143	4.4527898	10913	37.33	6	25.384022	0.20200001	0.39710474	27
soy_OGL_1992	1300	6.3401136	0	6802	33.53	7	20.061733	0.14300001	0.45751947	21

soy_OGL_2691	1021	9.7915058	9.108717	5715	29.97	7	6.0560789	0.185	0.48476851	21
soy_OGL_869	1629	1.0942405	0	4177	32.96	3	45.86763	0.192	0.57842129	9
soy_OGL_1299	1000	0.3178266	0	8849	26.5	2	5.7821312	0.285	0.51957369	2
soy_OGL_2007	1900	3.0006773	9.2631578	12194	34	3	29.05121	0.16500001	0.39754546	8
soy_OGL_2363	1442	9.6849852	0	8522	32.8	7	18.104433	0.14	0.12819532	8
soy_OGL_2773	1693	6.3025274	2.0673361	7083	29.65	5	1.7178241	0.142	0.29779372	6
soy_OGL_2793	1876	2.9072554	10.341151	1001	28.03	8	20.476891	0.18099999	0.1889414	5
soy_OGL_3424	1371	0.84260994	0	18154	30.7	2	1.8516887	0.19	0.40849674	5
soy_OGL_3842	1300	7.3592849	9.1538458	10474	30.07	5	4.3533444	0.20299999	0.52617598	17
soy_OGL_5080	1648	11.109388	0	1001	32.22	4	5.7465529	0.153	0.40472585	5
soy_OGL_5687	1200	1.4495741	14.083333	3129	26.5	6	33.138809	0.222	0.42821839	5
soy_OGL_6036	1727	0.88451302	2.6635785	6975	26.46	6	2.7673166	0.207	0.32278943	5
soy_OGL_6375	1146	0.28626621	18.411867	12891	24.86	1	1.0485927	0.237	0.32021081	1
soy_OGL_6695	1100	7.2336855	10.272727	3811	24.45	7	3.5120587	0.266	0.03736873	6
soy_OGL_6700	1651	0.69440275	0	9480	29.55	1	0.57246935	0.152	0.072106726	4
soy_OGL_867	1165	1.0942405	3.3476396	4055	27.55	2	6.4525518	0.222	0.57472658	7
soy_OGL_1621	1200	1.5494736	3.4166667	6709	26.66	4	5.5125756	0.21600001	0.41322336	7
soy_OGL_2328	1300	8.2941523	0	4150	31.84	3	2.2685249	0.132	0.51738071	15
soy_OGL_2357	1000	2.8688939	0	20524	34.2	2	9.7808437	0.14399999	0.19527982	8
soy_OGL_2772	1300	5.8838282	0	2180	29.23	6	8.2920771	0.186	0.29973078	6
soy_OGL_5721	1070	4.7354045	0	3675	28.13	1	0.035494115	0.259	0.4811756	7
soy_OGL_6094	1017	0.54288405	0	24121	29.99	4	1.8975407	0.142	0.65213758	8
soy_OGL_6378	1386	1.438513	5.2669554	4755	28.64	3	18.919813	0.134	0.18688558	2
soy_OGL_129	1182	1.4927685	10.913706	13613	26.39	2	0.88605857	0.24600001	0.59630328	9
soy_OGL_635	1300	5.2757597	0	14344	31.07	4	8.1170998	0.171	0.72435832	15
soy_OGL_1302	1014	1.5215753	0	35138	33.03	1	3.5079961	0.24600001	0.57009238	8
soy_OGL_2810	1500	0.41487023	0	9776	26.6	4	0.063233674	0.178	0.39079705	6
soy_OGL_3074	1200	0.57695127	6.25	25102	29.83	1	0.19895983	0.205	0.2197299	9
soy_OGL_3408	1424	2.4633574	13.202248	5253	26.26	5	18.27726	0.169	0.64278692	5
soy_OGL_3892	1580	0.8433677	0	13530	27.78	6	8.818634	0.20200001	0.57351005	6
soy_OGL_3897	1661	1.5956808	0	14629	29.86	3	1.95819	0.134	0.65350461	4

soy_OGL_4055	1800	0.25916085	0	4102	26.72	4	4.1910543	0.16599999	0.37820384	7
soy_OGL_5717	1300	7.9770703	6	14930	30.3	4	3.8798249	0.20999999	0.46353993	7
soy_OGL_6046	1750	1.461244	0	8123	29.71	1	9.5818462	0.13500001	0.19821939	10
soy_OGL_6098	1210	0.58113271	0	29007	33.05	4	9.8620348	0.13500001	0.65837389	11
soy_OGL_6386	1400	1.0395986	3.7857144	34885	32.42	2	1.8399013	0.17299999	0.34157547	4
soy_OGL_142	1052	1.3519406	0	26545	29.84	1	3.0468192	0.131	0.65349132	5
soy_OGL_1296	1007	0.3178266	0	32375	30.78	1	3.4559839	0.114	0.48561561	3
soy_OGL_2839	1000	5.5548873	0	15726	33.1	2	7.4029689	0.139	0.66804922	23
soy_OGL_4743	1400	0.54586262	0	11645	26.85	3	4.4792137	0.17	0.34115481	2
soy_OGL_4751	1400	0.12056544	0	12576	27.5	2	1.1733493	0.141	0.45586199	1
soy_OGL_5105	1300	9.3550339	0	17395	30.92	7	1.3406783	0.15000001	0.28485504	7
soy_OGL_5702	1350	0.11315778	0	16717	29.55	4	0.72006541	0.107	0.3819854	8
soy_OGL_6086	1078	0.40784842	0	23611	29.12	3	3.6954246	0.13	0.41788122	3
soy_OGL_6707	1000	0.14302784	0	26661	29.5	2	3.0458267	0.14	0.49588597	6
soy_OGL_872	1200	1.0942405	9.833333	3917	22.75	3	3.2151723	0.2	0.5879547	8
soy_OGL_3411	1005	2.4898665	0	6627	24.17	3	1.4286149	0.21699999	0.60979092	5
soy_OGL_4252	1204	9.7208376	0	8338	26.82	10	9.574605	0.19	0.31040198	11
soy_OGL_4256	1276	9.2218924	0	5229	26.33	9	10.72535	0.19499999	0.3120949	10
soy_OGL_482	1273	5.5002999	0	8328	28.12	7	7.5859642	0.145	0.51413184	20
soy_OGL_1646	1192	7.0483088	3.1879194	2001	27.93	4	12.103205	0.156	0.59027344	21
soy_OGL_4324	1177	2.2446182	0	5678	25.31	7	3.2430685	0.16	0.43787229	19
soy_OGL_4182	1200	14.989739	0	2686	30.25	10	7.7673149	0.146	0.18143567	16
soy_OGL_2029	1000	0.99519539	0	9411	25.6	2	10.61917	0.12899999	0.26690584	2
soy_OGL_4730	1763	4.8687081	0	2815	26.99	6	2.4621842	0.077	0.53954488	10
soy_OGL_2758	1292	3.639648	0	2001	31.26	8	26.164396	0.133	0.34033915	11
soy_OGL_1591	1500	5.281703	0	6701	29.66	6	6.1733923	0.082999997	0.72229165	10
soy_OGL_5989	1200	1.6204541	0	8455	26.58	6	7.0407257	0.15099999	0.59547448	13
soy_OGL_2633	1300	7.9126515	3.1538463	8390	31.23	10	7.2709088	0.097000003	0.56582171	22
soy_OGL_532	1200	10.494274	7.5	2429	28.66	8	3.5788407	0.134	0.38020721	20
soy_OGL_1964	1000	7.7554264	3.2	3184	30.5	4	7.364182	0.13	0.49334091	25
soy_OGL_2701	1400	3.3123655	2.6428571	6015	29.14	7	4.4287238	0.101	0.46511188	18

soy_OGL_2804	1132	0.8990916	0	8006	30.38	4	16.465038	0.119	0.32557911	10
soy_OGL_1610	1100	0.11835136	0	3454	31.18	2	33.836285	0.094999999	0.093303569	1
soy_OGL_2332	1054	7.2161794	0	2001	28.17	1	0.18883276	0.13600001	0.34066972	8
soy_OGL_2387	1000	7.888226	0	8414	31	6	10.42019	0.127	0.60354108	15
soy_OGL_3070	1100	1.0271347	0	4610	26.9	4	10.208003	0.132	0.20351292	6
soy_OGL_595	1000	0.5085156	0	20562	28.5	2	3.6889629	0.127	0.64065862	8
soy_OGL_1628	1456	3.0774791	0	2001	27.6	2	1.6911108	0.133	0.48834378	9
soy_OGL_2376	1300	0.74426717	5.8461537	11925	24.53	4	4.8498478	0.12	0.53459215	1
soy_OGL_4275	1000	5.9289575	8.3999996	6688	27.1	6	5.8574829	0.16500001	0.36269885	19
soy_OGL_5979	1300	7.1452026	0	7052	29.07	4	4.0401111	0.124	0.62012243	16
soy_OGL_6013	1546	1.5527503	0	1664	25.67	4	4.1339507	0.123	0.49477041	7
soy_OGL_94	1172	10.351217	6.9965868	14668	28.49	5	7.370636	0.213	0.76842594	23
soy_OGL_463	1600	5.5066857	0	9021	28.25	4	6.4880924	0.15099999	0.55087388	19
soy_OGL_1644	1065	7.0483088	17.746479	9743	24.97	4	13.197753	0.25799999	0.58983016	21
soy_OGL_3861	1600	9.8148384	8.125	4062	26.5	7	5.1581559	0.17200001	0.26036051	21
soy_OGL_6365	1800	1.2846644	0	12212	24.38	4	7.0842242	0.212	0.65285957	5
soy_OGL_5131	1600	6.3039489	0	6056	26.68	3	5.8196912	0.15899999	0.65378505	8
soy_OGL_498	1600	5.067452	0	9445	24.43	5	23.946774	0.16500001	0.4757928	24
soy_OGL_3858	1862	10.036083	1.5037594	5326	26.42	3	40.006241	0.214	0.27137768	24
soy_OGL_3862	1700	9.8148384	10.529411	9688	25.76	7	7.8303447	0.241	0.26010731	21
soy_OGL_6346	1471	5.6157908	0	21095	29.16	5	11.1084	0.197	0.89366931	24
soy_OGL_6422	1300	10.893449	0	11144	27.76	3	38.541115	0.20200001	0.54382116	33
soy_OGL_494	1700	4.9800091	0	7000	24.58	5	30.901804	0.12	0.47823423	24
soy_OGL_2001	1568	7.3541341	0	3701	23.91	3	2.8522375	0.17399999	0.44233978	15
soy_OGL_3060	1500	17.138634	3	1850	22.73	3	2.949698	0.192	0.47428936	3
soy_OGL_5164	1400	6.6491861	4.3571429	8299	24.57	3	8.2377243	0.169	0.83331966	15
soy_OGL_543	1300	10.749329	12.153846	6409	27.84	4	2.2191281	0.169	0.35933334	18
soy_OGL_577	2000	1.8986254	5.4499998	7499	23.6	3	1.9196731	0.175	0.25336915	2
soy_OGL_2039	2500	0.94065005	0	3374	27.92	2	14.193683	0.16	0.36654249	7
soy_OGL_2095	1100	1.3710024	3.3636363	30506	31	2	17.923897	0.115	0.76458663	15
soy_OGL_2805	1714	0.65297556	17.444574	9191	24.85	3	11.650559	0.31299999	0.33332723	12

soy_OGL_3893	1900	0.8433677	8.1578951	12041	24.57	6	8.818634	0.199	0.57363933	6
soy_OGL_6701	1276	0.69440275	7.9937305	37634	31.26	1	0.59971058	0.141	0.078639343	3
soy_OGL_861	1100	7.4204826	9.545455	9688	26.45	3	6.4279017	0.185	0.58033592	14
soy_OGL_1321	1400	0.24154867	5	5736	23.42	1	4.4111633	0.184	0.62211233	14
soy_OGL_1899	1227	9.4963474	6.3569684	11552	26.16	6	12.683743	0.163	0.649737	11
soy_OGL_5351	1529	2.9911871	7.7174625	10059	25.04	7	3.3538368	0.148	0.49102813	14
soy_OGL_580	1397	0.084886439	7.6592698	31304	25.34	2	6.7212424	0.197	0.4833608	2
soy_OGL_1619	1300	1.1600796	22.461538	26634	25.92	2	70.956757	0.18099999	0.40595475	7
soy_OGL_1990	1221	7.5878448	5.8149056	16259	21.45	6	8.008873	0.207	0.46064866	18
soy_OGL_2657	1297	6.8734031	8.0956049	8465	25.36	1	2.272202	0.20900001	0.5318706	25
soy_OGL_3075	1081	0.57695127	13.413506	32202	25.99	1	0.19895983	0.19499999	0.22003801	10
soy_OGL_3883	1100	0.027143367	0	38642	27.54	1	3.7395444	0.162	0.37996385	7
soy_OGL_4732	1425	1.3662759	0	36911	30.73	1	0.12047315	0.169	0.15653431	9
soy_OGL_5083	1480	7.9923754	9.6621618	2156	22.29	1	47.137802	0.15899999	0.37244385	3
soy_OGL_5740	1289	13.020522	0	12945	27.77	2	4.9311676	0.184	0.69343889	14
soy_OGL_6060	1481	2.0422838	0	25108	28.22	2	5.6778278	0.075999998	0.055807397	12
soy_OGL_6114	1800	2.5854952	2.6666667	14515	25.22	1	13.262783	0.186	0.71673077	7
soy_OGL_6116	1303	2.2216065	0	20659	24.63	3	3.8967295	0.19	0.72604966	13
soy_OGL_6133	1800	2.7482004	1.5555556	15946	32.16	2	30.513409	0.07	0.76204032	15
soy_OGL_6392	1300	3.7100728	8.9230766	18153	23.92	2	8.2213869	0.22	0.38539737	3
soy_OGL_6668	1600	12.019849	4.8125	3598	26.12	8	11.411879	0.154	0.010268705	22
soy_OGL_6686	1208	6.8529043	14.7351	15431	26.57	3	46.435875	0.219	0.022505013	20
soy_OGL_546	1000	10.749329	0	25909	30.1	3	3.5368268	0.114	0.35846847	18
soy_OGL_860	1295	5.045455	0	13292	23.55	4	0.77783704	0.193	0.58393753	13
soy_OGL_1298	1000	0.3178266	0	39482	22.5	1	2.9363437	0.13699999	0.5072791	2
soy_OGL_3086	1116	2.0021172	0	25737	24.91	1	0.0220751	0.123	0.27896535	7
soy_OGL_3094	1100	0.6157763	0	35078	29.45	2	5.0864921	0.092	0.34772989	7
soy_OGL_4257	1281	9.2218924	0	12508	20.68	6	6.2342315	0.21799999	0.31364393	11
soy_OGL_5114	1479	5.6311255	0	7423	23.05	4	15.299383	0.156	0.3694343	12
soy_OGL_5693	1200	1.387786	0	26590	24	2	25.497341	0.116	0.40315709	13
soy_OGL_1615	1700	0.42990735	23.117647	3509	26.17	6	56.79237	0.161	0.38481191	3

soy_OGL_6655	1300	15.964157	19	3809	26.23	7	7.0641665	0.21600001	0.19352518	19
soy_OGL_178	1600	4.2186117	0	7290	27	4	3.7915866	0.127	0.77040935	13
soy_OGL_4072	1400	5.8943801	3.2857144	6106	27	6	4.953814	0.13699999	0.52470118	19
soy_OGL_5372	1229	5.9304881	17.331163	4658	22.29	6	3.1755002	0.20100001	0.63047212	13
soy_OGL_5983	1479	6.6010385	0	14433	22.51	8	2.6207807	0.15899999	0.61435711	16
soy_OGL_6120	1400	2.3116186	2.8571429	8576	23.07	5	11.838049	0.171	0.72946703	12
soy_OGL_3169	1792	12.889535	0	8541	24.94	9	51.504616	0.086000003	0.6316337	15
soy_OGL_2062	1400	2.554987	0	10535	25.57	4	0.95077837	0.139	0.58254093	11
soy_OGL_4076	1100	5.8943801	9.181818	14095	26.27	6	5.7353821	0.15800001	0.53146845	19
soy_OGL_6122	1500	2.3054614	0	16578	27.6	4	0.51315057	0.109	0.73247123	13
soy_OGL_1284	1278	7.132494	0	16012	22.45	3	18.673264	0.139	0.6584456	18
soy_OGL_1603	1500	5.281703	0	17968	27.86	2	18.957331	0.068000004	0.68434525	14
soy_OGL_5115	1530	5.6311255	0	9373	22.09	4	15.299383	0.124	0.36959493	12
soy_OGL_6102	1313	0.477795	9.5201826	11579	21.47	4	2.1915698	0.182	0.66430151	11
soy_OGL_6675	1200	9.9655132	0	10318	27.16	3	0.40493882	0.131	0.0130971	27
soy_OGL_3046	1097	32.947975	0	19557	24.61	3	40.721748	0.106	0.6647746	10
soy_OGL_1303	1000	1.5215753	0	10158	24.2	2	7.2931638	0.27399999	0.57532585	12
soy_OGL_1997	1400	6.4805918	0	10048	29.14	4	6.4898047	0.20900001	0.44786689	19
soy_OGL_4353	1306	3.1938996	0	13316	24.27	7	3.4718399	0.2	0.48733181	17
soy_OGL_5153	1092	4.1436477	0	12835	26	3	4.971374	0.20100001	0.77393335	19
soy_OGL_5656	1200	6.3537583	0	8399	24.83	3	15.769091	0.198	0.50936782	20
soy_OGL_3391	1429	5.6634336	3.1490552	3680	28.9	4	40.834469	0.15700001	0.70214611	17
soy_OGL_2061	1213	2.3059373	0	19415	28.6	1	1.2095	0.176	0.57870322	11
soy_OGL_3846	1414	3.0571678	7.5671854	12120	24.96	3	9.686162	0.178	0.40632257	2
soy_OGL_4016	1169	7.0667925	0	22554	29.94	1	2.1888874	0.191	0.69944233	16
soy_OGL_5062	1400	3.1510634	0	35680	31.35	1	0.23491456	0.235	0.58155614	3
soy_OGL_5073	1500	0.16888668	0	31504	30.06	3	0.90148515	0.177	0.50925851	2
soy_OGL_5079	1000	11.011989	0	25558	32.4	1	5.9897971	0.146	0.41032636	5
soy_OGL_5703	1173	0.11315778	0	34086	30.77	1	0.40247896	0.176	0.38132671	8
soy_OGL_6050	1100	2.3951523	4.181818	19024	24.54	2	1.0488321	0.25	0.17105612	7
soy_OGL_6212	1000	6.6037278	0	31444	32.3	3	10.153718	0.249	0.8690244	29

soy_OGL_2031	1027	1.7172174	0	9546	25.12	3	21.232882	0.229	0.30004615	3
soy_OGL_2369	1260	0.67735338	0	19202	26.58	1	0.057518862	0.124	0.099602751	6
soy_OGL_5345	1377	2.1660724	0	2440	23.89	1	9.6324234	0.18799999	0.49453798	4
soy_OGL_2364	1644	9.6849852	0	13022	27.31	7	18.104433	0.236	0.12797964	8
soy_OGL_2762	1200	3.2010031	0	20051	23.16	5	14.784334	0.20299999	0.32982168	12
soy_OGL_2767	1093	4.6344571	0	21821	24.88	4	19.453714	0.19499999	0.32743382	12
soy_OGL_3063	1187	13.119327	0	11031	22.49	2	5.2104301	0.243	0.14106013	5
soy_OGL_3077	1056	0.69136071	0	31762	27.46	2	0.36628908	0.15800001	0.22759451	10
soy_OGL_5049	1409	6.5904026	0	21574	26.33	3	37.82695	0.243	0.61535853	11
soy_OGL_6088	1200	0.69722927	0	36732	28.75	1	11.883606	0.193	0.55703247	6
soy_OGL_593	1000	0.71430248	0	20269	21	2	0.61479425	0.212	0.6309936	7
soy_OGL_2807	1478	1.0325171	0	9081	26.38	1	32.970032	0.13500001	0.35478935	5
soy_OGL_3073	1215	2.1047292	0	13716	24.36	1	10.89752	0.163	0.21095096	8
soy_OGL_871	1714	1.0942405	0	2303	28.06	3	88.507225	0.215	0.58532852	8
soy_OGL_6681	1388	7.6147938	2.2334294	1001	26.87	7	38.067959	0.12899999	0.021496912	23
soy_OGL_1909	1041	14.749738	24.303555	5479	25.45	5	2.1920948	0.21600001	0.61707145	13
soy_OGL_1599	1051	5.281703	14.176974	20405	29.3	2	6.1763835	0.131	0.68975294	15
soy_OGL_2763	1167	3.2010031	19.708654	7611	23.9	5	11.306363	0.18799999	0.32938671	12
soy_OGL_3061	1000	16.283766	21.5	22206	31.3	1	3.4592695	0.13600001	0.35885531	1
soy_OGL_5122	1500	6.9515624	15.4	3339	25.73	3	4.8484769	0.199	0.40483865	13
soy_OGL_5704	1200	2.7745914	20.416666	27453	27.91	1	2.7280815	0.16599999	0.30301532	1
soy_OGL_6699	1698	0.69440275	6.1837454	8617	26.56	4	9.5528669	0.094999999	0.068272971	4
soy_OGL_6000	1300	3.0652781	13.384615	6972	24.46	7	5.8489618	0.15000001	0.54733163	18
soy_OGL_1624	1800	1.3796759	1.8333334	9949	26.77	3	1.3240128	0.056000002	0.44556019	2
soy_OGL_600	1393	5.0991559	11.414214	2458	24.04	7	16.944464	0.15000001	0.65909106	9
soy_OGL_4080	1200	5.8943801	0	5685	26.66	3	4.6108451	0.13600001	0.54248708	24
soy_OGL_2660	1424	6.8734031	0	3463	24.71	3	1.5135432	0.127	0.53135318	25
soy_OGL_2837	1283	5.5548873	0	7815	25.09	3	3.2647965	0.138	0.66591072	23
soy_OGL_538	1475	10.749329	0	2750	26.16	8	22.143547	0.108	0.36381233	21
soy_OGL_1940	1300	15.018729	0	8166	29.23	6	10.08659	0.108	0.5395487	21
soy_OGL_1968	1400	8.2513695	2.2857144	4436	29.78	4	9.5706692	0.097999997	0.49163312	25

soy_OGL_2798	1439	0.8990916	0	1001	22.93	1	0.004874148	0.127	0.32078108	10
soy_OGL_590	1133	1.0339187	0	24024	22.85	4	8.2659426	0.122	0.6090368	8
soy_OGL_2036	1000	0.62599713	0	21909	21.7	2	10.186376	0.14	0.35609052	8
soy_OGL_6692	1400	7.9217877	0	16832	24.21	4	17.263233	0.081	0.034273136	10
soy_OGL_822	1153	12.450212	0	10547	29.4	3	33.011215	0.089000002	0.74076933	23
soy_OGL_2006	1300	2.4300511	0	4797	22.15	4	3.2377954	0.204	0.40569806	4
soy_OGL_3879	1400	1.4084551	2.6428571	6081	18.78	8	80.576248	0.16	0.20529185	5
soy_OGL_2340	1117	11.84416	0	2865	24.97	7	12.045063	0.17200001	0.31362766	13
soy_OGL_2993	1100	9.2852879	0	9731	27.9	5	20.017591	0.13699999	0.80737448	25
soy_OGL_6662	1160	17.337919	0	2001	26.63	9	8.9174442	0.184	0.005641606	23
soy_OGL_2025	1071	1.2592741	3.0812325	14713	25.49	3	12.994309	0.111	0.3225269	5
soy_OGL_2797	1039	1.5446639	0	17768	27.23	1	0.49690655	0.121	0.30348989	8
soy_OGL_3064	1100	13.119327	0	8518	27.72	2	5.2104301	0.107	0.1409532	5
soy_OGL_3843	1243	7.3592849	0	8731	29.04	4	6.4019752	0.138	0.52549601	17
soy_OGL_4248	1288	9.7208376	0	5369	28.41	6	17.998335	0.107	0.29320714	16
soy_OGL_4263	1397	2.6787946	0	3227	24.55	6	10.362242	0.127	0.33831921	13
soy_OGL_5411	1200	9.4738331	0	14198	30.5	4	6.5322752	0.115	0.74952698	14
soy_OGL_5698	1398	1.1073029	0	3849	26.32	4	9.6700354	0.12	0.39759386	15
soy_OGL_6084	1235	0.14201316	0	17317	24.85	2	3.040158	0.104	0.22577515	1
soy_OGL_2356	1000	2.8688939	0	7574	27.7	1	19.558249	0.115	0.19655505	10
soy_OGL_3082	1085	0.30723089	0	2001	26.82	2	55.348843	0.118	0.25717351	8
soy_OGL_4737	1254	1.3662759	0	5265	21.77	2	9.5198784	0.14	0.14814679	10
soy_OGL_5116	1248	5.8165097	0	1001	22.75	3	16.42539	0.168	0.37099776	12
soy_OGL_5710	1000	8.3291292	0	16728	25.6	2	3.9659913	0.102	0.078835249	4
soy_OGL_6074	1072	1.3030386	0	14404	22.1	4	4.4355297	0.13600001	0.008813712	3
soy_OGL_6801	1211	4.8344703	22.295624	9890	43.76	10	116.29536	0.29800001	0.78603518	22
soy_OGL_3173	1372	11.789145	18.29446	1320	35.27	6	55.438042	0.141	0.64489073	21
soy_OGL_4427	1300	9.7329044	10.461538	7605	31.38	7	18.496197	0.146	0.61522472	23
soy_OGL_3390	1600	5.6634336	13.5	4649	33.62	4	40.834469	0.197	0.7026636	17
soy_OGL_1915	1311	4.1802773	24.637682	2523	26.23	9	50.414326	0.19499999	0.57165873	12
soy_OGL_122	1400	4.3635497	10.928572	9866	32.71	6	48.29842	0.068999998	0.56271821	6

soy_OGL_6097	1119	0.54288405	22.162645	3298	28.5	6	70.313675	0.119	0.65387458	10
soy_OGL_4819	1000	19.378592	15.7	5411	31.5	5	6.034955	0.134	0.96135575	16
soy_OGL_2686	1000	10.232581	0	4427	33.5	7	20.447409	0.175	0.49060139	24
soy_OGL_1921	1000	13.194177	0	6027	33.5	7	4.3148499	0.145	0.56094158	21
soy_OGL_5674	1100	10.021258	0	2292	32.63	4	21.700743	0.093999997	0.47259387	14
soy_OGL_1971	1100	8.7267275	7.7272725	7750	31.81	7	11.270623	0.109	0.48790261	26
soy_OGL_553	1200	18.677822	0	3171	38.91	8	32.428539	0.037999999	0.33040091	18
soy_OGL_3871	1000	9.8148384	7.9000001	2178	30.8	9	31.50157	0.127	0.25184977	17
soy_OGL_3807	1800	8.2365665	32	2389	30.33	8	63.81657	0.235	0.6117897	13
soy_OGL_1720	1596	34.72348	34.335838	3373	26	8	260.85187	0.219	0.83812189	25
soy_OGL_2895	1924	8.9753227	39.345116	3841	25.77	17	260.31473	0.126	0.88371807	13
soy_OGL_6814	1242	7.4979596	28.904991	4128	24.31	7	215.12354	0.097000003	0.80101377	29
soy_OGL_1951	1300	21.06424	19.923077	4848	28.84	9	11.231849	0.12800001	0.51579869	15
soy_OGL_3170	1100	12.889535	28.181818	5741	27.09	10	48.698517	0.15000001	0.63178521	15
soy_OGL_1361	1193	9.4480371	26.068735	1485	26.15	7	104.49555	0.126	0.77446717	21
soy_OGL_986	1472	9.9324665	8.491848	2675	33.89	9	194.09158	0.162	0.77140713	32
soy_OGL_1722	1107	36.117916	0	1001	23.48	9	232.60893	0.112	0.83908087	25
soy_OGL_1719	1425	34.72348	3.3684211	6835	32.42	8	262.78976	0.127	0.83727175	25
soy_OGL_2110	1800	6.7586851	0	3813	25.61	12	369.22458	0.207	0.9477523	14
soy_OGL_2571	1613	7.0306044	13.639182	1001	28.08	8	415.45572	0.088	0.68764073	18
soy_OGL_3513	1000	41.712101	0	7631	26.9	9	440.82959	0.027000001	0.73412389	23
soy_OGL_3514	1305	41.712101	13.02682	3626	27.27	9	440.82959	0.149	0.73425162	23
soy_OGL_3515	1030	41.712101	26.69903	2001	24.75	10	398.40335	0.072999999	0.73431718	23
soy_OGL_3591	1400	4.7033892	34	8650	26.07	7	390.31799	0.16599999	0.8580122	29
soy_OGL_3592	1100	4.7033892	9.727273	2336	24.9	8	369.88428	0.098999999	0.85848516	29
soy_OGL_3593	2426	4.7033892	23.042044	4570	29.18	9	328.94366	0.094999999	0.85881996	29
soy_OGL_4129	1100	10.342244	0	6301	22.81	7	399.76541	0.093999997	0.82752752	31
soy_OGL_4130	1289	10.342244	37.703648	7169	35.6	7	399.76541	0.162	0.82782733	31
soy_OGL_4171	1200	57.504368	18.833334	2287	33.25	8	28.093042	0.177	0.1569047	7
soy_OGL_4527	1686	7.9699202	38.078293	3067	23.84	6	816.21539	0	0.76256597	33
soy_OGL_4528	1000	7.9699202	29.299999	12953	23.3	7	700.88092	0.13	0.762914	33

soy_OGL_4529	1300	7.9699202	17.538462	2433	28.53	12	406.95377	0.197	0.76510692	32
soy_OGL_5417	1908	12.182234	0	2001	25.68	10	305.45093	0.097999997	0.95027298	7
soy_OGL_2568	1003	7.0306044	39.680958	6823	24.52	9	374.97421	0.142	0.68813276	18
soy_OGL_2569	1173	7.0306044	27.450981	5626	31.11	9	374.97421	0.122	0.68809092	18
soy_OGL_2570	1263	7.0306044	0	2926	30	9	374.97421	0.126	0.68799651	18
soy_OGL_3112	1516	2.5238051	35.620052	1001	22.55	10	288.16135	0.15700001	0.5128656	13
soy_OGL_4116	1012	7.7928329	11.264822	6543	27.86	7	220.96301	0.197	0.79469687	23
soy_OGL_4117	1338	7.7928329	25.635277	1451	23.76	4	381.7092	0.013	0.79662287	25
soy_OGL_4118	1000	7.7928329	20.5	4551	31.4	3	505.09924	0.118	0.79684895	25
soy_OGL_4346	1370	8.2939415	3.0656934	2443	19.12	9	506.5285	0.211	0.47565243	21
soy_OGL_4347	1200	6.3071108	0	4550	41.08	8	562.79303	0.22400001	0.47724012	23
soy_OGL_3594	1500	4.7033892	0	3029	23.6	9	328.94366	0	0.85895115	29
soy_OGL_5418	1253	12.182234	0	1957	28.81	11	278.11523	0.086999997	0.95040542	7
soy_OGL_4131	1090	10.342244	0	10160	24.12	7	187.36253	0.125	0.82924849	32
soy_OGL_4169	1100	61.380577	7.3636365	2742	33.18	8	21.560427	0.118	0.15582053	7
soy_OGL_1026	1196	6.3006811	37.207359	1001	33.44	9	95.040863	0.122	0.82687747	31
soy_OGL_57	1600	11.04541	2.3125	15116	31.37	5	50.815098	0.090999998	0.84422421	27
soy_OGL_5050	1700	6.5904026	12.117647	2362	29.35	2	55.679558	0.134	0.61448824	11
soy_OGL_5081	1101	21.920118	20.435966	17608	31.15	3	7.3182039	0.117	0.4030548	5
soy_OGL_2343	1746	16.299006	9.3928976	3089	28.57	10	23.043476	0.094999999	0.30506423	12
soy_OGL_6685	1400	7.6147938	27.214285	1055	27.78	4	38.883102	0.163	0.022192717	20
soy_OGL_1945	1135	23.406984	24.845816	12726	28.45	8	81.204422	0.124	0.53085923	18
soy_OGL_1315	1200	2.0239863	33.25	6606	28.75	3	79.697144	0.121	0.60559016	17
soy_OGL_2673	1600	6.8734031	19.9375	9770	29.68	7	54.572304	0.191	0.50548601	23
soy_OGL_4023	1500	7.0667925	9.6000004	9556	28.93	5	77.293755	0.117	0.6913923	16
soy_OGL_3835	1800	7.7801862	0	1844	29.16	8	56.086422	0.059	0.54102147	25
soy_OGL_3054	1274	30.750532	2.6687598	2806	31.55	4	4.0348716	0.199	0.57464367	3
soy_OGL_2527	1600	7.693583	6.125	4204	30.81	9	82.78508	0.12800001	0.7820664	5
soy_OGL_868	1600	1.0942405	13.1875	12374	32.12	1	88.766724	0.121	0.5764758	7
soy_OGL_4280	1500	5.0428143	1.8666667	4201	23.26	8	107.22707	0.167	0.36670813	20
soy_OGL_517	1268	2.3637695	3.1545742	18618	23.18	4	137.0737	0.086000003	0.42725676	14

soy_OGL_2082	1271	1.6845587	18.961447	2574	24.15	7	66.911461	0.163	0.70587683	8
soy_OGL_2721	2002	6.8279347	0	1015	27.12	9	168.88676	0.071999997	0.43251398	20
soy_OGL_2722	2162	6.7211156	0	2001	25.9	9	169.29041	0.111	0.43239993	20
soy_OGL_4200	1600	4.0633597	37.9375	1744	22.87	8	288.43118	0.17	0.21416126	19
soy_OGL_4348	1241	6.1021829	0	2001	24.73	5	872.71979	0.134	0.47835207	23
soy_OGL_516	1357	2.3637695	0	1001	28.88	3	180.95107	0.13500001	0.42850193	14
soy_OGL_3113	1033	5.6704493	0	17400	27.2	6	265.80106	0.093999997	0.51477736	12
soy_OGL_4199	1900	3.1617231	3.6315789	2423	28.36	7	329.61893	0.17299999	0.21370013	19
soy_OGL_4201	1496	3.907387	0	3077	27.87	8	291.63776	0.227	0.21539678	19
soy_OGL_4661	1231	8.5420761	0	11044	24.53	6	116.62761	0.19	0.67757601	26
soy_OGL_5333	1628	10.928795	39.373463	3776	23.52	4	311.36511	0.142	0.57067072	8
soy_OGL_2724	1400	6.7211156	2.3571429	3354	31.78	8	184.20576	0.061999999	0.43138811	19
soy_OGL_3529	1104	1.9912556	13.043478	6896	24.18	8	386.27237	0.024	0.76316452	12
soy_OGL_58	1199	11.04541	0	4716	32.27	4	63.474609	0.108	0.84359396	27
soy_OGL_1688	1720	9.1770983	14.360465	5399	29.41	8	29.928612	0.108	0.73888701	9
soy_OGL_3373	1381	10.989937	23.026793	7809	30.48	6	32.114395	0.12	0.75481009	13
soy_OGL_4175	1340	19.785273	27.38806	3889	29.1	10	8.9526358	0.168	0.17290528	17
soy_OGL_4213	1314	4.1915531	17.656012	5426	27.92	7	21.690073	0.089000002	0.25125167	23
soy_OGL_1981	1476	9.5797806	13.143631	5530	35.56	5	40.307369	0.003	0.47646832	25
soy_OGL_6677	1100	9.2386303	23.818182	5309	28.36	8	16.42305	0.109	0.015041351	29
soy_OGL_712	1016	8.4636536	18.110237	4512	29.62	8	48.681385	0.124	0.84763992	24
soy_OGL_6799	1000	4.8344703	0	2054	32.1	9	125.64165	0.126	0.78563792	21
soy_OGL_1649	1200	8.4981375	2.3333333	2408	23.5	10	104.0661	0.141	0.59413815	20
soy_OGL_4771	1285	6.7980485	8.1712065	2468	29.41	4	45.115665	0.092	0.84061533	9
soy_OGL_3040	1100	24.358362	7.909091	3939	29.72	5	33.396999	0.13	0.68250215	12
soy_OGL_2759	1332	3.540004	17.867868	3314	26.42	8	56.858444	0.089000002	0.33944294	12
soy_OGL_1648	1000	8.4981375	0	2673	33.4	9	118.38069	0.090000004	0.59331751	20
soy_OGL_5094	1083	1.4031272	0	1112	22.43	2	152.65868	0.082000002	0.089211486	1
soy_OGL_6636	1257	7.9076147	0	8372	28.32	9	8.3020058	0.13	0.97697055	22
soy_OGL_2480	1144	5.6079402	0	2001	24.56	11	7.6778784	0.207	0.89345646	24
soy_OGL_915	1100	6.3260517	0	6109	27.36	10	9.7425737	0.164	0.68313628	27

soy_OGL_3967	1267	8.0769224	0	3808	25.09	10	14.30653	0.167	0.94612306	10
soy_OGL_2523	1300	7.5373769	3.3846154	1254	25.3	14	22.276794	0.169	0.81426221	18
soy_OGL_3365	1354	12.993029	0	2478	26.88	13	12.154834	0.145	0.79446948	13
soy_OGL_6195	1058	6.222538	0	2001	23.44	11	5.025383	0.133	0.85484421	16
soy_OGL_3677	1059	6.1510382	0	1513	25.21	10	19.286514	0.13699999	0.93825322	12
soy_OGL_3294	1000	5.0341988	0	2229	25.9	9	15.380539	0.132	0.95541936	25
soy_OGL_304	1004	11.124907	4.2828684	3784	26.59	9	18.861059	0.13699999	0.93040532	8
soy_OGL_6271	1414	5.2232471	0	2001	27.72	8	8.778223	0.124	0.92648834	28
soy_OGL_2141	1405	6.6979451	0	2402	30.03	8	8.2604342	0.113	0.86515594	30
soy_OGL_6979	1273	4.8485398	0	7085	31.18	6	11.203269	0.108	0.94413447	33
soy_OGL_6335	1301	5.6879897	0	1818	29.43	6	4.5990534	0.097000003	0.90541273	30
soy_OGL_1742	1151	3.8039601	15.20417	2919	21.54	13	5.7125731	0.152	0.98683274	14
soy_OGL_5450	1359	5.0694704	0	2015	26.85	9	7.9279828	0.043000001	0.93124676	14
soy_OGL_300	1000	8.1388817	19.700001	4513	23.1	11	11.800037	0.145	0.92299765	12
soy_OGL_1705	1228	6.6742897	0	2180	28.01	9	3.4926043	0.035999998	0.81549662	29
soy_OGL_2458	1400	5.9070358	2.4285715	3989	27.07	11	12.493586	0.079000004	0.93053144	16
soy_OGL_4600	1383	5.497468	4.5553145	2001	24.07	13	10.823985	0.068000004	0.90992266	10
soy_OGL_6835	1139	3.9573007	5.2677789	2678	27.74	10	1.4578713	0.125	0.8147378	36
soy_OGL_3547	1246	8.9636507	0	1727	27.36	8	1.5426327	0.090999998	0.80588019	23
soy_OGL_6340	1007	5.6157908	3.9721947	2706	27.2	6	4.002429	0.097999997	0.89804256	29
soy_OGL_4648	1069	5.2841516	0	3889	27.78	10	4.413414	0	0.71360987	27
soy_OGL_6635	1000	7.9076147	13.1	9729	27.6	9	8.3020058	0.118	0.97692919	22
soy_OGL_6620	1564	8.7494211	0	1001	25.95	12	5.5700836	0.142	0.94802552	11
soy_OGL_1417	1000	11.014842	0	1188	27	8	3.7326677	0.19400001	0.85630578	17
soy_OGL_3713	1013	6.9130831	0	6377	27.54	9	7.6834545	0.142	0.83226335	24
soy_OGL_371	1400	7.7784052	0	1452	29.35	11	7.4445691	0.112	0.81357205	20
soy_OGL_3833	1079	7.7801862	6.6728454	2001	27.98	10	5.5863171	0.154	0.54320139	27
soy_OGL_718	1084	9.6048651	0	4125	28.78	8	6.5628285	0.124	0.85613757	26
soy_OGL_2144	1000	7.0482421	0	2405	28.8	7	7.1666994	0.146	0.86026144	30
soy_OGL_4464	1167	7.5555859	0	1001	26.64	12	5.8568654	0.164	0.69798732	25
soy_OGL_6841	1200	3.9573007	0	4185	29.08	9	13.630019	0.11	0.8175627	34

soy_OGL_397	1329	8.8643551	0	2597	30.39	8	6.614748	0.089000002	0.76095045	25
soy_OGL_1793	1259	5.5180402	3.7331216	2049	26.05	10	19.175663	0.13500001	0.82712471	11
soy_OGL_1195	1053	4.0395017	0	1001	26.02	10	4.2822032	0.13500001	0.8819012	17
soy_OGL_3607	1000	4.9169555	0	3038	25.1	11	0.86204904	0.122	0.88172668	16
soy_OGL_6646	1004	4.0469542	0	3885	25.89	10	10.091497	0.121	0.99174333	13
soy_OGL_1788	1100	5.2867265	0	2203	24.27	12	4.7111387	0.048999999	0.88430518	15
soy_OGL_2477	1100	3.3217475	0	3703	25.9	12	7.4025855	0.112	0.90196854	24
soy_OGL_4894	1108	9.0506868	5.0541515	3451	23.55	12	4.7913852	0.119	0.90524983	12
soy_OGL_5456	1233	6.9202266	0	1089	24.81	12	9.1461296	0.138	0.91237807	18
soy_OGL_6995	1093	5.9223719	0	2001	26.44	8	8.5473528	0.132	0.95482695	25
soy_OGL_1120	1082	2.2730639	0	2438	24.58	9	7.5355978	0.112	0.980232	15
soy_OGL_1110	1321	6.1349368	0	1231	27.17	14	12.503329	0.119	0.94773239	16
soy_OGL_1188	1100	4.3006682	0	3475	26.45	15	6.6610904	0.116	0.89130265	27
soy_OGL_5869	1073	7.2906718	0	1042	28.23	10	5.9647269	0.111	0.92002475	26
soy_OGL_1006	1000	6.5819335	0	1620	26.4	11	10.296087	0.115	0.79812407	15
soy_OGL_5440	1257	5.0618563	3.1821797	5147	27.76	11	12.076348	0.106	0.95200443	15
soy_OGL_742	1164	8.9459286	0	2523	25.6	14	7.4349446	0.089000002	0.91198885	11
soy_OGL_1416	1400	11.014842	0	2287	28.64	10	4.8395166	0.093999997	0.85435522	16
soy_OGL_1540	1028	8.1677341	0	5103	28.01	10	3.1849835	0.13	0.87585336	33
soy_OGL_1839	1122	7.2193756	0	3608	28.69	10	3.8830335	0.063000001	0.74348378	29
soy_OGL_3708	1032	7.1042829	0	1001	26.45	13	13.928825	0.13600001	0.83701718	23
soy_OGL_4005	1300	11.197123	0	2474	25.53	16	4.0283594	0.15000001	0.8048923	12
soy_OGL_4441	1045	8.6878357	0	2001	26.69	12	11.524039	0.139	0.63450032	19
soy_OGL_4647	1216	5.2841516	0	1001	26.23	14	8.354394	0.134	0.71694773	31
soy_OGL_5001	1167	8.9428253	0	2843	26.47	15	4.3572283	0.131	0.69795561	28
soy_OGL_6176	1268	8.6720114	2.9968455	1001	25.63	11	4.4388247	0.117	0.8218649	14
soy_OGL_6839	1119	3.9573007	0	2001	28.5	8	4.4479685	0.113	0.81582505	34
soy_OGL_1091	1142	6.4006157	0	1759	24.51	12	10.033394	0	0.91709059	9
soy_OGL_1104	1100	5.3018403	5.2727275	3563	26.9	9	10.97975	0.115	0.93793517	18
soy_OGL_1656	1100	8.9003105	0	1952	27.09	10	7.3009834	0.133	0.60528362	20
soy_OGL_2512	1050	7.4874678	0	3551	28.38	8	2.8637574	0.11	0.82431644	25

soy_OGL_3451	1042	10.103625	0	2225	26.29	12	10.304541	0.114	0.59103614	12
soy_OGL_4421	1055	9.7329044	0	2708	27.01	10	4.2733245	0.106	0.61105037	23
soy_OGL_6805	1200	6.6510434	0	4000	28.83	9	8.3991661	0.082999997	0.79177916	21
soy_OGL_2886	1000	7.0442643	0	2525	26.2	10	2.9160376	0.012	0.85429543	16
soy_OGL_6936	1027	8.8029718	0	2001	27.16	8	6.1774516	0.035	0.90606749	19
soy_OGL_2696	1183	8.1054287	0	2001	26.12	9	7.176785	0.163	0.47297046	19
soy_OGL_4010	1100	7.0667925	0	1199	24.36	9	5.6498094	0.121	0.70628846	15
soy_OGL_5378	1000	8.9067116	0	2724	23.6	11	2.8135331	0.141	0.675008	11
soy_OGL_609	1086	7.0958691	0	2001	26.24	8	10.636346	0.127	0.68318295	16
soy_OGL_3485	1000	5.426621	0	1859	27.8	8	18.634951	0.12800001	0.64995992	24
soy_OGL_1820	1112	0.91241473	0	9720	28.5	6	2.8681152	0.106	0.76882428	31
soy_OGL_6326	1100	6.7954488	13.909091	11492	27.18	8	4.6560478	0.132	0.91891491	22
soy_OGL_1205	1011	6.7576227	3.0662711	5680	26.4	7	0.92117059	0.13500001	0.82797366	25
soy_OGL_2442	1400	3.0977101	0	2225	25.42	8	8.1280537	0.068000004	0.97033215	11
soy_OGL_183	1290	5.00559	3.5658915	3008	26.74	7	6.037262	0.081	0.77739698	14
soy_OGL_2607	1117	5.8562093	17.099373	2481	23.45	10	3.4294314	0.121	0.60285252	15
soy_OGL_4342	1100	5.8494349	14.454545	2184	24	11	4.7673016	0.131	0.46644074	17
soy_OGL_4609	1200	6.7095437	0	1954	26.75	7	2.6326487	0.145	0.83378434	8
soy_OGL_173	1200	2.1532793	4.25	2719	21.91	8	3.5154796	0.183	0.76750463	12
soy_OGL_2240	1082	7.3392978	0	1001	27.91	9	6.8305616	0.133	0.69017971	15
soy_OGL_643	1103	7.5262041	0	5817	30.46	8	7.8696332	0.117	0.75054634	26
soy_OGL_1664	1095	8.7383938	0	2118	28.12	8	7.1383166	0.123	0.62637007	11
soy_OGL_1639	1043	4.9139419	0	2001	27.42	7	3.5944653	0.14	0.57276893	12
soy_OGL_6328	1100	6.7954488	0	11239	30.36	6	5.829483	0.119	0.91836172	23
soy_OGL_747	1117	7.9587779	2.6857655	3886	27.75	6	4.4863329	0.122	0.91947067	13
soy_OGL_6345	1100	5.6157908	0	4248	29.18	4	8.5079031	0.13600001	0.89471912	25
soy_OGL_743	1000	7.9587779	0	9995	27.9	7	2.6253722	0.134	0.91889888	13
soy_OGL_6464	1300	6.0830817	0	5299	25.76	9	3.1565604	0.111	0.60032105	15
soy_OGL_781	1059	9.4103231	6.3267231	4824	28.7	6	3.3774915	0.14	0.93205792	19
soy_OGL_3125	1027	6.3040566	0	2868	28.72	8	10.328381	0.131	0.54409117	24
soy_OGL_3955	1300	0.89052546	0	5055	23.53	12	7.937819	0.112	0.99089617	6

soy_OGL_611	1116	7.0958691	0	1001	27.24	7	2.5896988	0.12899999	0.68696266	21
soy_OGL_766	1013	3.116626	0	4543	23.49	9	4.9962993	0.11	0.99251777	6
soy_OGL_1801	1342	3.2149055	0	1115	26.3	9	8.9415369	0.094999999	0.7924422	14
soy_OGL_2586	1018	1.6719028	0	2913	22	11	3.3039491	0.12	0.64925873	14
soy_OGL_6730	1040	6.6663599	3.1730769	2692	24.03	10	5.8939729	0.139	0.71631396	14
soy_OGL_4008	1100	11.197123	0	3544	27.36	10	1.5451584	0.104	0.80219615	10
soy_OGL_1004	1056	6.542963	0	5736	26.23	9	11.025846	0.1	0.79704982	15
soy_OGL_4807	1000	5.6626678	0	8955	25.6	9	2.8795228	0.064000003	0.9367128	14
soy_OGL_6180	1111	7.406157	7.290729	2001	25.92	6	7.1629772	0.122	0.82770222	12
soy_OGL_6186	1000	6.0692587	0	4512	26.4	7	5.9620481	0.12	0.84066409	12
soy_OGL_1794	1266	5.5180402	0	2887	28.98	9	18.735395	0.090000004	0.82623053	11
soy_OGL_96	1000	10.343252	3.8	6269	28.4	8	6.6642113	0.101	0.76432121	19
soy_OGL_393	1000	8.4611053	0	2889	29.3	7	6.279315	0.101	0.76448196	24
soy_OGL_4322	1033	3.5637994	12.875121	2549	24.68	12	7.3511753	0.13699999	0.43033069	23
soy_OGL_4892	1000	9.0506868	3.5999999	6128	27.2	9	4.3883386	0.109	0.90697652	14
soy_OGL_6462	1000	5.1859083	0	1313	27.1	9	2.2665029	0.043000001	0.58891803	21
soy_OGL_2883	1390	7.0442643	0	4590	22.08	12	3.6073871	0.192	0.84933358	16
soy_OGL_3717	1227	7.065599	2.3634882	2890	23.79	9	8.9217615	0.18799999	0.82634336	27
soy_OGL_4588	1558	4.07375	4.4287548	2001	22.59	12	28.505186	0.145	0.97306156	12
soy_OGL_654	1433	6.4309473	0	3852	27.56	8	2.429085	0.121	0.76042163	29
soy_OGL_1067	1249	4.5279164	8.3266611	5081	23.61	8	3.1329453	0.145	0.86739236	23
soy_OGL_6768	1300	6.4668698	9.8461542	2962	22.92	8	7.071579	0.17299999	0.7485733	22
soy_OGL_4571	1344	5.6887312	0	3063	23.13	11	5.0945725	0.171	0.8233878	23
soy_OGL_3566	1351	5.4506187	0	5816	28.27	6	6.6481347	0.082000002	0.83514249	34
soy_OGL_63	1492	11.010665	0	1217	24.59	8	9.8884315	0.12800001	0.83664894	27
soy_OGL_1148	1400	5.8387361	0	4535	21.78	10	23.277988	0.161	0.96061844	28
soy_OGL_1431	1460	11.258756	0	1001	20.54	9	29.400101	0.155	0.87817818	21
soy_OGL_1569	1185	10.813619	0	2001	20.42	8	3.8238969	0.207	0.80749017	25
soy_OGL_2176	1239	8.9299202	8.3131561	2258	21.54	11	15.608394	0.17299999	0.8097477	27
soy_OGL_3312	1546	13.943912	0	2016	22.44	9	6.2724428	0.16	0.90862	19
soy_OGL_3531	1300	8.9636507	4.4615383	4583	23.84	11	22.125458	0.16500001	0.78864306	18

soy_OGL_4123	1264	9.6362591	0	5247	24.28	11	6.2611856	0.183	0.80515653	28
soy_OGL_6924	1419	8.8029718	0	1799	24.59	6	1.5437334	0.147	0.89740908	28
soy_OGL_6974	1300	4.5740175	0	2819	23.15	10	7.1771359	0.2	0.94196433	34
soy_OGL_269	1525	9.600378	0	1900	23.01	8	11.550646	0.139	0.88781226	17
soy_OGL_702	1469	8.118474	5.4458814	2440	22.87	8	18.015234	0.145	0.83542436	16
soy_OGL_2257	1349	6.0701208	0	7325	25.57	9	7.2798209	0.142	0.64817667	37
soy_OGL_3490	1560	5.426621	0	1853	21.21	10	18.830853	0.148	0.65261579	21
soy_OGL_6229	1467	8.3471193	0	4540	19.01	10	24.537083	0.18799999	0.88270897	15
soy_OGL_6316	1300	13.669057	0	4680	21.07	8	15.277287	0.189	0.94878298	14
soy_OGL_1182	1202	4.3006682	0	5692	22.29	12	9.2941637	0.191	0.90028566	29
soy_OGL_1395	1313	6.9438424	0	1001	23	10	4.7810822	0.162	0.81216967	32
soy_OGL_3247	1266	8.3858376	0	2091	22.9	11	10.410067	0.163	0.73401397	33
soy_OGL_5469	1186	4.9895315	0	2001	20.23	10	17.991777	0.20999999	0.87885821	27
soy_OGL_6759	1006	10.003958	0	3398	22.36	8	4.8079357	0.18700001	0.74053597	30
soy_OGL_1118	1317	2.8246608	0	3104	20.12	10	20.091202	0.17399999	0.97777069	16
soy_OGL_4122	1203	9.6362591	0	2640	21.03	7	4.6279554	0.185	0.80130452	26
soy_OGL_1538	1209	7.7790313	4.7973533	4542	25.31	12	11.322295	0.18700001	0.88121974	37
soy_OGL_4135	1200	10.646371	0	2410	26.08	11	5.6478987	0.15700001	0.83306968	31
soy_OGL_5888	1090	9.3344879	0	2118	26.23	10	13.706441	0.163	0.88698012	37
soy_OGL_5952	1437	11.551946	0	1216	24.91	12	9.3105898	0.145	0.70107466	22
soy_OGL_6537	1200	11.936101	0	3032	27.58	9	9.7252865	0.141	0.74462271	31
soy_OGL_2171	1641	8.2492304	0	2001	25.59	9	19.759336	0.086999997	0.81947464	21
soy_OGL_4816	1500	12.994103	0	1605	24.73	11	26.951105	0.149	0.95875835	16
soy_OGL_4828	1423	17.834297	0	4412	24.1	7	16.096285	0.125	0.97755277	17
soy_OGL_5526	1200	11.696812	9.416667	1297	23.33	9	12.411586	0.168	0.79240233	25
soy_OGL_4688	1200	10.870666	0	2789	27.33	5	2.6000493	0.13500001	0.63668627	39
soy_OGL_2951	1488	11.427831	0	2708	28.09	7	21.278648	0.081	0.89428985	17
soy_OGL_1655	1376	9.0782251	9.8110466	1224	25.87	8	10.100339	0.132	0.60382026	21
soy_OGL_6862	1300	10.103802	4.0769229	4714	28.23	5	7.2523332	0.119	0.83895165	28
soy_OGL_1175	1000	5.2192574	6.1999998	2018	22.9	8	6.6503263	0.109	0.90733331	26
soy_OGL_1196	1358	6.7576227	0	2266	23.63	12	4.8810558	0.089000002	0.8477149	12

soy_OGL_2108	1273	6.7726569	0	4344	22.54	12	4.9078932	0.116	0.95195079	14
soy_OGL_2459	1500	5.9070358	1.9333333	3602	24.26	11	12.493586	0.083999999	0.93047553	16
soy_OGL_2530	1119	7.693583	4.5576406	1207	19.3	14	6.2974586	0.109	0.76387763	9
soy_OGL_3606	1139	4.2983022	0	1295	20.54	11	3.4014645	0.123	0.87839907	18
soy_OGL_3733	1082	8.292532	0	3028	24.67	9	2.7641947	0.114	0.7968291	26
soy_OGL_4844	1500	6.4237089	0	1749	22.53	10	8.8825769	0.12800001	0.97751176	14
soy_OGL_998	1133	9.376277	5.1191525	1210	23.47	8	3.7583308	0.126	0.79042441	15
soy_OGL_1197	1200	6.7576227	0	2724	23.41	10	3.9776869	0.097999997	0.84272367	16
soy_OGL_1484	1070	5.6002989	4.5794392	1001	23.64	7	4.868824	0.082000002	0.95680165	21
soy_OGL_2439	1249	7.3556457	0	3601	23.29	11	6.6953406	0.009	0.97778499	10
soy_OGL_2848	1351	5.5548873	0	3307	25.09	9	6.9243832	0.107	0.67896575	26
soy_OGL_3261	1024	5.2893763	0	1001	22.16	10	4.6444116	0.079000004	0.83977348	19
soy_OGL_4577	1400	5.9374781	0	1825	25.42	7	5.9798493	0.090999998	0.83126211	21
soy_OGL_5439	1168	5.0618563	4.6232877	6322	23.45	11	12.076348	0.126	0.95205486	15
soy_OGL_6573	1100	4.8296428	0	1893	24.36	6	6.3806686	0.127	0.78129137	30
soy_OGL_6879	1291	4.5204587	0	1819	24.94	8	8.6290846	0.123	0.84870565	24
soy_OGL_28	1026	10.279623	0	2001	22.31	9	7.3927755	0.117	0.89936525	31
soy_OGL_251	1132	13.280943	0	2482	24.2	9	2.7782507	0.121	0.86641365	19
soy_OGL_388	1148	8.6352415	0	4332	23.51	10	7.2426195	0.145	0.77012396	28
soy_OGL_996	1500	7.1945324	0	2985	22.4	11	9.6904707	0.105	0.78430098	23
soy_OGL_1398	1200	13.123453	0	4087	22.58	8	5.579452	0.148	0.82397568	29
soy_OGL_1516	1200	6.1372461	0	2197	22.5	9	2.3529618	0.148	0.91025001	34
soy_OGL_1548	1031	7.6185937	0	2026	23.86	10	6.0570235	0.119	0.86186123	33
soy_OGL_2131	1445	8.6764479	0	3432	22.28	14	6.2823124	0.071000002	0.89048624	19
soy_OGL_2148	1100	7.3043337	0	1323	20.36	10	29.505194	0.112	0.85456425	29
soy_OGL_2423	1122	11.967738	0	1574	22.45	8	7.8382578	0.11	0.71920598	28
soy_OGL_2588	1438	1.7138728	0	2105	17.73	18	13.579116	0.017000001	0.64761889	15
soy_OGL_2851	1076	5.5548873	4.7397771	1001	21.46	10	12.49297	0.102	0.6905117	28
soy_OGL_3250	1371	9.1212559	2.69876	2690	22.24	11	22.320473	0.118	0.74469221	22
soy_OGL_3341	1228	10.878196	3.4201953	2001	22.63	10	1.3451328	0.164	0.85483909	26
soy_OGL_4460	1466	5.4048753	0	1538	20.32	14	13.442472	0.119	0.68319738	13

soy_OGL_4856	1311	6.8892426	0	4819	21.66	12	5.0714235	0.103	0.95908093	14
soy_OGL_5827	1035	14.406287	0	3985	22.99	9	6.9213305	0.13500001	0.92547268	20
soy_OGL_5870	1060	8.4256935	0	2207	21.13	12	5.6305022	0.121	0.91841018	26
soy_OGL_6315	1098	13.669057	0	2205	21.49	9	6.7253103	0.097999997	0.95150638	13
soy_OGL_6780	1685	11.277898	0	2308	22.43	13	17.330057	0.1	0.7676816	17
soy_OGL_6819	1050	6.6407022	0	2001	23.14	7	11.986353	0.12	0.80683309	35
soy_OGL_6925	1100	8.8029718	0	2594	22.9	11	1.6307318	0.126	0.89823061	29
soy_OGL_18	1000	10.21663	0	2193	22.2	6	5.6800199	0.079000004	0.91934544	26
soy_OGL_1119	1026	2.8246608	0	2001	21.83	10	20.091202	0	0.97783715	16
soy_OGL_1152	1132	5.8387361	0	6098	24.11	8	15.162896	0.122	0.95950878	28
soy_OGL_1161	1200	8.7633495	0	3314	21.75	9	14.453886	0.101	0.9415614	19
soy_OGL_1392	1000	6.9438424	0	3351	22	7	6.6973948	0.113	0.80912	32
soy_OGL_1760	1324	17.394621	0	3781	21.45	6	5.9724803	0.125	0.95799673	12
soy_OGL_1835	1100	8.3344145	0	3515	22.45	9	9.3286848	0.105	0.75597727	26
soy_OGL_1863	1090	5.4766021	0	5780	20.82	10	4.3317018	0.115	0.71919155	30
soy_OGL_2184	1060	9.8723383	0	2834	23.96	6	5.2317066	0.11	0.79620826	27
soy_OGL_2235	1512	7.2443314	0	1452	22.55	10	5.5046091	0.075999998	0.7048257	20
soy_OGL_2252	1005	4.5184188	0	3752	18.6	11	7.4144316	0.141	0.65505046	25
soy_OGL_2481	1111	7.0818982	0	3618	22.68	7	10.609393	0.126	0.89184266	23
soy_OGL_3196	1106	8.3576651	0	1988	23.86	8	13.64865	0.111	0.68767434	30
soy_OGL_3712	1109	6.9130831	0	4317	22	9	7.6834545	0.13	0.83234763	24
soy_OGL_3781	1100	13.260455	0	3238	19.9	10	9.6236525	0.097000003	0.69697428	18
soy_OGL_4655	1106	7.8542323	0	4817	23.59	9	6.7151036	0.108	0.69305187	26
soy_OGL_4683	1000	10.870666	0	2371	23.4	6	2.1210446	0.12800001	0.6415621	40
soy_OGL_5204	1090	6.245574	0	4165	21.37	8	3.4909284	0.085000001	0.97035366	20
soy_OGL_5824	1100	16.034658	0	5310	20.09	8	3.3637316	0.115	0.91747624	18
soy_OGL_6157	1162	5.245831	0	3264	21.42	10	6.3670201	0.122	0.79249614	19
soy_OGL_6519	1100	3.0955679	0	3463	21	11	3.5122933	0.118	0.70603663	26
soy_OGL_6551	1050	13.347547	0	2802	22.76	5	4.9122868	0.121	0.75651085	29
soy_OGL_6615	1300	8.5314484	2.4615386	4487	23.3	11	11.619727	0.097999997	0.88702506	14
soy_OGL_6935	1305	8.8029718	2.6053641	2207	24.13	7	6.5706534	0.064000003	0.9060241	19

soy_OGL_13	1391	10.132022	0	2340	25.73	9	10.755423	0.111	0.94366062	18
soy_OGL_365	1059	7.5258417	0	2001	25.02	10	5.0669246	0.057999998	0.82388288	27
soy_OGL_1049	1509	5.3472867	0	2086	24.51	15	8.8484955	0.056000002	0.85156506	29
soy_OGL_1058	1261	4.5279164	5.2339411	2001	23.55	11	9.1935968	0.096000001	0.86033779	27
soy_OGL_1076	1343	7.9827704	0	2001	24.05	12	18.522795	0.082999997	0.88968283	16
soy_OGL_1396	1100	6.9438424	5	2646	25.36	11	5.6556125	0.093999997	0.81247205	32
soy_OGL_1461	1048	9.1846943	0	3183	26.24	9	10.279806	0.123	0.92398393	31
soy_OGL_2264	1000	7.1234393	0	1611	28.1	6	6.4291024	0.12800001	0.6370092	44
soy_OGL_2507	1037	7.4874678	8.4860172	2534	21.69	14	4.0942936	0.141	0.83143008	27
soy_OGL_2922	1100	9.1610184	0	3039	25.27	12	6.7864761	0.11	0.96085531	26
soy_OGL_3460	1144	8.8430595	15.559441	1285	20.62	15	9.3329878	0.12800001	0.61553419	16
soy_OGL_3748	1059	6.8004804	7.5542965	2001	23.41	12	10.624949	0.123	0.77211761	24
soy_OGL_4814	1115	6.1591496	11.928251	6159	22.95	12	17.368975	0.109	0.95304173	15
soy_OGL_5396	1398	9.4848547	0	4789	25.89	12	6.8356376	0.094999999	0.71368307	19
soy_OGL_6225	1333	10.775764	3.0007503	1672	26.48	10	8.1916475	0.121	0.87718832	27
soy_OGL_6820	1175	6.4448819	5.1063828	1032	26.8	8	12.408299	0.105	0.80742973	34
soy_OGL_6825	1342	6.5125389	0	2887	27.71	10	12.43193	0.101	0.80908	36
soy_OGL_234	1394	9.1542082	7.7474895	2979	25.96	8	7.3071136	0.097999997	0.84413832	20
soy_OGL_717	1300	9.6048651	0	3998	28.61	7	5.8511581	0.072999999	0.85599148	26
soy_OGL_3565	1200	5.4506187	0	2443	27.25	6	6.6481347	0.057	0.83502609	33
soy_OGL_209	1180	14.722309	0	1001	25.5	7	3.9210536	0.066	0.8164348	24
soy_OGL_1163	1500	9.3865528	0	2456	22.73	10	34.685966	0.041999999	0.93221492	16
soy_OGL_1442	1078	8.1389084	0	7010	22.54	13	18.106047	0.082999997	0.89868128	22
soy_OGL_1671	1343	9.1770983	0	2206	23.08	14	12.37324	0	0.70244771	13
soy_OGL_1707	1006	7.9271779	0	1481	22.46	13	6.8885236	0.125	0.82022077	34
soy_OGL_1831	1100	8.2200718	0	2685	22.18	10	23.590605	0.094999999	0.75779545	27
soy_OGL_2258	1100	6.0701208	0	2496	23.18	10	22.539761	0.111	0.64665598	39
soy_OGL_2920	1100	9.3318186	2.6363637	7206	23.63	12	11.694722	0.12	0.96328938	29
soy_OGL_2923	1093	9.2812614	0	2001	23.69	10	7.8417754	0.097999997	0.96028543	26
soy_OGL_3583	1000	6.0902267	0	5307	25.2	7	19.78978	0.090000004	0.84698689	41
soy_OGL_3941	1000	8.8798027	8.1999998	2231	21.1	9	24.416506	0.139	0.86931968	27

soy_OGL_4521	1134	8.7941418	0	2348	22.22	11	18.249975	0.13	0.75677896	31
soy_OGL_4682	1016	10.870666	0	1041	27.26	6	2.1210446	0.14	0.64208394	41
soy_OGL_4697	1012	8.5891142	0	2009	23.22	11	13.431599	0.1	0.61413074	39
soy_OGL_4705	1238	9.078599	0	3516	24.71	12	2.4500916	0.081	0.60209554	32
soy_OGL_5833	1138	13.562174	0	5177	25.83	8	5.9149113	0.125	0.96099943	22
soy_OGL_5874	1076	9.8349943	0	1001	24.81	9	8.0013075	0.103	0.90858614	35
soy_OGL_6520	1021	21.291258	0	2467	21.64	9	5.8238935	0.106	0.70837444	21
soy_OGL_6787	1092	11.136688	0	2317	22.06	9	29.654833	0.125	0.77692461	27
soy_OGL_3316	1000	18.038614	0	11027	25.8	9	2.0417116	0.064999998	0.89663136	26
soy_OGL_4479	1400	7.5810852	0	6040	26.5	10	24.59482	0.079000004	0.71154994	30
soy_OGL_4972	1100	10.245035	12.272727	3058	21.36	10	13.928859	0.12899999	0.73033941	17
soy_OGL_5848	1000	9.6763773	0	1065	23.7	7	9.7075167	0.07	0.98163736	20
soy_OGL_3701	1206	7.5635667	12.106136	2001	20.64	11	13.507148	0.075999998	0.86730874	6
soy_OGL_650	1031	6.5986133	0	3176	25.99	8	2.2432523	0	0.75946975	30
soy_OGL_1414	1000	12.59621	8.6000004	7010	26.4	9	5.248415	0.119	0.85040802	19
soy_OGL_3209	1027	5.9144826	4.7711782	4220	25.8	7	2.0250385	0.071000002	0.69640464	35
soy_OGL_6252	1357	5.4503398	0	4211	27.56	8	19.218313	0	0.91391361	23
soy_OGL_6863	1200	10.103802	3.5833333	2332	27.16	5	7.2523332	0.082000002	0.83921665	27
soy_OGL_47	1000	9.9827271	0	4721	27.5	6	3.9571714	0.029999999	0.86362422	30
soy_OGL_226	1000	9.4661407	0	3539	24.2	9	6.0070243	0	0.83454925	22
soy_OGL_1814	1100	6.0240116	0	3553	23.45	10	18.918741	0	0.77477598	26
soy_OGL_2961	1099	10.851157	0	6790	25.38	10	9.8085117	0	0.86199576	19
soy_OGL_3123	1011	6.9868913	18.397627	1091	21.76	9	14.700299	0.145	0.54204679	23
soy_OGL_3171	1000	12.618308	5.5	3161	23.1	10	12.64767	0.11	0.64002174	18
soy_OGL_3363	1300	12.993029	4.5384617	2354	25.15	9	12.98272	0.059999999	0.80211061	15
soy_OGL_5763	1094	13.454047	0	3403	25.5	7	15.135885	0.093000002	0.78812826	20
soy_OGL_6570	1100	4.8296428	0	2077	25.18	8	2.9845872	0	0.77932817	32
soy_OGL_6600	1377	8.5314484	0	2001	22	11	17.30092	0	0.8582505	10
soy_OGL_6941	1023	11.24362	0	2001	22.67	8	6.0745077	0	0.91792732	18
soy_OGL_3830	1336	7.930079	0	2001	24.77	12	7.1796374	0.167	0.54532462	28
soy_OGL_2511	1149	7.4874678	0	3355	24.8	8	2.8637574	0.191	0.82444519	25

soy_OGL_773	1087	10.280827	3.9558418	2162	22.44	9	6.9784603	0.193	0.95040625	17
soy_OGL_1795	1236	5.5180402	0	3472	23.54	13	26.981222	0.175	0.82382673	11
soy_OGL_4885	1200	3.9014754	3.5	2536	23.83	11	24.040154	0.18099999	0.92188776	19
soy_OGL_6297	1275	6.0601311	0	7783	26.19	12	14.940119	0.146	0.94958365	18
soy_OGL_949	1048	6.087534	0	2274	21.75	10	5.1655254	0.23100001	0.73822254	15
soy_OGL_1670	1200	9.1770983	0	3981	24	13	12.644554	0.17900001	0.70229006	13
soy_OGL_2111	1314	6.2956948	0	4891	24.88	9	5.7009974	0.16	0.93963695	16
soy_OGL_3609	1162	5.1192613	0	5154	24.01	10	21.70985	0.15800001	0.88729113	16
soy_OGL_202	1070	11.890499	0	2230	25.14	6	6.6497402	0.184	0.81109506	28
soy_OGL_4466	1237	7.5555859	0	2001	20.69	15	30.275328	0.21699999	0.70052874	25
soy_OGL_6929	1171	8.8029718	0	1877	21.17	12	32.130795	0.207	0.90329564	28
soy_OGL_5545	1249	7.2413769	0	2648	22.49	9	19.547129	0.182	0.76497895	18
soy_OGL_204	1049	11.890499	0	2696	27.74	7	7.0201573	0.13500001	0.81138164	28
soy_OGL_221	1100	11.444668	0	2303	25.54	11	16.147816	0.16	0.82990736	24
soy_OGL_1246	1148	9.8108654	3.3972125	3322	25.52	11	3.4339721	0.161	0.74276227	25
soy_OGL_6755	1000	10.182024	0	2468	29.2	5	4.1971292	0.122	0.73824382	33
soy_OGL_694	1141	11.121198	0	3756	24.8	10	7.9367633	0.124	0.81380719	20
soy_OGL_724	1081	9.0755138	0	8048	22.94	14	5.5886073	0.12800001	0.86497098	19
soy_OGL_1214	1000	6.7576227	0	3785	23.5	10	10.383507	0.139	0.81748682	24
soy_OGL_1699	1000	6.9589791	0	1050	23.9	9	2.822082	0.12899999	0.81226516	27
soy_OGL_3979	1229	5.9596634	3.8242474	2123	21.88	11	3.9325228	0.17	0.89314228	14
soy_OGL_4465	1096	7.5555859	0	4341	24.72	13	4.6526146	0.126	0.6984238	25
soy_OGL_4875	1001	4.0852547	0	2001	22.77	13	5.6381521	0.141	0.93149608	27
soy_OGL_6849	1000	3.720983	0	1730	23.4	12	15.323351	0.147	0.82267642	23
soy_OGL_309	1012	10.227943	0	1452	24.5	8	6.2707047	0.122	0.94504631	13
soy_OGL_1355	1087	11.526744	0	1015	23.45	9	10.888006	0.12899999	0.75878805	13
soy_OGL_3543	1100	8.9636507	0	3299	27.36	7	2.4798691	0.103	0.80055553	24
soy_OGL_3663	1200	4.1581578	5.6666665	2156	22.25	9	21.538654	0.142	0.98798281	12
soy_OGL_3680	1192	6.1510382	0	2505	23.23	11	15.506551	0.078000002	0.93496776	11
soy_OGL_3758	1012	7.3212295	2.7667985	2502	25.19	8	14.347114	0.132	0.75019693	22
soy_OGL_3907	1000	9.3006687	3.8	2659	24.4	9	4.775373	0.117	0.77333182	21

soy_OGL_3973	1118	9.8309717	0	3073	23.7	10	8.1908779	0.107	0.93585384	10
soy_OGL_4006	1199	11.197123	0	3688	23.1	11	1.4170552	0.14	0.80231929	10
soy_OGL_4161	1083	9.3938532	0	2001	24.09	9	9.8772774	0.082000002	0.90237164	15
soy_OGL_4840	1000	5.6178126	0	4133	19.9	11	4.769515	0.097000003	0.98904175	9
soy_OGL_5511	1174	5.4987149	0	2001	24.02	9	6.8508983	0.101	0.82244635	17
soy_OGL_6616	1000	8.5314484	0	2006	23.3	11	10.877316	0.103	0.88993227	11
soy_OGL_6775	1000	10.365577	0	2680	24.2	12	10.181883	0.138	0.7634322	12
soy_OGL_403	1014	7.6263041	0	2001	20.71	14	9.4462318	0.13600001	0.75104731	23
soy_OGL_3721	1014	7.0987005	0	1703	23.57	9	14.301719	0.126	0.82221889	26
soy_OGL_401	1109	7.6530638	0	2868	23.98	9	10.638362	0.13	0.75399506	25
soy_OGL_2210	1000	6.4445391	0	2193	20.8	9	26.314205	0.14399999	0.75361007	26
soy_OGL_2422	1000	11.967738	0	4840	25	9	6.9859967	0.14399999	0.71900052	28
soy_OGL_3650	1100	1.8333012	0	6682	24.54	9	32.674976	0.124	0.94547969	24
soy_OGL_3965	1009	8.0769224	0	4182	21.5	11	14.906283	0.079000004	0.9475165	10
soy_OGL_5178	1075	10.392078	0	1183	22.32	8	2.5952768	0.131	0.88934702	16
soy_OGL_5391	1116	9.3595705	0	1001	22.49	9	6.1577964	0.114	0.70601594	17
soy_OGL_99	1000	11.199151	0	3182	26.5	9	8.8539562	0.133	0.75744849	24
soy_OGL_315	1000	12.282213	0	5402	25.5	14	11.158525	0.134	0.92966664	15
soy_OGL_790	1100	8.0895433	0	2730	25	11	10.022397	0.11	0.88307029	19
soy_OGL_1453	1031	9.2263308	0	1001	27.64	8	7.2276168	0.115	0.91414666	32
soy_OGL_2189	1000	10.96957	4.0999999	3847	27.8	8	6.9463873	0.132	0.79076147	29
soy_OGL_2196	1042	8.5738249	0	2375	26.87	9	3.626899	0.13	0.77564025	32
soy_OGL_2447	1038	7.4119039	4.5279384	1507	23.98	11	15.524823	0.107	0.96102798	15
soy_OGL_2489	1100	6.8494215	0	1541	23.54	12	15.236042	0.050999999	0.88390207	17
soy_OGL_2493	1000	7.548306	0	1347	22.7	12	9.33671	0.035	0.87032866	15
soy_OGL_2926	1153	8.7015877	0	2001	25.67	12	10.566432	0.094999999	0.95109695	22
soy_OGL_2942	1100	11.741648	0	2233	25.36	9	8.6707573	0.12	0.91506386	21
soy_OGL_3990	1089	11.197123	4.315886	2001	23.14	13	13.967981	0.116	0.83717245	11
soy_OGL_4585	1100	4.07375	5.6363635	3804	23.81	14	36.785587	0.125	0.97695422	10
soy_OGL_6314	1166	16.098692	0	1071	25.38	10	7.5000157	0.075000003	0.95396316	11
soy_OGL_1425	1077	11.581857	0	2579	26.09	7	4.976583	0.115	0.87509716	20

soy_OGL_2635	1115	7.9126515	0	2001	25.56	12	10.631259	0.041999999	0.56457293	22
soy_OGL_4108	1061	12.218921	0	3850	26.01	11	10.911925	0.107	0.70363909	16
soy_OGL_4443	1192	8.6510143	0	1153	26.34	10	13.702197	0.078000002	0.6350987	20
soy_OGL_6175	1000	9.6457357	0	1275	23.4	10	9.2655945	0.067000002	0.82034969	16
soy_OGL_6230	1100	9.5319738	0	2840	25.54	9	24.906801	0.097000003	0.88275808	15
soy_OGL_65	1000	11.49644	0	4967	25.7	8	17.917261	0.14300001	0.83196366	29
soy_OGL_1051	1065	5.3472867	0	1956	23.19	10	28.563259	0.113	0.8546114	29
soy_OGL_2149	1126	7.3043337	0	2001	24.6	11	26.886021	0.126	0.85423172	30
soy_OGL_3761	1000	10.661443	0	3203	23.6	13	18.2148	0.131	0.74437338	20
soy_OGL_5826	1000	16.034658	0	3468	24.7	10	5.8203039	0.101	0.92175537	19
soy_OGL_947	1040	11.357085	0	1001	23.26	10	18.130402	0.088	0.72310621	16
soy_OGL_1430	1100	11.258756	0	4942	24.45	8	31.03154	0.116	0.8772282	22
soy_OGL_1845	1013	5.552063	0	1024	22.8	9	32.676273	0.075999998	0.73705518	26
soy_OGL_1907	1000	14.749738	0	2184	24.6	11	20.122959	0.13699999	0.62027919	13
soy_OGL_6604	1189	8.5314484	0	2001	23.63	10	28.366709	0.074000001	0.86821753	16
soy_OGL_3772	1200	12.101471	0	2449	28.08	8	8.3230724	0.068999998	0.71785837	19
soy_OGL_1001	1100	7.2732038	0	4925	24.27	12	23.648502	0	0.79421991	15
soy_OGL_1092	1324	6.4006157	13.141994	1330	24.62	9	21.837635	0.145	0.92009544	13
soy_OGL_2451	1439	7.5294766	12.508687	1728	23.55	10	14.224622	0.142	0.94860488	13
soy_OGL_3752	1600	7.633616	0	2662	29.12	10	8.351757	0.075999998	0.76291847	26
soy_OGL_2116	1300	6.8356886	0	1577	24.15	10	4.4560003	0.067000002	0.93608713	15
soy_OGL_6837	1030	3.9573007	0	1389	24.95	10	1.4578713	0.093999997	0.81484228	35
soy_OGL_4568	1000	4.667098	4.0999999	2290	23.5	9	3.3282983	0.104	0.82186717	23
soy_OGL_2445	1304	6.659574	8.1288347	2582	22.92	12	5.0505848	0.079000004	0.96495104	14
soy_OGL_2882	1000	7.0442643	8.6999998	5051	23	14	1.8248138	0.008	0.84862179	17
soy_OGL_3716	1189	6.9130831	11.7746	2001	24.72	10	7.6231704	0.112	0.83180165	24
soy_OGL_2564	1130	4.5566983	0	3248	24.6	15	15.692022	0.005	0.69877625	17
soy_OGL_8	1167	8.163537	6.8551841	2855	23.56	6	10.688488	0.15700001	0.95832324	15
soy_OGL_3279	1155	1.0940363	0	4173	23.54	5	4.6100678	0.171	0.97792166	22
soy_OGL_665	1040	6.8420768	0	9238	22.5	6	4.8541975	0.176	0.76967192	33
soy_OGL_1084	1430	6.1470599	0	6348	23.42	8	9.4256601	0.138	0.9025346	15

soy_OGL_1382	1000	8.1746645	0	3714	27.2	3	4.5882316	0.146	0.80141759	35
soy_OGL_2700	1256	3.3123655	0	3151	17.51	9	5.5970707	0.193	0.46723232	19
soy_OGL_3923	1432	8.8987665	0	6506	28.21	6	1.5728644	0.07	0.82219827	19
soy_OGL_710	1300	8.4636536	0	10012	27	7	6.3578019	0.108	0.84741116	23
soy_OGL_4350	1604	6.5096278	0	4289	23.94	9	8.9396629	0.103	0.48394483	20
soy_OGL_4622	1321	4.2519794	0	5807	26.94	5	22.78409	0.104	0.75732541	29
soy_OGL_4329	1482	6.0304036	0	4799	20.44	8	1.9704498	0.139	0.44426787	18
soy_OGL_5700	1600	1.0714349	0	3297	21.18	8	7.0013595	0.121	0.39532951	15
soy_OGL_5921	1305	8.3593283	0	7482	21.6	5	17.435148	0.161	0.83367831	15
soy_OGL_6513	1200	7.4994183	0	8398	25.41	5	5.8478813	0.127	0.69273365	26
soy_OGL_3151	1153	9.2073507	0	7016	21.42	6	14.917093	0.163	0.58287609	19
soy_OGL_4440	1500	8.986455	0	3680	26.26	7	23.282284	0.107	0.6302411	25
soy_OGL_1817	1100	0.91241473	0	1159	24.81	4	4.1563892	0.131	0.7697565	32
soy_OGL_2219	1000	4.6833062	0	2426	23.3	8	8.4474306	0.086999997	0.74920183	23
soy_OGL_4582	1000	1.4350497	0	2177	21.1	7	4.6542816	0.109	0.83661604	19
soy_OGL_4813	1033	5.8693018	0	4419	23.91	5	6.4310737	0.125	0.9485476	18
soy_OGL_6302	1300	2.1871984	6.8461537	3536	20.61	8	6.4408102	0.145	0.99124253	8
soy_OGL_89	1031	7.4370308	0	2749	24.05	6	4.0077295	0.108	0.77486479	27
soy_OGL_358	1000	7.2958274	0	10320	25.9	8	3.7183652	0.109	0.83268917	29
soy_OGL_698	1121	11.121198	0	3718	21.49	8	11.040893	0.126	0.81648868	18
soy_OGL_1200	1243	6.7576227	0	4106	22.92	8	3.1760921	0.075000003	0.83559209	21
soy_OGL_1799	1300	5.5180402	4	3675	20.76	9	6.7496748	0.107	0.81379545	9
soy_OGL_2128	1000	9.2421608	0	7275	19.1	7	18.200476	0.141	0.89777523	17
soy_OGL_2166	1000	8.3071995	0	7096	22.7	7	20.497267	0.134	0.83149081	29
soy_OGL_2872	1000	6.2971745	0	4671	20.1	10	7.883625	0.114	0.80535549	17
soy_OGL_2887	1091	8.9753227	0	13579	21.81	12	9.1583328	0.12	0.86650401	21
soy_OGL_3159	1641	8.0538549	0	1657	22.79	10	1.7218801	0.078000002	0.60564798	15
soy_OGL_3185	1021	10.885145	0	4624	20.66	9	27.316723	0.13500001	0.6629048	24
soy_OGL_3671	1100	4.6051531	0	8645	21.09	11	12.22925	0.109	0.95821458	13
soy_OGL_3911	1000	9.3006687	0	2626	22.5	6	5.2159028	0.142	0.78463554	22
soy_OGL_4603	1000	5.7093301	0	3925	20	12	6.8016148	0.013	0.88228106	10

soy_OGL_4891	1462	9.0506868	0	4803	24.14	8	4.8738451	0.1	0.90701652	14
soy_OGL_5327	1036	7.7459235	0	3374	20.94	10	6.9189677	0.092	0.65118903	20
soy_OGL_5395	1203	9.4848547	0	2828	21.94	9	4.8316588	0.097000003	0.71328187	19
soy_OGL_5937	1012	7.4355073	0	2646	23.32	7	8.5883512	0.105	0.73636675	23
soy_OGL_6535	1030	10.313567	0	9446	22.13	9	5.7515612	0.141	0.73503619	21
soy_OGL_6593	1157	5.3763165	0	2720	18.15	8	11.473552	0.185	0.80272633	20
soy_OGL_6612	1156	8.5314484	0	4400	16.95	8	9.1538372	0.16	0.87877911	17
soy_OGL_6741	1235	9.1031542	0	3910	24.61	7	6.4467001	0.113	0.72956097	27
soy_OGL_6860	1000	10.103802	0	6465	24.3	7	4.7677336	0.123	0.83480901	25
soy_OGL_2996	1039	10.117564	0	2482	25.5	5	4.632237	0.096000001	0.80398983	21
soy_OGL_3654	1400	1.9542303	0	8715	24.28	10	15.281493	0.059	0.95387119	14
soy_OGL_4304	1400	4.4642582	0	2291	25.21	9	5.0807405	0.094999999	0.4001694	26
soy_OGL_4358	1300	5.3951726	0	1188	22.3	10	4.1547394	0.066	0.49451637	16
soy_OGL_6143	1300	4.9215565	0	2074	23.69	6	4.2990394	0.106	0.77052325	16
soy_OGL_2858	1200	5.5548873	6.4166665	3256	23.16	8	6.9590759	0.113	0.71467191	10
soy_OGL_4780	1400	3.6792157	0	4272	22.14	6	4.6919894	0.114	0.88008332	8
soy_OGL_664	1102	6.8420768	0	6538	26.86	6	4.8541975	0.093999997	0.76957834	33
soy_OGL_780	1000	9.4103231	0	4353	23.8	7	3.9127805	0	0.93336719	18
soy_OGL_833	1200	9.0662546	0	5219	23.5	6	5.8779864	0.093999997	0.71366405	22
soy_OGL_957	1050	13.85167	0	3701	20.76	5	7.143816	0.116	0.74691314	21
soy_OGL_1083	1244	6.1470599	0	8704	22.99	8	9.4256601	0.11	0.90247202	15
soy_OGL_1115	1040	4.3241005	0	4535	22.98	7	13.3234	0.071000002	0.97214192	16
soy_OGL_1244	1100	10.032667	0	5723	25.27	7	3.0019841	0.115	0.74627632	22
soy_OGL_2104	1000	4.8394938	4.5	5199	19.6	8	13.445053	0.071000002	0.9636789	10
soy_OGL_2650	1064	7.1323462	0	1139	23.49	7	16.657085	0.096000001	0.53437191	27
soy_OGL_2678	1471	10.232581	0	1001	25.96	7	9.0743437	0.066	0.50281918	23
soy_OGL_2698	1543	8.1054287	0	1044	24.75	8	6.2417569	0.086000003	0.4718042	19
soy_OGL_2968	1000	10.693128	10.1	1907	21.8	5	16.259047	0.133	0.85339147	19
soy_OGL_2978	1300	12.918274	2.3076923	4461	24.53	6	9.0673981	0.104	0.83086383	20
soy_OGL_2992	1000	9.2852879	0	8631	24.1	6	17.602253	0.134	0.80742556	25
soy_OGL_3007	1087	6.375104	0	2001	22.63	6	8.0146637	0.108	0.77958989	18

soy_OGL_4321	1118	3.5637994	2.6833632	1001	20.66	10	7.4079089	0.11	0.42882937	21
soy_OGL_4401	1100	8.6328869	5.4545455	3661	22.27	9	5.2014475	0.105	0.5619669	25
soy_OGL_5399	1000	9.4738331	0	2211	22.5	5	5.6082315	0.071000002	0.73511648	20
soy_OGL_6310	1100	18.142227	0	9136	23.81	5	10.879979	0.122	0.96122128	11
soy_OGL_6449	1100	8.9351873	6.3636365	6413	22.9	8	10.736296	0.122	0.57206172	29
soy_OGL_6499	1209	8.8186426	0	5186	25.47	7	3.1205337	0.097000003	0.68508399	26
soy_OGL_6507	1098	7.9388223	0	4071	23.13	7	8.3896561	0.103	0.68881863	23
soy_OGL_6592	1000	5.3763165	0	4120	22.1	8	11.473552	0.050000001	0.80267954	20
soy_OGL_672	1097	4.2763386	0	8382	23.33	6	1.8188249	0.112	0.77920878	23
soy_OGL_800	1000	9.380168	0	10308	24	4	1.8055148	0.13699999	0.84942967	24
soy_OGL_1271	1012	6.6517758	7.5098815	6028	22.03	7	4.5365448	0.125	0.68717855	19
soy_OGL_1666	1400	8.7383938	4.2142859	1501	23	8	11.893914	0.11	0.63229227	8
soy_OGL_1972	1100	8.7267275	0	3241	24.45	6	12.209159	0.115	0.48731494	27
soy_OGL_2298	1084	9.808919	0	6449	20.84	6	2.2282088	0.121	0.60087687	20
soy_OGL_3548	1100	8.9636507	0	10607	23.45	7	2.0246992	0.116	0.80656523	22
soy_OGL_3905	1000	9.3006687	0	8036	22.9	6	22.389164	0.133	0.76588649	20
soy_OGL_4330	1572	6.0304036	0	2001	23.79	7	1.4850141	0.082999997	0.44436318	20
soy_OGL_4970	1100	10.245035	0	6897	23.54	6	5.0703917	0.121	0.73286682	16
soy_OGL_5643	1018	9.2479429	0	1001	19.74	5	4.4369993	0.122	0.53974646	17
soy_OGL_6137	1400	3.3948011	0	3979	23.07	5	8.1777868	0.102	0.76730537	14
soy_OGL_653	1100	6.4309473	0	4763	26.36	8	2.429085	0	0.76036036	29
soy_OGL_909	1297	5.9492388	0	1001	28.37	5	12.264137	0.056000002	0.67727435	29
soy_OGL_3488	1000	5.426621	10	1924	23.2	8	20.128374	0.101	0.65233481	21
soy_OGL_4434	1200	8.4435787	0	3252	27	8	6.2117472	0.086000003	0.62232107	26
soy_OGL_4789	1329	13.341439	0	3596	28.44	6	5.8744464	0.025	0.90907586	15
soy_OGL_912	1200	6.1910648	0	1375	24.16	7	30.498451	0.061000001	0.68122745	26
soy_OGL_1550	1000	8.9413004	0	11600	25.9	8	16.843077	0.089000002	0.85888094	30
soy_OGL_5194	1161	13.332328	7.0628767	2328	25.49	4	6.7836704	0.077	0.95834804	16
soy_OGL_5257	1400	11.939192	0	6881	28.21	7	6.215343	0.055	0.85051221	19
soy_OGL_487	1263	4.9804826	0	1001	22.8	11	7.8100209	0.162	0.5041126	15
soy_OGL_1291	1400	6.4559865	0	1729	24.5	10	27.168205	0.147	0.64607018	15

soy_OGL_2542	1180	4.3840361	0	3638	21.77	9	3.1309779	0.193	0.73669648	19
soy_OGL_3456	1420	9.534853	0	2001	23.52	9	5.5341597	0.149	0.60203362	14
soy_OGL_4388	1189	7.6460648	0	3842	26.49	9	5.8016953	0.122	0.54539502	26
soy_OGL_2651	1082	7.1323462	0	2700	22.92	7	16.657085	0.15000001	0.53404194	27
soy_OGL_3022	1025	10.401243	0	3938	21.26	8	12.126117	0.19400001	0.75211674	20
soy_OGL_1959	1276	6.5777268	2.8996866	2399	26.48	8	4.8051248	0.131	0.49845532	24
soy_OGL_493	1300	4.9355707	0	2008	23.84	7	9.632616	0.15899999	0.48145044	21
soy_OGL_6188	1274	4.7146115	0	7288	24.64	6	3.2910631	0.152	0.84261918	12
soy_OGL_1790	1258	5.5180402	0	6611	23.92	9	24.380384	0.121	0.83340585	9
soy_OGL_1970	1003	8.7267275	0	4366	28.11	7	8.1822138	0.134	0.48879546	26
soy_OGL_511	1156	3.8568666	0	5360	24.39	7	9.7380648	0.149	0.45568216	22
soy_OGL_2753	1100	8.4189348	0	4078	24.63	12	26.415489	0.131	0.36846852	11
soy_OGL_1598	1180	5.281703	0	6584	21.1	8	31.528429	0.164	0.69575596	16
soy_OGL_5839	1000	13.562174	0	7141	28.4	5	7.0481896	0.13600001	0.96448809	22
soy_OGL_556	1179	20.895227	0	3157	22.9	10	14.341985	0.169	0.32605857	18
soy_OGL_1107	1195	6.4156709	0	7319	22.76	9	61.892998	0.119	0.94489861	18
soy_OGL_266	1000	6.2561297	0	5158	25.1	7	9.0979433	0.124	0.88642436	18
soy_OGL_2891	1001	8.9753227	0	5565	26.87	7	9.3781614	0.13699999	0.87061614	21
soy_OGL_3160	1195	8.0538549	0	2001	21.75	10	1.7218801	0.167	0.60606617	15
soy_OGL_4007	1207	11.197123	0	4981	24.02	11	1.4170552	0.097000003	0.80226922	10
soy_OGL_1003	1000	6.542963	0	5831	22	9	11.025846	0.121	0.79697359	15
soy_OGL_1588	1137	6.6485653	0	2697	22.69	9	15.728658	0.127	0.77001786	16
soy_OGL_2623	1000	8.794776	0	3154	23.2	9	4.4608855	0.118	0.5805909	24
soy_OGL_2866	1134	5.7699661	0	2992	21.6	10	29.133146	0.118	0.78542089	14
soy_OGL_2977	1000	12.918274	0	2161	25	5	10.880878	0.127	0.83097446	20
soy_OGL_3023	1028	10.401243	0	6278	24.02	8	12.126117	0.13	0.75201702	20
soy_OGL_6770	1143	7.4753222	0	3252	22.57	8	10.274889	0.126	0.7501722	17
soy_OGL_771	1010	10.71943	0	7320	26.73	6	8.9903688	0.077	0.9579922	16
soy_OGL_1897	1116	9.4963474	4.749104	2253	24.28	9	4.9972792	0.115	0.6534543	14
soy_OGL_2306	1063	7.6200151	0	2001	23.23	9	4.3208532	0.117	0.56637591	15
soy_OGL_2641	1051	7.9126515	0	2068	25.88	7	4.3148041	0.122	0.55085665	26

soy_OGL_2953	1041	9.0759773	0	1001	26.12	4	8.4233713	0.13	0.88580251	16
soy_OGL_3661	1011	4.1581578	0	3249	24.43	7	21.907316	0.039000001	0.98933047	12
soy_OGL_4458	1024	5.2578583	0	2161	23.73	9	20.440519	0.093000002	0.68226254	12
soy_OGL_5169	1028	8.0355263	0	5820	25.48	6	4.7568765	0.12800001	0.8496694	18
soy_OGL_5385	1015	9.3595705	0	4413	24.63	9	7.6504912	0.082999997	0.69111025	20
soy_OGL_6472	1084	4.584981	0	2427	24.44	10	23.816908	0.097000003	0.6175766	14
soy_OGL_1636	1200	3.861047	0	2184	22.25	8	4.1028008	0.148	0.56473625	9
soy_OGL_3267	1015	5.2893763	0	4349	23.74	4	3.9906518	0.132	0.84770495	19
soy_OGL_3520	1100	1.9912556	0	6107	23.72	7	11.352756	0.113	0.74891526	17
soy_OGL_3526	1161	1.9912556	0	1001	22.56	6	5.431469	0.116	0.75413102	14
soy_OGL_3812	1034	7.745584	0	2756	21.47	9	8.2033606	0.108	0.59044492	7
soy_OGL_5136	1109	0.82107258	0	8491	22	10	9.9586048	0.12800001	0.69155532	13
soy_OGL_5383	1146	9.3595705	0	3214	25.13	6	2.3728209	0.127	0.68839908	16
soy_OGL_6486	1098	8.5538664	0	5846	25.5	7	5.2517185	0.113	0.6486975	19
soy_OGL_475	1000	5.5857544	0	1137	22.5	7	8.1280136	0.12	0.53036487	26
soy_OGL_2620	1100	8.8686056	0	2314	20.54	8	37.93264	0.132	0.58382869	23
soy_OGL_3788	1096	13.802341	0	2001	23.17	8	18.067875	0.12800001	0.68422902	10
soy_OGL_6510	1000	7.9388223	0	4500	25.6	6	18.757362	0.12800001	0.69212443	26
soy_OGL_3129	1000	8.0850887	0	4105	24.8	6	15.405865	0.126	0.55145979	25
soy_OGL_4089	1083	12.218921	0	2001	22.89	7	15.850635	0.134	0.64212143	10
soy_OGL_1650	1078	8.4981375	3.9888682	3034	25.88	9	9.2293787	0.098999999	0.59749758	19
soy_OGL_1886	1041	9.2462587	0	2470	24.68	10	19.542131	0.104	0.67159933	15
soy_OGL_2554	1000	3.5880075	5.0999999	2454	24.6	7	23.783754	0.106	0.71965736	22
soy_OGL_2666	1100	6.8734031	0	2293	26.45	10	12.195951	0.097000003	0.52218533	25
soy_OGL_2979	1041	12.918274	0	6185	29.29	6	8.7957888	0.101	0.83055747	21
soy_OGL_3371	1084	12.902715	0	2001	28.78	5	8.0822678	0.107	0.77027726	17
soy_OGL_3440	1100	7.5834217	0	1765	24.9	11	21.444805	0.093999997	0.55410093	12
soy_OGL_4770	1000	6.7980485	0	2518	26.2	7	28.525553	0.117	0.83904696	9
soy_OGL_4996	1000	8.6126404	0	1195	27.5	5	4.6131344	0.086999997	0.70197648	26
soy_OGL_565	1000	21.491308	0	4316	23.3	10	3.492749	0.114	0.31026578	21
soy_OGL_5585	1170	5.8065071	0	4596	25.98	10	36.622448	0.061999999	0.68045688	19

soy_OGL_5929	1000	23.260778	0	9923	26.5	8	3.9835286	0.119	0.75172448	15
soy_OGL_6349	1000	5.6157908	14	3753	25.9	4	11.127664	0.139	0.8922298	23
soy_OGL_6918	1235	8.8029718	6.7206478	9369	29.47	7	8.8255606	0.111	0.89423931	24
soy_OGL_2090	1488	1.7034707	0	2001	25.4	6	3.9426556	0.050000001	0.76055437	15
soy_OGL_4725	1200	5.8001513	0	2993	26.5	8	5.4422164	0.077	0.5595817	22
soy_OGL_235	1018	9.1542082	0	4461	27.3	8	7.3071136	0.077	0.84417605	20
soy_OGL_1000	1234	5.6003585	0	3946	26.33	9	13.236205	0.037	0.79097039	14
soy_OGL_6488	1087	8.5538664	4.5078197	1348	25.85	8	7.0905499	0.109	0.64926952	20
soy_OGL_4665	1010	8.2117281	23.366337	6469	28.41	12	20.511387	0.14399999	0.66983294	34
soy_OGL_6934	1192	8.8029718	6.9630871	2001	29.61	11	37.949127	0.117	0.90414774	23
soy_OGL_638	1010	9.6527052	0	1001	29.3	10	34.510124	0.12	0.73719764	16
soy_OGL_409	1032	11.870942	4.263566	2775	25.77	14	17.667454	0.101	0.73366523	13
soy_OGL_4794	1100	13.341439	0	2510	28.45	9	12.505765	0.119	0.91731155	15
soy_OGL_6231	1200	9.1821709	0	4580	27.41	12	21.280247	0.104	0.88329005	15
soy_OGL_4392	1000	9.4882059	0	1039	29.1	11	30.956522	0.1	0.55610961	23
soy_OGL_237	1249	10.989239	10.168135	2001	26.82	10	9.9135027	0.16	0.8474564	21
soy_OGL_738	1200	8.9926348	15.833333	2669	25.66	10	18.078196	0.161	0.90347439	14
soy_OGL_1708	1619	7.9271779	2.6559606	2001	28.47	13	6.7546797	0.109	0.82117432	34
soy_OGL_2981	1245	11.277602	8.8353415	2438	28.99	8	6.6719174	0.13699999	0.82634896	23
soy_OGL_5420	1470	11.149388	13.809524	1695	24.48	13	8.2741852	0.15700001	0.96109825	14
soy_OGL_5480	1600	4.7314305	0	4542	31.31	10	8.8769779	0.074000001	0.86550194	33
soy_OGL_6298	1100	6.0601311	14.181818	4858	25.9	11	15.993726	0.14	0.94965726	18
soy_OGL_3338	1032	13.069633	17.44186	2229	29.16	7	10.811461	0.13500001	0.85970968	27
soy_OGL_1685	1736	9.1770983	5.4147468	2969	28.74	10	16.819216	0.057	0.73644459	10
soy_OGL_3997	1063	11.197123	14.581373	2001	26.99	8	8.555747	0.131	0.82479715	15
soy_OGL_1762	1291	17.394621	14.639814	1001	30.44	8	22.644669	0.090000004	0.95672107	11
soy_OGL_3308	1100	14.902535	13.909091	4939	29.18	8	8.5586987	0.111	0.91382027	19
soy_OGL_230	1097	9.9151058	14.949863	1134	26.16	10	12.934575	0.131	0.83905643	24
soy_OGL_1470	1121	9.2116108	0	2682	29.08	9	4.2702718	0.050000001	0.93394023	29
soy_OGL_2980	1084	12.228049	7.1033211	1001	28.41	9	5.8468137	0.096000001	0.82847726	22
soy_OGL_3442	1297	7.5834217	13.569777	2271	24.9	15	23.640272	0.097000003	0.55560595	12

soy_OGL_3556	1200	6.3657079	5.9166665	2884	27.91	11	7.5898356	0.108	0.82676917	26
soy_OGL_3598	1122	4.7033892	13.368984	2001	25.84	10	16.754353	0.123	0.86339718	24
soy_OGL_3969	1368	8.0769224	10.818713	2001	25.95	10	19.581486	0.075999998	0.94536239	10
soy_OGL_1711	1100	11.918611	0	3529	32.18	13	8.3774986	0	0.82582408	35
soy_OGL_1207	1098	6.7576227	0	3734	29.14	8	7.3372645	0	0.82582903	28
soy_OGL_312	1100	12.282213	2.909091	2416	30.45	9	18.71879	0.126	0.93663514	14
soy_OGL_432	1034	10.683906	0	1001	30.27	10	18.990097	0.132	0.67746067	20
soy_OGL_943	1249	12.449766	5.8446755	1997	28.74	10	13.368411	0.133	0.71565259	20
soy_OGL_3710	1100	7.0062461	0	4764	30.09	10	23.407564	0.104	0.83437341	23
soy_OGL_3942	1100	8.8798027	0	4189	30.36	9	8.6400642	0.115	0.87014049	27
soy_OGL_24	1004	11.015924	0	2001	31.87	11	13.073587	0.13	0.90916216	29
soy_OGL_4795	1200	13.341439	4.9166665	1017	30.16	9	12.505765	0.109	0.91749918	15
soy_OGL_6866	1341	8.3950586	4.6979866	4593	31.39	9	19.843878	0.1	0.83991742	26
soy_OGL_4704	1053	9.078599	0	3076	31.14	10	16.502283	0.122	0.60951287	38
soy_OGL_5830	1069	15.318932	0	9177	31.05	13	11.695643	0.13600001	0.94032228	20
soy_OGL_2212	1000	6.4445391	9.3999996	9193	30.7	10	23.85778	0.12800001	0.75328898	27
soy_OGL_106	1200	15.306171	6.0833335	6641	29.41	10	4.6881604	0.115	0.73382425	14
soy_OGL_2498	1200	7.4874678	0	2390	26.75	14	7.5474539	0.029999999	0.8426888	14
soy_OGL_4101	1237	12.218921	0	2001	29.74	11	3.1830208	0.090999998	0.68535733	20
soy_OGL_4976	1036	11.117381	0	1001	27.99	12	5.0272541	0.13	0.72110182	18
soy_OGL_5582	1100	5.9725876	0	2050	28.54	13	16.471968	0.107	0.68455553	19
soy_OGL_6778	1100	10.637803	0	1565	26.36	15	11.171764	0.111	0.76605636	13
soy_OGL_6872	1000	8.3950586	0	4020	30.3	9	6.546947	0.115	0.8437525	26
soy_OGL_26	1100	10.054278	0	1026	29.81	10	6.4305115	0.108	0.9036606	31
soy_OGL_104	1053	12.394506	0	2001	28.86	10	10.714575	0.090999998	0.73984885	19
soy_OGL_303	1367	10.392898	0	2303	27.13	12	20.041241	0.071000002	0.92925733	8
soy_OGL_691	1185	11.121198	0	3652	28.1	12	3.1362998	0.039000001	0.81192547	21
soy_OGL_1030	1067	6.3006811	0	2602	29.05	10	9.6499834	0.01	0.83157456	28
soy_OGL_1080	1000	7.9827704	9.8000002	3562	24.5	12	17.474819	0.104	0.89251846	15
soy_OGL_3153	1343	10.090086	0	1001	29.18	11	3.6960595	0.075999998	0.58659816	22
soy_OGL_3345	1000	10.744705	0	1801	29.2	9	1.0350329	0.082999997	0.85253453	24

soy_OGL_3750	1067	7.254467	0	2911	28.02	12	5.2717485	0.072999999	0.7708841	25
soy_OGL_4099	1100	12.218921	4.2727275	2807	27.81	14	10.204226	0.133	0.67892551	22
soy_OGL_4136	1173	10.646371	0	1001	29.24	11	5.6478987	0.096000001	0.83317906	31
soy_OGL_4519	1100	8.9862776	0	1081	29.45	8	8.9939518	0.111	0.75461727	34
soy_OGL_4793	1100	13.341439	2.5454545	2235	28.18	9	12.505765	0.11	0.91724998	15
soy_OGL_1437	1138	7.9350634	0	2001	32.33	10	25.745865	0.079999998	0.89466655	27
soy_OGL_3760	1202	10.661443	0	1001	28.78	14	17.046877	0.07	0.74445921	20
soy_OGL_1153	1000	5.8387361	0	4898	31	8	15.162896	0.033	0.95945615	28
soy_OGL_1658	1277	8.8195906	0	1001	29.28	9	7.1597362	0.035999998	0.60708261	22
soy_OGL_3931	1019	9.5840302	0	7406	31.01	9	9.741559	0.066	0.85099393	24
soy_OGL_4403	1123	9.3176165	0	2750	28.94	11	9.6504068	0.067000002	0.56451535	23
soy_OGL_2898	1041	8.9753227	6.5321808	1001	29.39	10	29.182426	0.071000002	0.89131021	13
soy_OGL_423	1000	14.106673	0	3924	29.5	12	3.0399926	0	0.69538289	24
soy_OGL_1918	1244	4.4789438	0	2001	30.46	9	26.535799	0.104	0.56515455	17
soy_OGL_5517	1000	8.5462761	5.3000002	5309	29.6	7	7.5655503	0.082999997	0.80545592	25
soy_OGL_1410	1300	14.723554	5	4621	27.07	11	5.5957627	0.139	0.83899653	22
soy_OGL_2139	1556	6.2898784	0	6017	26.6	9	48.985847	0.083999999	0.87263507	29
soy_OGL_2284	1049	12.293853	4.6711154	2001	28.59	6	19.724258	0.138	0.62378842	41
soy_OGL_5519	1300	8.5462761	15.384615	2186	25.07	9	34.112244	0.133	0.80262452	24
soy_OGL_6869	1800	8.3950586	0	1470	30.66	8	29.280153	0.039999999	0.84212327	27
soy_OGL_5303	1100	24.034395	9.636364	2222	28.72	9	19.907883	0.108	0.70329881	27
soy_OGL_3353	1200	12.108066	18.25	2654	26	8	32.483772	0.12800001	0.82629496	16
soy_OGL_107	1440	15.306171	0	1001	27.77	11	4.7782288	0.046	0.73348242	14
soy_OGL_1709	1349	11.838197	0	1001	28.24	13	7.2853689	0.094999999	0.8241753	36
soy_OGL_1710	1328	11.918611	3.5391567	2001	27.18	13	8.3774986	0.124	0.82576233	35
soy_OGL_3304	1189	14.744515	0	1001	24.13	16	11.831074	0.050999999	0.93083	17
soy_OGL_4920	1000	13.037633	0	3578	26.4	12	4.8079066	0.061000001	0.77632374	28
soy_OGL_5228	1000	10.151151	0	1280	25.3	10	12.757979	0.022	0.91928661	20
soy_OGL_5876	1218	10.178902	0	3217	27.83	9	8.8167181	0.061999999	0.90314287	31
soy_OGL_6546	1200	13.347547	0	1435	27.91	11	10.112593	0.094999999	0.7519564	30
soy_OGL_1432	1311	10.901735	2.3646071	3674	25.09	11	25.839436	0	0.87896597	21

soy_OGL_1447	1100	10.671152	0	2996	26.18	9	22.412865	0.118	0.90821052	32
soy_OGL_1728	1143	28.425341	0	4449	24.23	10	11.559277	0.125	0.84914589	24
soy_OGL_4953	1052	12.134647	2.756654	2733	27.75	7	9.4563179	0.097000003	0.751517	33
soy_OGL_5775	1100	19.448713	0	3591	23.81	11	9.3744669	0.127	0.82539934	33
soy_OGL_5777	1070	14.783132	0	2001	24.85	10	5.9458609	0.108	0.83181578	41
soy_OGL_5802	1002	12.976668	0	2593	24.75	8	16.874744	0.096000001	0.85904443	37
soy_OGL_5296	1000	23.831551	0	4662	25.6	6	10.197484	0.13600001	0.72791463	26
soy_OGL_2287	1001	12.293853	0	2128	29.27	9	12.359873	0.079000004	0.6218394	40
soy_OGL_4834	1391	17.834297	10.064702	2001	26.24	12	8.2830744	0.103	0.98206764	14
soy_OGL_3945	1046	26.245321	4.9713192	1127	27.53	7	4.525774	0.061999999	0.87866861	25
soy_OGL_4633	1014	19.448103	2.7613413	2001	27.21	11	9.3156013	0.125	0.74045753	39
soy_OGL_5626	1073	36.55751	4.1938491	1763	28.89	12	7.809288	0.090000004	0.61478925	29
soy_OGL_5829	1000	15.470398	0	2141	24.8	14	8.1802664	0.016000001	0.93177706	24
soy_OGL_5889	1000	10.038893	0	1325	26.9	8	16.84602	0.012	0.88580614	38
soy_OGL_1454	1000	9.5077581	0	4152	28.7	6	5.6339574	0	0.91559809	31
soy_OGL_105	1121	14.445976	0	3266	24.88	12	10.452209	0	0.73687881	16
soy_OGL_3328	1056	11.347876	0	1001	26.79	7	11.357668	0	0.87530619	30
soy_OGL_4694	1097	8.5891142	0	8809	29.8	11	13.639303	0.032000002	0.61457515	40
soy_OGL_1108	1333	6.187727	0	4814	24.15	10	55.712246	0.059999999	0.94496685	18
soy_OGL_1233	1093	9.0944204	6.495883	2892	26.44	9	21.672363	0.029999999	0.76068521	23
soy_OGL_2163	1043	8.4397182	0	2237	25.69	7	18.042578	0	0.84238076	31
soy_OGL_5280	1027	10.270111	9.5423565	3696	25.8	8	19.714537	0.090999998	0.7560488	24
soy_OGL_5292	1200	21.185158	0	7280	25.91	7	17.332621	0.078000002	0.7327683	24
soy_OGL_6947	1300	10.483934	0	2052	26.15	7	26.166666	0	0.92287809	22
soy_OGL_1937	1000	18.530302	15.7	2106	28.1	9	10.987101	0.106	0.54420131	24
soy_OGL_2137	1200	6.2898784	3.9166667	2791	25.25	8	54.58247	0.015	0.87283945	29
soy_OGL_4139	1000	10.988504	8.1000004	2739	26.1	9	29.574678	0.037999999	0.84156519	28
soy_OGL_5765	1151	20.418718	2.5195482	4125	28.84	9	6.7981439	0	0.80824018	21
soy_OGL_4917	1000	16.032492	0	2873	25.3	8	32.786858	0.014	0.77889031	24
soy_OGL_2903	1200	13.152136	0	3195	28.16	10	13.800819	0.155	0.98419148	22
soy_OGL_3535	1296	8.9636507	0	3050	28.54	10	22.555202	0.097999997	0.79239523	23

soy_OGL_4506	1000	8.4976664	0	4903	28	10	33.485977	0.13500001	0.744807	36
soy_OGL_1905	1154	23.127859	0	2891	28.07	10	18.671026	0.125	0.62413877	13
soy_OGL_5437	1000	5.1846781	11.8	4248	25.6	15	82.934662	0.145	0.95892721	16
soy_OGL_5615	1000	27.974483	0	4450	28.5	8	13.770544	0.138	0.62757856	24
soy_OGL_3604	1200	4.7843852	0	4319	23	9	87.196495	0.109	0.87526476	22
soy_OGL_6745	1000	23.582851	0	2603	35.1	7	18.519163	0.082999997	0.73336041	26
soy_OGL_1757	1000	17.394621	13.9	2431	26.9	9	47.797859	0.14300001	0.95918185	13
soy_OGL_3322	1074	10.753889	0	2001	23.55	9	118.84104	0.117	0.88623041	24
soy_OGL_4864	1047	5.5955515	0	2001	24.06	14	177.73097	0.118	0.94412094	17
soy_OGL_1070	1100	7.9827704	0	2136	26.9	13	35.503689	0.12800001	0.87642902	18
soy_OGL_2147	1000	7.0482421	0	1627	27.2	10	23.847639	0.14399999	0.85576606	28
soy_OGL_4901	1214	9.0506868	0	1001	25.53	12	18.996721	0	0.89281166	14
soy_OGL_6868	1104	8.3950586	0	1001	26.53	10	18.295338	0.108	0.84037888	25
soy_OGL_6911	1123	8.8029718	3.1166518	1001	27.15	7	28.266319	0.111	0.8903836	17
soy_OGL_2679	1200	10.232581	4.5	1078	24.33	12	36.708504	0.104	0.5012657	26
soy_OGL_4468	1139	7.5555859	0	1123	24.75	12	46.203907	0.125	0.7018699	24
soy_OGL_5287	1068	17.785692	0	2001	25.28	11	18.701477	0.121	0.73876417	22
soy_OGL_5841	1100	13.472019	0	2089	25.81	10	23.143742	0.132	0.96970797	21
soy_OGL_1902	1187	26.684738	2.9486098	1744	23.25	14	13.202422	0.118	0.63195175	10
soy_OGL_2919	1060	9.3426876	0	1001	24.62	14	112.99213	0.106	0.96525276	30
soy_OGL_4001	1065	11.197123	0	2001	23.66	10	73.137901	0.12	0.81754291	19
soy_OGL_5832	1057	13.562174	0	1001	27.71	10	34.664627	0.097000003	0.95683479	24
soy_OGL_5864	1021	9.1074429	0	2001	27.71	7	47.607845	0.113	0.93192345	24
soy_OGL_4140	1000	11.063471	0	6059	29.4	7	13.007035	0.107	0.85298485	26
soy_OGL_5583	1100	5.8065071	0	3766	28.36	11	33.820923	0.072999999	0.68079692	19
soy_OGL_2138	1000	6.2898784	0	4491	25.5	8	54.58247	0.085000001	0.87277067	29
soy_OGL_3492	1084	5.426621	0	1812	23.06	11	62.650448	0.086000003	0.65590459	21
soy_OGL_5258	1000	11.51429	0	5638	28.7	14	35.497784	0.007	0.83181095	18
soy_OGL_1563	1015	10.973433	0	4470	29.35	9	20.774496	0	0.82482648	25
soy_OGL_3339	1400	13.069633	8.9285717	1113	29.5	7	10.720885	0.114	0.85784793	26
soy_OGL_1418	1354	11.014842	18.833088	1001	28.36	11	38.421307	0.102	0.85820258	21

soy_OGL_1433	1004	10.901735	20.318726	4384	26.09	11	25.839436	0.145	0.87907815	22
soy_OGL_1729	1116	27.671904	20.430107	1001	30.91	13	7.3364964	0.123	0.85191941	24
soy_OGL_5518	1138	8.5462761	18.717047	3178	26.8	10	30.789223	0.124	0.8038314	25
soy_OGL_6877	1147	8.3950586	12.816042	3193	27.63	8	20.305794	0.115	0.84656036	23
soy_OGL_4957	1000	12.134647	10.7	6377	29.5	7	8.9455986	0.103	0.75104964	33
soy_OGL_1571	1000	10.813619	7.4000001	1058	26.4	9	5.2788277	0.072999999	0.80672026	25
soy_OGL_2178	1096	8.9299202	17.062044	2511	25.82	10	14.85498	0.126	0.80641741	25
soy_OGL_2909	1000	10.078434	14.2	1001	26.2	7	10.433558	0.114	0.97512764	26
soy_OGL_3648	1200	1.8333012	13.25	2182	25.5	10	30.089041	0.064999998	0.94532436	24
soy_OGL_4493	1100	9.6481829	7	1867	26.72	11	6.6839652	0.118	0.73098391	30
soy_OGL_4543	1500	6.9025164	0	2045	28.33	12	7.4001799	0.068999998	0.78662479	32
soy_OGL_6637	1100	7.9076147	11.181818	2161	24.09	12	9.6977797	0.097000003	0.97858775	21
soy_OGL_5875	1100	10.178902	0	1867	29.9	11	11.392278	0	0.90676022	32
soy_OGL_2933	1500	9.9275036	0	1022	30.66	8	19.6761	0	0.93353617	18
soy_OGL_4695	1000	8.5891142	0	7709	31.3	11	13.639303	0.079000004	0.61450326	40
soy_OGL_3769	1037	12.172926	0	2001	28.92	9	8.2572451	0	0.72992426	21
soy_OGL_821	1096	12.059816	0	1001	27.46	4	32.642231	0.117	0.74237531	23
soy_OGL_5632	1021	24.815081	0	5880	28.59	8	8.7208033	0.142	0.60224378	13
soy_OGL_637	1000	9.6527052	0	2492	26.7	9	34.220394	0.071000002	0.73629665	15
soy_OGL_1674	1084	9.1770983	0	2572	25	9	43.348198	0.1	0.70606184	16
soy_OGL_2648	1200	7.4653587	0	3961	27.16	9	31.573944	0.090000004	0.5417937	29
soy_OGL_3399	1000	2.8635902	0	5908	27.8	7	23.058424	0.125	0.69523042	18
soy_OGL_4086	1032	7.4914689	0	3993	28.19	4	15.127453	0.117	0.57482594	11
soy_OGL_6049	1006	2.1657593	0	4809	25.64	2	5.0487928	0.118	0.19574459	9
soy_OGL_4727	1121	4.8687081	0	2427	25.06	7	5.6268392	0.113	0.55009151	16
soy_OGL_3057	1000	5.589066	0	4826	24.6	3	4.6132493	0.121	0.52424258	2
soy_OGL_813	1456	8.8038511	0	10172	30.08	7	6.2943654	0.077	0.76978904	12
soy_OGL_6189	1500	4.7146115	0	5075	29.6	5	5.088841	0.066	0.84293443	12
soy_OGL_4351	1200	6.5096278	13.25	2251	26.41	9	8.9396629	0.115	0.48407951	19
soy_OGL_847	1000	5.9970145	16	4894	25.2	4	4.9579091	0.14	0.6391328	15
soy_OGL_1330	1300	4.7698789	11.769231	14730	28.07	5	7.4703107	0.077	0.67965758	6

soy_OGL_5356	1064	2.9911871	12.781955	3877	25.09	4	13.562528	0.133	0.4942545	14
soy_OGL_6021	1200	2.3629057	15.916667	2476	25.25	5	19.742716	0.103	0.39507142	12
soy_OGL_3090	1108	2.0621765	28.33935	1075	24	4	34.27924	0.118	0.30529723	3
soy_OGL_883	1128	4.0211573	17.996454	1485	25.17	7	25.438444	0.116	0.63954479	8
soy_OGL_671	1000	4.2763386	11.8	7540	26.5	7	2.299463	0.106	0.77912205	23
soy_OGL_6358	1000	5.9217067	14.3	3742	22.4	7	8.2972088	0.125	0.8550213	6
soy_OGL_848	1326	5.9970145	0	1919	28.8	4	4.9579091	0	0.6389004	15
soy_OGL_2046	1000	2.835119	12.8	4816	24	5	1.5439975	0.097999997	0.47718978	11
soy_OGL_3402	1088	2.5044255	15.900735	6864	23.25	7	8.0952644	0.115	0.66889399	7
soy_OGL_3425	1317	0.84260994	0	2963	25.2	3	1.258257	0	0.40951502	5
soy_OGL_4207	1400	3.6840379	3.6428571	2207	25.5	8	4.4533992	0.048999999	0.23435558	13
soy_OGL_4731	1000	1.3662759	18.5	1010	20.6	6	1.9281696	0.106	0.16275163	9
soy_OGL_1916	1100	4.1864786	6.4545455	1104	26.09	8	11.145372	0	0.56912661	14
soy_OGL_2330	1000	10.115131	9.6000004	9533	29.6	3	2.3743284	0.057999998	0.50329357	11
soy_OGL_5756	1046	6.5565777	12.141491	5638	28.58	2	9.074852	0.079000004	0.76183623	14
soy_OGL_2748	1300	4.8816667	0	1237	27.23	8	1.7404139	0.108	0.38494056	14
soy_OGL_5377	1300	3.6074958	0	2808	27	7	6.1835999	0.111	0.65506798	8
soy_OGL_841	1238	5.8473277	2.6655896	4434	26.81	6	7.9451857	0.117	0.64547658	15
soy_OGL_1805	1100	4.1940126	0	9729	29	5	5.0153661	0.121	0.78578895	17
soy_OGL_2065	1400	4.2405567	0	2565	27.21	5	10.303807	0.090000004	0.63353205	10
soy_OGL_2386	1300	7.888226	0	3937	29.38	6	10.42019	0.094999999	0.60329878	15
soy_OGL_2434	1300	0.78866917	0	4193	24.23	5	5.297039	0.124	0.75097531	7
soy_OGL_4337	1100	5.0690784	0	4979	28.9	9	14.914173	0.131	0.46187174	20
soy_OGL_5662	1000	7.3934207	0	1768	28.6	5	10.580032	0.111	0.50163603	20
soy_OGL_4038	1000	4.4449058	5	7047	27.7	1	0.063361578	0.116	0.43828076	5
soy_OGL_4755	1104	0.93389368	0	5815	25.27	3	0.3509987	0.11	0.57583427	1
soy_OGL_5978	1200	7.1452026	0	2752	30.83	3	5.0927401	0.071000002	0.62034696	16
soy_OGL_6101	1058	0.477795	0	4120	27.12	2	3.1772857	0.12899999	0.66290748	13
soy_OGL_6708	1046	0.14302784	7.0745697	1001	24.95	1	6.0629549	0.115	0.501647	7
soy_OGL_6039	1400	1.4594702	10.428572	3491	27.42	3	29.08709	0.056000002	0.25300509	2
soy_OGL_6698	1163	0.69440275	16.680998	2001	22.95	3	11.249501	0.121	0.067550749	3

soy_OGL_2010	1400	4.9582324	3.3571429	1502	26.85	6	1.5695053	0.107	0.3868669	10
soy_OGL_2360	1106	2.8688939	0	7441	24.05	8	1.9295732	0.119	0.18380789	6
soy_OGL_2437	1186	0.78866917	0	10450	26.98	5	7.5610828	0.11	0.75422055	6
soy_OGL_3069	1084	4.8104396	4.1512914	1001	23.43	5	5.1263027	0.125	0.006311319	1
soy_OGL_4747	1100	1.3206984	0	12005	27.36	3	1.3007599	0.097000003	0.39071918	7
soy_OGL_5113	1100	5.6311255	7.909091	2702	26.9	5	12.240232	0.122	0.36904538	12
soy_OGL_6360	1100	1.2353655	0	11379	26.27	2	0.87763846	0.12800001	0.78752768	5
soy_OGL_6407	1061	6.8150654	6.0320454	4426	25.25	4	1.727953	0.12	0.49330789	9
soy_OGL_599	1000	5.0991559	6.5999999	2383	28	5	20.055241	0.124	0.65827668	9
soy_OGL_2392	1372	7.888226	0	7339	32.06	5	5.822619	0.044	0.62321216	14
soy_OGL_4359	1248	5.3951726	3.3653846	1523	27.48	8	4.4683743	0.071000002	0.49456564	17
soy_OGL_6118	1142	2.2216065	0	2130	23.73	4	0.7171675	0.126	0.72771817	13
soy_OGL_6121	1104	2.3116186	6.3405795	3805	24.9	6	10.668534	0.109	0.73075658	13
soy_OGL_2757	1047	8.2878428	0	2542	28.55	12	20.797125	0.097000003	0.359855	7
soy_OGL_2653	1049	6.8734031	0	1001	29.64	5	13.038914	0.085000001	0.53363466	27
soy_OGL_2826	1000	2.0155141	0	2396	26.3	5	7.7421126	0.113	0.57933277	6
soy_OGL_3107	1000	1.7647178	7.1999998	3554	23.9	7	5.2799706	0.13600001	0.48206133	5
soy_OGL_4056	1000	0.2840631	0	2048	24.6	6	1.3367742	0.077	0.37445	7
soy_OGL_6361	1000	1.2353655	0	10338	26.6	5	5.9802036	0.088	0.77418721	5
soy_OGL_127	1000	1.5303117	0	3227	24.8	6	6.279346	0.101	0.5911293	9
soy_OGL_592	1180	0.71430248	0	4615	26.77	2	6.3579936	0.079999998	0.62895316	7
soy_OGL_2038	1300	0.96399927	0	1656	23.69	5	5.1476526	0.085000001	0.36296311	7
soy_OGL_3078	1100	1.2740204	0	7314	26	6	0.4828369	0.086000003	0.23990023	10
soy_OGL_3414	1350	0.37037379	0	2001	26.74	2	12.978787	0.035999998	0.54227191	6
soy_OGL_3797	1078	1.26052	11.410019	7958	25.13	10	16.02688	0.079999998	0.65010822	11
soy_OGL_4269	1000	3.4015584	0	1051	24.6	6	4.2908292	0.105	0.34461302	16
soy_OGL_5086	1000	0.3779718	0	2067	22.4	2	0.69363242	0.139	0.35439688	3
soy_OGL_5349	1400	2.9911871	0	1370	26	5	3.0381651	0.078000002	0.48468119	14
soy_OGL_5701	1064	0.91327834	0	3713	26.97	3	7.4935555	0.071000002	0.38833088	12
soy_OGL_5725	1000	2.7392509	0	2416	23.9	6	5.6872263	0.088	0.5632866	5
soy_OGL_5731	1000	1.4187498	0	6526	24.3	3	3.9451611	0.088	0.62440991	5

soy_OGL_6025	1007	1.8328881	0	13114	28.59	5	0.92227334	0	0.38521904	15
soy_OGL_6034	1034	1.099659	5.319149	2131	22.05	4	1.6876011	0.134	0.33438602	4
soy_OGL_6035	1000	1.4335037	0	10321	24.9	6	2.1787734	0.107	0.33232144	5
soy_OGL_6712	1100	0.12902215	0	10534	27.09	2	2.8166242	0	0.60834616	2
soy_OGL_2749	1000	6.5649028	8.6999998	1550	26.1	8	8.7687416	0.116	0.38194406	13
soy_OGL_3847	1100	7.4157596	7.7272725	3937	27.09	7	6.9344282	0	0.29754078	9
soy_OGL_489	1232	5.3632855	11.607142	3033	24.1	8	11.631506	0.127	0.49342167	19
soy_OGL_1360	1500	7.8114729	0	4134	28.33	5	9.6006079	0.088	0.76687968	12
soy_OGL_4455	1500	4.7464509	9.1999998	4257	22.46	7	18.105949	0.13	0.67466718	12
soy_OGL_5374	1258	6.2914834	9.4594593	4526	20.42	5	4.3402677	0.162	0.63957155	13
soy_OGL_5743	1135	13.020522	0	13949	24.49	6	6.3172998	0.12800001	0.70248431	16
soy_OGL_819	1000	10.47439	0	11734	23.4	5	10.749363	0.145	0.7468906	23
soy_OGL_907	1051	5.9492388	0	12168	24.07	6	11.862093	0.139	0.6768043	29
soy_OGL_2750	1600	5.7574492	0	3521	23.87	9	23.117178	0.075999998	0.38069579	13
soy_OGL_5171	1078	8.0355263	0	11048	25.97	5	5.5722823	0.13500001	0.8501001	18
soy_OGL_6425	1000	10.893449	0	10809	24.1	4	4.7814307	0.131	0.54491186	33
soy_OGL_870	1000	1.0942405	21.9	5913	23.3	4	33.87426	0.14300001	0.5803684	9
soy_OGL_5174	1189	6.9958062	0	10147	29.52	2	4.1228566	0.101	0.87088406	19
soy_OGL_6367	1704	2.5912349	0	7967	26.29	3	7.0199561	0.059999999	0.64927644	6
soy_OGL_478	1189	5.5857544	0	10944	27.92	4	5.4824595	0.082999997	0.52649099	21
soy_OGL_5719	1503	3.9622605	0	2256	23.02	4	3.1535113	0.097000003	0.47060516	7
soy_OGL_2003	1000	6.9207196	14.9	8733	23.7	4	12.901971	0.14399999	0.44150001	14
soy_OGL_2751	1553	8.9011316	1.8673536	6656	23.69	8	8.4175739	0.093999997	0.37679255	13
soy_OGL_3137	1100	8.3777838	0	15838	26.81	4	7.6506586	0.114	0.55908006	27
soy_OGL_3150	1344	9.2073507	0	11376	28.42	6	14.180368	0.075999998	0.58228809	19
soy_OGL_3374	1332	10.989937	0	9469	25.37	5	36.175362	0.1	0.75473583	13
soy_OGL_4042	1331	0.43014365	0	2001	17.95	1	2.1280773	0.17200001	0.41702911	11
soy_OGL_5176	1200	7.2353287	0	12303	25.25	3	5.303761	0.113	0.87782854	17
soy_OGL_5726	1379	2.8807406	0	10434	19.94	3	11.017958	0.127	0.5693832	5
soy_OGL_6131	1000	2.167546	5.0999999	17631	23	5	4.8117104	0.14399999	0.75324392	9
soy_OGL_6383	1100	0.26723456	8.272727	24046	25.45	2	3.6599655	0.056000002	0.28102511	3

soy_OGL_453	1127	3.0446455	0	17920	24.22	5	3.875406	0.109	0.58378255	14
soy_OGL_477	1100	5.5857544	5.5454545	4169	24.63	3	7.1762877	0.126	0.52730179	21
soy_OGL_823	1104	12.450212	0	9400	23.91	3	33.011215	0.103	0.74067968	23
soy_OGL_6070	1100	0.788831	0	12341	18.27	1	8.3341627	0.126	0.025127551	7
soy_OGL_6320	1000	9.4922562	0	16479	28	4	4.8501863	0.108	0.93137449	18
soy_OGL_5084	1000	6.0809145	23.9	8836	22.9	1	47.137802	0.104	0.372282	3
soy_OGL_6656	1011	15.964157	14.935707	4845	24.03	7	6.9593258	0.14399999	0.18804173	19
soy_OGL_1789	1250	5.5180402	8	4808	23.6	8	22.087742	0.061000001	0.83349675	9
soy_OGL_2534	1402	7.4369493	0	3645	27.24	7	12.214153	0.067000002	0.75785893	13
soy_OGL_1870	1100	5.0498676	0	8415	27.18	6	13.168991	0.089000002	0.71321428	26
soy_OGL_3006	1110	6.375104	3.5135136	6341	25.49	6	7.1134319	0.107	0.78075075	18
soy_OGL_3793	1400	3.1278274	0	4374	25.07	10	22.52689	0	0.65516311	10
soy_OGL_4380	1300	6.6147962	0	2669	27.84	6	6.3849044	0.072999999	0.53125477	25
soy_OGL_5373	1327	6.0673037	2.2607386	2001	24.64	5	13.436002	0.079999998	0.63270462	13
soy_OGL_5963	1100	7.1839008	5.5454545	5506	25.72	6	0.46636611	0.119	0.67312753	21
soy_OGL_2582	1223	5.237216	0	2001	21.91	9	10.85631	0	0.66298521	15
soy_OGL_6736	1157	6.7172632	0	5178	22.99	10	16.82708	0	0.72152853	19
soy_OGL_483	1059	5.5002999	0	7733	18.22	8	7.4007506	0.071999997	0.51375675	19
soy_OGL_507	1300	4.4821186	0	4655	24.38	6	7.6541381	0.064999998	0.45955855	23
soy_OGL_534	1000	10.494274	0	2145	20.9	6	3.8230314	0.102	0.37721622	21
soy_OGL_851	1128	7.4370508	2.5709219	10078	23.84	6	1.761797	0.12	0.62350565	22
soy_OGL_881	1128	2.4722638	0	5080	20.03	4	2.5074496	0.127	0.6269356	9
soy_OGL_1345	1480	7.3499031	4.189189	1001	23.58	4	9.9313774	0.078000002	0.73111004	12
soy_OGL_2074	1000	3.6825252	0	5499	19.4	7	6.3011012	0.109	0.6612978	13
soy_OGL_2230	1400	7.2320971	0	3813	26	6	10.571854	0.046999998	0.7133165	17
soy_OGL_2608	1326	8.0021572	0	7128	23.37	7	4.1500378	0.092	0.5991956	21
soy_OGL_2658	1000	6.8734031	0	2765	23.7	2	2.2202265	0.12800001	0.53167135	25
soy_OGL_3447	1200	11.627316	0	4654	21.83	9	12.988303	0.088	0.57746673	9
soy_OGL_3856	1100	10.036083	0	4392	22	8	6.2464828	0.115	0.27424893	22
soy_OGL_3915	1100	9.3006687	0	8081	24	3	4.3032303	0.121	0.79184175	23
soy_OGL_4340	1149	5.0690784	0	5040	16.79	8	16.733919	0.105	0.46210092	18

soy_OGL_4775	1044	6.7980485	0	1079	21.36	5	18.943016	0.061000001	0.84491307	10
soy_OGL_5392	1000	9.4848547	0	5631	23.6	3	5.7213116	0.1	0.71152699	18
soy_OGL_6172	1024	9.6413136	0	7429	21.58	7	5.7411976	0.048999999	0.81466377	15
soy_OGL_6664	1330	12.137495	0	2001	24.96	9	4.1647635	0.092	0.006542761	25
soy_OGL_3268	1400	5.2893763	7.2142859	2109	26.07	6	24.440109	0.064000003	0.84921944	17
soy_OGL_4710	1200	5.5082192	0	3099	28.58	7	9.7356339	0	0.59000653	34
soy_OGL_928	1009	12.140412	0	4442	24.97	7	11.472142	0	0.70153826	25
soy_OGL_2402	1000	11.483459	0	5082	24.1	8	10.186023	0	0.68876243	18
soy_OGL_2970	1000	11.978155	0	6264	25.4	7	4.8957019	0	0.85020852	21
soy_OGL_3025	1202	11.296754	0	7062	27.53	7	10.117967	0.075000003	0.74936163	19
soy_OGL_3146	1000	8.65382	0	2386	25.3	9	8.7032461	0	0.57880342	22
soy_OGL_3174	1035	11.789145	6.0869565	5266	21.06	6	55.180843	0.122	0.64550543	20
soy_OGL_3486	1000	5.426621	0	1795	22.3	7	30.976269	0.007	0.65057433	21
soy_OGL_3904	1206	9.3006687	0	1001	25.04	7	20.078566	0	0.76431602	18
soy_OGL_5398	1059	9.4738331	0	4034	24.17	7	20.096918	0	0.73344803	20
soy_OGL_5951	1000	11.551946	0	8961	26	9	6.3989983	0	0.704449	23
soy_OGL_6255	1000	5.2737613	0	6166	26.1	5	27.882589	0.052999999	0.91490149	25
soy_OGL_490	1098	5.023427	0	3780	24.22	9	3.092375	0	0.48935136	18
soy_OGL_878	1173	2.4722638	0	2438	21.99	2	1.446648	0.086999997	0.62485951	8
soy_OGL_1625	1686	2.688483	0	3079	24.91	2	0.22139801	0.028000001	0.47535881	6
soy_OGL_3808	1200	8.2365665	0	9175	27.41	7	9.617568	0	0.61045063	13
soy_OGL_4058	1100	1.3664422	9.181818	5016	21.72	3	9.6577978	0.093999997	0.34116924	3
soy_OGL_4077	1042	5.8943801	3.9347408	3079	24.56	4	5.1087947	0.074000001	0.53447282	20
soy_OGL_4079	1265	5.8943801	0	2385	28.45	2	6.8761353	0.002	0.5422464	24
soy_OGL_4762	1197	0.4713738	0	15584	25.06	4	1.3624809	0.079000004	0.79686725	6
soy_OGL_5047	1300	6.5904026	2.1538463	3446	24.07	3	6.145885	0.090000004	0.62034726	8
soy_OGL_6007	1100	3.6136997	7.7272725	9505	26	4	11.002473	0.078000002	0.53263265	14
soy_OGL_6711	1208	0.12902215	0	14488	25.16	3	9.9533958	0	0.60060394	2
soy_OGL_479	1075	5.5857544	3.7209303	9146	22.69	4	5.6402006	0.096000001	0.52545607	20
soy_OGL_583	1328	0.57824314	0	4942	19.8	5	1.1029658	0.097999997	0.58030868	4
soy_OGL_634	1232	5.2757597	0	21512	30.11	3	10.495376	0	0.72391593	15

soy_OGL_885	1000	8.0451517	2.8	10497	20.8	4	44.938602	0	0.65344864	14
soy_OGL_888	1031	8.0451517	0	7063	24.15	4	5.3364706	0.098999999	0.65680212	19
soy_OGL_1329	1000	4.3766484	0	4095	18.5	1	4.8465109	0.054000001	0.66980112	4
soy_OGL_1344	1000	7.3499031	0	7905	20.8	3	11.38693	0.097999997	0.73037201	13
soy_OGL_1979	1181	10.00319	0	5188	25.06	7	7.1430211	0.024	0.47748053	26
soy_OGL_2342	1049	16.299006	2.9551954	2001	20.78	3	5.4646826	0.108	0.30993927	12
soy_OGL_2734	1056	6.8346286	0	9381	22.15	6	8.8036394	0.085000001	0.40880069	18
soy_OGL_2774	1130	6.5037332	0	5076	18.67	4	3.1557326	0.12800001	0.29522273	6
soy_OGL_3055	1100	10.730741	17.90909	2946	20.81	4	4.7569385	0.132	0.55509365	2
soy_OGL_3404	1325	2.5044255	0	13157	23.77	6	1.6901937	0.064999998	0.66355705	9
soy_OGL_4015	1025	7.0667925	0	14663	20.97	2	8.6197004	0.126	0.70076829	15
soy_OGL_4024	1000	7.0667925	0	2539	23.4	5	6.9599576	0.001	0.6875	16
soy_OGL_4085	1100	7.4914689	11.818182	3328	22	4	15.127453	0.097999997	0.57474393	11
soy_OGL_4250	1000	9.7208376	0	6486	21.4	6	2.8104815	0.083999999	0.30388293	14
soy_OGL_5095	1323	0.43929935	0	8374	21.61	2	6.3194327	0	0.041673228	3
soy_OGL_5132	1100	6.2508564	3	4656	21.54	3	5.8196912	0.115	0.65394151	8
soy_OGL_5664	1000	7.7668753	5.1999998	11898	21.3	8	5.776186	0.123	0.49721074	20
soy_OGL_5699	1100	1.1073029	6.2727275	4562	20.63	5	6.1025939	0.092	0.39677012	15
soy_OGL_5737	1000	13.165402	0	7856	24.2	4	4.3080115	0.075999998	0.68650001	13
soy_OGL_5954	1090	8.8384924	0	1424	23.76	4	12.318757	0	0.69158673	20
soy_OGL_6008	1032	3.6136997	0	7273	20.44	6	7.962605	0.115	0.5325188	14
soy_OGL_6027	1518	1.5537344	0	1001	20.35	4	0.74820036	0.093999997	0.38283673	15
soy_OGL_6373	1009	2.0298591	5.1536174	4743	17.44	3	2.6871159	0.117	0.48018804	2
soy_OGL_6393	1288	2.3906288	0	4020	20.96	9	13.914756	0	0.40003794	3
soy_OGL_6674	1037	9.9655132	0	9130	20.73	2	0.48499602	0.116	0.013036274	27
soy_OGL_6676	1000	9.9655132	0	2520	21.6	9	2.0579996	0	0.014348372	28
soy_OGL_3031	1000	9.2140102	11.6	1239	23.3	5	10.172854	0.043000001	0.73355317	15
soy_OGL_3256	1282	5.2893763	0	5195	22.77	6	44.641861	0	0.8280822	15
soy_OGL_5955	1300	8.8384924	0	3214	28.15	5	13.26694	0	0.69148469	20
soy_OGL_5958	1158	9.0571718	0	2490	26.42	4	15.920022	0	0.69050002	17
soy_OGL_5175	1084	7.2353287	0	10903	27.39	3	5.303761	0.13500001	0.8777132	17

soy_OGL_5371	1301	5.8088784	0	6847	25.9	6	6.1033521	0.126	0.62772799	13
soy_OGL_3149	1096	8.65382	0	4280	27.09	5	13.490625	0.118	0.58198017	19
soy_OGL_3454	1000	9.8757811	0	7366	25	5	4.8191204	0.146	0.59569961	12
soy_OGL_3455	1000	9.8757811	0	7394	25.3	7	4.9815359	0.13500001	0.59772247	12
soy_OGL_6723	1071	8.8704958	7.1895423	4235	25.02	6	10.131293	0.152	0.70640004	8
soy_OGL_606	1300	7.1531291	0	5178	25.07	7	24.819769	0.102	0.68169928	15
soy_OGL_2706	1031	3.4366314	0	8317	23.47	7	16.701143	0.133	0.45181009	21
soy_OGL_4412	1300	6.3518429	0	9085	24.07	8	41.276947	0.102	0.5778985	18
soy_OGL_5922	1105	8.3593283	0	11134	24.16	5	26.938509	0.131	0.83254057	15
soy_OGL_5013	1194	11.339603	0	6198	30.23	7	10.370746	0.103	0.67610979	21
soy_OGL_2790	1521	6.0796947	0	2936	27.15	5	11.82972	0.077	0.21462165	8
soy_OGL_4054	1416	0.29615524	0	3498	23.87	4	8.8046713	0.121	0.38743076	11
soy_OGL_6163	1100	6.0707769	0	12769	28.9	3	8.1698351	0.105	0.79912579	17
soy_OGL_1322	1027	0.24154867	0	15336	25.7	1	4.4111633	0.112	0.62248093	14
soy_OGL_2350	1181	2.8688939	0	8854	24.89	5	10.649649	0.115	0.22560638	8
soy_OGL_2354	1235	2.8688939	0	2001	21.78	5	0.90948188	0.145	0.2089984	12
soy_OGL_3889	1500	0.027143367	0	5239	26.53	4	26.578051	0.054000001	0.40974519	8
soy_OGL_4192	1056	5.3633652	0	8001	26.51	7	6.3852444	0.125	0.20391801	22
soy_OGL_5353	1072	2.9911871	0	7753	24.9	5	3.7688153	0.121	0.4915244	14
soy_OGL_5705	1100	3.4428258	0	8984	22.63	2	2.8887174	0.117	0.28015324	1
soy_OGL_4061	1087	0.41162741	2.7598896	18367	23.45	2	3.6812937	0.096000001	0.066223077	3
soy_OGL_4247	1083	9.9370441	0	11358	21.97	5	39.775558	0.13500001	0.29179227	17
soy_OGL_6067	1147	1.6618187	0	12842	20.05	3	24.153093	0.12800001	0.042897958	12
soy_OGL_1618	1000	1.1600796	0	15434	19.7	2	70.956757	0.102	0.40550196	7
soy_OGL_2054	1000	3.3452113	0	8258	21.9	3	2.3851016	0.145	0.55976361	10
soy_OGL_3855	1126	10.560259	0	3879	25.39	6	26.159727	0.121	0.277677	19
soy_OGL_3888	1137	0.027143367	0	6928	23.04	3	34.64098	0.125	0.40965948	8
soy_OGL_5070	1174	2.1815977	0	7354	24.36	2	37.435596	0.081	0.54320174	4
soy_OGL_5088	1061	14.498571	0	5083	25.16	2	5.1088223	0.104	0.22606678	2
soy_OGL_5676	1141	10.021258	0	2039	25.41	4	11.160657	0.125	0.47173181	13
soy_OGL_5677	1100	9.7722187	0	10684	27	4	6.0011139	0.115	0.47104597	13

soy_OGL_5688	1078	2.0145493	0	7014	24.3	6	48.635571	0.12	0.42259005	6
soy_OGL_5712	1176	7.4721704	0	13158	26.44	1	1.4047815	0.057999998	0.068885975	3
soy_OGL_5728	1000	4.5680037	0	17936	22.2	2	33.222359	0.107	0.57322341	5
soy_OGL_3436	1003	7.3611813	0	10784	25.72	8	50.337318	0.123	0.5438832	13
soy_OGL_4411	1235	8.6647367	0	7414	25.91	8	41.276947	0.090999998	0.57783967	17
soy_OGL_171	1109	2.0941939	0	1573	21.82	3	0.088223323	0.12	0.72973824	9
soy_OGL_484	1000	5.5002999	0	6033	24	8	7.4007506	0.13	0.51368016	19
soy_OGL_530	1060	11.005226	3.1132076	1001	24.15	9	7.9638166	0.123	0.38500267	11
soy_OGL_1337	1000	2.2828174	0	8580	21.2	8	7.2052855	0.132	0.70409328	10
soy_OGL_2066	1000	4.2405567	0	6765	23.4	6	9.1758356	0.13699999	0.63375878	10
soy_OGL_2351	1395	2.8688939	0	2462	22.5	10	0.36916527	0.077	0.21912386	9
soy_OGL_2381	1030	7.888226	0	5795	24.07	9	4.6613426	0.097000003	0.59824878	12
soy_OGL_3115	1000	5.6704493	0	3364	22.6	6	0.19280368	0.131	0.51788014	11
soy_OGL_3392	1095	5.6634336	0	5073	25.11	4	2.2405198	0.118	0.7015115	17
soy_OGL_3686	1056	7.5635667	0	10237	25.75	6	8.6794538	0.121	0.90241045	15
soy_OGL_3796	1300	1.26052	0	6558	22.76	10	16.02688	0.081	0.65015882	11
soy_OGL_5161	1100	6.6482263	0	5541	27.18	4	5.5673146	0.107	0.82030398	16
soy_OGL_5427	1031	12.267535	0	8324	27.06	4	5.1141095	0.114	0.98187828	11
soy_OGL_5663	1075	7.5133257	0	3180	25.39	6	4.9121294	0.079000004	0.49811766	20
soy_OGL_2390	1004	7.888226	0	2001	23	9	10.803274	0.033	0.60671622	16
soy_OGL_2600	1000	3.365438	0	2381	22.5	10	24.525871	0.044	0.62280768	14
soy_OGL_459	1100	3.5637314	0	1467	24.27	7	35.078716	0.107	0.56276578	17
soy_OGL_633	1000	5.7509642	0	7886	22.5	5	16.059563	0.12899999	0.72190487	15
soy_OGL_1288	1000	7.3108006	0	3682	24.5	5	11.307076	0.094999999	0.65600002	16
soy_OGL_1590	1110	5.281703	0	7544	21.62	5	18.044056	0.12899999	0.72974998	9
soy_OGL_2718	1024	4.0992632	0	2302	23.14	7	6.5822368	0.105	0.44523427	24
soy_OGL_2752	1063	8.4189348	0	2378	18.15	12	26.415489	0.077	0.36852926	11
soy_OGL_2756	1011	8.2878428	0	4278	19.58	12	20.797125	0.122	0.3599157	7
soy_OGL_2823	1100	2.0155141	0	3938	20.27	7	39.179367	0.133	0.55225378	8
soy_OGL_6453	1008	5.9874048	0	13907	24.7	8	4.3669896	0.121	0.57971483	20
soy_OGL_491	1100	5.023427	0	1022	25.18	8	29.607697	0.105	0.48638287	19

soy_OGL_5744	1000	13.020522	0	1909	25.9	6	10.894938	0.077	0.70695502	15
soy_OGL_138	1140	0.16197154	0	4223	22.89	3	5.1872706	0.124	0.63303381	6
soy_OGL_159	1040	3.0367718	0	3107	22.3	2	6.8817439	0.090999998	0.7021082	9
soy_OGL_576	1017	1.8716706	0	6907	20.74	3	1.9196731	0.12899999	0.25308439	2
soy_OGL_1614	1000	1.1756582	0	3209	21.4	4	0.2740078	0.021	0.35268933	4
soy_OGL_2033	1124	2.137743	0	8354	21.53	5	2.1294034	0.113	0.31872579	4
soy_OGL_2806	1033	1.3742812	0	2992	22.94	3	1.511838	0.101	0.34291112	12
soy_OGL_4209	1000	3.1847808	0	4967	24.3	8	11.697232	0.017999999	0.23976937	12
soy_OGL_4265	1222	2.6787946	0	3743	22.58	9	9.1986389	0.061000001	0.34018591	15
soy_OGL_5124	1100	7.9918165	0	3360	22.72	6	2.5150437	0.126	0.41757429	8
soy_OGL_5708	1100	2.51285	0	2879	21.54	2	2.0775414	0.115	0.10624521	2
soy_OGL_5711	1000	7.4721704	0	1603	25.3	2	9.7870359	0.039999999	0.073735632	3
soy_OGL_6003	1069	3.4906964	0	7571	27.12	5	15.25239	0	0.54077041	14
soy_OGL_6056	1030	0.099082492	0	2387	22.23	2	0.099147908	0.105	0.12822796	3
soy_OGL_6096	1021	0.54288405	0	2365	21.35	4	2.1916099	0.059	0.6532039	10
soy_OGL_2015	1087	3.2330246	0	12248	22.26	4	5.3407445	0.11	0.38017899	9
soy_OGL_2345	1000	7.3284101	4.0999999	5798	23.1	9	11.870274	0.005	0.29481652	8
soy_OGL_2766	1032	3.4072301	0	13021	24.22	5	15.568583	0.037999999	0.32774365	12
soy_OGL_3114	1000	5.6704493	0	6232	21.4	5	0.56697917	0.14300001	0.51662171	11
soy_OGL_4214	1000	4.1915531	0	3040	21.5	6	24.610453	0.138	0.25134671	23
soy_OGL_4258	1000	9.2218924	0	4224	26.9	3	9.4156761	0.004	0.31445	12
soy_OGL_4753	1160	0.28445095	0	2962	21.46	5	35.15202	0.090000004	0.54875612	3
soy_OGL_6693	1100	7.9217877	0	2187	23.27	4	3.1462631	0	0.035504855	10
soy_OGL_1667	1398	8.7383938	0	2235	27.32	7	13.357824	0.018999999	0.6326279	8
soy_OGL_4301	1000	4.1622143	0	3078	28.8	6	24.815271	0.082000002	0.39790252	25
soy_OGL_5667	1008	7.7668753	0	4638	27.48	6	7.3109965	0.022	0.49686974	20
soy_OGL_2081	1042	1.6845587	0	2818	23.8	8	58.58371	0.064999998	0.7057488	8
soy_OGL_3110	1000	2.0293322	17.4	3842	22.2	8	43.710621	0.085000001	0.49373046	7
soy_OGL_5970	1000	8.3158064	15.4	4212	24.2	6	3.5982468	0.16500001	0.65666324	15
soy_OGL_2034	1145	1.2525767	18.951965	12284	23.31	6	6.3328848	0.109	0.32916453	4
soy_OGL_3849	1000	7.4157596	20.9	6444	24.6	6	7.6047039	0.11	0.29259229	12

soy_OGL_4242	1400	4.520647	3.5	4994	29.21	7	5.3271694	0.082999997	0.27694425	30
soy_OGL_3790	1037	4.9141068	9.5467691	1239	20.92	10	6.9171467	0.052000001	0.65777254	10
soy_OGL_6181	1100	6.9349771	0	4908	25.72	7	6.5201569	0	0.82816058	12
soy_OGL_898	1136	6.5197372	0	7803	30.19	6	10.092576	0.045000002	0.67042041	30
soy_OGL_2590	1133	4.7435961	7.5022063	2788	24.62	10	12.386198	0.022	0.64226109	15
soy_OGL_6344	1100	5.6157908	0	1848	27.45	4	8.5079031	0	0.89482129	24
soy_OGL_2023	1168	1.3061663	12.243151	2001	22.08	3	0.11210825	0.064999998	0.32881168	6
soy_OGL_3079	1100	0.87092143	13.272727	4605	22.18	2	0.8469364	0.104	0.24157096	10
soy_OGL_3433	1261	3.656785	0	3533	24.82	6	6.0135217	0	0.52981365	8
soy_OGL_5064	1072	5.2891674	16.231344	2786	21.54	6	1.4199408	0.082999997	0.56600595	6
soy_OGL_908	1000	5.9492388	6.0999999	11771	29.6	6	11.862093	0.061999999	0.6768533	29
soy_OGL_2231	1000	7.2320971	13	8413	26.6	6	10.878972	0.093000002	0.71312386	19
soy_OGL_5370	1198	7.9470868	0	2055	28.29	4	5.8800211	0	0.62579036	14
soy_OGL_6401	1828	6.8150654	0	2001	29.59	8	17.361572	0	0.47215739	12
soy_OGL_3412	1356	2.0739	0	8754	24.92	4	0.90955061	0.113	0.60055763	5
soy_OGL_449	1093	4.76688	3.3851783	6131	25.89	3	4.9207854	0.112	0.59151351	12
soy_OGL_2346	1100	6.5047197	11.909091	5125	24.81	4	9.1229477	0.118	0.28405964	5
soy_OGL_3845	1515	3.0571678	0	1121	26.66	2	13.761656	0.050999999	0.40775967	2
soy_OGL_6042	1084	0.95590049	0	28918	30.62	4	4.9632807	0.007	0.2191947	10
soy_OGL_2631	1000	7.9126515	0	3998	27.4	9	3.4251685	0	0.56601751	22
soy_OGL_6601	1000	8.5314484	0	6364	27	8	8.0275812	0	0.86219567	15
soy_OGL_581	1185	0.092011556	0	6625	22.7	5	0.45920998	0.041000001	0.5207662	1
soy_OGL_2707	1000	3.4366314	0	8968	27.7	8	14.728556	0.017000001	0.45176223	21
soy_OGL_3405	1200	2.5044255	0	4115	24.58	4	5.0360589	0.082000002	0.66018891	9
soy_OGL_5125	1000	0.49185139	7.6999998	3087	25	3	20.96353	0	0.43362975	5
soy_OGL_2676	1000	10.232581	3.5999999	7137	30	5	6.2725334	0.075000003	0.50357693	23
soy_OGL_3877	1275	1.2656252	5.1764708	1268	27.76	4	34.178806	0.01	0.2254646	7
soy_OGL_5645	1000	9.2479429	0	6266	28.6	6	7.4155326	0.061000001	0.53706896	17
soy_OGL_4222	1178	4.0722065	3.7351444	1001	29.79	8	30.099712	0.107	0.26311839	31
soy_OGL_1986	1000	9.6599522	11.5	2246	25.8	11	4.1451063	0	0.4679383	18
soy_OGL_5039	1100	7.3473787	10.181818	1189	27.9	6	8.6203337	0	0.65057439	22

soy_OGL_101	1100	10.922771	0	2340	32.45	5	9.3287001	0.079999998	0.75046664	24
soy_OGL_4394	1047	8.5982914	4.1069722	5744	31.32	8	12.647203	0.082999997	0.5584206	22
soy_OGL_827	1034	10.746717	10.058027	2886	30.17	5	12.543222	0.12800001	0.72308326	23
soy_OGL_6670	1200	9.9655132	7.9166665	4274	32.08	7	13.592624	0.048	0.010698829	22
soy_OGL_5423	1258	12.267535	0	2001	31.08	5	8.4590149	0.032000002	0.97992814	12
soy_OGL_3448	1065	9.7242231	2.629108	9518	29.2	11	18.791903	0.061999999	0.58393276	11
soy_OGL_4176	1000	18.91416	0	2584	32.2	12	19.369682	0	0.17538829	14
soy_OGL_1936	1093	18.530302	17.200365	5013	28.63	9	10.872908	0.096000001	0.54429567	24
soy_OGL_3497	1148	47.600048	0	3133	27.09	4	41.480244	0.097999997	0.71131033	17
soy_OGL_5620	1000	29.539919	0	2289	28.5	7	5.7219605	0	0.62391955	22
soy_OGL_1746	1100	13.638608	12.545455	9801	28.63	9	29.064001	0.048	0.98149675	16
soy_OGL_5621	1000	29.539919	0	4991	27.3	6	7.3525524	0.071999997	0.62339461	24
soy_OGL_6808	1000	6.2792668	33.099998	2011	30.4	8	123.16982	0	0.79655832	21
soy_OGL_720	1000	9.1615238	26.299999	1263	29.7	7	115.34366	0.018999999	0.86001831	19
soy_OGL_1759	1000	17.394621	12.5	1905	28.8	7	60.377228	0	0.95806819	12
soy_OGL_6813	1077	7.7418113	13.927577	5773	29.8	11	93.153671	0.088	0.79895055	23
soy_OGL_6804	1235	4.8344703	17.894737	1001	33.19	10	115.33292	0	0.78714907	24
soy_OGL_2938	1127	9.9764471	0	1096	29.63	8	46.767273	0.007	0.92487299	17
soy_OGL_6803	1196	4.8344703	0	2001	21.23	9	127.67606	0.077	0.7869674	24
soy_OGL_5856	1200	8.370719	24.166666	2430	29.91	8	56.567776	0.061999999	0.94608676	18
soy_OGL_2158	1058	7.9192505	11.342155	6339	29.01	7	15.730636	0.07	0.84929359	29
soy_OGL_982	1000	6.2075529	8.1999998	1771	28.9	7	12.345994	0	0.76909381	32
soy_OGL_1250	1179	14.230903	7.6335878	2825	29.68	7	10.48095	0.078000002	0.72770613	19
soy_OGL_5675	1600	10.021258	0	3492	31.31	4	21.700743	0	0.47252873	14
soy_OGL_559	1012	21.124374	10.770751	5543	24.6	7	7.5583582	0.125	0.32334632	18
soy_OGL_563	1152	21.491308	0	8057	28.73	8	9.4132662	0.077	0.31508192	23
soy_OGL_3872	1077	9.8148384	22.376972	1001	23.86	10	28.358847	0.134	0.25179926	17
soy_OGL_3803	1200	8.2365665	21	3427	22.91	7	112.4017	0.082000002	0.62365663	12
soy_OGL_3068	1185	38.188908	11.392406	2001	30.46	6	5.5605326	0.046	0.11348936	2
soy_OGL_6511	1200	7.9388223	0	2900	29.16	6	18.757362	0.021	0.69217706	26
soy_OGL_4499	1000	8.7435341	0	5377	27.6	6	22.891724	0	0.73800987	35

soy_OGL_6256	1317	4.9920311	0	2001	27.03	3	54.334961	0.037	0.9159959	25
soy_OGL_4658	1027	9.0728102	0	2001	18.3	7	97.924576	0.050000001	0.67941654	26
soy_OGL_188	1309	7.50841	11.535523	3708	26.2	6	26.560663	0.043000001	0.79238278	12
soy_OGL_4174	1010	20.926271	4.7524753	6649	26.53	8	5.5188723	0	0.17193128	17
soy_OGL_3869	1051	9.8148384	8.2778311	1001	26.26	10	28.193409	0.123	0.252794	19
soy_OGL_5003	1047	7.1169462	0	1783	21.39	6	98.534592	0.13500001	0.69341391	22
soy_OGL_2760	1200	3.9935622	0	3997	25.41	6	77.651344	0.067000002	0.33887762	12
soy_OGL_4183	1000	14.27253	8.8999996	1372	24.4	6	32.739742	0.122	0.18337521	17
soy_OGL_5673	1300	9.4097462	12.153846	4511	33.84	8	63.865719	0.023	0.47709578	17
soy_OGL_2723	1260	6.7211156	0	1979	24.52	8	182.79167	0	0.43215874	20
soy_OGL_639	1041	9.6527052	5.3794427	2001	24.78	8	41.22665	0.066	0.73822343	17
soy_OGL_5324	1000	11.453777	0	2523	28.2	7	20.157156	0.007	0.66098779	25
soy_OGL_4288	1000	5.7368112	0	2203	27.7	9	31.219425	0	0.3798202	26
soy_OGL_4177	1000	18.090168	0	3645	26.6	6	18.464994	0	0.17745806	15
soy_OGL_4246	1126	9.9370441	2.4866786	1226	27.61	7	30.374676	0.048999999	0.29112899	17
soy_OGL_6800	1000	4.8344703	0	7601	32.6	10	116.29536	0	0.78598547	22
soy_OGL_2677	1100	10.232581	11.181818	3205	27.72	7	9.0743437	0.116	0.50293005	23
soy_OGL_2994	1000	9.2852879	13.2	9121	29.8	6	19.040201	0.122	0.80714893	24
soy_OGL_5401	1408	9.4738331	8.522727	6135	29.11	7	14.80544	0.078000002	0.73637629	19
soy_OGL_1225	1300	9.0944204	0	3322	29.15	7	12.818521	0	0.76959652	20
soy_OGL_4235	1000	4.7568674	15.9	2582	25.1	9	12.839015	0.067000002	0.27444854	30
soy_OGL_4302	1028	4.4824991	10.311284	4484	27.91	6	24.815271	0.032000002	0.39804232	25
soy_OGL_5006	1300	10.049834	0	1672	29.69	7	14.42519	0	0.68795562	15
soy_OGL_2543	2800	4.3840361	17.178572	5320	31.25	9	3.1309779	0.221	0.73654544	19
soy_OGL_753	2825	5.9034243	27.504425	2091	27.5	8	5.1130219	0.17299999	0.93979782	12
soy_OGL_4889	2519	3.9014754	21.516476	4086	27.19	10	4.831213	0.168	0.91933948	19
soy_OGL_3655	1360	1.9542303	31.617647	7513	22.35	10	15.281493	0.208	0.95392781	13
soy_OGL_777	1758	8.9971619	20.477816	3619	28.27	7	2.3860292	0.18799999	0.94234264	17
soy_OGL_4873	2053	4.0852547	27.910376	1470	26.74	10	2.551672	0.18099999	0.93353385	25
soy_OGL_5206	2800	6.245574	15.321428	2962	31.89	10	5.3054276	0.178	0.96972561	20
soy_OGL_5591	2300	3.3001637	22.913044	4513	28.52	13	6.5985422	0.206	0.66344059	22

soy_OGL_282	2111	7.6405764	30.412127	5269	29.74	5	1.7817541	0.20100001	0.9036361	26
soy_OGL_1515	2700	6.1372461	25.814816	2145	28.96	10	3.1155977	0.186	0.91179764	32
soy_OGL_1782	2531	5.2867265	20.545238	3294	28.4	9	6.035562	0.142	0.89500976	21
soy_OGL_1783	2500	5.2867265	31.76	3508	28.16	8	5.4910989	0.23199999	0.89464611	21
soy_OGL_3679	2630	6.1510382	5.5893536	1318	30.68	12	14.364848	0.067000002	0.93502015	11
soy_OGL_5459	2717	6.9202266	18.881119	1001	28.26	11	4.9198666	0.14300001	0.91095012	17
soy_OGL_6831	1200	4.1189404	25.5	3220	25.75	7	4.7817822	0.205	0.81125206	35
soy_OGL_745	2023	7.9587779	18.240238	3956	28.57	7	3.5118289	0.12800001	0.91907483	13
soy_OGL_2107	1387	5.4921489	27.829849	3923	24.51	7	9.8257122	0.182	0.95651835	15
soy_OGL_1477	1543	5.5293665	21.062864	2758	26.63	7	9.4120817	0.132	0.94649434	19
soy_OGL_350	1560	3.5052428	24.871796	5439	26.53	8	6.7967172	0.124	0.84514415	29
soy_OGL_4881	2313	3.9014754	3.7181151	3439	28.66	13	2.1338425	0.171	0.924483	19
soy_OGL_2842	1518	5.5548873	22.727272	2328	25.95	8	2.6364913	0.245	0.67271149	24
soy_OGL_2462	1765	5.2698236	12.351274	6487	28.04	8	4.5364461	0.17299999	0.92486835	17
soy_OGL_286	1598	6.6751828	21.401752	3463	28.34	8	4.98703	0.25999999	0.90535331	26
soy_OGL_4420	1900	9.7329044	22.894737	2755	29.47	9	4.1380081	0.257	0.61012071	23
soy_OGL_6589	1894	5.3763165	6.969377	4161	31.46	10	4.6465006	0.115	0.8003217	26
soy_OGL_814	2800	8.7106552	3.7857144	2729	37.39	5	2.4152937	0.169	0.75408596	20
soy_OGL_2841	1336	5.5548873	19.985029	1001	26.79	7	5.109859	0.177	0.67088127	24
soy_OGL_3685	1498	7.5635667	21.094793	4857	28.03	7	8.593318	0.212	0.9026224	15
soy_OGL_7007	1628	7.3327656	26.289927	8053	26.53	10	5.1769238	0.22400001	0.9754858	9
soy_OGL_1803	1700	3.2149055	20.82353	4457	27.76	9	8.9583912	0.154	0.79133117	14
soy_OGL_4382	1395	6.9435525	26.666666	2001	25.8	9	3.361932	0.193	0.53405315	22
soy_OGL_4621	1788	9.8585806	12.695749	1930	32.04	3	1.3956103	0.16599999	0.76094848	28
soy_OGL_3264	1300	5.2893763	26.692308	2214	25.69	9	4.2489977	0.184	0.84477574	19
soy_OGL_1020	1430	5.5723405	20.979021	2632	26.5	8	4.9283142	0.168	0.82104057	25
soy_OGL_6167	1197	10.100551	22.305765	1038	25.64	6	5.3899522	0.17	0.80778682	14
soy_OGL_1777	2000	5.2867265	20.549999	1450	29.8	8	3.2902884	0.16599999	0.89696103	21
soy_OGL_1912	1845	2.9864438	29.701897	2101	24.98	13	7.3506708	0.15099999	0.61208767	12
soy_OGL_763	1927	3.7801154	17.6959	4360	28.07	9	9.5529604	0.061000001	0.97863191	7
soy_OGL_5151	1800	4.1436477	20.222221	4235	28.16	5	3.0128195	0.17399999	0.77322489	19

soy_OGL_5982	2400	6.6010385	18.875	4776	29.45	7	3.2864971	0.17	0.61775512	16
soy_OGL_320	1958	10.951384	25.791624	7661	30.74	5	5.1659575	0.18799999	0.91070724	14
soy_OGL_571	2600	5.1880841	20.884615	1525	27.8	12	9.5375795	0.13600001	0.2956036	12
soy_OGL_2737	1980	6.8346286	28.585859	2851	26.66	8	3.700469	0.205	0.40772799	19
soy_OGL_5962	2100	7.1839008	19.904762	3306	29	6	0.46636611	0.145	0.67318881	21
soy_OGL_2232	1521	7.2443314	23.734385	5669	29.45	7	3.7931798	0.223	0.70842564	19
soy_OGL_4414	2400	5.6794109	25.625	9300	30.54	11	2.8084068	0.219	0.58797628	15
soy_OGL_767	1825	3.116626	34.410957	6983	28	8	5.3038955	0.18700001	0.99270493	5
soy_OGL_2091	2150	1.7034707	11.209302	3799	32.37	6	3.9426556	0.15099999	0.76078588	15
soy_OGL_6322	1300	6.3246384	26.076923	2415	27.84	3	0.31802765	0.185	0.93002552	18
soy_OGL_413	2500	10.858807	35.759998	6817	26.48	10	2.2123041	0.176	0.7236802	15
soy_OGL_4566	3500	5.8248348	34.085712	3080	31.85	6	7.3551612	0.186	0.81967419	26
soy_OGL_5594	2168	4.3595667	34.040592	1001	23.98	8	4.8219814	0.18000001	0.6572656	18
soy_OGL_1064	2500	4.5279164	25.32	5150	27.88	7	5.4305205	0.057	0.86442822	24
soy_OGL_2238	2000	7.3392978	29.6	2921	24.75	9	3.4720438	0.104	0.69176745	16
soy_OGL_2544	2675	5.5435143	36.785046	6078	28.63	7	11.36973	0.184	0.73279458	19
soy_OGL_6115	3300	2.335758	37.363636	3070	26.57	5	2.0084639	0.20100001	0.72528023	13
soy_OGL_275	1200	9.6343765	33.333332	2882	26.58	7	2.1959488	0.23199999	0.89707917	28
soy_OGL_349	1175	3.5052428	34.042553	3871	24.93	8	7.1576614	0.23100001	0.84531647	29
soy_OGL_378	2124	7.3028045	28.342749	2001	29.09	7	4.4505782	0.184	0.79062504	19
soy_OGL_384	2300	7.1420999	22.695652	1352	28.56	15	4.3599367	0.17	0.77780181	26
soy_OGL_1696	1441	6.8353257	31.089521	1001	26.02	9	1.9882516	0.252	0.81071925	26
soy_OGL_3207	1400	5.9144826	23.142857	2707	28.57	8	1.8208869	0.156	0.69593281	34
soy_OGL_3208	1700	5.9144826	20.235294	2666	30.41	8	1.8208869	0.169	0.69627124	35
soy_OGL_4535	1400	7.1095409	37.92857	3145	26.64	7	3.2377396	0.248	0.77667022	30
soy_OGL_4623	1700	4.2519794	21.705883	3635	28.58	11	11.093511	0.199	0.75422221	31
soy_OGL_6992	2400	5.2089171	19.666666	5215	33.33	8	12.888945	0.13600001	0.9535777	27
soy_OGL_279	1813	6.375752	36.679535	3945	26.8	8	3.6431577	0.148	0.90322179	27
soy_OGL_390	2700	8.8540125	20.518518	1880	32.07	11	5.3395548	0.147	0.76802254	28
soy_OGL_3573	1240	5.4506187	30.483871	2188	25.24	11	4.666224	0.21699999	0.83753908	37
soy_OGL_3724	2400	7.0879893	29.791666	4202	29.33	11	2.2625737	0.18799999	0.81624037	26

soy_OGL_3909	1808	9.3006687	24.778761	3042	28.26	9	4.7741895	0.116	0.78190118	22
soy_OGL_4565	1497	6.1890826	37.474949	1315	24.78	7	13.661819	0.237	0.81775242	25
soy_OGL_5270	1875	8.2448311	21.706667	2647	29.01	9	9.8052635	0.152	0.79362804	20
soy_OGL_6269	1500	5.2232471	24.133333	8033	27.33	11	6.7974467	0.185	0.92601812	30
soy_OGL_6562	1587	3.7855389	21.676119	3908	29.17	9	13.323902	0.161	0.76865852	39
soy_OGL_6976	1500	4.5740175	29	7615	26.33	10	6.145299	0.222	0.94226629	33
soy_OGL_1035	1293	6.3006811	34.029388	1001	25.13	10	10.821136	0.205	0.83587992	26
soy_OGL_1242	1400	8.69104	30.214285	3987	28.35	10	14.715106	0.178	0.75244737	25
soy_OGL_2164	1800	7.8468871	35.611111	1309	28.44	12	17.498936	0.222	0.83608258	29
soy_OGL_2902	1800	13.152136	24.277779	1295	30.66	10	13.800819	0.162	0.98424679	22
soy_OGL_3012	1617	11.587709	33.704391	1001	29.06	6	5.0912633	0.252	0.77129328	24
soy_OGL_4646	1620	5.2841516	24.25926	2249	27.4	14	8.8265572	0.163	0.71764576	32
soy_OGL_290	1684	10.362462	36.045132	5404	28.8	10	5.2226124	0.15099999	0.90783823	29
soy_OGL_353	2500	8.5371962	30.68	1908	30.88	11	11.746054	0.106	0.84206307	31
soy_OGL_931	2204	12.449766	8.3938293	3092	33.39	12	3.3207929	0.043000001	0.70564121	25
soy_OGL_1165	1499	9.6878195	35.223484	1490	26.28	12	23.937103	0.228	0.92604828	20
soy_OGL_1402	2200	14.041171	9.863636	2252	33.59	8	4.8340292	0.037	0.82867163	21
soy_OGL_1452	1780	9.5029097	26.235954	5416	30.56	10	8.2948456	0.111	0.91195118	33
soy_OGL_1500	2153	8.5456972	33.813282	1001	27.96	8	6.7173271	0.139	0.98393846	19
soy_OGL_2457	1700	9.9290686	28.352942	6679	27.58	12	15.7273	0.142	0.93747902	16
soy_OGL_2914	1900	9.6217709	23.105263	2230	29.15	10	11.610849	0.19400001	0.97003829	28
soy_OGL_3237	1400	9.7670603	22.214285	2984	30.28	8	9.5203953	0.142	0.72772449	36
soy_OGL_3951	1833	23.835562	37.315876	1001	29.45	14	4.3481884	0.19599999	0.89783859	16
soy_OGL_4515	1400	8.9862776	33.5	2085	27.14	9	7.4261656	0.185	0.75297344	35
soy_OGL_4821	1200	19.378592	34.333332	2448	26.83	9	5.066865	0.21699999	0.96374202	16
soy_OGL_4928	1401	14.560184	30.763741	3584	29.12	9	3.7084348	0.20299999	0.76791292	37
soy_OGL_5525	1797	11.696812	29.382303	1719	29.32	10	11.500789	0.134	0.7928046	25
soy_OGL_6734	2500	6.7172632	30.959999	2511	29	11	12.566297	0.133	0.72130603	19
soy_OGL_6847	1890	3.9573007	34.444443	1001	25.71	12	10.150598	0.164	0.82087308	27
soy_OGL_6878	1392	8.3950586	37.212643	2840	24.85	9	17.783716	0.19499999	0.84697711	23
soy_OGL_1014	1357	6.0355277	31.466471	1001	26.08	6	7.3983121	0.198	0.81478858	20

soy_OGL_1204	1636	6.7576227	21.882641	4962	29.7	7	0.92117059	0.114	0.82802474	25
soy_OGL_1263	1600	9.3204823	23.0625	1440	29.62	6	5.4890232	0.156	0.70081139	24
soy_OGL_3459	2139	8.9865389	30.528284	3454	28.84	8	3.0388246	0.16599999	0.61095011	14
soy_OGL_6492	1500	9.3050442	27.200001	4044	27	9	2.8666909	0.15000001	0.66366196	15
soy_OGL_6608	1400	8.5314484	29.142857	6693	28.5	7	4.1436224	0.191	0.87438846	18
soy_OGL_640	1472	8.197032	31.861414	2001	25.4	9	10.607157	0.17299999	0.74252146	15
soy_OGL_1860	1600	5.4766021	29.125	5723	29.93	7	2.442523	0.15099999	0.72241235	36
soy_OGL_2214	2300	6.4445391	26.565218	4523	29.6	7	2.1450982	0.093000002	0.75188988	25
soy_OGL_4126	1156	10.237288	31.487888	5204	28.02	5	1.8427024	0.22499999	0.81819665	32
soy_OGL_6280	1991	5.7888355	17.478655	8551	32.34	7	9.8850412	0.064000003	0.93718201	28
soy_OGL_6281	1337	5.7888355	32.460732	6104	26.7	7	9.8850412	0.17399999	0.93725562	28
soy_OGL_6731	2791	7.8205519	34.826225	6144	31.45	9	11.943333	0.191	0.71847332	16
soy_OGL_273	1400	9.3673096	33.214287	10673	28.21	6	5.0966506	0.237	0.89656031	26
soy_OGL_1825	1634	9.0145245	33.353733	7079	27.53	7	10.264588	0.206	0.76459414	24
soy_OGL_3936	1433	8.8798027	26.936497	4710	28.89	4	2.4579394	0.197	0.86373419	26
soy_OGL_3937	1240	8.8798027	33.387096	2420	25.4	4	2.4579394	0.19499999	0.8638947	26
soy_OGL_4486	1500	7.7733254	21.733334	8630	30.6	7	5.8588023	0.16500001	0.721237	30
soy_OGL_4798	1694	13.103085	26.564344	4829	27.56	7	3.996104	0.126	0.91924071	13
soy_OGL_5250	1624	9.1176739	35.160099	2333	27.21	4	8.0974693	0.17900001	0.86185217	22
soy_OGL_3785	2106	14.043512	38.129154	2012	30.95	8	13.267465	0.169	0.69453192	16
soy_OGL_6876	1200	8.3950586	39.75	2317	26.91	8	20.305794	0.185	0.84653097	23
soy_OGL_7002	1463	6.3244863	35.133289	9059	26.52	12	19.719011	0.156	0.96405059	15
soy_OGL_85	1680	7.5146651	35.535713	1001	27.73	7	11.462914	0.12	0.79543638	27
soy_OGL_210	1600	12.431113	38.5	5482	27.93	9	3.7211483	0.161	0.81892443	26
soy_OGL_737	2243	9.5748711	37.628178	3832	28.84	12	36.307308	0.121	0.89013457	11
soy_OGL_806	1400	9.2155247	30.642857	5905	27.92	8	13.347414	0.20100001	0.84158593	21
soy_OGL_1384	1200	6.9438424	35.583332	4865	28.41	7	20.920994	0.192	0.80632854	37
soy_OGL_1830	1500	8.2200718	34.933334	3838	28.06	10	24.508057	0.13600001	0.7583766	27
soy_OGL_2263	1558	7.1234393	24.197689	3871	31.38	6	6.4291024	0.098999999	0.63766974	44
soy_OGL_3327	1800	11.347876	37.055557	3376	29.5	9	10.898246	0.115	0.87649769	28
soy_OGL_4141	1163	11.063471	31.814274	4796	28.54	7	13.007035	0.192	0.85306507	26

soy_OGL_4404	1463	9.3176165	31.237185	2116	26.24	10	13.547401	0.16599999	0.56542706	24
soy_OGL_4666	1000	8.714469	37.599998	5308	26.6	8	14.779904	0.213	0.66639155	35
soy_OGL_4812	2228	5.9010963	25.583483	2078	30.87	6	19.875843	0.085000001	0.94697547	18
soy_OGL_4963	1920	9.1757927	31.927084	3837	30.57	7	11.269644	0.15700001	0.74231851	23
soy_OGL_5033	1458	9.2836533	35.253773	1001	26.95	6	3.9742978	0.198	0.65893209	28
soy_OGL_5805	1300	12.976668	36.923077	7527	31.3	7	5.616302	0.147	0.86204976	39
soy_OGL_642	1431	8.429347	27.183788	2640	24.38	11	2.7592614	0.182	0.74539918	21
soy_OGL_799	1500	9.380168	22.266666	1844	26.26	10	3.4051304	0.15800001	0.85383594	23
soy_OGL_6295	1212	6.0601311	36.056107	2616	23.1	10	9.1623478	0.199	0.9490301	21
soy_OGL_6909	2021	7.0806479	20.484909	1001	27.75	9	5.3221707	0.057	0.87761074	18
soy_OGL_6996	1506	5.9223719	26.494024	2001	25.03	8	6.4813943	0.142	0.95537037	22
soy_OGL_6203	1330	6.3214092	26.842106	6146	25.86	9	4.4309134	0.13600001	0.86171937	27
soy_OGL_6561	1540	3.7855389	18.116882	2613	28.31	10	12.152939	0.121	0.76839375	39
soy_OGL_729	1563	9.9542494	26.935381	1001	27.31	10	4.5963016	0.142	0.87815619	17
soy_OGL_6854	1500	8.3716021	25.133333	1141	27.33	10	4.1282163	0.156	0.82944763	26
soy_OGL_1147	1500	5.8387361	25.4	2826	28.66	11	19.53536	0.118	0.96536845	28
soy_OGL_2907	1677	13.152136	32.91592	3038	25.1	15	3.312923	0.17299999	0.98071063	24
soy_OGL_3248	1474	8.6051903	36.838535	1001	27.2	12	23.614962	0.12800001	0.73642617	28
soy_OGL_3530	2042	8.9636507	29.285015	2001	27.52	14	22.494814	0.063000001	0.78644621	17
soy_OGL_3697	1500	7.5635667	33.733334	3279	24.46	13	11.703513	0.167	0.88579828	19
soy_OGL_6284	1466	6.7950077	31.787176	2241	24.62	12	7.6781287	0.16599999	0.94071352	29
soy_OGL_6927	1200	8.8029718	34.666668	2723	26.16	8	5.3530412	0.16500001	0.899836	30
soy_OGL_6626	1612	9.2474756	25.434242	1001	27.79	10	6.3023319	0.108	0.96141601	22
soy_OGL_5554	1657	6.151978	25.890163	3391	24.92	11	12.935363	0.12899999	0.73637909	17
soy_OGL_6610	1313	8.5314484	32.673267	2001	25.74	7	11.005042	0.17299999	0.87815642	17
soy_OGL_341	1453	9.9017172	39.160358	4179	26.49	9	9.5062189	0.152	0.86034685	27
soy_OGL_695	1800	11.121198	25.444445	1196	29.11	9	7.7289896	0.07	0.81387305	20
soy_OGL_5222	1376	11.680604	31.10465	2884	30.23	7	21.756847	0.117	0.9341417	27
soy_OGL_5806	1007	12.015316	35.153923	3607	30.18	9	18.797022	0.13699999	0.86601323	38
soy_OGL_333	1615	10.351954	21.052631	4391	29.96	8	2.3670864	0.182	0.87573421	22
soy_OGL_1509	1852	6.1372461	18.304535	2001	29.69	11	12.823114	0.192	0.92555642	21

soy_OGL_1542	1400	8.1677341	21.642857	1467	28	10	3.1849835	0.208	0.87563688	33
soy_OGL_2561	1570	5.5703273	25.796179	4558	27.19	11	6.6759591	0.16500001	0.70590317	18
soy_OGL_3767	1125	12.172926	27.733334	2449	24.8	12	2.0676868	0.233	0.73213017	21
soy_OGL_5238	1187	9.4519281	24.599831	2001	28.81	6	8.4082203	0.205	0.88620478	24
soy_OGL_5559	1505	7.472156	23.32226	2275	27.64	10	8.9863348	0.162	0.72548658	17
soy_OGL_6627	1500	9.3168287	16.333334	3390	28.66	10	7.9379802	0.18099999	0.9640218	23
soy_OGL_6968	1261	5.001214	23.394131	1179	28.07	8	3.3976319	0.22499999	0.93984061	34
soy_OGL_6987	1485	5.3196578	17.373737	8624	31.44	9	8.9931927	0.168	0.95060408	33
soy_OGL_5540	2164	8.6397324	11.737523	2001	30.77	12	11.217363	0.154	0.77698225	23
soy_OGL_1160	1494	8.7633495	31.994646	1001	31.05	8	30.546175	0.19	0.94476342	21
soy_OGL_1733	1439	19.930004	27.51911	2001	29.18	12	5.7090888	0.16500001	0.8647989	14
soy_OGL_2133	1974	7.899683	15.602837	3185	30.64	13	9.3199682	0.106	0.88835442	19
soy_OGL_2177	1600	8.9299202	24.1875	1747	28.81	11	15.608394	0.23999999	0.80962843	27
soy_OGL_3674	1900	6.1510382	19.052631	4064	30.42	10	22.133448	0.11	0.94278538	13
soy_OGL_3952	1300	21.498575	27.615385	4230	29.76	9	2.6350734	0.215	0.90783894	12
soy_OGL_5892	1238	10.038893	20.840065	5292	33.11	8	16.84602	0.155	0.88542664	38
soy_OGL_5602	1401	4.5532155	22.698072	1010	28.05	8	9.1971941	0.17399999	0.64680314	24
soy_OGL_2966	1500	10.693128	24.799999	4043	29.86	5	16.259047	0.19599999	0.85362554	19
soy_OGL_4422	2200	9.7329044	0	5382	34.45	10	4.2733245	0.037999999	0.61120486	24
soy_OGL_3926	1405	8.1360826	27.829182	2001	30.39	6	26.604071	0.17399999	0.84477949	21
soy_OGL_707	1094	9.20959	34.369286	2303	26.78	6	14.093465	0.212	0.84146476	19
soy_OGL_5017	1197	8.4612236	32.49791	6805	28.15	8	16.434469	0.243	0.66965544	25
soy_OGL_1934	1475	17.808937	21.898306	3003	31.93	9	5.8219919	0.112	0.54738313	26
soy_OGL_3536	1300	8.9636507	21.538462	3073	29.07	7	14.48832	0.155	0.79290265	24
soy_OGL_6617	1415	8.5314484	29.893993	1022	24.45	10	8.5576782	0.183	0.89102668	10
soy_OGL_1201	1500	6.7576227	17	2395	28.73	9	3.0309799	0.12899999	0.83273685	23
soy_OGL_2504	1845	7.4874678	12.520326	1562	30.56	11	4.7028208	0.1	0.83537412	21
soy_OGL_2464	1500	5.6777735	23.4	2001	24.4	12	13.476362	0.18099999	0.92002761	20
soy_OGL_662	1196	5.3564477	15.802675	2654	26.92	11	2.8700936	0.171	0.76761156	36
soy_OGL_4792	1277	13.341439	30.305403	2001	26.54	12	10.344243	0.191	0.91639167	15
soy_OGL_1177	1200	4.3006682	22.916666	3171	29.25	8	17.891899	0.154	0.90463597	30

soy_OGL_3691	1052	7.5635667	34.695816	2727	24.9	11	15.487956	0.19	0.89630675	17
soy_OGL_3751	1010	13.611315	33.762375	1357	25.84	11	7.7570949	0.197	0.76443964	24
soy_OGL_6773	1502	7.5508246	20.639149	2010	27.69	8	5.406249	0.127	0.75231409	14
soy_OGL_6313	1474	16.098692	21.913162	2001	31.27	8	7:6755629	0.085000001	0.95434153	11
soy_OGL_5221	1034	11.744185	31.624758	1001	29.98	8	32.159695	0.138	0.93508941	27
soy_OGL_1007	1900	6.9552069	23.631578	2616	29.05	10	3.4522197	0.175	0.79922265	16
soy_OGL_1155	2525	5.8387361	22.930693	2001	31.68	9	8.0585003	0.149	0.95458537	24
soy_OGL_1191	1600	4.0395017	35.1875	3909	27.31	9	8.0431252	0.213	0.8840614	20
soy_OGL_2125	1468	8.9817944	34.128067	3976	28.33	8	5.6505122	0.22400001	0.90156108	18
soy_OGL_2488	1832	6.8494215	28.111353	2001	27.45	11	4.8780851	0.12800001	0.88515544	18
soy_OGL_2506	2300	7.4874678	32.913044	1120	28.43	10	6.6803579	0.178	0.83481818	21
soy_OGL_3622	2129	3.8661525	33.255051	1593	28.08	10	7.19487	0.146	0.91605574	23
soy_OGL_3639	1086	5.7721701	34.346226	1001	26.51	5	5.5774856	0.259	0.93350852	29
soy_OGL_5209	1700	6.245574	24.941177	3172	29.41	8	4.365047	0.121	0.96392685	24
soy_OGL_5276	1900	8.3274832	32.736843	2289	27.84	10	5.3482847	0.20200001	0.77687806	20
soy_OGL_5455	2000	5.4725728	31.549999	2536	28.15	11	6.5938716	0.169	0.92515326	12
soy_OGL_6844	2037	3.9573007	36.818851	1001	29.3	5	5.4934878	0.22400001	0.81926072	32
soy_OGL_5508	2051	5.4987149	36.372501	1864	24.81	11	6.4213028	0.108	0.82596934	16
soy_OGL_660	1200	5.3564477	34.666668	3755	29.58	11	2.8155937	0.183	0.76734662	36
soy_OGL_749	2839	5.0048141	21.768229	1001	35.47	14	3.9690888	0.030999999	0.9316588	14
soy_OGL_759	1631	5.8962474	39.668915	2838	25.81	12	11.059538	0.15899999	0.95625585	11
soy_OGL_959	1800	13.073158	37.722221	3560	30.55	9	6.3087397	0.198	0.74964517	27
soy_OGL_1053	2400	4.5279164	31.25	3047	34.25	8	4.2976089	0.15000001	0.85741574	27
soy_OGL_1133	1295	5.8739777	39.227798	2001	25.55	9	6.0100608	0.205	0.98555934	18
soy_OGL_1137	2473	5.6738558	36.59523	1081	30.44	12	4.0370731	0.055	0.97758192	25
soy_OGL_1143	1900	5.6311908	23.052631	4581	32	7	11.555932	0.119	0.97119296	29
soy_OGL_1523	2200	6.1372461	19.454546	1750	37.31	9	6.1719604	0.17299999	0.90382737	37
soy_OGL_1524	1200	6.1372461	39.5	6584	29.16	9	8.663496	0.18799999	0.90305954	38
soy_OGL_1680	1781	9.1770983	35.317238	1095	28.69	13	5.3619161	0.119	0.72216028	19
soy_OGL_1779	1584	5.2867265	32.891415	2096	28.34	9	3.0771959	0.164	0.89663959	21
soy_OGL_1864	1442	5.0498676	36.407768	1637	26.69	9	6.2936125	0.176	0.7170195	30

soy_OGL_1877	1304	5.170598	37.960121	3051	27.68	12	6.581502	0.192	0.70758104	21
soy_OGL_2129	2104	8.6764479	23.193916	2001	29.8	12	8.2669115	0.107	0.89179796	18
soy_OGL_2132	1931	7.899683	24.184361	1433	28.17	14	7.6301556	0.176	0.88971877	19
soy_OGL_2206	1300	6.2900872	35.307693	3057	28.07	9	6.1407647	0.211	0.76186699	28
soy_OGL_2446	1700	6.659574	36.470589	2013	28.76	11	11.394419	0.13500001	0.96382165	16
soy_OGL_2509	1680	7.4874678	28.095238	1391	31.54	9	8.0339956	0.13	0.82624197	26
soy_OGL_2584	2481	4.0981293	18.379686	2001	34.26	13	13.263859	0.068000004	0.65519035	13
soy_OGL_2901	2100	13.152136	34.761906	2237	31.71	9	15.397767	0.13699999	0.9846468	20
soy_OGL_2927	1811	7.6108041	32.744339	2001	29.37	11	11.086601	0.17299999	0.94877398	23
soy_OGL_3230	1950	8.2360296	35.641026	1702	32.41	8	16.696682	0.197	0.72198892	37
soy_OGL_3242	1667	9.3938437	26.814636	4989	34.13	9	8.8448887	0.18799999	0.73021281	36
soy_OGL_3263	1834	5.2893763	31.515812	2007	30.42	11	3.1937933	0.168	0.84377885	19
soy_OGL_3291	1476	3.2396839	30.894308	7276	30.75	10	5.6620264	0.156	0.96098846	23
soy_OGL_3299	1800	7.5410056	39	1729	33.44	9	13.238162	0.20200001	0.94243777	18
soy_OGL_3342	1711	10.878196	24.254822	1209	31.91	9	0.94170183	0.127	0.85423964	26
soy_OGL_3575	1357	5.4506187	30.508474	1160	29.91	8	4.9807382	0.178	0.84032279	37
soy_OGL_3576	1100	5.4506187	38.909092	4060	29.18	7	5.1038799	0.234	0.84166753	41
soy_OGL_3638	1800	5.0647411	36.555557	3097	30.72	6	4.7504911	0.182	0.93311155	30
soy_OGL_3700	1900	7.5635667	35.736843	2628	29.26	13	13.457724	0.176	0.8711459	8
soy_OGL_3722	1364	7.1902876	35.483871	1053	29.54	10	7.1970778	0.186	0.81718612	26
soy_OGL_3747	1799	7.8206534	34.630352	4318	29.51	13	11.235866	0.213	0.77606881	24
soy_OGL_3749	1868	6.8004804	31.905781	1001	32.11	13	6.4169011	0.20200001	0.77133906	25
soy_OGL_4551	1500	5.245616	31.200001	1816	30.33	11	8.0169706	0.17200001	0.79393941	30
soy_OGL_4554	1588	3.8827412	36.020149	2465	30.41	11	7.590044	0.148	0.79470676	27
soy_OGL_4564	2000	7.0163956	31.549999	1311	29	11	4.964077	0.097999997	0.81533051	24
soy_OGL_4590	2000	4.07375	37.099998	2942	35.75	12	5.1281962	0.141	0.9640131	13
soy_OGL_4594	1400	5.2460666	37.642857	2406	28.07	11	8.6308327	0.163	0.94486928	15
soy_OGL_4895	2209	9.0506868	37.166138	2001	27.38	12	7.0352101	0.16599999	0.90197366	13
soy_OGL_5494	1500	4.8364692	38.799999	3705	29.4	8	8.4420538	0.23800001	0.85314178	30
soy_OGL_5506	2100	5.7864904	18.857143	4512	32.52	12	10.167773	0.11	0.8287701	19
soy_OGL_5877	1398	10.178902	29.184549	5935	32.18	9	8.8167181	0.134	0.90299499	31

soy_OGL_5903	1354	9.19067	33.013294	5822	29.83	13	0.22578724	0.215	0.86977786	34
soy_OGL_6582	1500	5.2729778	36.666668	1199	30.06	9	16.620815	0.211	0.78574425	35
soy_OGL_6586	1900	4.9233418	39.473682	1647	34	14	6.9401822	0.071000002	0.79250634	35
soy_OGL_6812	1732	6.2792668	32.04388	1128	28.11	11	10.132987	0.226	0.79868287	23
soy_OGL_6983	1800	4.6887946	25.888889	4598	31.61	10	5.5530095	0.156	0.94713014	33
soy_OGL_224	2700	9.4661407	38.851852	2184	31	10	6.2298059	0.133	0.83419573	24
soy_OGL_2844	1758	5.5548873	29.977247	1001	28.1	7	3.2662811	0.186	0.67405593	24
soy_OGL_3148	2100	8.65382	34.380951	4668	30.23	9	6.0400505	0.20200001	0.58039606	22
soy_OGL_3265	1400	5.2893763	36.785713	3088	26.64	8	3.6838903	0.207	0.84544837	19
soy_OGL_356	1229	4.0336118	35.964199	8227	29.45	7	1.0748448	0.20100001	0.83687836	29
soy_OGL_2223	2000	1.0696845	22.200001	3014	29	11	10.658498	0.094999999	0.72664678	17
soy_OGL_4452	1530	4.4197712	35.816994	3231	25.35	12	12.034771	0.17299999	0.66250801	11
soy_OGL_5467	1979	6.4554529	33.602829	3732	29.25	6	6.4385815	0.152	0.89454103	16
soy_OGL_6571	1400	4.8296428	31.357143	6356	29.5	6	2.5219452	0.184	0.78082877	32
soy_OGL_748	2733	7.9587779	36.955727	1001	28.83	6	4.4863329	0.098999999	0.91956079	13
soy_OGL_2854	2956	5.5548873	33.457375	3391	27.7	11	1.6990417	0.078000002	0.70418286	15
soy_OGL_23	1475	11.015924	32.135593	2001	32	8	16.512674	0.122	0.91019547	29
soy_OGL_62	1400	11.010665	35.5	3032	29.42	6	4.1295204	0.19	0.83754545	27
soy_OGL_192	1421	8.3450031	38.775509	2366	28.71	7	3.1677914	0.193	0.80054951	20
soy_OGL_229	1200	9.9151058	37	7625	28.08	9	2.5803294	0.197	0.83872825	24
soy_OGL_310	2000	10.227943	24.950001	2792	31.6	9	5.858089	0.089000002	0.94494146	13
soy_OGL_376	1500	11.080396	32.066666	2940	28.66	9	8.0077686	0.162	0.79810363	18
soy_OGL_940	1900	12.449766	38.210526	7073	35.36	8	9.1880684	0.206	0.7097531	28
soy_OGL_1017	1859	6.0355277	33.942982	1867	31.36	8	9.8752213	0.092	0.81925905	24
soy_OGL_1269	1618	6.6517758	36.71199	2337	26.76	9	4.4153686	0.145	0.68766147	19
soy_OGL_1377	1250	5.7269979	38.880001	1932	32.16	6	8.1114607	0.186	0.79470968	35
soy_OGL_1388	1100	6.9438424	37.81818	7716	32.18	6	10.681188	0.235	0.80857474	34
soy_OGL_1651	1400	8.6515789	32.714287	3084	27.28	12	8.1764889	0.169	0.59970081	21
soy_OGL_1766	1537	5.2867265	38.776836	3512	27.39	10	6.0978651	0.15099999	0.91373581	13
soy_OGL_1780	2200	5.2867265	25.454546	5063	35.68	8	6.7899122	0.105	0.89518505	21
soy_OGL_1858	1500	5.4487619	30.4	4528	31.93	7	10.368548	0.145	0.72750324	37

soy_OGL_2113	1853	6.8356886	35.078251	2248	33.83	8	4.9216523	0.15000001	0.93796331	17
soy_OGL_2122	1800	8.9625301	38.611111	3202	29.61	8	2.5877657	0.139	0.90342659	17
soy_OGL_2195	2018	8.5738249	29.534193	1001	33.34	8	7.9601226	0.113	0.77851838	27
soy_OGL_2610	1879	8.0021572	38.584354	2001	28.31	8	4.6701937	0.199	0.59879094	21
soy_OGL_2910	1500	10.078434	39.599998	7756	31.4	8	12.391597	0.149	0.97465533	26
soy_OGL_3015	2090	12.769964	30.047848	1001	32.96	5	2.2231066	0.15000001	0.76323831	24
soy_OGL_3206	1325	5.9144826	38.566036	3418	29.96	9	3.4957027	0.154	0.69581997	34
soy_OGL_3704	1800	8.5720577	32.111111	7602	30.61	9	5.6318908	0.189	0.84252363	20
soy_OGL_3705	2300	8.5720577	36.130436	6569	31.6	10	9.1912813	0.14	0.84238625	20
soy_OGL_3919	1500	9.3006687	39.266666	3495	27.86	9	5.4696169	0.18000001	0.79759377	20
soy_OGL_4003	1879	11.197123	27.993614	1624	33.74	10	7.3501225	0.082999997	0.81007391	17
soy_OGL_4372	1621	8.4425459	31.955584	2001	31.83	10	13.866102	0.15000001	0.52256382	25
soy_OGL_4550	2300	3.6987016	39.47826	4958	34.69	12	2.2732141	0.056000002	0.79265809	31
soy_OGL_4608	1815	6.9008231	31.955923	1987	32.12	13	8.3270483	0.1	0.85609806	10
soy_OGL_4907	2184	15.417212	32.967033	1572	34.06	11	13.692621	0.066	0.78492731	17
soy_OGL_5263	2200	10.745309	29.272728	3256	30.18	10	3.2209492	0.109	0.81570733	15
soy_OGL_5272	2100	7.2727275	18.714285	4609	33.47	8	12.134956	0.101	0.7891829	20
soy_OGL_5443	1898	5.0694704	36.986301	4144	30.61	9	2.9772601	0.126	0.94993109	15
soy_OGL_5470	2100	4.9895315	32.333332	1992	31.28	10	18.040922	0.057999998	0.87847894	27
soy_OGL_5498	1555	4.4415636	31.318329	2001	31.63	8	11.508561	0.12	0.84793103	28
soy_OGL_5891	1300	10.038893	28	6825	34.92	8	16.84602	0.142	0.88551021	38
soy_OGL_6534	1500	10.313567	33.866665	2546	29.73	10	5.8639178	0.133	0.73477668	21
soy_OGL_6549	1706	13.347547	39.097305	2648	31.53	6	3.684001	0.205	0.75496733	29
soy_OGL_6574	1574	4.8296428	35.514614	1175	29.6	6	5.7237091	0.199	0.78167874	30
soy_OGL_6771	1645	7.4753222	31.671732	2001	30.15	9	8.9303398	0.15000001	0.7503438	17
soy_OGL_6846	2100	3.9573007	36.42857	8537	32.66	7	5.8448825	0.139	0.81952214	32
soy_OGL_6943	1462	11.24362	38.78249	3065	30.84	9	5.235003	0.18799999	0.91908962	18
soy_OGL_6980	1200	4.8485398	26.916666	6032	30.75	5	10.968753	0.176	0.94418663	33
soy_OGL_7006	1700	6.3107963	38.588234	2762	32.76	12	3.466634	0.133	0.9710477	9
soy_OGL_227	1000	8.7488394	39.200001	4823	28	6	3.5075991	0.227	0.83586681	24
soy_OGL_4345	1880	8.2939415	28.138298	3262	31.59	9	8.6995745	0.17399999	0.47516331	22

soy_OGL_5899	1485	10.121329	32.121212	3899	30.3	6	4.4611826	0.142	0.87643367	31
soy_OGL_3695	1168	7.5635667	37.5	3084	23.88	13	6.1042523	0.21600001	0.88906145	18
soy_OGL_4879	1828	3.9014754	23.194748	1542	30.14	11	5.8338423	0.082999997	0.92718798	23
soy_OGL_5503	1326	5.1489553	36.802414	1136	26.62	12	4.8553581	0.178	0.84011775	19
soy_OGL_5885	1312	10.300918	34.832317	2001	30.25	11	6.2801309	0.13699999	0.89271426	35
soy_OGL_2547	1300	4.2873001	32.615383	2275	25.69	10	4.6002922	0.177	0.72836012	20
soy_OGL_6797	1200	4.8344703	35.583332	3255	25.25	9	2.9671144	0.193	0.7851426	21
soy_OGL_332	1760	10.351954	38.06818	2001	28.69	9	2.5174747	0.094999999	0.87628561	22
soy_OGL_348	1505	3.5052428	29.501661	1122	30.83	7	5.6318388	0.107	0.84606284	30
soy_OGL_1394	1300	6.9438424	38.384617	3416	28.38	9	4.1619854	0.141	0.81206119	32
soy_OGL_1503	1400	8.5456972	38.42857	1125	31.71	8	7.715251	0.126	0.98651308	17
soy_OGL_1815	1223	0.91241473	37.857727	2024	28.29	9	24.58066	0.16	0.77280444	29
soy_OGL_2871	1528	7.6317539	36.191101	1001	25.98	9	7.2904625	0.111	0.80111271	18
soy_OGL_3203	1543	8.2018318	36.616982	4320	31.3	10	5.8514123	0.082999997	0.69290918	36
soy_OGL_3239	1266	9.3938437	27.962086	1001	31.12	6	7.5521336	0.13600001	0.72908711	36
soy_OGL_3971	1500	9.8309717	34.733334	2910	25.73	10	8.7942953	0.121	0.93605769	10
soy_OGL_3995	1800	11.197123	29.722221	3381	29.5	10	4.6630955	0.093999997	0.82622308	15
soy_OGL_4536	1670	7.1064296	28.982037	1001	33.65	8	2.8805695	0.057	0.77698547	32
soy_OGL_4537	1247	7.1064296	30.232557	6045	29.59	9	5.4473419	0.139	0.77765417	33
soy_OGL_5879	1100	10.269903	37.363636	2853	30.45	9	20.935802	0.126	0.89907146	34
soy_OGL_5881	1100	10.300918	38.454544	6703	29.63	9	8.461566	0.131	0.89763778	35
soy_OGL_6277	1600	5.9430509	37.5	3560	29.56	10	6.0706854	0.119	0.93437994	22
soy_OGL_1519	1200	6.1372461	27.416666	7829	30.33	8	3.877233	0.12	0.9085595	34
soy_OGL_6852	1545	7.945219	36.31068	4498	27.05	10	10.707836	0.131	0.82816809	22
soy_OGL_1090	1284	6.6428576	31.853582	2001	25.07	9	5.0487909	0.226	0.91418564	12
soy_OGL_1482	1731	5.904388	16.002312	1286	30.56	9	6.1733298	0.149	0.95096803	20
soy_OGL_1785	1357	5.2867265	31.245394	4021	25.79	12	9.6896906	0.189	0.88893646	18
soy_OGL_3612	1500	5.6934285	28.933332	2994	27.33	11	12.080242	0.178	0.89136785	17
soy_OGL_5384	1473	9.3595705	28.581127	1001	28.37	8	2.9686544	0.259	0.69009775	20
soy_OGL_5441	1258	5.0618563	35.532593	3373	25.91	11	11.630589	0.23	0.95193648	15
soy_OGL_5850	1800	9.6763773	20.388889	3764	31.77	7	4.1667891	0.176	0.98444659	19

soy_OGL_6296	1274	6.0601311	31.632652	3217	26.92	11	7.7848797	0.22	0.94943643	18
soy_OGL_6907	1523	7.0806479	30.531845	4426	29.08	9	10.897634	0.266	0.87634134	23
soy_OGL_66	1200	12.433825	23.666666	3741	31.75	10	5.3344183	0.186	0.82703638	33
soy_OGL_313	1300	12.282213	33.53846	3381	29.38	13	13.501177	0.19	0.93422073	14
soy_OGL_728	1410	10.898283	36.666668	2911	32.19	14	4.3951149	0.16599999	0.87069666	20
soy_OGL_758	1200	5.5111747	39.083332	1794	26.25	10	25.064493	0.228	0.95407957	10
soy_OGL_778	1700	8.7557526	21.235294	3367	31.52	9	3.840348	0.12	0.93916404	18
soy_OGL_1060	1400	4.5279164	32.92857	1349	27.92	13	13.21634	0.18000001	0.86260015	25
soy_OGL_1093	1300	8.3440781	34.615383	3232	28.92	12	17.751846	0.20100001	0.92674464	16
soy_OGL_1158	1034	8.7633495	38.684719	1001	25.24	13	18.325819	0.26300001	0.94944113	22
soy_OGL_1240	1600	8.8961325	33.375	1138	34.18	10	18.504833	0.22	0.75438595	25
soy_OGL_1486	1878	7.653698	23.588924	1001	36.04	10	4.5054879	0.169	0.96350402	21
soy_OGL_1559	1581	11.818582	25.490196	2001	32.82	8	7.7541118	0.20299999	0.83773214	21
soy_OGL_1570	1460	10.813619	38.082191	2001	32.8	8	4.8831601	0.243	0.8071869	25
soy_OGL_2175	1490	8.9299202	38.657719	1001	32.95	11	15.309572	0.227	0.81011516	27
soy_OGL_2485	1605	6.4331512	35.576324	1082	33.27	8	5.3510995	0.25	0.88666415	21
soy_OGL_2958	1300	11.014667	36.46154	2488	32.46	10	11.522526	0.197	0.87355322	19
soy_OGL_3200	1100	8.3908644	39.81818	5124	31.09	10	5.7195139	0.26499999	0.69193172	34
soy_OGL_3343	1165	10.878196	38.111588	3120	29.52	9	0.94170183	0.249	0.8541767	26
soy_OGL_3569	1167	5.4506187	31.276777	2001	31.53	9	8.9046755	0.20299999	0.8360306	35
soy_OGL_3572	1151	5.4506187	35.273674	1186	30.58	10	4.9779515	0.20900001	0.83734232	37
soy_OGL_3587	1000	5.4232616	38.799999	2734	30.6	8	16.685156	0.212	0.85237873	36
soy_OGL_3734	1516	9.0400381	23.548813	2990	33.24	9	10.638314	0.152	0.79009873	26
soy_OGL_4483	1958	7.5806398	25.434116	1733	32.83	11	4.4121923	0.235	0.7161243	28
soy_OGL_4533	1370	7.5105057	30.072992	7614	32.55	10	8.6480942	0.20900001	0.77603412	29
soy_OGL_5513	1032	5.2083502	39.922482	1001	26.45	11	5.245666	0.24699999	0.81752491	18
soy_OGL_6985	1440	4.8170056	27.986111	2141	29.51	15	7.8443623	0.20100001	0.94902366	35
soy_OGL_1764	1182	5.2867265	33.756344	6772	25.63	9	8.7708807	0.207	0.91570777	10
soy_OGL_4450	1441	3.2397017	28.105482	3519	27.13	11	8.9315691	0.15899999	0.65239257	13
soy_OGL_5444	1300	5.0694704	33.53846	8944	29.61	9	2.9772601	0.20299999	0.94977009	15
soy_OGL_6190	1062	5.6346884	33.333332	2099	26.27	8	2.2918994	0.22400001	0.84635508	15

soy_OGL_33	1264	10.486021	30.45886	2001	35.99	7	9.3417883	0.13600001	0.8958022	31
soy_OGL_276	1486	9.7329025	24.966352	1001	37.88	7	4.51651	0.114	0.89778882	29
soy_OGL_437	1362	10.683906	37.665199	1001	29	11	13.631361	0.185	0.67403758	19
soy_OGL_896	1254	7.0074801	31.578947	1430	30.14	7	7.0969319	0.17200001	0.66767383	29
soy_OGL_1375	1300	5.7269979	24.846153	3883	34.07	6	4.3216019	0.115	0.79377663	35
soy_OGL_1561	1600	10.973433	24.5625	2617	33.25	7	11.790428	0.161	0.82570237	25
soy_OGL_2106	1600	5.1327806	34.375	4526	34.06	11	2.7473176	0.146	0.96026146	13
soy_OGL_2126	1226	8.6662102	31.402937	2677	28.79	7	6.3209705	0.193	0.90076631	17
soy_OGL_2211	1400	6.4445391	29.857143	3293	32.35	9	26.314205	0.146	0.75354129	27
soy_OGL_3329	1200	11.347876	32.25	3076	33.25	9	14.164609	0.152	0.87444699	30
soy_OGL_3545	1200	8.9636507	33.666668	3331	29.58	7	5.8104205	0.21600001	0.80193627	24
soy_OGL_3642	1246	5.6271753	31.781702	4443	31.54	6	12.814153	0.207	0.93535531	27
soy_OGL_5020	1639	8.8939037	26.723612	3706	32.88	8	14.040364	0.155	0.66891646	26
soy_OGL_5242	2163	8.6306667	15.811373	2349	36.19	4	11.693774	0.14399999	0.87980103	24
soy_OGL_5321	1212	11.453777	37.541256	2800	31.93	11	15.395656	0.153	0.66332853	25
soy_OGL_5466	1200	6.4554529	34.416668	4777	27.66	10	6.4948754	0.184	0.89552104	16
soy_OGL_5516	1132	8.4901819	39.399292	3371	33.39	9	6.4590673	0.198	0.8098647	22
soy_OGL_5576	1960	6.2863836	20.05102	3892	34.23	10	23.416119	0.123	0.69180995	22
soy_OGL_6444	1081	9.0478334	33.024979	1780	29.32	8	9.2391119	0.175	0.56525338	32
soy_OGL_6508	1600	7.9388223	30.6875	2119	32.93	7	14.346871	0.169	0.69144368	26
soy_OGL_6842	1100	3.9573007	33.81818	3421	33.63	6	8.1664724	0.214	0.81871408	33
soy_OGL_6922	1480	8.8029718	35.270271	4036	35.13	4	8.976058	0.25	0.89668685	26
soy_OGL_1895	1605	9.4963474	26.728971	2814	29.28	9	8.7804966	0.14399999	0.65655828	16
soy_OGL_6810	1200	6.2792668	33.083332	5765	29.16	7	16.7729	0.234	0.79776829	21
soy_OGL_760	1366	5.8962474	38.726208	1045	27.81	13	8.780448	0.17	0.95718807	9
soy_OGL_1069	1200	4.5279164	35.166668	1201	28.25	10	10.718622	0.178	0.87040555	23
soy_OGL_1490	1200	7.4780941	34.083332	3933	28.58	12	26.393402	0.16500001	0.97199142	23
soy_OGL_2121	1430	9.8124828	25.944056	1306	30.48	10	18.041445	0.133	0.91605502	16
soy_OGL_3623	1372	3.8661525	26.093294	2204	28.35	11	6.6992178	0.163	0.91622239	24
soy_OGL_3667	1900	4.1581578	18.105263	4230	30.31	12	17.44483	0.086000003	0.97899139	14
soy_OGL_4858	1600	6.8892426	32.75	1441	32.75	12	4.2034168	0.093000002	0.95855874	13

soy_OGL_6629	1293	8.8137932	32.559937	1342	29	12	10.811676	0.15800001	0.96832079	24
soy_OGL_405	1300	7.9741797	26.923077	2899	27.15	12	2.4156163	0.148	0.74763966	25
soy_OGL_4522	1058	7.9699202	28.355387	2637	31.28	10	5.7836566	0.13600001	0.76129276	34
soy_OGL_4556	1300	7.340271	33.384617	1504	31.38	13	16.315704	0.112	0.8014124	23
soy_OGL_5548	1186	7.1524053	33.558178	3706	26.72	14	11.281716	0.156	0.75298452	15
soy_OGL_675	1100	3.8562949	25	4194	27.81	8	6.1691256	0.15099999	0.78098989	25
soy_OGL_263	1200	9.6228313	39.166668	2430	31.41	12	11.061611	0.156	0.88147974	15
soy_OGL_1767	1411	5.2867265	33.876682	2001	29.62	11	5.5929375	0.138	0.91368473	13
soy_OGL_4160	1100	9.3938532	37.545456	1411	28.9	9	7.7105131	0.167	0.90028989	16
soy_OGL_278	1000	6.375752	39.599998	2866	31.6	9	4.0111594	0.141	0.90268254	27
soy_OGL_1412	1127	16.339678	27.15173	1001	31.67	7	2.6472139	0.123	0.84270567	22
soy_OGL_5521	1000	8.5462761	38	1507	32.3	9	9.9577217	0.13600001	0.80102301	27
soy_OGL_284	1900	7.6405764	26.947369	4729	28.21	7	6.1887593	0.141	0.90446043	26
soy_OGL_5485	2100	4.7314305	39.095238	6240	27.85	6	14.019121	0.257	0.8635211	33
soy_OGL_6789	1518	9.1081762	32.608696	1001	24.24	9	3.6096735	0.191	0.77749342	25
soy_OGL_35	1900	9.8391256	25.842106	7236	30.36	10	11.044274	0.12899999	0.89304847	31
soy_OGL_37	2000	9.7632828	29.65	2612	28.2	10	10.990569	0.145	0.89088488	30
soy_OGL_3223	1193	9.7705011	39.81559	4422	28.24	7	10.248329	0.178	0.71346927	49
soy_OGL_4549	2122	5.7242432	36.286522	2001	25.44	11	7.0814981	0.132	0.79163861	32
soy_OGL_5244	2284	8.810091	35.332748	3075	27.97	7	10.20177	0.146	0.87740242	24
soy_OGL_4105	2100	12.218921	28	3425	28.71	8	5.2611556	0.147	0.69396222	20
soy_OGL_102	2800	10.922771	27.142857	2869	33.14	6	8.0376854	0.12	0.74958181	24
soy_OGL_1463	1378	9.5639515	30.841799	2939	28.44	6	15.966932	0.154	0.92563969	31
soy_OGL_4627	2017	3.3767221	34.506695	1001	27.56	7	7.6949282	0.081	0.74963397	33
soy_OGL_4679	2000	10.891823	33.299999	3918	32.5	8	17.022524	0.13	0.64468628	39
soy_OGL_6312	1861	21.00876	33.745296	4013	29.12	9	2.9941256	0.117	0.95730376	11
soy_OGL_1700	1933	6.9589791	29.125711	3395	26.02	8	2.8418443	0.104	0.81245112	28
soy_OGL_3933	2231	8.8798027	11.788436	1630	31.01	8	2.8647604	0.041999999	0.86127132	26
soy_OGL_5887	1387	9.3344879	35.61644	2624	25.09	11	9.2722082	0.15000001	0.88783741	36
soy_OGL_2603	1815	6.5441737	37.52066	1001	22.97	10	13.103658	0.119	0.61406243	18
soy_OGL_3727	1200	7.6693859	38.666668	5036	22	9	6.6042786	0.171	0.81009442	19

soy_OGL_818	1495	10.47439	31.438128	1211	26.22	6	4.2819037	0.13	0.74811757	23
soy_OGL_1481	2220	5.904388	36.126125	5006	25.54	9	13.204861	0.050000001	0.95008916	20
soy_OGL_3932	1546	9.3250446	39.327297	2001	24.51	8	4.6850519	0.14	0.85395724	25
soy_OGL_5860	1986	9.3926363	32.880161	2001	27.94	6	5.7022986	0.068999998	0.93410355	23
soy_OGL_598	2300	2.6747844	23.130434	3759	27.65	4	1.4532186	0.152	0.65376818	9
soy_OGL_382	1147	8.0134726	32.868351	10445	25.19	7	1.7226105	0.185	0.78768432	20
soy_OGL_5566	1513	7.8096585	27.825512	8802	26.76	8	8.5647755	0.167	0.71209913	17
soy_OGL_6148	2100	5.4320879	28.190475	6727	28.47	5	0.96236831	0.123	0.78190821	17
soy_OGL_6609	1813	8.5314484	23.110867	13798	30.11	6	5.6109757	0.145	0.87646449	18
soy_OGL_1311	1140	2.0239863	33.508774	21258	29.03	2	4.3383112	0.167	0.59195405	13
soy_OGL_2814	1600	0.37861791	29.875	2901	24	3	1.5661993	0.167	0.41210791	6
soy_OGL_120	1195	0.65264124	37.405857	12957	23.26	2	2.9170091	0.153	0.55986017	6
soy_OGL_132	1870	1.6597055	7.9679146	16763	31.55	1	0.77871293	0.01	0.59865129	9
soy_OGL_591	1356	0.81641358	30.38348	14039	25.51	2	3.9726629	0.192	0.62593067	10
soy_OGL_1320	1263	0.24154867	34.362629	20978	27.55	1	0.078865454	0.213	0.61970627	14
soy_OGL_2349	2041	2.8688939	26.555611	11635	28.85	5	10.649649	0.133	0.22573395	8
soy_OGL_2828	1900	2.0155141	19.526316	3442	26.57	3	4.0432391	0.111	0.58846837	5
soy_OGL_3109	2171	1.7917838	21.234455	8268	26.99	6	8.7883358	0.127	0.49184707	6
soy_OGL_4053	3064	0.29615524	17.199739	9587	32.14	5	1.6782029	0.16500001	0.38954368	13
soy_OGL_5085	1600	4.0220618	25.5625	8984	28.37	1	0.79523319	0.092	0.36701566	4
soy_OGL_6076	2900	1.7462445	37.517242	3881	29.79	2	20.435745	0.20299999	0.012365804	3
soy_OGL_6109	1891	0.20972228	36.805923	3079	22.1	3	0.040088061	0.198	0.68302238	7
soy_OGL_6718	1800	2.7221162	31.444445	25540	31.5	1	0.028711028	0.093000002	0.6639626	10
soy_OGL_631	1400	5.4129052	33.92857	8489	26.21	5	4.5430431	0.17900001	0.71882755	17
soy_OGL_849	1700	6.0357013	24.235294	10741	31.17	3	10.845319	0.086999997	0.63698435	16
soy_OGL_2304	1900	6.8934898	22.842106	16247	31.26	7	3.4569345	0.085000001	0.57131195	16
soy_OGL_4276	1532	5.4117041	28.524805	10456	28.91	6	5.8574829	0.185	0.36283147	19
soy_OGL_5042	1600	6.568222	26.5	7606	27.43	5	0.7715233	0.108	0.64958745	20
soy_OGL_5110	1200	9.5241146	30.416666	20203	31.33	1	0.60522556	0.103	0.32255122	8
soy_OGL_5121	1696	6.9515624	36.379719	12706	30.54	2	6.2405739	0.141	0.40155998	13
soy_OGL_111	1550	0.17572904	32	3272	22.64	2	0.89984494	0.103	0.087409362	1

soy_OGL_2801	1000	0.8990916	36.200001	16681	26.9	2	12.59503	0.111	0.32197997	10
soy_OGL_6063	1510	2.0422838	34.105961	1001	23.5	4	6.9026737	0.124	0.052362245	11
soy_OGL_835	1959	5.7850161	27.003572	3030	26.44	6	2.7668867	0.075000003	0.69822657	13
soy_OGL_5053	1649	6.5904026	25.106125	1001	26.07	6	9.6989374	0.097999997	0.60813838	13
soy_OGL_1333	1642	3.8014758	22.655298	2920	27.1	5	12.227235	0.184	0.69192755	9
soy_OGL_4783	1219	3.5324056	27.727646	3865	24.36	5	10.622014	0.19400001	0.88725394	8
soy_OGL_2573	1300	6.4692268	25.307692	11247	25.84	9	3.7323456	0.184	0.68103147	16
soy_OGL_2728	1856	6.995357	21.066811	2100	30.06	7	3.7543066	0.153	0.42426655	18
soy_OGL_380	1500	8.0134726	20.666666	12186	29.66	7	1.7226105	0.183	0.78814417	20
soy_OGL_510	1241	4.4821186	28.364222	4144	24.65	6	4.6850696	0.19499999	0.45660627	22
soy_OGL_116	1693	0.27173504	7.2061429	26432	34.96	1	2.9251781	0	0.52052647	4
soy_OGL_877	1900	2.4722638	12	3711	28.94	2	1.446648	0.127	0.62480187	8
soy_OGL_2361	1300	4.2267075	29.692308	5027	25.84	3	0.24580364	0.14300001	0.13588533	7
soy_OGL_3417	1500	0.4680596	31.133333	2361	26.53	1	19.78817	0.186	0.53541476	6
soy_OGL_3423	1088	0.84260994	23.161764	20849	28.86	2	1.8516887	0.097999997	0.40841347	5
soy_OGL_4046	1368	0.37265155	27.850878	12097	27.48	5	4.8614759	0.184	0.40662432	16
soy_OGL_4164	1815	0.61671168	20.93664	5082	29.53	2	17.722666	0.074000001	0.4335385	2
soy_OGL_2093	1492	1.3710024	17.493298	9614	27.27	2	3.648881	0.13500001	0.76345873	15
soy_OGL_2094	1444	1.3710024	15.858726	15262	30.67	2	3.648881	0.088	0.76376361	15
soy_OGL_2791	1605	5.7500677	27.663551	2001	25.42	5	10.639784	0.15899999	0.21344388	8
soy_OGL_4043	2000	0.43234766	9.5	1103	27.95	3	1.9635891	0.083999999	0.41063845	13
soy_OGL_5104	1104	9.3550339	35.326088	16864	27.26	2	0.10046821	0.22400001	0.27991202	6
soy_OGL_6099	1036	0.5669629	23.648649	26092	29.44	1	9.8100948	0.141	0.66161948	13
soy_OGL_2746	1400	5.0142555	28.642857	3235	26.28	7	10.81669	0.168	0.39027622	15
soy_OGL_4721	1422	5.8001513	21.940928	5100	29.32	4	1.7162265	0.139	0.5678497	24
soy_OGL_4765	1187	5.1086917	30.32856	5185	26.28	3	20.754265	0.17200001	0.80966067	6
soy_OGL_3857	1200	10.036083	29.5	11613	28.83	8	4.0294867	0.237	0.27342919	23
soy_OGL_4578	1400	5.9374781	19.142857	4864	28.14	5	5.2967024	0.111	0.83193094	21
soy_OGL_2821	1100	2.0155141	28.181818	9224	25	4	6.8987455	0.123	0.54000634	7
soy_OGL_4050	1121	0.26952159	20.16057	14127	26.76	4	2.2347946	0.104	0.39376193	13
soy_OGL_2840	1200	5.5548873	21.833334	10153	30.16	5	6.0993161	0.125	0.66974962	24

soy_OGL_6140	1200	3.3948011	26.583334	7632	26.66	5	3.4324322	0.141	0.76982743	15
soy_OGL_3120	1722	6.0844588	15.62137	7057	31.01	7	6.5341625	0.059999999	0.52944511	18
soy_OGL_5980	1500	7.1452026	19.933332	8452	29.86	4	4.0401111	0.090999998	0.62004083	16
soy_OGL_1594	2219	5.281703	26.543488	5090	32.22	2	0.30541286	0.18799999	0.7077108	18
soy_OGL_4051	3270	0.26952159	33.333332	10730	44.58	4	2.2347946	0.38499999	0.39363128	14
soy_OGL_139	2606	2.8892014	34.574059	20343	37.37	2	0.2146938	0.315	0.63930345	6
soy_OGL_1317	2480	0.24154867	37.459679	14714	35.48	2	0.46186057	0.176	0.61800337	14
soy_OGL_1323	1213	0.24154867	35.366859	16423	30.33	1	4.4111633	0.141	0.62252265	14
soy_OGL_1341	1700	0.32211781	32.176472	16412	31.05	2	1.8734994	0.30599999	0.7197361	14
soy_OGL_2035	1300	0.62599713	25.615385	25409	31.61	1	0.00487084	0.066	0.35588536	8
soy_OGL_2812	1700	0.16320086	39	1510	27.23	2	1.387175	0.17200001	0.40319458	6
soy_OGL_4030	1906	0.4967483	31.164743	8343	27.07	3	2.7892387	0.176	0.63671541	7
soy_OGL_4039	2000	0.4582673	23.700001	5272	29.65	4	8.349618	0.127	0.42558461	9
soy_OGL_4047	2347	0.37265155	23.178526	18291	35.06	5	4.8614759	0.20299999	0.40624616	15
soy_OGL_4733	1500	1.3662759	32.200001	17536	31.86	1	0.12047315	0.133	0.15526797	9
soy_OGL_5087	1796	0.37127793	39.420937	5466	27.89	1	11.438566	0.145	0.34403577	2
soy_OGL_5993	1915	0.28763628	22.924282	7604	27.98	6	1.0639614	0.13600001	0.56898904	12
soy_OGL_6033	2616	0.48655906	29.013762	1248	32.56	2	6.1329522	0.118	0.34721348	7
soy_OGL_6083	1312	1.5192883	36.661587	21117	29.95	3	0.024011277	0.109	0.083318546	2
soy_OGL_6110	1000	0.21376705	38.299999	19854	28	2	0.058298897	0.141	0.68382269	7
soy_OGL_6123	1803	2.099159	33.000553	29684	36.71	2	0.14236361	0.106	0.73327577	13
soy_OGL_6722	2300	2.7221162	28.826086	10463	35.17	3	1.9520746	0.215	0.67119867	5
soy_OGL_2358	1100	2.8688939	38.454544	15400	27.09	1	0.00343914	0.106	0.19348165	8
soy_OGL_5996	4087	0.28763628	27.134817	6031	34.76	2	0.24454311	0.079999998	0.56326479	15
soy_OGL_179	1397	4.2186117	36.864712	1051	26.27	3	2.3765297	0.16599999	0.77303934	13
soy_OGL_154	1278	7.7098465	32.707355	19578	32.86	2	4.5510955	0.14300001	0.68487841	13
soy_OGL_156	2471	4.1056633	24.443544	1971	33.95	3	2.893321	0.14	0.69676423	12
soy_OGL_177	1200	4.2186117	34.416668	4790	26	4	3.7915866	0.168	0.77034575	13
soy_OGL_5991	2158	0.28763628	29.471733	7984	29.1	6	1.0639614	0.035999998	0.56931633	11
soy_OGL_6010	2100	1.7006036	27.761906	5792	30.23	7	2.2093465	0.090000004	0.508699	9
soy_OGL_6410	3008	6.8150654	32.380318	3353	34.64	4	3.5344493	0.19400001	0.49414355	9

soy_OGL_525	1400	2.3637695	28.428572	5568	27.42	3	1.4523289	0.112	0.4115901	12
soy_OGL_4041	1071	0.47341603	35.480858	10018	25.21	4	7.2885089	0.116	0.42476293	11
soy_OGL_3098	1089	1.1479118	38.383839	24468	30.11	2	7.23174	0.039000001	0.39772612	5
soy_OGL_485	1102	4.9804826	36.569874	14944	27.76	3	1.3756965	0.090999998	0.50930727	17
soy_OGL_4194	1238	4.6005397	33.037155	1001	24.47	10	1.5854977	0.197	0.20999223	20
soy_OGL_115	2209	0.51387459	25.2603	9630	33.09	2	4.9686456	0.204	0.51893127	5
soy_OGL_1318	1994	0.24154867	14.593781	11156	32.39	2	0.46186057	0.177	0.61828732	14
soy_OGL_1623	1800	1.3796759	29.111111	12469	29.77	4	1.1885607	0.241	0.44456568	2
soy_OGL_2353	2032	2.8688939	32.775589	4512	32.33	4	1.6800938	0.244	0.21116729	12
soy_OGL_2818	1942	0.18303733	18.434603	7351	30.32	4	1.6579659	0.124	0.50267249	1
soy_OGL_3100	1022	1.1479118	32.97456	28199	32.58	3	2.2566531	0.088	0.40311587	5
soy_OGL_3105	1200	1.1479118	33.166668	22127	33.16	1	0.097443491	0.139	0.43644378	3
soy_OGL_3899	1400	1.5956808	24.285715	3806	27.35	2	0.61079943	0.132	0.67660075	4
soy_OGL_4049	1031	0.26952159	24.733269	26522	33.55	1	0.1010604	0.067000002	0.39801922	13
soy_OGL_6011	1500	1.4287384	27.866667	14115	31.6	4	2.9913032	0.113	0.50185716	6
soy_OGL_6015	1300	2.4418838	25.461538	20069	30.23	2	0.026753051	0.108	0.47084695	6
soy_OGL_6090	1875	0.69722927	26.08	5484	29.38	2	5.961226	0.215	0.55827689	6
soy_OGL_6132	1140	2.167546	31.052631	5731	25.7	3	5.0926108	0.223	0.75352323	10
soy_OGL_6371	2000	1.9526396	16.65	18170	33.25	2	1.9247146	0.14300001	0.62199152	3
soy_OGL_2012	1000	2.7130883	34.799999	14403	29.5	4	10.420037	0.115	0.3836039	10
soy_OGL_2784	1400	2.5057061	32.214287	3476	26	6	7.8973269	0.153	0.2333986	10
soy_OGL_3097	1100	0.6157763	37.18182	13742	27.36	6	4.3848529	0.13	0.3596811	7
soy_OGL_4268	1669	3.4015584	26.003595	3636	28.34	7	4.4090805	0.19499999	0.34434307	16
soy_OGL_5091	1200	1.092412	38.416668	7224	26.58	3	24.474054	0.116	0.13039948	2
soy_OGL_2064	1670	1.6292684	26.706587	2008	29.34	8	1.0126131	0.093000002	0.6144799	7
soy_OGL_5990	1757	1.5043266	14.797951	1001	29.99	6	0.95313317	0.057999998	0.57857275	13
soy_OGL_3521	2100	1.9912556	28.142857	3737	25.76	6	10.433919	0.14	0.74900842	17
soy_OGL_158	2352	3.5756059	32.738094	16632	27.67	3	1.6175621	0.20999999	0.69844043	9
soy_OGL_2069	2149	3.4504049	39.97208	3813	23.96	3	3.316045	0.142	0.64140618	12
soy_OGL_4756	2449	0.84740651	28.256432	12063	27.35	3	6.0787153	0.054000001	0.73169953	5
soy_OGL_5147	1700	4.3001404	29.058823	11002	27.47	3	2.1245944	0.15000001	0.76554728	21

soy_OGL_837	3588	5.3767109	31.96767	8722	32.74	3	3.6326334	0.041999999	0.65431345	16
soy_OGL_842	2101	5.8473277	32.413136	11672	28.7	4	0.95956695	0.082999997	0.64209819	15
soy_OGL_4354	2400	3.1938996	38.083332	4407	26.66	6	5.9255471	0.077	0.48768049	17
soy_OGL_119	1310	0.65264124	33.282444	11622	23.05	2	2.9170091	0.103	0.5598262	6
soy_OGL_5102	1328	1.5646205	37.123493	21558	25.07	3	0.2273265	0.066	0.16769472	3
soy_OGL_5043	1387	6.568222	36.986301	14013	25.37	4	0.084836803	0.074000001	0.64941514	19
soy_OGL_1894	1500	9.4963474	29.933332	3167	27.06	8	9.3912697	0.167	0.65771753	16
soy_OGL_4082	2000	7.4914689	33.549999	2821	26.95	9	2.6208673	0.121	0.55830401	17
soy_OGL_5143	1944	4.3852158	36.985596	2001	26.08	6	8.8222466	0.105	0.74051261	21
soy_OGL_830	1208	9.6582899	39.238411	1001	26.65	4	12.011958	0.182	0.72028852	23
soy_OGL_1260	1300	10.37138	36.53846	3102	25.76	6	9.984498	0.18799999	0.71008331	20
soy_OGL_3801	1447	8.0413237	35.03801	2612	25.36	9	24.895399	0.17200001	0.6246506	12
soy_OGL_555	2200	20.895227	39.954544	1975	33.18	9	11.331004	0.107	0.32723874	18
soy_OGL_911	1200	5.9492388	39.916668	1280	26.33	4	17.813278	0.17299999	0.67786539	27
soy_OGL_6428	1264	10.893449	36.867088	6417	30.06	7	10.394678	0.14	0.54696661	34
soy_OGL_2545	1227	4.2833328	32.681335	7227	25.42	10	9.9429626	0.163	0.7312727	20
soy_OGL_6461	1554	5.8666077	29.729731	3471	26.64	9	2.4051576	0.138	0.58726323	22
soy_OGL_74	1491	9.8974447	36.619717	3318	29.17	8	18.235809	0.079999998	0.8057394	25
soy_OGL_1379	1500	5.7269979	37.466667	7828	28.33	8	11.415756	0.114	0.79667944	35
soy_OGL_3929	1289	8.2275667	37.31575	6724	26.84	8	11.241423	0.131	0.84759194	24
soy_OGL_6865	1200	10.103802	36.916668	4041	29	6	13.561954	0.148	0.83942521	27
soy_OGL_429	1451	12.23607	29.290144	2001	29.08	6	6.4540882	0.118	0.6838941	22
soy_OGL_1683	1427	9.1770983	37.070778	3554	25.78	8	9.673048	0.14300001	0.72595549	15
soy_OGL_5593	1700	3.6134067	35.64706	3081	25.7	10	21.232048	0.075999998	0.66015708	20
soy_OGL_5181	1600	14.145021	19.75	4061	32.12	6	5.6671896	0.102	0.9051286	17
soy_OGL_3774	1264	13.809534	26.028481	7676	31.09	7	9.0123625	0.183	0.71568269	21
soy_OGL_4371	1700	5.4403811	26	1241	29.94	11	37.492428	0.122	0.52103615	23
soy_OGL_245	1100	15.037194	36.272728	9634	31.9	7	20.349678	0.167	0.85776907	20
soy_OGL_3819	1451	7.7295065	24.259132	2745	28.87	11	15.803836	0.1	0.56278968	21
soy_OGL_5312	1000	18.329891	26.200001	3511	31.9	7	6.0563107	0.139	0.68156099	27
soy_OGL_4669	1400	8.714469	15.5	3372	33.78	7	17.332151	0.077	0.66522223	35

soy_OGL_1573	1007	9.8763494	35.749752	3023	31.87	5	43.074696	0.125	0.79664838	28
soy_OGL_1274	2800	6.6517758	39.42857	6118	32.42	6	4.8338232	0.13600001	0.68664032	20
soy_OGL_2531	1624	7.7228384	36.391624	3543	25.61	8	4.2208781	0.168	0.75845021	13
soy_OGL_6241	2095	5.4170856	21.861576	2816	31.02	5	5.9789271	0.079000004	0.90055037	19
soy_OGL_281	1500	6.375752	39.866665	3580	31	6	1.5545734	0.119	0.90359312	26
soy_OGL_402	1800	7.6530638	38.833332	5158	30.83	9	10.638362	0.13600001	0.75372523	25
soy_OGL_407	1622	9.0930395	39.087547	3490	31.62	9	8.2230444	0.132	0.73865664	17
soy_OGL_1265	1385	9.6259041	37.97834	2153	29.02	8	14.336401	0.154	0.6979956	23
soy_OGL_1781	1475	5.2867265	35.254238	5866	30.77	9	6.035562	0.118	0.89509326	21
soy_OGL_3192	1600	9.9972277	33	3404	31.18	7	2.8999982	0.14300001	0.67332792	29
soy_OGL_3235	1157	9.8079872	33.102852	6052	33.79	7	10.026531	0.125	0.72500354	39
soy_OGL_3302	1900	9.4088583	39.736843	4907	30.05	8	7.8754659	0.108	0.93522578	18
soy_OGL_4558	1600	8.4823227	33.5	2894	32.25	6	23.34544	0.145	0.80342585	24
soy_OGL_6652	1800	15.119693	38.111111	2285	32.94	10	2.2254882	0.092	0.66474819	13
soy_OGL_6840	1542	3.9573007	35.343708	4700	32.87	8	14.624803	0.112	0.81659728	33
soy_OGL_1278	1355	7.387959	34.538746	2953	29.52	7	5.4666343	0.18000001	0.67483091	24
soy_OGL_1282	1389	6.1225662	39.236862	1002	29.01	6	1.28658	0.21799999	0.66358852	19
soy_OGL_1819	1500	0.91241473	39.733334	5920	29.93	7	3.8595233	0.17299999	0.76893508	31
soy_OGL_1868	1400	5.0498676	35.142857	4469	30.21	5	15.760678	0.168	0.7138409	28
soy_OGL_2215	1300	6.4445391	37.384617	5629	31.3	6	1.0916889	0.20100001	0.75182569	25
soy_OGL_2316	1368	7.0776219	38.66959	2268	29.16	9	5.6599402	0.163	0.54272562	19
soy_OGL_3005	1900	6.9705009	31.789474	1294	29.42	6	7.0310016	0.112	0.78525108	20
soy_OGL_3564	1200	5.4506187	38.25	11032	33.66	7	11.909006	0.177	0.83431154	33
soy_OGL_4719	1456	5.318872	37.843407	2001	30.63	7	7.5893664	0.14399999	0.57842773	27
soy_OGL_5483	1200	4.7314305	37.833332	12740	33.58	7	12.18399	0.206	0.86377013	33
soy_OGL_6474	1700	7.1733117	38.117645	2561	28.82	9	2.8096616	0.13699999	0.62274349	15
soy_OGL_6493	1701	9.3050442	38.095238	3464	29.98	6	6.5714922	0.191	0.66720539	17
soy_OGL_1253	1500	11.432598	37.400002	2094	33.66	7	10.696194	0.097000003	0.72214037	19
soy_OGL_4668	1243	8.714469	33.708771	5172	36.36	7	17.332151	0.086000003	0.66533989	35
soy_OGL_1871	1700	5.0498676	25.764706	3315	34.94	6	12.445052	0.086999997	0.7130487	25
soy_OGL_2319	1532	11.954895	37.793736	1981	32.76	8	9.8207293	0.13699999	0.53210092	18

soy_OGL_2668	1500	6.8734031	39.400002	3833	29.93	7	7.7067723	0.15700001	0.51526576	29
soy_OGL_4155	1400	9.8956871	34.357143	5211	31.78	5	23.62254	0.145	0.89317989	18
soy_OGL_336	1250	9.2740116	38.400002	2001	30.8	6	19.809711	0.115	0.8679902	24
soy_OGL_755	1500	6.1331749	37.466667	3297	31.66	10	12.102518	0.108	0.94771367	12
soy_OGL_1033	1768	6.3006811	39.366516	2461	31.67	11	27.496244	0.050999999	0.83462328	28
soy_OGL_1784	1800	5.2867265	35.666668	1265	32.38	11	19.410498	0.043000001	0.88968831	18
soy_OGL_3620	2100	3.8661525	37.380951	5998	32.9	12	5.9635634	0.011	0.91466117	22
soy_OGL_3999	1300	11.197123	38.923077	2136	29.46	8	11.044416	0.13600001	0.82304233	16
soy_OGL_6939	1700	10.270773	37.823528	5523	33.47	10	4.8847728	0.059	0.90894681	19
soy_OGL_1089	1800	7.5212369	22.944445	2258	30.22	8	12.072728	0.068000004	0.91189504	11
soy_OGL_2248	1401	3.1746132	36.830833	1350	27.12	7	13.218222	0.142	0.65821093	27
soy_OGL_4990	1038	8.6126404	36.705204	2248	29.47	6	2.9812658	0.15899999	0.70526534	27
soy_OGL_2984	1174	11.277602	32.793869	2001	30.32	7	5.5188746	0.117	0.82573193	22
soy_OGL_5577	1200	6.1746764	38.833332	7880	25.25	11	8.3671646	0.149	0.68990421	21
soy_OGL_1019	1700	6.0227766	38.823528	2596	29.41	6	5.7743216	0.071999997	0.82064933	25
soy_OGL_744	1600	7.9587779	37.625	8356	27.75	8	3.0853879	0.102	0.91893697	13
soy_OGL_2452	1419	7.4458432	33.967583	8979	29.52	9	18.21773	0.098999999	0.94666368	14
soy_OGL_2502	1399	7.4874678	37.955681	2874	28.44	6	11.289385	0.096000001	0.83938468	18
soy_OGL_3389	1300	5.6634336	38.307693	2258	28.07	8	28.678377	0.121	0.70476037	17
soy_OGL_3461	1900	8.8457031	33.789474	3462	32.31	9	3.9476848	0.030999999	0.61815763	18
soy_OGL_4654	1315	7.2297339	37.794678	4537	30.41	6	3.6025734	0.098999999	0.69660133	29
soy_OGL_6343	1149	5.6157908	36.118362	3300	31.07	4	8.5079031	0.116	0.895383	24
soy_OGL_1349	1200	10.258554	36.833332	2966	30.75	7	3.0385489	0.106	0.74211377	16
soy_OGL_3935	1452	8.8798027	37.878788	6168	28.71	4	2.4579394	0.097000003	0.86363876	26
soy_OGL_331	1375	10.351954	26.4	1846	34.69	5	4.2924633	0.113	0.8774516	23
soy_OGL_391	1200	8.4611053	37.5	3797	36.5	9	4.5653815	0.134	0.76659912	27
soy_OGL_1558	1337	9.3490543	34.405384	3367	35.75	7	8.3081532	0.14	0.84012878	24
soy_OGL_5179	1500	10.392078	32.666668	2303	31.6	7	14.263038	0.13500001	0.89628947	14
soy_OGL_6858	1400	8.4172974	27.357143	3527	35.64	6	3.6870041	0.131	0.83439404	25
soy_OGL_1262	1200	9.7057629	37	2147	31.08	5	6.0552659	0.227	0.7013377	24
soy_OGL_2595	1434	5.1120324	29.358438	3281	28.31	10	18.197117	0.153	0.63026571	16

soy_OGL_3382	1200	10.989937	39.416668	3470	29.33	7	13.16286	0.20100001	0.75125349	12
soy_OGL_6169	1400	9.8931875	24.5	1177	29.64	6	9.6710539	0.148	0.80978644	14
soy_OGL_6306	1471	5.4021316	34.262405	5308	34.33	8	5.0833626	0.123	0.98435867	9
soy_OGL_1676	1500	9.1770983	35.666668	5976	36.4	9	10.886816	0.064999998	0.71075934	16
soy_OGL_4296	1499	3.9414778	34.956638	2590	31.68	10	32.912186	0.122	0.39045417	23
soy_OGL_6654	1921	15.746664	27.27746	1001	37.89	8	3.4302859	0.034000002	0.38748202	15
soy_OGL_3762	1131	10.661443	39.08046	3597	29.26	11	16.785376	0.15800001	0.74265665	19
soy_OGL_4898	1200	9.0506868	36.916668	3698	35.08	9	5.3020058	0.113	0.89464229	17
soy_OGL_322	1000	10.951405	38.799999	7422	30.3	9	5.3449636	0.13600001	0.89768469	16
soy_OGL_2467	1001	4.3606744	38.761238	5587	29.97	10	26.413948	0.141	0.91309088	21
soy_OGL_4104	1263	12.218921	27.078384	1001	33.33	7	5.6422768	0.093999997	0.69151819	20
soy_OGL_6603	1600	8.5314484	25.8125	4312	31.81	11	14.870426	0.059	0.86590391	15
soy_OGL_4093	1000	12.218921	33.400002	3378	28.5	8	6.5368748	0.14399999	0.66251063	19
soy_OGL_4845	1000	6.4237089	36.900002	5390	30.2	8	4.2559252	0.142	0.97683549	13
soy_OGL_5912	1124	8.0339689	23.042706	2928	30.87	5	3.6988883	0.123	0.84763265	24
soy_OGL_6221	1000	9.7941818	36.599998	9137	35	8	9.6013689	0.115	0.87358886	29
soy_OGL_971	1000	13.568718	23.799999	9992	35.4	6	0.96079314	0.090000004	0.76326931	36
soy_OGL_1585	1100	7.7159863	32.909092	3219	31.09	7	6.9662991	0.113	0.77786309	20
soy_OGL_2553	1007	3.931226	39.821251	2060	30.68	8	34.417099	0.124	0.72073752	22
soy_OGL_6577	1039	4.8296428	31.18383	2772	33.1	5	10.865314	0.106	0.78308147	31
soy_OGL_1643	1500	5.7636523	39.333332	5217	24.8	9	5.5965042	0.17900001	0.5841974	20
soy_OGL_3984	1374	4.8896408	37.554585	4765	24.3	7	23.772984	0.184	0.88727021	12
soy_OGL_4370	1197	5.2109051	36.257309	2017	24.97	7	13.397062	0.18099999	0.51763242	22
soy_OGL_4409	1900	8.6647367	23.105263	2065	29.36	7	6.1728191	0.112	0.57658553	20
soy_OGL_4945	1500	9.4054356	26.200001	12716	32.6	5	9.1168709	0.152	0.75675976	36
soy_OGL_2388	1800	7.888226	39.055557	2014	27.88	5	12.294239	0.182	0.60379243	15
soy_OGL_4333	1671	6.1024008	38.300419	7599	25.49	9	4.7635403	0.14300001	0.44654208	19
soy_OGL_5911	1646	8.0339689	39.611179	5050	27.64	3	0.87221313	0.119	0.84875643	24
soy_OGL_1663	1395	8.7383938	36.487453	7760	26.81	7	5.5784245	0.15000001	0.62400919	13
soy_OGL_2326	1601	11.537634	27.170519	16207	32.66	4	4.1983199	0.089000002	0.51875681	14
soy_OGL_2337	1479	10.937825	29.885057	3261	27.92	5	0.32979381	0.115	0.32213303	12

soy_OGL_4078	1552	5.8943801	37.306702	2001	26.8	3	4.5319543	0.118	0.53912884	24
soy_OGL_4231	1500	4.3900228	33.266666	2619	26.53	6	10.13053	0.132	0.27034423	28
soy_OGL_5736	1604	12.080498	33.229427	5049	27.8	3	1.2523483	0.141	0.6717971	12
soy_OGL_1283	1817	7.132494	33.571823	10332	31.31	4	20.78879	0.102	0.65867108	18
soy_OGL_4726	1100	4.8687081	39.636364	2032	22.45	8	5.9448047	0.189	0.55075818	16
soy_OGL_1266	1553	6.6517758	26.400515	5847	29.87	5	5.9171333	0.064000003	0.69220173	24
soy_OGL_2385	1700	7.888226	31.941177	3873	27.52	7	9.7627163	0.075999998	0.60269743	14
soy_OGL_3916	1026	9.3006687	28.947369	11655	30.4	2	1.4564432	0.097999997	0.79207271	23
soy_OGL_417	1163	12.999779	35.511608	5408	27.68	5	6.2568727	0.15000001	0.70795661	17
soy_OGL_3522	1142	1.9912556	39.667252	7882	27.84	7	44.820503	0.11	0.75094694	17
soy_OGL_3524	1600	1.9912556	33.6875	3320	31.37	6	51.933178	0.039000001	0.75260186	14
soy_OGL_4978	1503	11.98569	30.605455	8586	28.87	8	5.8967414	0.094999999	0.71815228	19
soy_OGL_2732	1500	7.717042	30.933332	2896	28.8	5	10.466733	0.077	0.40951398	18
soy_OGL_3431	1549	12.258618	28.921885	2613	28.79	4	6.9084163	0.07	0.51872784	8
soy_OGL_5641	1088	9.2479429	39.889706	8031	26.65	5	5.4362521	0.114	0.54001576	17
soy_OGL_4084	1951	7.4914689	19.272167	1001	31.06	6	24.521713	0.133	0.57418656	11
soy_OGL_6505	1200	7.9388223	26.166666	11220	31.58	6	9.4914494	0.182	0.68853652	23
soy_OGL_2795	1532	2.55638	36.357704	6103	27.08	9	28.69561	0.15700001	0.17904808	4
soy_OGL_862	1300	7.9338479	30.153847	2285	25.38	6	8.3454552	0.167	0.56888282	14
soy_OGL_4243	1600	9.1415434	27.125	8297	28.93	11	12.667691	0.15099999	0.28521979	21
soy_OGL_531	1605	11.936089	28.971962	1296	30.52	5	25.43294	0.112	0.38213491	15
soy_OGL_4178	1261	18.090168	28.548771	13178	35.28	5	18.232113	0.033	0.17817752	15
soy_OGL_4238	1210	4.9720435	28.842976	2052	27.27	8	2.8756092	0.161	0.27557847	31
soy_OGL_6452	1287	5.9874048	24.242424	8428	28.9	8	4.9064341	0.134	0.57950878	21
soy_OGL_2835	1100	5.5548873	29.272728	1289	27.54	4	9.2260847	0.131	0.66523743	23
soy_OGL_3809	1000	8.2365665	30.4	14175	27.7	8	8.8775711	0.117	0.61024463	12
soy_OGL_680	1024	10.042812	25.976563	4346	30.46	4	8.2521095	0.124	0.79502046	23
soy_OGL_6430	1127	10.893449	24.489796	8994	32.91	6	11.624411	0.097000003	0.54810005	34
soy_OGL_537	1244	10.749329	29.421223	3209	29.26	8	15.578804	0.113	0.36581784	21
soy_OGL_4944	1064	9.4054356	20.300753	11404	33.64	6	9.0005159	0.093999997	0.7568329	36
soy_OGL_3002	1688	6.4039621	33.945499	8148	31.33	4	8.3077583	0.243	0.78711492	23

soy_OGL_2642	2000	7.9126515	16.200001	4819	35.5	7	4.3148041	0.086000003	0.55072725	26
soy_OGL_4075	1946	5.8943801	33.556011	2143	30.06	6	5.6086822	0.13699999	0.52592295	19
soy_OGL_6456	1487	5.9874048	29.791527	7365	28.78	7	4.9803023	0.14399999	0.57994527	20
soy_OGL_1273	1797	6.6517758	23.038397	11814	32.27	7	4.5365448	0.12800001	0.68689036	20
soy_OGL_1309	1334	2.0239863	36.95652	13996	32.15	3	2.9055865	0.098999999	0.59167516	13
soy_OGL_2435	1408	0.78866917	38.778408	13830	32.1	6	7.2378469	0.101	0.75395477	6
soy_OGL_2830	1100	5.5548873	35.545456	15864	29.81	5	7.9335485	0.15000001	0.66182542	22
soy_OGL_5355	2000	2.9911871	25.950001	1777	31.3	4	13.562528	0.104	0.49415353	14
soy_OGL_850	1835	7.4370508	28.065395	2216	36.13	4	2.2509887	0.132	0.62637782	21
soy_OGL_1272	1300	6.6517758	38.46154	7811	30.07	7	4.5365448	0.134	0.68708771	19
soy_OGL_2639	1500	7.9126515	27.666666	3650	30.53	5	8.3028603	0.1	0.55578321	22
soy_OGL_3028	1700	9.7849836	32.764706	8884	31.64	6	9.7906981	0.12899999	0.74699575	18
soy_OGL_3863	1700	9.8148384	34.882355	3788	33.58	7	7.8303447	0.082999997	0.25985408	21
soy_OGL_4298	1600	4.904017	34.75	6153	31.06	7	5.5141559	0.090000004	0.39409387	26
soy_OGL_5167	1700	8.5415621	32.529411	7594	33.82	5	0.87491685	0.146	0.83925092	17
soy_OGL_6514	1100	7.4994183	38.909092	9698	30.81	5	5.8478813	0.17399999	0.69278258	26
soy_OGL_1597	1118	5.281703	38.46154	4449	29.78	3	6.8124475	0.148	0.70168346	18
soy_OGL_2222	1621	1.0696845	33.62122	11335	37.13	5	4.8676686	0.113	0.73056424	22
soy_OGL_3469	1796	8.2846069	36.525612	14051	35.41	4	3.5675933	0.098999999	0.6322242	25
soy_OGL_5056	1400	6.5904026	37.642857	3310	29.78	3	14.78289	0.149	0.60353005	11
soy_OGL_5134	1600	4.9704185	32.6875	8266	32.31	3	15.330687	0.079000004	0.67547518	11
soy_OGL_5910	1155	8.0339689	38.18182	23516	34.89	3	8.0654459	0.109	0.84973699	24
soy_OGL_6672	1400	9.9655132	38.857143	2973	32.92	4	4.0290499	0.139	0.011867552	27
soy_OGL_1602	1200	5.281703	37.666668	22168	33.75	2	18.957331	0.030999999	0.68459523	14
soy_OGL_3008	1800	6.7379055	18.666666	5992	34.05	5	2.2741725	0.041000001	0.77650213	20
soy_OGL_515	1300	2.5546122	39.53846	7545	27.92	5	1.0999035	0.1	0.44129729	17
soy_OGL_2059	1197	1.5917815	39.515457	8530	31.74	1	1.5149444	0.068000004	0.57392454	11
soy_OGL_3095	1700	0.6157763	33.64706	2355	28.23	5	12.612445	0.054000001	0.35672149	7
soy_OGL_5148	1400	4.3001404	24.714285	7002	32.28	3	2.1245944	0.078000002	0.76590151	21
soy_OGL_5697	1400	1.1854842	37.57143	3261	29.28	5	3.9784093	0.068000004	0.39816859	15
soy_OGL_4784	1494	3.5324056	31.392235	1884	26.43	4	13.208198	0.097000003	0.88730395	8

soy_OGL_2336	1011	10.937825	39.366962	16179	29.67	3	0.005394727	0.085000001	0.32299083	12
soy_OGL_1062	1000	4.5279164	38.099998	12169	30.3	7	8.0657921	0.124	0.86423218	24
soy_OGL_1797	2000	5.5180402	37.099998	4212	29.85	7	4.3183627	0.030999999	0.82065582	12
soy_OGL_2311	1519	7.6886683	29.756418	1001	28.9	6	12.268929	0.085000001	0.55974686	17
soy_OGL_2833	1400	5.5548873	34.357143	2393	30.42	5	8.2488346	0.090999998	0.66307575	23
soy_OGL_4081	1693	7.4914689	27.93857	2300	30.95	7	7.1773844	0.072999999	0.54891884	23
soy_OGL_4253	1572	9.7208376	39.821884	1752	27.98	10	9.574605	0.083999999	0.31063432	11
soy_OGL_5752	1300	6.5565777	38.692307	3329	31.15	6	4.4782968	0.114	0.75371212	14
soy_OGL_440	1200	6.6230578	39.75	11181	29.83	7	3.1428249	0.106	0.66198647	14
soy_OGL_5654	1400	5.120719	35.857143	8895	33.07	6	4.6775832	0.029999999	0.51054406	21
soy_OGL_5973	1258	8.3158064	36.804451	7199	28.13	6	8.2260561	0.116	0.65374488	15
soy_OGL_6357	1400	5.3133087	36.857143	7336	30.35	6	4.197186	0.086999997	0.85897022	7
soy_OGL_843	1800	5.9970145	21.5	1047	34.66	5	3.9663272	0	0.64046878	15
soy_OGL_2843	1100	5.5548873	35.454544	6928	30.09	8	2.6364913	0.117	0.67296708	24
soy_OGL_4236	1100	4.8173609	37.636364	3234	27.09	9	5.9152117	0.12800001	0.2751244	30
soy_OGL_462	1343	5.5066857	38.198063	12498	30.23	5	9.2167234	0.041000001	0.55127931	19
soy_OGL_6667	1500	12.019849	38.799999	2408	30.2	6	4.5736804	0.07	0.009032639	22
soy_OGL_2538	1623	4.4041967	21.565002	3405	30.68	7	8.5509663	0.119	0.74277544	19
soy_OGL_3274	1214	2.1021929	34.678749	4688	29.15	7	6.5205121	0.18799999	0.99087095	10
soy_OGL_3816	1800	7.7295065	26.166666	3270	30.72	8	8.1365385	0.163	0.56757939	16
soy_OGL_3016	1200	8.9994106	31	5899	32.83	4	3.8317091	0.19400001	0.76160848	24
soy_OGL_2037	1900	0.62599713	34.315788	14609	40.26	2	10.186376	0.149	0.35643604	7
soy_OGL_2043	1300	1.0022501	36.46154	2886	32	3	0.26432887	0.105	0.46741265	10
soy_OGL_2347	1500	6.5047197	35.799999	1417	28.86	5	10.892324	0.183	0.28304586	5
soy_OGL_2359	1442	2.8688939	36.893204	4007	30.3	3	11.980911	0.17900001	0.19163109	8
soy_OGL_4752	1529	0.28445095	36.102028	6206	34.79	2	0.93980998	0.098999999	0.54574066	3
soy_OGL_5669	1182	7.7953877	33.24873	4110	28.68	5	2.1201828	0.18700001	0.49346361	20
soy_OGL_6009	1900	3.6008489	24.578947	4758	33.73	7	3.7294328	0.117	0.51710206	13
soy_OGL_6721	1608	2.7221162	28.980099	2955	31.65	3	1.9520746	0.089000002	0.67103559	5
soy_OGL_298	1144	8.1388817	30.594406	10708	30.68	8	15.568912	0.148	0.91988581	17
soy_OGL_542	1600	10.749329	32.9375	1109	32.56	5	6.046639	0.149	0.35955855	19

soy_OGL_1888	1428	9.2462587	31.162464	2042	30.95	7	4.9330006	0.126	0.66823936	12
soy_OGL_3902	1400	9.3006687	32.642857	2483	31.35	4	11.012568	0.148	0.76045114	16
soy_OGL_4232	1407	4.5469155	32.125088	4269	30.49	8	13.434469	0.163	0.27247736	29
soy_OGL_4385	1200	5.5947452	36.25	3459	30.41	8	15.917703	0.18099999	0.53924167	21
soy_OGL_1359	1031	10.431696	36.275459	11195	32.58	4	4.2564344	0.116	0.76191497	12
soy_OGL_1987	1600	8.9979553	29.8125	11944	36.87	5	3.2884071	0.132	0.46228248	19
soy_OGL_3890	2064	0.027143367	36.627907	3043	36.62	5	6.571012	0.138	0.41332799	7
soy_OGL_4326	1351	2.6155119	30.866026	6193	33.23	5	3.1601844	0.079999998	0.43881387	19
soy_OGL_5038	1000	7.2364998	37.099998	8957	30.2	5	10.617906	0.228	0.65181983	22
soy_OGL_6682	1400	7.6147938	39.785713	2182	33.35	5	33.679317	0.145	0.021819072	20
soy_OGL_3458	1353	8.9865389	27.050999	2001	28.3	8	3.0388246	0.139	0.61089993	14
soy_OGL_1613	1600	1.1756582	26.1875	5306	31.56	1	19.402168	0.02	0.34572795	4
soy_OGL_1267	1000	6.6517758	38.700001	3415	33.2	5	3.0947754	0.109	0.6906535	24
soy_OGL_2380	1500	7.888226	28.733334	2352	30.46	9	4.498013	0.105	0.59680057	12
soy_OGL_5044	1137	5.904129	37.906773	2099	30.16	4	1.0236262	0.142	0.64838117	17
soy_OGL_2496	1200	7.548306	36.666668	7628	30	6	4.7242727	0.133	0.86420977	6
soy_OGL_6161	1475	7.8820863	19.254238	9636	36	5	6.7067142	0.048	0.79743552	17
soy_OGL_1654	1398	9.0782251	29.256081	5250	36.33	7	2.6960566	0.025	0.60245383	19
soy_OGL_520	1392	2.3637695	32.183907	2287	30.96	6	6.027391	0.074000001	0.42432433	14
soy_OGL_4312	1000	2.3265874	38.799999	2131	30.2	6	20.723942	0.121	0.41323569	24
soy_OGL_5997	1000	3.0450165	37	8667	34	7	0.1472452	0.088	0.55690306	19
soy_OGL_1853	1435	5.259068	29.268293	8433	26.96	7	8.3523855	0.13600001	0.72982144	31
soy_OGL_1224	2112	9.0944204	29.592804	1001	30.77	9	36.138916	0.057999998	0.77175879	19
soy_OGL_1832	1790	8.2200718	39.16201	2516	26.75	8	21.450394	0.115	0.75676334	27
soy_OGL_2288	1700	10.317506	26.117647	6644	31.35	7	5.5287166	0.074000001	0.619578	40
soy_OGL_5822	2271	13.314646	34.654339	2001	30.73	5	10.571586	0.059999999	0.9068684	23
soy_OGL_1252	1600	11.432598	28.5	2888	28	8	17.469496	0.118	0.72410089	17
soy_OGL_6260	2400	4.8768115	34.458332	6956	27.54	5	3.1589792	0.024	0.91750908	23
soy_OGL_4157	2163	8.5009871	39.389736	2001	28.2	6	21.292664	0.046	0.89483881	17
soy_OGL_39	1290	10.190989	35.891472	3937	27.75	4	14.20615	0.109	0.88510972	29
soy_OGL_820	1540	11.020067	37.922077	2001	26.88	4	10.331572	0.106	0.74591166	23

soy_OGL_1856	1100	5.259068	38.909092	9219	26.45	6	10.718579	0.124	0.7286396	37
soy_OGL_5282	1566	16.257269	39.399746	11208	28.73	8	8.2016125	0.055	0.74813622	22
soy_OGL_4290	2187	4.9876347	34.15638	4062	27.2	8	5.9398146	0.124	0.38404116	26
soy_OGL_4313	2000	2.3265874	29.25	7731	29.95	6	21.823156	0.041000001	0.41399249	24
soy_OGL_4983	1600	9.9015322	36.8125	10458	29.37	2	2.6295288	0.149	0.71061099	26
soy_OGL_5961	1463	6.6949921	32.672592	25836	33.01	4	9.1681395	0.068000004	0.67963773	21
soy_OGL_4283	1649	5.4775915	28.441479	2908	25.16	10	7.1021528	0.115	0.37072799	22
soy_OGL_2204	1474	6.9489923	24.287653	4724	29.17	4	8.3576164	0.079999998	0.76482224	30
soy_OGL_2643	1755	7.9126515	37.777779	4406	27.92	5	2.4849603	0.078000002	0.55051905	26
soy_OGL_793	1225	9.3835421	39.7551	21525	29.95	3	9.8881006	0.061999999	0.87189978	22
soy_OGL_3132	1400	8.0850887	35.214287	5753	29.21	4	15.712978	0.086000003	0.55487067	24
soy_OGL_5454	1700	5.4725728	18.82353	2001	24.82	11	6.666903	0.118	0.9254483	12
soy_OGL_4809	1800	5.6626678	12.777778	2542	28.38	8	10.380248	0.057	0.94153523	15
soy_OGL_5438	1320	5.1586671	23.560606	3237	22.42	13	11.392112	0.183	0.95317423	15
soy_OGL_3285	1122	2.9900167	18.894831	4207	26.29	9	3.1217964	0.121	0.96719253	23
soy_OGL_3669	1900	4.1581578	2.2631578	2420	28.84	10	10.043108	0	0.97312444	14
soy_OGL_5510	1197	5.4987149	15.455305	2839	23.72	11	4.5422359	0.089000002	0.82355183	17
soy_OGL_2105	1180	5.1327806	12.457627	2563	24.23	11	3.5010452	0	0.96046788	13
soy_OGL_1198	1067	6.7576227	20.805998	4024	23.52	10	3.9776869	0.097999997	0.84267253	16
soy_OGL_6882	1300	4.5204587	15.615385	1322	24.53	8	5.6007686	0.086999997	0.85423625	17
soy_OGL_1008	1164	3.2276397	23.453608	1392	24.05	10	3.2238803	0.085000001	0.79946876	16
soy_OGL_2874	1258	6.2971745	17.726549	3123	26.55	7	5.9396	0.125	0.80692816	17
soy_OGL_1192	2090	4.0395017	13.110048	1861	27.08	10	7.3737984	0.028999999	0.88357061	20
soy_OGL_2220	1232	3.8589771	29.626623	2602	21.99	9	2.7527812	0.171	0.74392217	26
soy_OGL_6838	1379	3.9573007	23.930384	1001	25.52	9	1.8689986	0.133	0.81514966	34
soy_OGL_5849	1700	9.6763773	12.352942	2785	30.41	7	10.176773	0.050000001	0.98259771	20
soy_OGL_3684	1061	7.5635667	33.553253	5602	24.12	9	7.4015532	0.15000001	0.90349954	15
soy_OGL_274	1086	9.6343765	29.742172	2158	28.08	6	2.5270452	0.124	0.89700031	28
soy_OGL_6536	1521	11.936101	35.50296	2001	28.07	10	12.170489	0.089000002	0.74282497	28
soy_OGL_32	1259	10.486021	25.814138	4506	29.07	7	9.3417883	0.113	0.89595401	31
soy_OGL_1039	1497	8.4023438	25.317301	2781	27.65	9	9.7894964	0.088	0.83961928	26

soy_OGL_3706	1768	7.8270955	18.325792	2001	28.78	9	9.0887985	0.044	0.84219021	20
soy_OGL_4478	1500	7.5810852	31.200001	2340	28.33	10	17.934263	0.077	0.7114197	30
soy_OGL_4921	1100	15.567796	30.09091	8162	30.09	12	4.3991876	0.118	0.77498955	30
soy_OGL_5878	1100	10.178902	36.81818	2021	28.45	8	25.564205	0.12	0.90262246	31
soy_OGL_6914	1854	8.8029718	22.384035	3369	28.74	10	5.6880126	0.052999999	0.89257699	20
soy_OGL_980	1300	6.2075529	17.23077	4957	29.07	9	0.87586629	0.111	0.76849407	32
soy_OGL_6791	1400	9.1081762	15.214286	2300	29	10	2.9844103	0.119	0.77781963	25
soy_OGL_1142	1900	5.5214667	9.7368422	1601	31.94	11	28.441126	0.022	0.97519296	26
soy_OGL_5267	1300	11.202606	19	3139	27.84	8	3.5827279	0.123	0.80569512	19
soy_OGL_1874	1500	5.0498676	15.8	3398	29	8	10.197219	0.088	0.71241885	24
soy_OGL_50	1000	10.004758	24.799999	4145	28	6	11.393287	0.145	0.85781211	28
soy_OGL_3582	1062	6.0902267	29.096045	4593	30.5	9	30.134411	0.109	0.84590429	38
soy_OGL_4888	1849	3.9014754	32.125473	2001	25.79	10	4.831213	0.075999998	0.91942561	19
soy_OGL_1541	1539	8.1677341	25.146198	2967	32.55	10	3.1849835	0.044	0.87572616	33
soy_OGL_2497	1440	7.4874678	33.888889	1849	26.31	13	8.3287125	0.123	0.84472239	12
soy_OGL_3570	1026	5.4506187	33.723198	1708	29.33	9	8.9046755	0.14	0.83626443	36
soy_OGL_3736	1440	9.0400381	36.458332	2928	31.38	15	11.725889	0.082000002	0.78849357	23
soy_OGL_4547	1400	5.584516	39.07143	1583	30.57	13	7.7160745	0.090000004	0.79095793	31
soy_OGL_5871	1302	12.403051	33.410137	2001	29.1	11	11.711566	0.111	0.91433662	28
soy_OGL_5904	1175	9.19067	34.723404	1001	29.87	12	0.24460284	0.12	0.86953187	35
soy_OGL_6584	1000	4.8956351	32.700001	2344	26.7	11	4.584064	0.18000001	0.78918546	34
soy_OGL_280	1200	6.375752	31.25	4873	28.5	8	3.6431577	0.098999999	0.90329295	27
soy_OGL_1029	1359	6.3006811	35.393673	3397	31.64	12	5.9736485	0.059999999	0.83069342	28
soy_OGL_1703	1100	6.6742897	34	2536	29.09	8	1.9143391	0.124	0.81456542	28
soy_OGL_2197	1100	8.5738249	33.363636	2031	29.45	9	3.626899	0.133	0.7753486	32
soy_OGL_2930	1300	8.8428612	32.846153	4206	30.84	11	7.110621	0.075999998	0.94317448	21
soy_OGL_4098	1400	12.218921	33.57143	1166	28.92	11	11.463666	0.075999998	0.67648262	23
soy_OGL_4539	1249	5.1131511	33.226582	3231	30.74	11	8.199007	0.086000003	0.78007489	29
soy_OGL_5208	1171	6.245574	36.720753	1001	30.14	8	4.365047	0.086000003	0.96409148	24
soy_OGL_6265	1100	6.2808328	34.454544	3273	28.63	9	6.6781569	0.119	0.92201418	26
soy_OGL_981	1068	6.2075529	37.921349	4378	26.02	10	9.1885967	0.125	0.76882279	32

soy_OGL_2112	1469	6.2956948	34.989788	2705	25.18	9	5.7009974	0.089000002	0.93953669	16
soy_OGL_2492	1542	7.9044895	33.852139	2001	26.26	11	13.351936	0.071000002	0.87647754	17
soy_OGL_3335	1100	13.069633	36.272728	5019	28.81	8	2.517653	0.12800001	0.86092627	28
soy_OGL_289	1200	6.9669991	36.5	1785	29.41	10	5.5374942	0.088	0.90752542	29
soy_OGL_5213	1063	7.9554181	36.594543	2001	27.75	7	6.7835627	0.105	0.95321953	26
soy_OGL_2945	1700	10.354479	28.470589	2639	28	9	1.9723843	0.027000001	0.90696168	18
soy_OGL_3218	1322	10.210989	38.880486	2154	31.92	10	7.2093325	0.021	0.71027845	48
soy_OGL_5896	1089	10.420918	26.538109	2001	30.57	9	10.423428	0.131	0.87860715	34
soy_OGL_54	1000	9.9992008	36.400002	1267	31.5	9	13.457255	0.13	0.85087878	27
soy_OGL_3259	1114	5.2893763	32.315979	2592	28.9	10	15.589121	0.13500001	0.83794957	19
soy_OGL_4125	1083	9.3277731	30.009233	2001	30.28	8	10.440394	0.123	0.81304634	27
soy_OGL_6904	1000	7.0806479	31.4	2975	29.7	8	6.2199335	0.13	0.87247527	23
soy_OGL_1852	1098	4.8108158	24.863388	2001	25.77	7	8.3523855	0.125	0.73009741	31
soy_OGL_3289	1200	3.2396839	21.916666	1187	24.83	8	4.7380238	0.089000002	0.96151614	23
soy_OGL_25	1100	10.054278	38.18182	3370	25	11	4.2496204	0.101	0.9046424	31
soy_OGL_1525	1217	6.1372461	28.841413	3962	26.7	9	5.0543828	0.097999997	0.90040374	37
soy_OGL_3229	1101	7.8257403	25.249773	1001	27.7	10	14.75468	0.114	0.72057396	37
soy_OGL_1047	1200	5.36303	39.416668	3839	21.33	17	5.8870568	0.101	0.85095692	28
soy_OGL_4148	1322	12.139669	22.617247	1408	27.91	11	4.5712953	0.041000001	0.87228751	25
soy_OGL_5226	1199	11.269387	28.940784	2001	26.1	12	5.4324217	0.07	0.92140251	22
soy_OGL_1501	1000	8.5456972	30.700001	7854	24.7	9	6.5388808	0.134	0.98420161	19
soy_OGL_3633	1079	6.7273793	20.94532	3772	27.43	5	6.614028	0.093999997	0.92744601	29
soy_OGL_3286	1643	2.9900167	14.607426	3597	26.84	10	9.1381111	0	0.96711057	23
soy_OGL_4847	1200	6.3971152	26.75	3648	24.58	11	10.903081	0.097000003	0.97332639	14
soy_OGL_1420	1100	11.385625	27.363636	3385	27.63	8	4.9389911	0.097999997	0.86613154	22
soy_OGL_1478	1063	5.5293665	34.807148	2291	23.7	8	16.798189	0.12800001	0.94836974	19
soy_OGL_2950	1100	10.830427	33.090908	1001	24.72	8	13.047966	0.124	0.89628482	17
soy_OGL_5216	1063	9.5305462	33.019756	2001	25.39	8	5.916985	0.115	0.9499169	28
soy_OGL_6790	1100	9.1081762	34	4719	24.45	10	3.2543292	0.117	0.77757418	25
soy_OGL_6942	1025	11.24362	30.829268	2220	24.09	9	7.3132744	0.13600001	0.91832429	19
soy_OGL_337	1300	9.5033493	19.384615	2514	29.23	9	5.3064847	0.028999999	0.86280179	26

soy_OGL_4492	1146	7.9822183	17.277487	1001	27.22	11	5.8206005	0	0.72901464	31
soy_OGL_6264	1042	5.1741633	18.714012	2510	26.1	9	6.6781569	0	0.92196804	26
soy_OGL_4886	1353	3.9014754	20.103474	2340	25.64	12	22.560701	0.11	0.92076576	17
soy_OGL_5265	1444	11.202606	19.736841	1001	27.97	10	10.512206	0.089000002	0.80650002	19
soy_OGL_3538	1319	8.9636507	13.419257	3093	29.79	7	8.2012806	0.071000002	0.79357237	24
soy_OGL_6491	1300	9.3050442	19.76923	3467	26.53	10	3.3995843	0.113	0.66320693	15
soy_OGL_1236	1580	9.0944204	13.670886	1001	29.49	9	8.4777269	0.056000002	0.75836051	23
soy_OGL_1419	1252	11.385625	16.613419	5393	29.55	9	6.4319448	0.092	0.8630501	22
soy_OGL_3297	1434	6.8884773	13.807531	2001	26.56	10	4.1186504	0.1	0.95038712	24
soy_OGL_4850	1200	6.2278233	22.333334	3619	23.41	14	14.140126	0.15000001	0.96787989	17
soy_OGL_5479	1812	3.8617556	2.8145695	2114	30.84	9	7.8933344	0.02	0.86700386	32
soy_OGL_1024	1108	5.5469222	18.321301	2315	25.63	9	1.7632167	0.075999998	0.82530314	29
soy_OGL_6289	1222	6.5515571	18.739771	2108	26.75	9	5.8705468	0.086000003	0.94667208	23
soy_OGL_2522	1206	7.5373769	19.237148	1001	25.95	15	11.446577	0	0.8155148	18
soy_OGL_1827	1300	8.1920242	19.461538	1955	26.3	11	6.6337647	0.090000004	0.76124352	24
soy_OGL_4827	1556	16.127125	14.524422	1001	31.87	11	10.967538	0	0.96934134	21
soy_OGL_5421	1100	11.149388	25	3339	24.9	12	14.780683	0.121	0.96186137	14
soy_OGL_5034	1100	9.4548454	24.727272	2435	28.36	11	6.4039435	0.101	0.65667105	28
soy_OGL_3193	1000	9.1204634	21	2166	28	9	3.9198883	0.103	0.67930788	29
soy_OGL_6952	1127	8.566577	16.858917	1001	28.74	11	9.8069944	0	0.92789841	25
soy_OGL_1235	1278	9.0944204	22.065727	2001	26.76	9	6.0819559	0.101	0.75946492	23
soy_OGL_1829	1100	8.4640703	25	2190	25.54	10	6.1747704	0.118	0.76050323	24
soy_OGL_1750	1105	13.638608	21.266968	1794	27.42	10	3.1023819	0.052999999	0.9762727	16
soy_OGL_4664	1100	8.1218634	20.545454	1153	27.09	10	11.204393	0.090999998	0.67433333	29
soy_OGL_1075	1891	7.9827704	24.431519	2216	28.29	18	15.38994	0.048	0.88627875	13
soy_OGL_4546	1100	5.584516	33.363636	3613	31.36	11	8.8927221	0.086000003	0.78978223	31
soy_OGL_4897	1128	9.0506868	35.549644	1001	26.15	10	15.410324	0.124	0.89874935	15
soy_OGL_6588	1135	4.9233418	31.013216	2040	26.69	9	5.4339504	0.124	0.79862404	29
soy_OGL_1028	1114	6.3006811	34.64991	1189	24.59	14	1.5578821	0.115	0.82917798	29
soy_OGL_2130	1300	8.6764479	27.923077	2779	26.69	13	8.3711691	0.088	0.89107341	18
soy_OGL_5882	1002	10.300918	27.44511	2001	29.64	10	7.8115005	0.097999997	0.89739788	35

soy_OGL_5902	1139	10.121329	31.957857	1001	29.49	15	1.3518513	0.119	0.87205923	31
soy_OGL_2472	1581	4.7689786	17.204302	2001	27.95	13	2.2604568	0.027000001	0.9044205	21
soy_OGL_5473	1179	4.9895315	31.63698	2001	27.05	13	14.221847	0.078000002	0.87287438	26
soy_OGL_725	1400	9.0755138	36.357143	2592	24.5	16	13.143567	0.093000002	0.86516786	18
soy_OGL_757	1799	5.3959246	29.016121	2420	30.68	14	14.111177	0.009	0.95123851	11
soy_OGL_797	1055	10.399013	31.374407	4284	28.24	11	4.4232435	0.079000004	0.86495662	23
soy_OGL_1713	1030	8.4408894	37.864079	2001	29.7	11	8.4678297	0.097999997	0.82658005	34
soy_OGL_1828	1300	8.1920242	24.153847	3355	28.61	10	6.1064987	0.054000001	0.76119804	24
soy_OGL_3310	1025	14.038661	36.682926	2001	29.07	11	6.8535175	0.083999999	0.91051149	17
soy_OGL_4860	1100	5.903389	31	2729	26.09	9	4.1208076	0.116	0.95220888	19
soy_OGL_1774	1093	5.2867265	31.198536	1001	25.25	8	3.5245461	0.092	0.89799356	23
soy_OGL_2103	1229	4.9611359	30.838079	1530	23.84	13	9.8718243	0.075999998	0.97392201	8
soy_OGL_5901	1036	10.121329	27.220078	2235	31.46	12	2.3039031	0	0.87314099	33
soy_OGL_6287	1100	6.8574758	37.272728	1165	29.54	12	3.1026711	0	0.9420293	28
soy_OGL_6928	1090	8.8029718	34.128441	1046	29.35	11	3.6931036	0	0.9022432	28
soy_OGL_1130	1500	5.8739777	28.666666	1759	25.93	12	17.381674	0.024	0.99274123	14
soy_OGL_668	1266	4.2763386	18.878357	1982	28.98	10	3.8762839	0.097999997	0.77511722	31
soy_OGL_1183	1014	4.3006682	32.051281	6993	28.2	13	8.8226728	0.12899999	0.90023685	29
soy_OGL_4868	1087	5.4112797	27.690893	3803	27.23	8	5.8455935	0.134	0.93985903	21
soy_OGL_5515	1302	5.3180718	25.422426	1908	28.26	8	2.8295076	0.092	0.81362069	20
soy_OGL_1528	1000	7.269011	21.200001	5074	30.6	7	4.8118658	0.125	0.89096427	35
soy_OGL_1786	1448	5.2867265	26.79558	4289	32.87	14	6.7515893	0.050999999	0.88709909	18
soy_OGL_2259	1084	6.9284716	20.479704	1505	34.04	8	9.3609991	0.082999997	0.64006424	43
soy_OGL_2471	1032	4.7094264	32.55814	4607	27.9	10	9.2792969	0.139	0.90701872	18
soy_OGL_3603	1217	4.9321332	26.294167	3545	31.22	9	9.1518507	0.092	0.87473661	22
soy_OGL_3608	1300	4.9169555	29	4079	29.3	12	3.5043459	0.093999997	0.88336289	15
soy_OGL_3616	1229	4.6640544	27.3393	4581	28.96	12	15.472368	0.106	0.90152675	18
soy_OGL_3711	1100	6.9130831	27.272728	1829	30.18	9	8.9447412	0.119	0.8327468	24
soy_OGL_4555	1400	3.923111	19.928572	3086	30.28	10	10.649964	0.075000003	0.79590708	26
soy_OGL_6765	1117	7.5721488	34.55685	1001	29.27	10	1.1294932	0.115	0.74680901	23
soy_OGL_73	1300	10.741905	22.307692	1639	32.84	12	16.360569	0.057	0.80906665	28

soy_OGL_287	1200	6.9669991	27.25	1855	30.83	11	4.8002825	0.063000001	0.90645713	26
soy_OGL_6954	1200	8.566577	26.083334	2155	29.08	12	9.6288357	0.088	0.92818731	25
soy_OGL_1048	1034	5.36303	29.01354	3054	25.24	17	7.700727	0.106	0.85104245	29
soy_OGL_2466	1049	4.4513826	27.645376	4021	26.5	12	13.851441	0.117	0.91596156	21
soy_OGL_4805	1000	5.6626678	31.1	4025	23.9	15	3.7497084	0.117	0.93489522	14
soy_OGL_4877	1578	4.2808261	12.103929	2001	29.21	12	3.9599187	0.002	0.92998695	24
soy_OGL_4883	1018	3.9014754	31.925344	1186	25.83	13	2.3942809	0.13699999	0.92346996	19
soy_OGL_6848	1058	3.6363637	27.693762	1001	29.39	12	6.673058	0.097000003	0.82190269	26
soy_OGL_294	1000	11.654119	30.4	2655	32.1	12	11.059482	0.085000001	0.9114297	24
soy_OGL_2161	1229	8.3984585	19.528072	2001	32.3	8	6.54849	0.064000003	0.84490234	30
soy_OGL_2885	1204	7.0442643	31.561462	2001	27.49	12	3.6073871	0.083999999	0.84948778	16
soy_OGL_2957	1083	9.701272	33.518005	1229	26.4	11	11.950677	0.12	0.87649858	18
soy_OGL_1505	1080	8.5456972	22.222221	2276	27.68	11	4.3103132	0.006	0.98922849	16
soy_OGL_3958	1400	0.89052546	26.357143	2071	29.71	11	2.1452339	0.033	0.98579228	9
soy_OGL_4100	1200	12.218921	25.916666	1739	29.41	14	10.5591	0.071999997	0.68023813	22
soy_OGL_4532	1000	7.5105057	32.599998	1638	32.2	12	13.212505	0.043000001	0.77438569	29
soy_OGL_4596	1000	5.2460666	32.299999	1311	26.5	11	12.125014	0.068999998	0.94122225	15
soy_OGL_4616	1100	8.1715069	26.272728	2080	27.54	12	8.1040792	0.035999998	0.76932681	23
soy_OGL_4801	1000	12.748341	29.1	2008	27.9	9	6.3562126	0.098999999	0.92717338	18
soy_OGL_6262	1000	5.7831564	27.200001	3134	28.4	9	9.5907526	0.071999997	0.92006916	26
soy_OGL_6639	1000	6.8812695	26.4	1546	29.3	11	11.991331	0	0.98026133	21
soy_OGL_2487	1569	6.4331512	27.278521	1001	23	10	5.21243	0.106	0.88544512	19
soy_OGL_6288	1406	6.5515571	34.566147	3430	23.68	9	5.8705468	0.13500001	0.94663632	23
soy_OGL_4922	1424	11.86034	32.58427	4566	26.82	12	4.2537355	0.103	0.77484334	30
soy_OGL_5247	1300	8.8967266	28.538462	1385	25.46	5	4.147193	0.131	0.86817074	22
soy_OGL_4981	1128	13.183422	39.007092	1800	25.53	11	20.656652	0.122	0.71388698	24
soy_OGL_1508	1615	6.1372461	31.145512	2084	23.83	12	11.86626	0.072999999	0.92576152	20
soy_OGL_3586	1424	5.4232616	36.516853	2001	25.49	12	24.995909	0.071999997	0.85147715	38
soy_OGL_1460	1334	9.1846943	35.832085	4331	26.68	9	10.279806	0.063000001	0.92392886	30
soy_OGL_1471	1200	9.2116108	34.25	2429	25.16	6	3.5414145	0.1	0.93593687	27
soy_OGL_4961	1300	9.1757927	36.923077	1760	24.76	10	11.192761	0.097000003	0.74546736	31

soy_OGL_2894	1400	8.9753227	25	5146	26.21	9	8.762866	0.086000003	0.87320012	19
soy_OGL_3307	1200	13.733257	27.916666	3290	25.58	9	4.6859384	0.125	0.91585255	18
soy_OGL_1535	1011	7.5677972	35.905045	1001	25.12	9	7.8578978	0.083999999	0.88317901	38
soy_OGL_1189	1038	4.3006682	39.402699	4173	19.46	16	4.1306386	0.061000001	0.89085525	27
soy_OGL_3283	1730	2.9420857	21.040462	5188	26.58	9	3.1279457	0	0.96771753	24
soy_OGL_6621	1672	9.2474756	24.401915	2001	25.29	9	6.4616547	0.046	0.95124233	15
soy_OGL_4572	1100	5.7964573	34.18182	2162	21.81	9	11.969826	0.097000003	0.82568288	22
soy_OGL_975	1140	11.69048	20.438597	2538	28.85	8	4.2506504	0.075999998	0.76429176	34
soy_OGL_6993	1430	5.2089171	26.503496	4080	26.85	8	12.888945	0.041000001	0.95363414	27
soy_OGL_318	1200	11.325543	30.916666	2104	24.75	12	19.947781	0.039999999	0.91497296	13
soy_OGL_5535	1109	11.696812	24.977457	1001	25.96	10	4.4428473	0	0.78589618	27
soy_OGL_6971	1200	4.3050809	28.583334	3387	24.91	9	3.2637677	0	0.94018084	33
soy_OGL_1248	1177	11.287494	16.567545	2001	25.48	12	3.4113688	0	0.73501515	19
soy_OGL_4779	1400	3.6792157	25.357143	9033	25.28	7	3.4828656	0.088	0.87497061	7
soy_OGL_864	1400	6.6630006	25.428572	4675	26.14	4	7.9757037	0.082000002	0.55413282	10
soy_OGL_5718	1000	7.9770703	35.5	12431	26.5	2	2.6548409	0.086000003	0.46559784	7
soy_OGL_6162	1155	6.0707769	29.870131	7529	26.06	4	7.913063	0.11	0.79846323	18
soy_OGL_2022	1085	0.84533012	30.599079	2971	23.13	2	13.124487	0.125	0.3326368	6
soy_OGL_4746	1100	1.3206984	29.454546	6305	22.63	3	1.3007599	0.127	0.39055207	7
soy_OGL_5346	1484	2.9911871	28.234501	3876	26.41	5	0.93452901	0.048	0.47313645	12
soy_OGL_6031	1013	2.5894165	35.241856	10707	25.17	4	2.3842518	0.085000001	0.36875379	12
soy_OGL_5715	1202	3.1764436	34.525791	5508	23.96	6	5.282856	0.116	0.38575071	1
soy_OGL_6377	1176	1.438513	30.357143	4081	23.97	1	0.0135002	0.107	0.17454015	2
soy_OGL_5350	1100	2.9911871	32.363636	1552	25.81	3	0.42951852	0.115	0.48624867	14
soy_OGL_2096	1453	2.4134915	18.719891	3346	25.18	6	8.687602	0.093999997	0.77953297	17
soy_OGL_6126	1522	1.8159347	18.462549	3788	25.49	6	0.066800021	0.081	0.73475528	14
soy_OGL_2539	1051	4.4041967	30.827784	2618	22.45	7	4.7407203	0.122	0.74243879	19
soy_OGL_112	1000	0.25185886	39.900002	3968	18.5	5	2.5764351	0.122	0.49774399	3
soy_OGL_2375	1406	0.23807999	26.813656	1643	22.19	4	5.4332561	0	0.31413838	1
soy_OGL_4029	1186	0.4967483	27.403036	2736	22.68	3	2.7892387	0	0.63696921	7
soy_OGL_149	1652	4.6668854	19.854721	3795	27.36	4	5.8429809	0	0.6831488	11

soy_OGL_1596	1092	5.281703	26.098902	4047	24.9	4	2.333339	0.083999999	0.70581549	18
soy_OGL_1331	1111	4.7278967	29.072906	8944	26.01	3	4.0483918	0.028000001	0.6833936	7
soy_OGL_4066	1400	0.90285671	19.785715	1035	25.78	5	0.22337551	0	0.51262522	18
soy_OGL_6243	1137	5.7421308	22.691294	2001	25.85	5	5.9681554	0.124	0.90086973	19
soy_OGL_3894	1100	0.99678105	21.454546	7978	23.36	3	3.6502311	0.132	0.5943079	6
soy_OGL_464	1200	5.5066857	21.083334	1731	25.91	5	6.1500635	0.097999997	0.55027479	20
soy_OGL_470	1000	5.8758793	20.1	12543	28.5	7	5.3401031	0.094999999	0.53667116	23
soy_OGL_3385	1144	5.6634336	23.426573	3594	27.36	3	3.4944127	0.1	0.71089864	17
soy_OGL_1300	1107	1.5215753	27.371273	5554	22.94	4	6.5680704	0.097999997	0.56437123	8
soy_OGL_5126	1322	0.22202559	17.322239	6282	25.34	2	10.136082	0.02	0.50507623	1
soy_OGL_521	1050	2.3637695	21.333334	1259	25.33	4	4.8164101	0	0.42220721	14
soy_OGL_522	1235	2.3637695	23.724697	2001	25.18	5	4.1141157	0.068999998	0.41995969	13
soy_OGL_4761	1073	0.4713738	34.855545	3568	23.11	2	2.7016947	0.133	0.79403466	3
soy_OGL_3900	1033	1.5956808	27.395935	24066	28.65	3	0.28770074	0	0.6811744	4
soy_OGL_597	1208	0.51163197	31.953642	1757	24.75	4	2.2958295	0.075999998	0.64208978	10
soy_OGL_879	1100	2.4722638	26	4242	25.81	3	1.4719762	0	0.62532955	9
soy_OGL_1325	1164	0.24154867	37.628864	2001	22.85	3	0.88891345	0.075999998	0.62832874	13
soy_OGL_2055	1000	3.3452113	39.900002	5358	23.9	3	2.3851016	0.071000002	0.55992019	10
soy_OGL_6363	1358	1.2353655	36.450665	2549	22.82	5	6.0668812	0	0.7732954	5
soy_OGL_3527	1281	1.9912556	21.701796	5166	26.3	8	5.8078794	0.118	0.75451076	14
soy_OGL_3525	1243	1.9912556	23.411102	4298	26.87	5	6.8073158	0.104	0.75345939	14
soy_OGL_5689	1800	2.4935195	10.666667	2754	32.22	4	1.0342195	0	0.41404599	14
soy_OGL_131	1000	1.5132793	30.299999	3001	24.5	1	0.64800018	0.101	0.59704554	9
soy_OGL_3407	1354	2.4633574	22.968981	4940	26.29	4	3.6811199	0.032000002	0.64346462	5
soy_OGL_6043	1000	1.3499382	36.5	1492	26.2	4	0.055895533	0.074000001	0.21207653	10
soy_OGL_6394	1100	2.3906288	37.81818	2709	23.9	7	5.9159074	0.102	0.41031706	2
soy_OGL_6152	1564	5.8023572	31.585678	2933	23.91	6	2.3370771	0.103	0.78661126	18
soy_OGL_4357	1300	5.8076673	35.307693	5400	23.07	7	5.0094395	0.090999998	0.49120402	18
soy_OGL_752	1489	5.9034243	26.796507	3325	22.16	8	5.2423201	0.041000001	0.93953568	11
soy_OGL_140	1000	2.8892014	37.700001	7002	20.2	2	0.24974069	0.094999999	0.64402437	7
soy_OGL_589	1000	1.0339187	26.200001	28450	27.8	2	5.3180141	0	0.60865909	8

soy_OGL_1632	1200	3.0774791	29.333334	17359	26.58	2	0.23421018	0.02	0.50343817	6
soy_OGL_2825	1014	2.0155141	39.250492	6080	20.71	4	7.5382504	0.094999999	0.56765956	8
soy_OGL_5376	1860	3.6074958	19.623655	3245	25.43	6	3.8732035	0.015	0.65336776	7
soy_OGL_123	1600	4.455246	13.5	3269	25.68	4	1.8888183	0	0.56419343	6
soy_OGL_3884	1300	0.027143367	32.307693	5038	19.61	5	2.8973658	0	0.38367361	8
soy_OGL_2303	1500	6.6531658	23.933332	3318	25.26	6	3.1006184	0.039000001	0.57860094	14
soy_OGL_2009	1008	5.4989123	33.73016	1189	20.93	4	1.8844742	0.085000001	0.3930617	11
soy_OGL_2747	1570	4.6842942	15.66879	4009	26.24	7	3.7472563	0	0.38548008	14
soy_OGL_3384	1437	5.6634336	18.371607	1001	26.09	3	3.4944127	0	0.71100461	17
soy_OGL_1804	1040	4.1940126	39.51923	13385	21.25	6	4.2540841	0.071000002	0.78625196	15
soy_OGL_3333	1100	13.000942	26.181818	8189	30.45	7	5.7824192	0.11	0.86397237	29
soy_OGL_6614	1913	8.5314484	15.263984	3575	30.89	9	12.296352	0	0.87996215	17
soy_OGL_6959	1100	6.068716	31.272728	7452	29.18	7	13.79142	0.106	0.93143064	33
soy_OGL_411	1200	11.590738	34.583332	2067	26.25	8	10.521846	0.123	0.72821623	16
soy_OGL_924	1445	11.929564	31.487888	3265	31.34	6	15.610137	0.041000001	0.69926322	26
soy_OGL_4436	1260	10.04345	34.444443	3400	27.06	7	7.0708647	0.092	0.62289274	26
soy_OGL_4437	1000	10.04345	34.900002	5160	27.6	7	7.0708647	0.125	0.62295467	26
soy_OGL_4715	1400	5.6724916	27.214285	3818	29.78	6	8.0756674	0.056000002	0.58228761	35
soy_OGL_5792	1000	14.27938	29.9	3149	31.6	6	11.499333	0.075999998	0.85317791	40
soy_OGL_5584	1100	5.8065071	38.545456	4966	26.81	11	33.820923	0.12	0.68075097	19
soy_OGL_612	1363	7.0958691	31.181217	1001	26.77	7	2.5896988	0.113	0.68713653	21
soy_OGL_386	1647	7.2147717	32.422588	5592	30.23	10	2.6520898	0.059	0.77512163	26
soy_OGL_1255	1473	10.965915	39.918533	2001	30.75	10	5.4617119	0.067000002	0.71353626	19
soy_OGL_1397	1286	13.123453	35.92535	2001	31.57	8	5.579452	0.086999997	0.82389557	29
soy_OGL_6533	1900	10.313567	27.631578	1505	30.57	10	6.3225303	0.028999999	0.73428398	20
soy_OGL_225	1389	9.4661407	35.13319	2001	31.46	9	6.0070243	0.046999998	0.83451015	22
soy_OGL_330	1068	10.351954	38.764046	2001	27.8	6	5.5050864	0.13699999	0.87800485	22
soy_OGL_368	1019	8.2798424	34.936211	7613	27.18	10	6.9757533	0.12899999	0.81670719	24
soy_OGL_696	1254	11.121198	33.333332	2088	30.78	10	7.348392	0.078000002	0.81407458	20
soy_OGL_722	1348	9.0755138	38.575668	1001	30.93	10	12.343993	0.067000002	0.86374724	21
soy_OGL_1237	1412	9.0944204	34.206799	2001	31.01	11	8.6183767	0.057	0.75679827	25

soy_OGL_1493	1100	7.3526444	37.454544	6035	26.09	8	2.8377819	0.127	0.97588873	22
soy_OGL_1859	1400	5.4766021	22.214285	3085	34.5	6	1.3028004	0.055	0.72316557	36
soy_OGL_2482	1567	6.4331512	29.291639	1001	33.31	8	5.0468569	0.054000001	0.88778085	22
soy_OGL_3759	1099	7.0757174	38.944496	1687	27.66	9	15.338108	0.106	0.74928325	20
soy_OGL_4574	1300	5.7964573	35.076923	2117	27.76	9	23.26643	0.106	0.8270064	21
soy_OGL_5016	1397	6.9104013	32.641373	1100	31.85	9	7.3707919	0.067000002	0.67313313	23
soy_OGL_5490	1035	4.7314305	31.787439	2083	30.43	6	13.208591	0.122	0.86080325	33
soy_OGL_5774	1024	19.448713	38.769531	2001	33.59	9	6.3970661	0.07	0.82345247	33
soy_OGL_6653	1300	15.119693	35.615383	1600	27.23	11	2.3868272	0.090999998	0.63021582	13
soy_OGL_7004	1396	5.9776316	38.610313	3556	30.65	11	5.9652596	0.079999998	0.96749383	11
soy_OGL_779	1113	9.4103231	34.591194	3742	27.04	6	4.8176455	0.104	0.93457711	19
soy_OGL_5818	1370	12.84843	36.934307	2670	29.12	7	4.5892253	0.090999998	0.9032557	23
soy_OGL_6845	1284	3.9573007	36.526482	3554	26.86	5	5.4934878	0.111	0.81931615	32
soy_OGL_86	1377	7.2984715	39.724037	1006	26.65	7	11.462914	0.086999997	0.79531515	27
soy_OGL_4890	1592	9.0506868	39.635677	3097	30.65	8	4.8738451	0.050999999	0.90705764	14
soy_OGL_5205	2000	6.245574	39.150002	5355	30.7	8	3.4909284	0	0.97022563	20
soy_OGL_1057	1400	4.5279164	38.214287	3167	36.57	9	11.270129	0.023	0.8594197	27
soy_OGL_1176	1300	4.3006682	37.384617	4971	31.61	8	17.891899	0.039999999	0.90471488	29
soy_OGL_3588	1000	5.4232616	39.099998	2396	34.8	7	18.802017	0.055	0.85299665	34
soy_OGL_4112	1300	8.8810902	39.153847	4139	28.38	11	17.208344	0.07	0.77411163	13
soy_OGL_6859	1000	10.103802	35.799999	5365	30.5	7	4.7677336	0.082999997	0.8347851	25
soy_OGL_435	1400	10.683906	34.357143	3874	32.35	9	16.094362	0.052999999	0.67447299	18
soy_OGL_1567	1100	10.710433	39.909092	4399	36.54	5	12.924914	0.01	0.81719047	27
soy_OGL_1824	1024	8.2052183	36.425781	2832	28.71	5	12.484703	0.093999997	0.76585335	24
soy_OGL_3493	1300	5.7129383	38.692307	2069	30.53	8	4.5083146	0.083999999	0.6593318	18
soy_OGL_3974	1800	4.0018716	35.611111	2149	30.16	10	14.349566	0.013	0.91317308	5
soy_OGL_4810	1584	5.6626678	36.742424	3892	27.96	8	27.753366	0.066	0.94258976	14
soy_OGL_6173	1900	9.5013762	39.052631	3675	28.47	8	9.0924816	0	0.81491846	15
soy_OGL_6735	2000	6.7172632	30.25	5911	30.15	10	13.822927	0	0.72137988	19
soy_OGL_802	1200	9.4385977	37.25	2386	28.58	5	13.813766	0.071000002	0.84466404	22
soy_OGL_1498	1781	8.5456972	38.46154	1001	30.71	9	5.823802	0	0.98323089	19

soy_OGL_2430	1332	11.372036	33.70871	1783	28.75	10	8.0971947	0.07	0.72793484	24
soy_OGL_3715	1516	6.9130831	38.192612	3306	31.33	11	7.7734132	0.018999999	0.83185768	24
soy_OGL_354	1400	4.6800423	30.142857	4933	29.57	7	12.047234	0.035999998	0.83849096	31
soy_OGL_2510	1409	7.4874678	36.550747	2000	26.82	9	7.8490939	0.056000002	0.82599187	26
soy_OGL_6767	1500	6.4668698	33.733334	1736	33.06	8	6.2936726	0	0.74813884	23
soy_OGL_261	1567	9.1737165	35.481812	6936	28.33	7	3.0910013	0.021	0.87613636	21
soy_OGL_1861	1600	5.4766021	29.4375	4513	29.56	6	2.2283258	0.012	0.72217858	36
soy_OGL_2169	1300	7.2302747	25.846153	1432	31.3	8	17.161777	0.092	0.82420182	22
soy_OGL_2491	1100	7.5006652	34.81818	2987	29.09	8	12.027684	0.11	0.87881118	18
soy_OGL_2742	1223	5.5531497	37.857727	2880	28.53	14	6.4566407	0.097000003	0.39797553	20
soy_OGL_3987	1242	4.9341402	36.151367	1625	28.82	11	11.916531	0.106	0.87494457	11
soy_OGL_5269	1126	8.472044	30.994671	2724	30.19	8	4.6549139	0.122	0.79446185	20
soy_OGL_5575	1391	6.2863836	27.677929	1001	30.33	9	25.614187	0.068000004	0.69194251	22
soy_OGL_190	1003	7.8639984	38.085743	5470	30.2	11	5.4138069	0.134	0.7965973	12
soy_OGL_5026	1038	7.1732235	30.924856	2115	32.27	7	10.715862	0.086000003	0.66310185	30
soy_OGL_2669	1017	6.8734031	39.921337	2639	28.9	9	11.20086	0.121	0.51056933	21
soy_OGL_5012	1016	11.339603	35.531498	4182	30.51	7	10.370746	0.112	0.67616713	21
soy_OGL_5966	1338	7.5982332	26.457399	2001	24.51	7	8.0538568	0.11	0.6631664	14
soy_OGL_466	1400	5.5066857	33.57143	2484	26.64	4	5.1121802	0.085000001	0.54986489	21
soy_OGL_1063	1400	4.5279164	25.285715	11050	29.57	6	5.3425212	0.056000002	0.86428982	24
soy_OGL_3349	1175	10.722426	26.638298	5676	28.51	4	3.1831048	0.114	0.84665555	25
soy_OGL_1961	1093	6.5777268	31.564501	3391	25.8	5	5.313314	0.133	0.49623576	23
soy_OGL_2321	1081	11.537634	38.482887	2012	24.6	5	4.2836637	0.134	0.52592748	16
soy_OGL_2638	1100	7.9126515	35.090908	3397	26.36	6	7.040236	0.118	0.55735314	21
soy_OGL_2652	1000	6.8734031	36.099998	7082	28.1	7	16.657085	0.103	0.53389162	27
soy_OGL_4091	1064	12.218921	39.473682	1354	25.46	7	10.351935	0.13500001	0.64654052	12
soy_OGL_5739	1000	13.047664	33.700001	2968	28.4	3	4.5349264	0.121	0.69166118	16
soy_OGL_6495	1268	9.6257772	36.198738	4344	25.39	6	7.0207953	0.101	0.66837555	14
soy_OGL_1939	1100	15.018729	37.636364	12595	32.18	7	12.779578	0.046999998	0.53977275	21
soy_OGL_3017	1000	10.088968	38	2404	28	4	19.607084	0.082999997	0.75825107	22
soy_OGL_2393	1100	7.888226	27	5624	26.36	6	7.1855588	0.12899999	0.62530643	13

soy_OGL_2709	1090	3.4366314	31.009174	5770	25.22	8	14.728556	0.133	0.45165041	21
soy_OGL_3066	1372	13.119327	29.008747	1780	27.55	4	3.5996175	0.048	0.1391149	5
soy_OGL_1339	1261	1.8587455	37.272007	1001	26.24	7	2.4450462	0.103	0.71150535	11
soy_OGL_6468	1580	5.4733601	27.151899	2295	27.72	8	14.152258	0.071000002	0.60822642	11
soy_OGL_845	1000	5.9970145	35.400002	6347	27	5	3.9663272	0.118	0.64011717	15
soy_OGL_5128	1226	4.8358898	36.867863	11306	27.32	6	2.2444372	0.046	0.59422356	2
soy_OGL_630	1480	5.4129052	28.581081	10369	29.05	6	4.6456919	0.055	0.71868896	17
soy_OGL_625	1002	3.0260718	36.726547	4149	29.24	6	1.6672305	0.108	0.70764524	23
soy_OGL_1358	1200	10.431696	32.833332	5695	30.91	6	7.3614545	0.054000001	0.76170379	12
soy_OGL_2227	1419	6.4599118	34.954193	6096	28.89	8	2.9117713	0.046999998	0.7211138	17
soy_OGL_2499	1000	7.4874678	37.400002	5279	28.3	6	13.23301	0.12800001	0.84028322	18
soy_OGL_5172	1007	4.208581	36.345581	4532	29.89	4	8.3199539	0.1	0.85108042	18
soy_OGL_6147	1045	5.6423368	36.650719	6096	28.7	5	1.2239078	0.119	0.78135854	19
soy_OGL_6494	1081	9.5896463	39.222942	1001	29.13	5	8.3718452	0.088	0.66779143	15
soy_OGL_2244	1055	6.1071477	38.767773	7681	28.05	6	7.2030563	0.097999997	0.68010759	14
soy_OGL_6347	1100	5.6157908	32.363636	9866	32.54	3	10.773394	0.027000001	0.89319152	23
soy_OGL_4369	1088	4.5123296	36.488972	3437	25.82	7	12.017664	0.116	0.51733553	23
soy_OGL_2333	1197	7.7122221	36.842106	13484	31.16	2	7.4499002	0	0.33477065	9
soy_OGL_627	1382	4.6759496	36.10709	3935	30.82	4	3.6091535	0	0.71136719	22
soy_OGL_2323	1157	11.537634	39.066551	2756	27.91	6	5.5224876	0.064000003	0.52111924	15
soy_OGL_5665	1300	7.7668753	31.76923	11038	32.23	7	6.363791	0	0.49711496	20
soy_OGL_3874	1075	1.7204038	33.860466	2262	27.72	5	5.3376584	0.097999997	0.23943026	18
soy_OGL_4095	1000	12.218921	32.200001	3499	30.4	5	7.8378673	0.090999998	0.66603279	19
soy_OGL_4239	1000	4.9720435	33.599998	5152	29.9	8	2.8756092	0.103	0.27568761	31
soy_OGL_5141	1000	4.0574603	38.400002	2091	25.9	6	23.476313	0.131	0.73011649	14
soy_OGL_5339	1200	24.68428	30.833334	1965	33.58	6	2.0121195	0.059999999	0.54237807	11
soy_OGL_2182	1200	9.9214792	23.5	4114	29.41	8	6.9547796	0.077	0.79786241	27
soy_OGL_3766	1057	12.325804	38.978241	2001	24.21	11	9.4557104	0.093999997	0.73548681	21
soy_OGL_4650	1200	6.4945478	28.416666	2382	26.08	8	2.5747933	0.093999997	0.71239215	27
soy_OGL_6902	1501	7.0806479	23.451033	4713	28.51	8	4.7884359	0.032000002	0.87189275	24
soy_OGL_4709	1125	5.5082192	21.51111	2001	28.71	6	8.5233583	0.061000001	0.59064543	34

soy_OGL_6826	1142	6.5125389	19.614712	2691	29.33	8	15.405775	0.002	0.80941767	35
soy_OGL_5203	1055	6.245574	32.511848	2839	24.36	6	6.3846922	0.061999999	0.97267348	20
soy_OGL_5934	1100	7.3944454	35.636364	5219	24.63	8	6.4855895	0.093999997	0.73776323	22
soy_OGL_4480	1000	7.5810852	27.700001	7640	30.7	10	24.59482	0.012	0.71160626	30
soy_OGL_5320	1059	11.453777	25.873465	1210	28.23	8	5.9652185	0	0.66615492	26
soy_OGL_1275	1092	7.1094861	26.373627	2854	25.54	9	4.7157788	0	0.68308806	21
soy_OGL_1922	1194	13.194177	28.056952	1073	29.14	7	4.6119018	0	0.56034416	23
soy_OGL_3446	1199	11.217252	31.77648	2001	24.68	11	11.298009	0.050000001	0.57632458	9
soy_OGL_5390	1300	9.3595705	27.307692	1017	28.53	7	19.726143	0	0.70171809	18
soy_OGL_6253	1100	5.4503398	24.727272	2074	28.63	7	22.261189	0	0.91415107	23
soy_OGL_4968	1374	10.245035	19.723434	3324	26.78	9	6.803565	0.085000001	0.73583096	16
soy_OGL_2962	1109	11.020073	26.871056	6692	28.76	9	10.473337	0.11	0.86176986	19
soy_OGL_701	1100	10.328465	28.09091	2020	28.9	6	15.270476	0.112	0.83429813	16
soy_OGL_434	1000	10.683906	35.700001	1849	26.8	9	21.173643	0.122	0.67526126	20
soy_OGL_705	1300	9.8149738	19.538462	2307	30.38	6	13.156789	0.066	0.84076452	20
soy_OGL_2529	1100	7.693583	32.090908	3089	25.81	10	36.318314	0.105	0.76931816	11
soy_OGL_1684	1111	9.1770983	29.342934	1346	23.85	10	3.3504198	0.116	0.73533392	10
soy_OGL_6480	1100	9.90658	24	2123	26	9	4.1425934	0.122	0.64105904	17
soy_OGL_1245	1062	9.7408285	20.903955	5039	27.02	9	2.5718105	0.088	0.7452932	23
soy_OGL_1499	1000	8.5456972	15.1	3399	28.4	8	4.5551753	0	0.98349512	19
soy_OGL_3739	1400	9.2037325	18.285715	4499	30.85	10	18.966543	0.041999999	0.78279829	24
soy_OGL_4693	1156	8.4898815	17.214533	10053	32.78	11	13.639303	0.034000002	0.61465645	41
soy_OGL_2598	1300	3.365438	29.692308	2727	24.23	12	22.699167	0.101	0.62383914	14
soy_OGL_2664	1115	6.8734031	22.869955	1482	27.17	13	19.145262	0	0.52532816	26
soy_OGL_5504	1130	5.7864904	20.176991	1001	26.99	9	24.05625	0	0.83224815	21
soy_OGL_5278	1291	8.150281	22.463207	1001	29.51	7	20.742928	0.057	0.7698549	18
soy_OGL_3777	1289	16.465231	17.53297	6972	31.26	10	3.6274905	0	0.71182448	19
soy_OGL_385	1000	7.2905135	37.599998	4615	29.8	10	3.6484663	0.103	0.77673423	26
soy_OGL_6	1000	6.2179899	36	3995	23.5	8	4.0740528	0.132	0.96763033	13
soy_OGL_4869	1047	5.4112797	27.889208	5598	26.36	8	5.8455935	0.101	0.93977994	21
soy_OGL_5446	1057	5.0694704	34.34248	2937	23.93	9	2.8753231	0.082999997	0.94917405	15

soy_OGL_2575	1393	4.5845432	27.422829	3185	25.05	12	1.6769795	0.035	0.67625785	18
soy_OGL_52	1051	9.9992008	38.915318	1001	28.82	7	15.097126	0.081	0.85318184	28
soy_OGL_370	1300	8.2798424	31.461538	2195	31.46	10	4.8072214	0.023	0.81640542	24
soy_OGL_2136	1440	8.1029568	36.319443	1001	31.04	10	3.0574043	0.006	0.87979817	22
soy_OGL_2218	1100	4.6833062	31.272728	2814	27.63	9	5.0174546	0.1	0.74987155	24
soy_OGL_2954	1035	9.1648493	36.038647	2545	28.4	8	4.6936259	0.101	0.8800298	18
soy_OGL_3597	1644	4.7033892	29.379562	1451	29.8	10	16.754353	0	0.86329556	24
soy_OGL_4617	1037	7.723742	33.365479	3248	28.06	10	7.4496236	0.105	0.76700002	24
soy_OGL_5823	1000	16.034658	34.400002	4921	29	10	5.9508739	0.093000002	0.91415089	20
soy_OGL_6299	1589	6.0601311	39.395847	2858	26.55	12	14.682072	0.02	0.94969314	18
soy_OGL_267	1100	6.2561297	32.81818	2258	27.18	6	9.8589449	0.101	0.88649559	18
soy_OGL_670	1000	4.2763386	34.200001	1896	26.6	8	3.7067518	0.106	0.77855027	23
soy_OGL_6192	1579	6.6425095	22.862572	3560	29.89	9	7.7466416	0	0.84899741	17
soy_OGL_730	1000	9.9542494	38.599998	3575	26.7	14	7.470922	0.037	0.88034284	17
soy_OGL_1103	1066	9.3077898	36.866791	1454	26.64	13	9.7475166	0	0.93695867	18
soy_OGL_1771	1247	5.2867265	38.412189	3086	29.91	12	10.118288	0	0.90236861	23
soy_OGL_3632	1100	8.0571461	31.818182	4440	32.27	10	2.7943213	0	0.92440242	29
soy_OGL_5442	1300	5.0618563	33.692307	2918	26.61	10	5.7005367	0	0.95154023	15
soy_OGL_5471	1098	4.9895315	37.795994	1001	27.41	11	4.8459635	0	0.87741768	27
soy_OGL_6197	1100	6.3268976	39.636364	2488	30.81	13	4.4146981	0.026000001	0.85526931	16
soy_OGL_6638	1257	7.9076147	37.788383	3361	31.34	12	9.6977797	0	0.97863287	21
soy_OGL_6931	1200	8.8029718	34.75	3012	33	14	30.285088	0.002	0.90348774	26
soy_OGL_7014	1500	7.0298228	34.466667	4288	29.33	14	12.962764	0	0.9884004	10
soy_OGL_7005	1300	6.3107963	22.923077	4043	26.38	10	5.8476701	0	0.97060889	11
soy_OGL_1247	1120	11.287494	35.892857	2858	26.16	11	5.8838816	0.057999998	0.73601192	18
soy_OGL_2915	1100	9.6217709	38.727272	7198	33.81	10	10.522021	0	0.96982127	28
soy_OGL_5262	1000	10.745309	39.799999	5860	27.9	10	3.2209492	0.097000003	0.81595731	15
soy_OGL_2853	1411	5.5548873	38.058113	6480	27.71	11	3.017633	0	0.70409703	15
soy_OGL_4651	1000	6.4945478	35.400002	4315	30.5	8	2.5747933	0.079999998	0.71180391	26
soy_OGL_1479	1100	5.5293665	31.636364	3524	28.72	8	16.798189	0.034000002	0.9484235	19
soy_OGL_2473	1100	4.7351184	32.272728	9440	31.54	11	3.8617861	0	0.90335315	22

soy_OGL_3829	1077	7.930079	30.91922	2103	31.01	11	7.3061476	0	0.5455246	28
soy_OGL_4836	1000	17.834297	39.5	6692	32.8	13	8.9488058	0	0.98220515	14
soy_OGL_5578	1068	6.1746764	39.794006	3153	30.99	11	8.3671646	0	0.68972152	21
soy_OGL_359	1060	7.2958274	25	9160	31.5	8	3.7183652	0	0.83263695	29
soy_OGL_1854	1143	5.259068	27.909012	1001	29.74	6	2.7197783	0	0.72934413	33
soy_OGL_2089	1410	1.7034707	32.482269	1001	26.31	9	2.6821935	0	0.75955242	15
soy_OGL_2876	1004	7.7406311	35.856575	1001	25	9	12.333274	0.057	0.81918675	14
soy_OGL_2948	1134	10.877373	33.333332	7420	29.54	8	7.6163063	0	0.8976596	17
soy_OGL_3827	1000	7.7698202	36.599998	2401	32.2	9	15.207882	0.003	0.55200428	27
soy_OGL_4626	1004	3.3767221	32.270916	2001	32.96	6	6.6404576	0	0.75009125	32
soy_OGL_5915	1000	8.4431925	27.1	5535	31.4	7	3.1001492	0	0.84524488	22
soy_OGL_6611	1010	8.5314484	30.693069	2001	28.11	8	9.6731186	0	0.87829226	17
soy_OGL_1930	1200	15.236115	39	1152	29.5	8	10.461191	0.004	0.55190587	25
soy_OGL_923	1102	11.336674	37.023594	4473	29.85	9	12.736386	0	0.69753319	28
soy_OGL_2159	1110	8.3984585	34.324326	2151	27.56	7	6.6593947	0	0.84727478	29
soy_OGL_3126	1000	6.2185674	38.200001	4220	24.3	12	6.1868887	0.068000004	0.5474717	24
soy_OGL_1560	1300	11.818582	23.461538	5882	31.3	8	7.7541118	0	0.83751786	21
soy_OGL_5570	1200	7.2933631	28.833334	2278	27.16	8	7.8546281	0	0.70647508	20
soy_OGL_5253	1394	11.726306	21.592539	2341	33.85	9	7.3045521	0.035	0.85909754	23
soy_OGL_6966	1343	4.4204926	21.667908	3955	36.11	7	3.7845838	0.028000001	0.93958682	32
soy_OGL_4652	1074	6.4945478	27.281191	4939	32.12	8	2.5747933	0.086000003	0.7116732	26
soy_OGL_233	1000	8.6488714	28	3089	29.4	8	10.901311	0.098999999	0.84234005	23
soy_OGL_1045	1146	5.3530307	33.682373	2001	36.21	10	17.354546	0.023	0.84796393	27
soy_OGL_6726	1100	7.836133	34	3320	28.54	11	11.444066	0.086999997	0.71130019	14
soy_OGL_1855	1162	5.259068	17.728056	2001	32.78	7	9.4332457	0.007	0.72909093	34
soy_OGL_2117	1200	6.8356886	25.833334	2082	27.41	14	32.858276	0	0.92691743	12
soy_OGL_2861	1100	6.8715682	31.818182	2045	27.27	11	3.2756555	0.096000001	0.77586484	11
soy_OGL_3553	1300	8.6066322	27	2139	34.61	13	5.993433	0	0.80987215	22
soy_OGL_3953	1074	18.983805	36.312851	2909	27.18	14	13.244849	0.059	0.92532766	4
soy_OGL_4884	1400	3.9014754	27.071428	3202	31.42	11	21.418276	0	0.92235512	19
soy_OGL_6290	1300	6.0841422	18.846153	3255	30.38	9	5.6112552	0	0.94720882	22

soy_OGL_1012	1000	6.8298855	30.299999	1454	27	8	12.053946	0.072999999	0.81315821	20
soy_OGL_1194	1106	4.0395017	23.056057	3242	29.11	9	6.3637576	0	0.88272047	19
soy_OGL_4576	1344	5.9374781	16.741072	2001	29.46	8	5.7659278	0.034000002	0.83039111	21
soy_OGL_1277	1190	7.387959	32.941177	1001	34.2	8	9.3452148	0	0.67798686	23
soy_OGL_3817	1310	7.7295065	34.045803	2830	33.12	12	7.7207742	0.021	0.56539011	19
soy_OGL_4561	1100	8.4823227	27.727272	6202	35.81	7	22.48382	0	0.80421078	25
soy_OGL_6418	1000	10.893449	28.700001	3591	36.8	6	20.151438	0.014	0.54213631	33
soy_OGL_231	1000	8.2410164	28.200001	5333	33.5	9	18.512213	0	0.83947098	24
soy_OGL_756	1100	5.3959246	36.636364	3100	32.18	11	3.9482379	0.013	0.94906861	12
soy_OGL_1772	1000	5.2867265	28.200001	1311	33.2	8	12.686503	0	0.90137988	24
soy_OGL_1942	1000	16.56954	31	1276	33.3	9	16.817846	0	0.53501946	20
soy_OGL_2536	1511	7.2488356	22.832561	1001	31.17	9	4.4289412	0.011	0.75513947	13
soy_OGL_4614	1160	11.743592	30.431034	2001	26.63	10	13.467242	0.059	0.81273907	6
soy_OGL_6178	1100	8.6720114	33.272728	2951	32	8	10.958734	0.029999999	0.82310456	13
soy_OGL_6431	1000	10.893449	23.799999	1313	33	5	4.3273172	0	0.54976714	35
soy_OGL_4724	1073	5.8001513	28.704567	1001	24.41	5	7.0608091	0.133	0.560817	22
soy_OGL_657	1200	6.5693884	24.166666	5651	28.16	6	2.9733	0.050999999	0.7608906	29
soy_OGL_1890	1198	9.4963474	31.96995	3443	25.29	7	5.6270695	0.085000001	0.66681594	13
soy_OGL_6160	1100	7.8820863	29.636364	4413	25	5	1.2645833	0.105	0.79490572	18
soy_OGL_3682	1200	6.1510382	31.333334	3962	23.16	8	3.170373	0.01	0.93206865	11
soy_OGL_480	1100	5.5857544	24.727272	2169	25.81	5	4.5130606	0.016000001	0.52497751	20
soy_OGL_1362	1400	4.9044428	27.714285	7609	27.92	8	7.5806904	0.009	0.78382421	24
soy_OGL_1865	1000	5.0498676	29.200001	2660	27.2	5	14.265493	0.097999997	0.71437663	28
soy_OGL_4286	1257	5.7368112	31.105808	1675	29.67	9	30.704748	0	0.3791177	25
soy_OGL_4217	1004	3.9072664	30.976095	3679	24.9	9	12.788445	0.067000002	0.25616208	26
soy_OGL_6134	1139	3.4754949	25.109745	2195	27.56	3	21.362064	0	0.76261979	15
soy_OGL_5550	1100	7.1524053	23	3281	26.27	8	2.2616808	0.13	0.74956322	17
soy_OGL_3912	1200	9.3006687	24.583334	4642	30.08	6	7.673697	0.067000002	0.78611559	22
soy_OGL_4287	1026	5.7368112	32.261208	3803	27.48	9	31.219425	0.101	0.37976298	26
soy_OGL_4212	1270	4.0856552	31.023623	2058	25.51	10	27.720919	0.089000002	0.24594699	17
soy_OGL_5592	1000	3.3001637	28.700001	9585	24.7	12	6.2489743	0.125	0.66329122	22

soy_OGL_4995	1009	8.6126404	21.010902	1001	29.33	5	4.6131344	0.081	0.70200521	26
soy_OGL_2084	1043	1.2674509	25.69511	1694	23.01	7	19.354525	0.052000001	0.75368422	14
soy_OGL_2247	1200	3.1746132	12.083333	2794	28.41	6	5.9703498	0.005	0.65947247	25
soy_OGL_2004	1082	5.9681087	24.491682	3821	27.63	6	11.518134	0.015	0.44101763	13
soy_OGL_4185	1300	8.7795687	15.923077	2985	27.76	10	6.873323	0	0.18813778	19
soy_OGL_2317	1000	8.2685928	28.4	2848	27.4	5	5.3491883	0.094999999	0.54010093	22
soy_OGL_4854	1214	7.4514632	21.99341	1796	27.92	5	23.752285	0.064000003	0.96089518	15
soy_OGL_2661	1200	6.8734031	19	3322	30	7	8.2685928	0	0.52868533	24
soy_OGL_3776	1164	13.809534	19.158075	4624	30.58	7	9.0123625	0.009	0.71543342	21
soy_OGL_3873	1168	9.8148384	23.287672	1176	26.62	10	6.0560851	0	0.24967381	17
soy_OGL_5019	1000	8.8939037	22.4	5906	29.3	8	14.040364	0	0.66897386	26
soy_OGL_2777	1200	6.7741928	31.416666	2777	24.91	9	14.95116	0	0.27055943	4
soy_OGL_3850	1000	9.9024754	26.299999	2481	26.2	8	11.515729	0	0.29037338	13
soy_OGL_1796	1716	5.5180402	18.881119	2287	28.78	8	4.5740261	0.046999998	0.82152224	12
soy_OGL_4018	1000	7.0667925	29.299999	9454	29.6	2	2.973582	0.07	0.69893849	16
soy_OGL_4356	1471	6.4631786	26.648539	1001	28.34	7	11.409381	0.050999999	0.49049753	17
soy_OGL_5658	1027	7.3934207	37.195717	4826	24.63	9	2.4102149	0.122	0.50535691	20
soy_OGL_5165	1035	8.5415621	28.405798	4740	27.24	4	1.5505449	0.090999998	0.83597934	15
soy_OGL_2068	1200	3.4504049	31.75	8113	29.66	3	3.316045	0	0.64122528	12
soy_OGL_163	1455	3.7334805	25.635738	1793	27.97	6	10.66058	0.001	0.70987213	8
soy_OGL_6119	1034	2.2216065	33.752419	2518	25.04	4	1.8792801	0	0.72883773	12
soy_OGL_5150	1014	4.1436477	39.94083	3121	22.87	5	3.0128195	0.115	0.77313316	19
soy_OGL_1914	1059	2.9864438	28.328611	2984	24.45	6	5.4765091	0	0.60928625	11
soy_OGL_6019	1034	2.0301862	35.396519	6661	26.01	5	11.22037	0	0.40235204	12
soy_OGL_1270	1048	6.6517758	39.885498	2722	25.76	7	3.8620455	0.079999998	0.68732196	19
soy_OGL_1965	1300	7.7554264	29.384615	1123	30.92	4	7.364182	0.028999999	0.49318182	25
soy_OGL_2315	1258	8.6314869	35.930046	1001	32.9	6	5.1578045	0	0.54595608	16
soy_OGL_4121	1000	7.7928329	27.200001	6141	32.6	4	6.2932639	0.022	0.79991901	26
soy_OGL_4306	1200	4.7367835	36	1095	30.41	7	3.5999022	0.041999999	0.40419629	24
soy_OGL_6198	1400	6.1686234	35.857143	8789	31.57	9	4.3396277	0	0.85655648	17
soy_OGL_2824	1100	2.0155141	38.272728	11301	30.9	2	14.489349	0	0.56133938	10

soy_OGL_3085	1221	1.6525757	39.39394	1001	30.05	3	14.43321	0	0.26457694	8
soy_OGL_840	1015	5.4804659	37.044334	3023	28.96	9	10.409371	0	0.64802915	15
soy_OGL_889	1044	8.0451517	35.440613	1989	27.58	6	4.7180138	0	0.65993917	19
soy_OGL_2225	1000	6.3921266	29	4114	26.9	10	5.2993641	0	0.72455508	16
soy_OGL_2239	1100	7.3392978	33.81818	2183	27.54	8	4.065176	0	0.69023395	15
soy_OGL_2857	1200	5.5548873	27.166666	4728	27.75	9	2.6199462	0	0.71080983	11
soy_OGL_3795	1111	3.1278274	35.373539	2001	25.47	8	9.5389528	0.057999998	0.6528514	11
soy_OGL_6649	1058	13.28592	34.499054	3002	27.59	7	3.1761291	0.035999998	0.7469669	12
soy_OGL_3111	1300	2.9160867	37.23077	2485	27.92	9	5.5294046	0	0.50814652	12
soy_OGL_4272	1000	4.9097567	31.799999	1281	28.1	6	12.881095	0	0.3562361	21
soy_OGL_5057	1000	6.5904026	37.200001	2745	28.4	5	9.9822159	0	0.60292953	11
soy_OGL_894	1279	7.0074801	37.294762	3590	29.63	5	2.7779937	0	0.66696894	29
soy_OGL_6509	1058	7.9388223	35.916824	5842	30.05	6	18.757362	0.029999999	0.69207174	26
soy_OGL_616	1100	3.2326741	29.727272	9956	30.09	3	12.9627	0.030999999	0.69712031	22
soy_OGL_1967	1200	8.2513695	24.5	7636	32.83	4	9.5706692	0	0.49173701	25
soy_OGL_2838	1000	5.5548873	36.400002	13898	30.2	3	3.2647965	0	0.66624874	23
soy_OGL_4308	1300	3.4580755	24.923077	8340	29.76	8	9.3970079	0	0.40836751	23
soy_OGL_4377	1000	6.6361041	35.099998	10249	32.2	5	23.373892	0.007	0.52814656	26
soy_OGL_1218	1000	6.7576227	39.5	8478	27.6	8	6.9760079	0.012	0.812307	23
soy_OGL_4379	1049	6.6361041	35.271687	4029	27.74	6	9.5556746	0	0.5289104	27
soy_OGL_4580	1100	5.9374781	35.090908	5384	25.45	8	5.3811183	0	0.83404291	20
soy_OGL_6476	1100	8.1601791	35.81818	5288	26.18	7	3.8115737	0	0.633793	17
soy_OGL_6594	1100	5.3763165	24.90909	6574	27	9	8.4346094	0	0.80453366	18
soy_OGL_2579	1300	4.4795728	21.461538	2681	28.61	8	7.5280809	0.079999998	0.67370629	17
soy_OGL_2860	1500	5.5548873	22.6	5388	28	9	6.1930103	0.048999999	0.71499419	10
soy_OGL_1595	1148	5.281703	20.6446	2001	30.05	2	0.30541286	0.078000002	0.70752692	18
soy_OGL_626	1030	3.6668093	34.757282	2001	35.63	4	1.7843091	0.041000001	0.70880914	24
soy_OGL_3660	1085	4.1581578	31.520737	8052	27.09	8	19.77438	0.096000001	0.98957574	12
soy_OGL_4417	1400	6.6752057	25.928572	4252	28.57	10	4.1184883	0.075999998	0.5975613	14
soy_OGL_4241	1020	4.9720435	29.019608	4722	29.5	7	2.9945648	0.093000002	0.27579319	31
soy_OGL_5363	1159	8.8681479	27.610008	8774	29.76	8	5.5288363	0.071000002	0.60488379	12

soy_OGL_6398	1419	6.8150654	29.457365	1001	30.3	6	14.611404	0.033	0.46976218	12
soy_OGL_3275	1000	2.1021929	32.200001	2288	25.6	7	6.5205121	0.092	0.99076039	11
soy_OGL_3004	1000	6.9705009	29.4	4691	33	6	6.9477706	0.059	0.78613615	22
soy_OGL_5191	1300	13.332328	19.307692	6918	34.69	5	7.7614179	0.003	0.95594764	16
soy_OGL_2703	1300	3.5302119	27.692308	2078	32.53	9	4.1011667	0	0.45894405	25
soy_OGL_5145	1186	4.3852158	21.500843	1113	29.76	5	5.2467408	0	0.7529611	22
soy_OGL_5603	1000	4.5532155	23.4	5373	29.5	8	10.107425	0	0.64665133	26
soy_OGL_1328	1029	0.24154867	33.916424	2422	29.64	4	3.7314844	0	0.63898385	8
soy_OGL_2708	1062	3.4366314	28.625235	6906	30.13	8	14.728556	0	0.45169014	21
soy_OGL_5986	1001	2.8841054	33.466534	1624	29.87	6	1.8306508	0.028000001	0.60658669	14
soy_OGL_424	1400	14.106673	37.07143	7483	26.57	10	4.9398742	0.103	0.69177026	24
soy_OGL_784	1876	10.419619	31.556503	3886	28.62	8	9.0316353	0.01	0.91734564	19
soy_OGL_3181	1707	12.374106	33.977737	1001	26.77	9	6.4075074	0.067000002	0.65593463	22
soy_OGL_4670	1543	10.891823	30.58976	1436	29.81	9	16.134077	0.055	0.65243137	35
soy_OGL_5814	1500	12.729729	34.266666	4159	27.86	7	4.8185945	0.072999999	0.89322549	25
soy_OGL_3595	1104	4.7033892	36.141304	5101	25	9	27.753897	0.11	0.86060792	26
soy_OGL_5243	1600	8.6306667	26	2273	28.06	6	11.928915	0.048	0.87906706	24
soy_OGL_5531	1327	11.696812	30.896759	5750	27.88	8	5.6984758	0.072999999	0.78765798	24
soy_OGL_709	1800	9.20959	22.166666	3438	28.94	7	12.110048	0.027000001	0.84181803	19
soy_OGL_3590	1416	5.1424751	35.310734	8381	26.27	6	4.3581886	0.056000002	0.85370535	31
soy_OGL_1887	1518	9.2462587	39.657444	2411	25.95	8	23.329348	0.079999998	0.67025268	13
soy_OGL_3024	1300	10.401243	39.846153	2869	25.38	7	13.511984	0.109	0.75165957	20
soy_OGL_6441	1077	9.537591	34.54039	2670	27.29	5	9.3301973	0.124	0.55868131	36
soy_OGL_5769	1271	20.915419	27.537373	7569	32.02	6	3.0320652	0.064999998	0.81194967	23
soy_OGL_1042	1390	8.4023438	30.071943	5227	27.33	6	14.116157	0.071999997	0.84176743	25
soy_OGL_5944	1100	9.668354	37.909092	3388	25.45	7	13.009373	0.123	0.7204439	24
soy_OGL_2167	1756	8.3071995	29.669704	1001	29.44	8	18.131691	0.002	0.83108002	28
soy_OGL_4510	1300	8.8380184	35.615383	10923	27.69	9	4.3237667	0.048999999	0.74801022	37
soy_OGL_5762	1241	13.454047	36.422241	2001	26.91	7	14.876851	0.064999998	0.78746843	20
soy_OGL_414	1500	13.282036	36.466667	4481	26.46	9	5.1671476	0.035999998	0.70942342	17
soy_OGL_4899	1700	9.0506868	32.823528	8090	25.35	9	5.3020058	0	0.89449346	17

soy_OGL_2468	1122	4.321734	38.85918	10226	22.37	9	11.171393	0.13	0.91285312	19
soy_OGL_3393	1599	5.6634336	32.20763	8548	27.45	5	3.1401823	0.041000001	0.69715863	18
soy_OGL_2729	1423	7.584291	30.850317	4095	25.5	9	6.3944831	0.075999998	0.42316005	19
soy_OGL_3163	1370	8.1492577	30.510948	2736	24.37	6	6.8318419	0.117	0.60985434	15
soy_OGL_3388	1371	5.6634336	39.970825	2854	23.7	4	6.4024534	0.090000004	0.70935035	17
soy_OGL_4969	1760	10.245035	27.272728	5723	28.01	6	5.0703917	0.014	0.73302871	16
soy_OGL_948	1943	6.087534	31.70355	3250	23.67	8	3.0212498	0.012	0.73745984	16
soy_OGL_1809	1079	5.8060555	39.944393	6466	21.96	8	5.2184553	0.116	0.78323448	21
soy_OGL_2391	1200	7.888226	37.25	3712	22.25	6	0.82651174	0.104	0.62085015	17
soy_OGL_3934	1300	8.8798027	36.923077	12220	26.38	6	1.9840223	0.024	0.86325741	26
soy_OGL_4999	1300	8.9428253	30.307692	4772	27.61	6	12.333051	0.052999999	0.70053524	26
soy_OGL_1178	1160	4.3006682	38.965519	2240	24.91	7	20.302364	0.071000002	0.90413332	30
soy_OGL_2975	1000	10.933967	29.799999	4381	26.5	8	12.300834	0.089000002	0.83326381	23
soy_OGL_5907	1177	7.9141469	39.42226	2001	25.65	8	14.775337	0.046	0.86283165	33
soy_OGL_1040	1100	8.4023438	27.454546	4899	26.54	7	10.371768	0.085000001	0.84085339	26
soy_OGL_5007	1370	10.049834	33.430656	1001	24.3	8	9.5612946	0.085000001	0.68765873	15
soy_OGL_55	1082	9.9992008	24.029575	1001	27.72	7	17.025173	0	0.85038787	27
soy_OGL_419	1038	13.982355	28.420038	1964	25.72	10	3.7455225	0.055	0.70588118	20
soy_OGL_798	1000	9.1312065	27.5	1418	23.9	8	3.6550336	0.064000003	0.85473436	22
soy_OGL_2478	1098	2.6678751	29.143898	3812	23.49	9	6.615449	0	0.8995595	26
soy_OGL_3474	1347	7.0972891	17.668894	5260	28.87	12	15.494199	0	0.64037931	30
soy_OGL_3560	1100	6.3657079	29.363636	4961	24.36	8	4.9975595	0.02	0.83101499	30
soy_OGL_4848	1300	6.3971152	30.23077	4948	23.84	10	11.060342	0.039999999	0.97328979	14
soy_OGL_6270	1200	5.2232471	22.833334	8865	26.66	10	6.65906	0	0.92607039	29
soy_OGL_6550	1339	13.347547	22.404779	3044	29.27	7	5.2706313	0	0.75551635	29
soy_OGL_6884	1392	6.5062184	35.632183	1001	24.2	10	10.30632	0	0.85899806	22
soy_OGL_2198	1398	8.5738249	34.83548	2001	25.17	8	7.2360826	0	0.77338535	34
soy_OGL_1386	1026	6.9438424	30.116959	4297	27.97	6	15.37778	0.048	0.80703402	37
soy_OGL_903	1300	6.8591065	37.46154	2617	26.07	7	12.832253	0	0.67457831	30
soy_OGL_3147	1214	8.65382	39.044479	2001	22.98	8	8.9139729	0.064000003	0.57893395	22
soy_OGL_930	1054	12.449766	36.622391	2108	23.81	10	2.8315191	0	0.70385206	24

soy_OGL_941	1005	12.449766	37.213932	1013	26.06	7	6.0048332	0.006	0.71047091	28
soy_OGL_945	1202	12.186299	28.618969	2001	25.37	10	11.475168	0	0.7206437	16
soy_OGL_1100	1097	8.7746096	31.267092	6706	27.62	12	36.20726	0.009	0.93525082	18
soy_OGL_6217	1000	7.4032087	35.299999	1766	24.7	8	17.573677	0	0.87033528	30
soy_OGL_241	1000	10.989239	37.799999	7825	24.5	9	5.9469886	0.035999998	0.84783918	21
soy_OGL_902	1000	6.5197372	32.700001	5978	26.6	9	7.3360667	0	0.6708529	31
soy_OGL_1422	1055	11.385625	27.109005	6035	27.86	6	6.2150521	0	0.86808378	23
soy_OGL_2982	1000	11.277602	27	5135	27.5	8	5.3049178	0	0.82624257	23
soy_OGL_3164	1200	10.987015	27.083334	2857	24.33	10	3.490643	0	0.61400598	16
soy_OGL_3662	1300	4.1581578	30.538462	4265	23.53	9	21.538654	0	0.98816311	12
soy_OGL_3972	1100	9.8309717	35.545456	4473	22.54	9	8.3480854	0.048999999	0.93590772	10
soy_OGL_5569	1300	7.2933631	28.846153	1933	25.53	8	7.8546281	0	0.7066322	20
soy_OGL_6843	1130	3.9573007	39.469025	2001	23.71	5	9.1800728	0	0.81906164	32
soy_OGL_2190	1100	10.96957	39.545456	6160	24.45	8	6.9463873	0	0.79052293	29
soy_OGL_3234	1000	8.3343325	38.900002	1425	25.5	5	8.7026739	0	0.72432661	39
soy_OGL_4910	1000	14.910236	39.200001	6428	24.2	11	11.803347	0	0.78347522	18
soy_OGL_2200	1086	8.5738249	37.200737	7072	25.69	6	7.8922873	0	0.77234012	34
soy_OGL_3050	1100	26.725401	33.454544	3296	27.81	9	0.67581522	0.093999997	0.60085958	4
soy_OGL_6697	1460	7.5215936	35.958904	2001	24.72	4	12.631207	0.02	0.050237343	1
soy_OGL_283	1087	7.6405764	24.195032	8050	26.67	5	1.7817541	0	0.90374607	26
soy_OGL_3794	1049	3.1278274	33.269779	3049	22.02	9	23.034557	0.071999997	0.65463293	10
soy_OGL_5364	1326	8.8681479	26.621418	2001	23.52	8	2.3438122	0.023	0.60823035	13
soy_OGL_5394	1216	9.4848547	21.875	5824	27.22	6	2.8943503	0.004	0.71256	19
soy_OGL_5556	1301	6.151978	37.202152	5976	22.98	7	2.9970751	0	0.73234481	16
soy_OGL_6576	1100	4.8296428	17.545454	5803	28.63	4	7.2312274	0.032000002	0.78213757	31
soy_OGL_4277	1263	5.4117041	30.87886	7194	25.09	6	7.5144176	0	0.36331132	19
soy_OGL_1286	1000	7.3108006	31	10089	28.8	3	16.074305	0.025	0.65743858	17
soy_OGL_2313	1400	7.6951575	33.214287	1209	25.28	5	9.0762024	0	0.55294037	17
soy_OGL_79	1100	9.6598225	28.90909	7802	28.36	5	15.03484	0	0.80025452	26
soy_OGL_2599	1020	3.365438	34.019608	1001	22.84	9	26.87641	0.027000001	0.62302172	14
soy_OGL_3027	1200	9.7849836	31.083334	3484	24.91	6	9.7922449	0	0.7472468	18

soy_OGL_3466	1050	8.5749073	30.285715	2849	24	8	7.0864296	0.041000001	0.62739664	19
soy_OGL_5604	1100	4.5532155	26.727272	3280	25.18	8	9.7567759	0	0.64616477	26
soy_OGL_5838	1000	13.562174	35.599998	8241	26.5	5	7.0481896	0	0.96441621	22
soy_OGL_857	1019	7.1209521	22.473013	2581	26.2	4	11.032272	0.029999999	0.59169531	15
soy_OGL_3867	1000	9.8148384	23.799999	5708	28.5	6	12.314476	0	0.25545064	19
soy_OGL_2546	1626	4.2873001	15.498155	1282	27.98	9	4.6070786	0.23800001	0.72840911	20
soy_OGL_4872	1630	4.7057142	10.858895	2001	27.42	10	4.3556657	0.22499999	0.93411893	24
soy_OGL_3288	1400	2.9993556	12.928572	6087	27.64	8	4.7380238	0.199	0.96174192	23
soy_OGL_1511	1427	6.1372461	16.117729	2194	28.94	7	6.2125831	0.17	0.92201191	22
soy_OGL_1775	1700	5.2867265	10.882353	2377	29.23	9	3.8106372	0.19499999	0.89775974	23
soy_OGL_2929	2036	7.6890759	1.7681729	1001	31.77	11	4.8766356	0.176	0.94638145	19
soy_OGL_4867	1989	5.4112797	9.4519863	1001	31.27	8	5.8455935	0.204	0.93990862	21
soy_OGL_5507	1578	5.7864904	17.237009	2834	26.93	12	10.167773	0.22499999	0.82870585	18
soy_OGL_6732	1935	6.0688667	9.2506456	3700	30.43	11	8.5558825	0.21600001	0.71990705	19
soy_OGL_6969	1567	5.001214	10.274409	2572	31.14	7	3.3775938	0.189	0.93990058	33
soy_OGL_2172	1300	8.2492304	18.692308	3037	28.61	6	4.3577433	0.204	0.81554586	24
soy_OGL_4993	1700	8.6126404	13.352942	2359	31.41	6	5.2710009	0.185	0.70473105	26
soy_OGL_5200	1452	4.7585993	17.011019	2583	28.09	6	6.496882	0.17399999	0.97971636	18
soy_OGL_5605	1198	3.8285015	18.614357	6083	26.62	10	6.6550746	0.227	0.64371657	27
soy_OGL_6908	1101	7.0806479	22.161671	3699	28.7	6	6.5324221	0.24699999	0.87700027	22
soy_OGL_7010	1401	7.1566463	20.842255	2001	26.55	10	6.0455103	0.192	0.98260456	11
soy_OGL_2449	1500	8.1517172	9.666667	2159	30.6	5	12.908495	0.142	0.9526853	15
soy_OGL_2486	1354	6.4331512	14.623339	2001	26.58	10	5.21243	0.171	0.88554543	19
soy_OGL_4853	1549	7.6953392	13.879923	2001	25.24	14	5.4102669	0.18799999	0.9628917	15
soy_OGL_603	1597	6.4707346	17.845961	2001	25.1	12	9.5476437	0.16599999	0.66858983	13
soy_OGL_2475	1461	4.7351184	0	2667	30.73	11	5.8343067	0.23199999	0.9027161	24
soy_OGL_2743	1467	5.5531497	0	1001	30.53	13	4.9064364	0.27000001	0.39762938	20
soy_OGL_5918	1600	8.4431925	0	1873	31.25	8	3.4913862	0.21799999	0.8437143	20
soy_OGL_3922	1350	9.3006687	15.259259	6165	28.74	9	5.1926866	0.31	0.80719125	16
soy_OGL_673	1206	3.8562949	0	1676	30.26	7	5.501626	0.213	0.77943736	23
soy_OGL_228	1400	9.9151058	0	3825	34.07	9	2.5803294	0.22499999	0.83863163	24

soy_OGL_288	1361	6.9669991	0	1001	32.4	10	5.5374942	0.237	0.90747041	29
soy_OGL_389	1060	8.6352415	0	6621	34.52	9	7.598371	0.244	0.76986665	28
soy_OGL_2226	1800	6.3921266	5.5555553	1314	31.38	10	5.3973646	0.15700001	0.72442663	16
soy_OGL_2956	1400	9.1648493	15.357142	2138	30	8	3.8872061	0.259	0.87935317	17
soy_OGL_3596	1787	4.7033892	2.1264689	4130	32.84	9	7.2468271	0.212	0.86269873	26
soy_OGL_5866	1500	9.3869944	0	2147	33.33	11	7.3247914	0.26100001	0.92713267	26
soy_OGL_2629	1409	7.9126515	0	5150	33.78	9	6.3275552	0.252	0.56671679	26
soy_OGL_2438	1766	7.3556457	4.360136	1001	28.65	11	8.5985079	0.15099999	0.97988927	9
soy_OGL_2897	1100	8.9753227	8.636364	2040	29.18	11	7.6505427	0.234	0.8888818	13
soy_OGL_4871	1539	4.7057142	1.8193632	2359	29.56	11	6.4036565	0.18099999	0.93477702	24
soy_OGL_5008	1467	8.6055784	6.9529653	1001	27.94	13	8.0708723	0.18000001	0.68672544	14
soy_OGL_6170	1017	10.292652	14.650934	2279	28.61	9	8.353816	0.259	0.81110525	14
soy_OGL_6590	1404	5.3763165	0	1949	32.76	9	5.8532834	0.154	0.80090064	24
soy_OGL_4462	1129	6.0359983	0	4945	34.36	9	11.768971	0.233	0.69172966	20
soy_OGL_6481	1219	8.3500423	9.0237904	1001	28.87	10	3.6997089	0.20100001	0.64292818	16
soy_OGL_788	1100	6.6936736	11.909091	4465	27.9	8	8.8841038	0.192	0.88770312	17
soy_OGL_6641	1257	6.8812695	9.2283211	4136	29.43	7	12.377577	0.168	0.98224497	20
soy_OGL_3161	2300	8.0538549	11.782609	1276	33.3	10	2.8836112	0.278	0.60623819	15
soy_OGL_5552	1700	6.9108586	16.411764	3071	30.58	10	5.8215423	0.191	0.74639082	14
soy_OGL_2229	1517	6.7853222	22.017139	1240	28.74	7	2.9559057	0.18000001	0.71989906	15
soy_OGL_5432	1160	4.0297146	29.137932	3865	24.65	10	15.865607	0.207	0.97820687	6
soy_OGL_6351	1200	5.8339896	14.083333	3620	30.08	7	2.3207331	0.154	0.88671064	23
soy_OGL_1821	1600	0.91241473	17.4375	5093	35.62	7	6.7093005	0.41299999	0.76856816	29
soy_OGL_1849	2000	4.9061704	4.5999999	3946	38.15	8	7.1346512	0.38800001	0.73181492	27
soy_OGL_3659	1200	4.1581578	0	3693	30.41	9	3.9261444	0.23899999	0.99098712	12
soy_OGL_1114	1736	3.9013312	2.4193549	1001	31.33	12	11.070081	0.186	0.9635216	9
soy_OGL_4887	2089	3.9014754	7.4676881	2001	36.57	10	4.5972743	0.24699999	0.91993499	19
soy_OGL_5201	1345	4.7585993	0	2014	34.57	8	5.5711198	0.26800001	0.97823876	18
soy_OGL_6596	1689	5.3763165	0	2001	34.39	11	11.175644	0.23999999	0.80651569	17
soy_OGL_6597	1400	3.883358	0	1144	36.07	10	11.927189	0.23999999	0.80822313	14
soy_OGL_3798	1552	1.880484	18.170103	2001	28.73	11	17.568901	0.19599999	0.64760512	11

soy_OGL_4285	1010	5.7368112	24.653465	1847	26.93	11	2.3900347	0.266	0.37852561	24
soy_OGL_4456	1331	4.9608045	2.3290758	6190	37.71	13	14.110181	0.32600001	0.67773205	11
soy_OGL_5599	1000	4.7505159	22	2359	28.7	8	2.6405492	0.27599999	0.65225673	20
soy_OGL_1875	1323	5.0498676	2.6455026	2872	31.82	10	3.7636225	0.17	0.70951492	21
soy_OGL_3672	1200	6.1510382	14.25	1066	28.66	10	3.5866263	0.20200001	0.94535196	13
soy_OGL_175	2300	2.1532793	5.9565215	4091	31.91	6	2.9661741	0.17200001	0.76820153	12
soy_OGL_2712	1600	4.0992632	12.5625	2108	27.87	10	4.3808403	0.154	0.44745803	23
soy_OGL_180	2118	4.2186117	5.6185079	3111	31.53	5	4.0171909	0.161	0.77375615	13
soy_OGL_3009	1716	6.7379055	19.172495	10204	32.63	5	2.2741725	0.30000001	0.77619022	20
soy_OGL_5368	1209	8.8879547	28.039701	2411	26.96	7	4.0375304	0.229	0.62183243	15
soy_OGL_6496	1700	9.6257772	5.5294118	3179	32.82	6	3.0519502	0.13	0.66932589	15
soy_OGL_2852	1325	5.5548873	12.377358	1001	27.62	6	6.4075227	0.15899999	0.696284	21
soy_OGL_4716	1209	5.4552517	17.369726	3097	27.62	7	8.5509129	0.161	0.5793981	27
soy_OGL_513	1457	3.8568666	5.284832	1001	29.23	10	8.8398666	0.245	0.45245945	17
soy_OGL_3266	1600	5.2893763	0	4805	32.56	4	3.9906518	0.18799999	0.84733611	19
soy_OGL_6153	2329	5.245831	3.6925719	2001	40.27	2	24.528133	0.38999999	0.78870338	18
soy_OGL_3468	1215	8.2846069	9.794239	11347	34.23	5	2.9586349	0.338	0.63213086	25
soy_OGL_6402	2094	6.8150654	0	4937	34.24	6	5.1427941	0.28299999	0.47592601	16
soy_OGL_1881	1200	4.2531829	12	4920	27.33	11	5.7057323	0.22400001	0.68691885	8
soy_OGL_2711	1259	4.1133008	9.2136612	2388	28.91	10	4.2648339	0.208	0.4492867	23
soy_OGL_6465	1000	6.0830817	17.799999	2731	25.8	9	3.9916718	0.26899999	0.60166746	15
soy_OGL_618	1165	3.2326741	0	2001	33.99	7	18.753477	0.19499999	0.69939709	23
soy_OGL_834	1169	9.0662546	0	3219	33.53	6	5.8779864	0.213	0.71350783	22
soy_OGL_2241	1400	7.3392978	2.8571429	2930	30.64	9	4.1277523	0.16	0.68433487	14
soy_OGL_2495	1100	7.548306	15.181818	3641	27.72	8	11.227009	0.235	0.86461538	6
soy_OGL_3121	1000	6.2578096	19.299999	2917	25.7	10	2.5148289	0.241	0.53177983	19
soy_OGL_3457	1100	9.328948	0	2247	33.36	8	12.535951	0.23800001	0.60400832	13
soy_OGL_836	1110	5.5400124	14.864865	2781	27.47	6	7.9798813	0.252	0.69163984	15
soy_OGL_4362	1693	3.9915023	6.261075	1677	30.06	8	10.736074	0.147	0.50825852	17
soy_OGL_160	1500	3.8654892	9.8666668	4357	28.6	5	0.9019385	0.191	0.70701718	10
soy_OGL_2242	1559	7.3392978	2.245029	7883	31.94	6	4.9433613	0.222	0.68218535	13

soy_OGL_4772	1400	6.7980485	0	6068	36.85	3	20.501026	0.30700001	0.84072089	9
soy_OGL_5045	1000	2.4656436	20.9	2007	25.3	5	4.3523922	0.26499999	0.64138901	11
soy_OGL_636	1308	6.0811286	0	2716	30.27	4	2.079932	0.17399999	0.72513777	14
soy_OGL_2305	1000	7.0116496	0	1810	32	5	6.3017454	0.23100001	0.56968349	15
soy_OGL_2533	1269	7.4369493	3.4672971	5879	32.54	7	12.214153	0.205	0.75793707	13
soy_OGL_5407	1000	9.4738331	23.4	2984	27.4	7	6.2979851	0.25299999	0.74745941	14
soy_OGL_5972	1030	8.3158064	15.728155	6301	29.8	7	7.9495077	0.24699999	0.65383011	15
soy_OGL_1347	1381	8.5493393	0	4696	34.9	5	7.0776377	0.18099999	0.73701155	14
soy_OGL_999	1070	6.697526	16.82243	5027	26.91	7	7.0448895	0.206	0.79080516	14
soy_OGL_4367	1523	7.6906767	4.4648719	3751	32.17	8	8.6053123	0.112	0.51479083	22
soy_OGL_5367	1200	8.8820086	16.416666	2240	29.25	7	2.5822415	0.184	0.61982799	15
soy_OGL_568	1542	5.1880841	8.2360573	2001	27.36	11	2.9672434	0.14	0.29684046	12
soy_OGL_3449	1400	9.8075924	9.3571424	1964	28.5	10	7.99231	0.16	0.58547169	12
soy_OGL_2441	1821	3.0977101	9.7199345	1833	32.45	6	10.072269	0.15800001	0.97184265	11
soy_OGL_4259	2200	2.2741857	20.636364	2725	31.5	9	5.0040531	0.21600001	0.3298395	13
soy_OGL_6355	1700	5.3719535	17.117647	1787	31.17	3	1.9461498	0.22499999	0.87337869	14
soy_OGL_619	1090	2.9936664	31.376146	4716	27.06	8	4.6007853	0.22	0.7011925	20
soy_OGL_134	1173	0.20161225	0	1001	41.6	3	4.4709792	0.39899999	0.61967057	4
soy_OGL_5724	1600	0.67194265	0	1377	33.62	6	1.5239898	0.29300001	0.54610467	6
soy_OGL_10	1200	8.163537	5.25	7702	34.75	7	4.408102	0.206	0.95652729	15
soy_OGL_455	1000	3.3159945	5.5999999	1181	34.9	7	4.7494693	0.287	0.57729727	12
soy_OGL_6184	1000	6.60361	0	3432	37.2	4	2.0916536	0.29800001	0.83830112	15
soy_OGL_6301	1063	2.1871984	21.260584	2831	30.1	7	5.6620235	0.264	0.9928782	8
soy_OGL_165	1800	2.0258014	2.9444444	2608	38.77	3	0.18654387	0.23999999	0.71958977	12
soy_OGL_4195	2400	3.415179	0	1318	36.87	7	1.1403224	0.169	0.21087709	20
soy_OGL_4328	1800	2.6155119	4.1111112	4399	36.83	6	2.3745637	0.20100001	0.43935421	19
soy_OGL_2739	2100	6.7385716	13.047619	6547	36.47	10	6.5636549	0.23100001	0.40543705	17
soy_OGL_4336	1261	5.7029614	18.794607	2780	33.22	7	3.1006455	0.31600001	0.45772165	17
soy_OGL_4778	1400	3.9707932	24.857143	1337	31.28	6	6.5839758	0.25799999	0.86774427	5
soy_OGL_5052	1818	6.5904026	5.9955997	9976	39.6	6	12.022698	0.28	0.60927105	13
soy_OGL_5358	1700	2.9911871	15.235294	1225	34.7	5	9.4991331	0.266	0.5034672	12

soy_OGL_6400	1100	6.8150654	8.181818	3288	37.09	7	7.6458845	0.31299999	0.47207466	12
soy_OGL_2578	1100	4.5751367	18.818182	4144	28.72	9	6.8155174	0.186	0.67469233	18
soy_OGL_4316	1200	1.3122375	14.333333	3573	30	11	14.637931	0.207	0.42070517	20
soy_OGL_2440	1407	3.0977101	7.7469792	2001	25.15	9	5.8634219	0.175	0.97404194	11
soy_OGL_1066	1066	4.5279164	16.228893	2001	25.98	9	3.4468975	0.20900001	0.8672809	23
soy_OGL_1506	1116	4.9607878	8.6021509	1914	27.68	8	12.715701	0.212	0.93205857	19
soy_OGL_4607	1455	6.8955364	0	2920	30.58	14	8.1866112	0.171	0.85663694	10
soy_OGL_4903	1000	9.0506868	0	1052	30.2	13	8.8072739	0.23999999	0.88877022	11
soy_OGL_5458	1235	6.9202266	2.5101213	1412	29.14	12	8.5473814	0.223	0.91163468	17
soy_OGL_3963	1200	8.0179386	3.5	3157	30	8	12.10102	0.182	0.96995002	9
soy_OGL_1740	1400	3.8039601	5.5	2203	26.85	11	8.9504814	0.17	0.9875617	13
soy_OGL_3656	1319	1.9542303	12.206217	2001	24.33	10	10.02743	0.20200001	0.95532382	10
soy_OGL_3273	1200	2.1021929	0	2350	27.16	9	9.1833601	0.19400001	0.99190325	10
soy_OGL_677	1106	3.8562949	6.4195299	1944	27.84	9	6.0950122	0.189	0.78108639	25
soy_OGL_1770	1200	5.2867265	9.5	4570	29.58	11	10.710917	0.182	0.90901947	20
soy_OGL_3678	1618	6.1510382	0	2227	30.34	10	4.7480102	0.123	0.93725324	12
soy_OGL_4866	1400	5.9310865	2.1428571	2130	29.64	11	7.2640986	0.13600001	0.9414987	19
soy_OGL_6245	1360	5.8414173	0	1259	29.19	13	3.1639693	0.186	0.90205437	20
soy_OGL_6633	1066	7.7989373	0	2807	29.54	12	5.9299784	0.21699999	0.97164267	21
soy_OGL_1071	1317	7.9827704	0	2039	32.57	8	8.9208374	0.14300001	0.87936383	16
soy_OGL_1787	1090	5.2867265	0	2001	31.83	14	8.0019579	0.219	0.88546324	17
soy_OGL_2135	1000	8.1029568	3.7	1227	31.2	10	2.6885068	0.23899999	0.88027984	22
soy_OGL_4553	1083	3.8827412	2.5854108	3091	32.31	11	7.590044	0.207	0.79443985	28
soy_OGL_5453	1215	5.0694704	6.0905352	1001	28.55	11	6.4665613	0.215	0.92561305	12
soy_OGL_4366	1200	6.5855064	15.666667	2464	27.5	9	6.0385346	0.141	0.51414746	22
soy_OGL_4416	1260	6.3058491	15.555555	2967	26.11	10	5.8599586	0.153	0.59552109	12
soy_OGL_6156	1762	5.245831	2.7241771	2001	31.89	6	7.9552803	0.048999999	0.79173064	19
soy_OGL_2087	1200	1.7034707	0	3160	30.33	9	9.7982893	0.212	0.75850761	15
soy_OGL_4349	1244	6.5096278	0	2787	30.22	10	7.4607339	0.191	0.48356208	19
soy_OGL_5009	1000	6.5572796	0	5061	29.1	10	3.8612299	0.23199999	0.68535507	16
soy_OGL_5553	1200	6.9108586	0	5471	29.33	10	5.8215423	0.20900001	0.74631798	14

soy_OGL_6179	1024	7.1503053	0	1414	31.93	5	6.0960512	0.21799999	0.82481623	13
soy_OGL_2383	1129	7.888226	0	2001	31.44	9	4.6613426	0.2	0.59843856	13
soy_OGL_1635	1169	1.074288	6.7579126	3177	27.37	9	9.2670822	0.211	0.54723305	4
soy_OGL_3032	1118	2.1420259	2.5044723	2914	26.11	5	3.5947635	0.227	0.72303325	7
soy_OGL_4267	1004	3.4015584	4.4820719	1001	30.07	7	4.4090805	0.223	0.34425032	16
soy_OGL_5412	1200	4.7039185	0	2304	25.91	8	1.5398402	0.177	0.82290161	4
soy_OGL_6307	1000	5.4021316	0	4136	29	8	3.2731328	0.17900001	0.98412341	9
soy_OGL_2710	1564	3.5777133	0	2001	31.52	11	7.4942803	0.104	0.45013413	21
soy_OGL_457	1000	4.091258	11	7898	28.8	10	4.8010712	0.189	0.56754953	19
soy_OGL_186	1034	4.0351768	0	2394	28.14	3	2.8309391	0.193	0.78732032	10
soy_OGL_704	1400	9.8199148	0	4922	33.14	6	2.9262235	0.081	0.84005064	20
soy_OGL_1578	1298	8.3843002	0	2691	32.28	5	3.2208574	0.109	0.79190475	24
soy_OGL_6325	1200	6.7954488	0	9392	32.25	7	5.3137331	0.106	0.91900003	22
soy_OGL_1882	1200	4.2531829	0	3064	32.5	10	4.9506712	0.20999999	0.6867857	8
soy_OGL_441	1300	0.60040933	6.0769229	3247	27.23	11	7.8062592	0.164	0.65176123	6
soy_OGL_5046	1000	2.4656436	0	1316	31.2	6	0.66742569	0.186	0.64061356	9
soy_OGL_443	1000	3.0958874	0	1642	33.3	9	9.1333189	0.146	0.62206757	7
soy_OGL_796	1100	10.399013	18.636364	2284	27.27	9	4.7534523	0.245	0.86510938	23
soy_OGL_3628	1100	3.2073443	23.818182	6001	27	10	10.198528	0.222	0.91983211	29
soy_OGL_3954	1412	10.1953	22.946177	4044	27.19	11	16.991886	0.19400001	0.93005133	4
soy_OGL_3964	1618	10.740408	20.148331	1678	28.43	13	7.2090006	0.20900001	0.9543801	14
soy_OGL_4387	1761	6.6198244	22.316866	1001	31.17	10	17.719301	0.234	0.54094183	23
soy_OGL_5854	1463	8.370719	21.531101	2193	28.09	8	9.8039131	0.208	0.94652742	17
soy_OGL_6832	1506	4.1189404	15.537848	4053	31.87	8	5.0814543	0.23199999	0.81153011	35
soy_OGL_992	1289	9.5245228	9.3095427	1001	31.8	4	2.0967381	0.168	0.77295625	30
soy_OGL_4962	1349	9.1757927	21.497406	4414	31.57	7	11.269644	0.266	0.74236947	23
soy_OGL_6794	1500	8.7524481	10.2	2047	30.93	11	0.57349163	0.169	0.78166687	23
soy_OGL_3743	1600	7.8206534	11.0625	4289	29.62	10	6.3432636	0.153	0.77850646	26
soy_OGL_1208	1997	6.7576227	13.570355	1001	33.5	11	15.979332	0.17900001	0.82343638	27
soy_OGL_1239	1139	8.8961325	29.587357	3477	29.32	9	19.53434	0.23800001	0.75473076	25
soy_OGL_1551	1177	8.9413004	19.286322	8000	31.35	8	16.843077	0.223	0.85866666	30

soy_OGL_5782	1026	14.565392	30.409357	1180	35.57	6	41.542435	0.227	0.84207171	41
soy_OGL_5834	1042	13.562174	19.577736	6535	31.86	8	5.9149113	0.20999999	0.96108812	22
soy_OGL_6962	1100	14.672769	22.09091	2743	32.27	9	8.5872898	0.214	0.93297297	34
soy_OGL_1403	1200	14.041171	15.083333	1092	32	7	5.1393661	0.16	0.82902485	21
soy_OGL_3306	1233	14.446834	17.923763	1336	28.22	11	3.4472017	0.207	0.91690475	18
soy_OGL_4461	1229	6.0359983	28.885273	2001	26.85	8	12.493958	0.208	0.69029957	19
soy_OGL_4009	1338	11.197123	22.421524	4202	27.57	9	3.7158775	0.17	0.80061156	10
soy_OGL_3780	1755	17.509209	15.384615	2667	35.95	9	13.015154	0.139	0.70166522	19
soy_OGL_4818	1300	19.378592	21.692308	1715	33.3	5	7.432395	0.169	0.96097463	16
soy_OGL_5298	1000	23.178028	29	3073	32.7	8	12.565261	0.21799999	0.7130549	25
soy_OGL_6416	1153	10.893449	29.748482	1596	30.87	7	19.070353	0.227	0.54154009	32
soy_OGL_3453	1200	10.348036	31.916666	4272	24.91	12	17.242237	0.20999999	0.59302098	12
soy_OGL_2935	1047	11.020795	22.063038	2001	27.12	8	6.6533151	0.20100001	0.92978859	19
soy_OGL_6618	1312	8.7494211	18.064024	4954	29.03	11	15.759034	0.141	0.94406605	9
soy_OGL_3770	1282	12.172926	22.464899	2001	28	10	8.6127348	0.161	0.72927165	20
soy_OGL_3238	1000	9.3938437	19.5	2367	30.5	6	7.5521336	0.14399999	0.72903937	36
soy_OGL_3787	1473	14.057844	21.249151	1169	29.53	9	10.959369	0.133	0.68752044	12
soy_OGL_4796	1500	13.341439	16.133333	2517	31.46	7	13.280596	0.092	0.91754311	15
soy_OGL_334	1200	10.148783	12.5	6028	31.66	9	4.3387933	0.192	0.87252253	21
soy_OGL_973	1600	13.568718	0	6854	37.43	7	0.83586955	0.16500001	0.76350862	36
soy_OGL_1264	1000	9.6259041	14.3	2078	31.4	8	12.934092	0.278	0.70023686	24
soy_OGL_3755	1600	7.7082705	8.3125	6871	33.31	10	17.958826	0.23800001	0.75833476	22
soy_OGL_3768	1339	12.172926	9.4846897	3466	31.51	9	5.5406032	0.18700001	0.72998714	21
soy_OGL_5388	1210	9.3595705	18.429752	2001	28.26	9	15.551739	0.219	0.70001066	19
soy_OGL_5820	1300	13.314646	0	1859	36.53	5	8.3399916	0.22	0.90585393	23
soy_OGL_6222	1260	10.025082	0	3777	34.6	8	9.6013689	0.23199999	0.87370998	28
soy_OGL_6273	1734	6.1533623	9.9192619	1001	32.41	9	13.75345	0.244	0.93099815	26
soy_OGL_1391	1400	6.9438424	0	4451	35.14	6	7.5768118	0.16599999	0.80906236	32
soy_OGL_1898	1100	9.4963474	24.90909	1366	27.18	9	12.409434	0.264	0.65129548	13
soy_OGL_2646	1111	7.4653587	0	1001	37.17	7	17.586126	0.245	0.54281819	29
soy_OGL_4613	1019	11.743592	16.584887	3456	29.44	10	14.869697	0.259	0.81782353	6

soy_OGL_6647	1734	13.28592	4.4405999	1001	34.83	7	5.4989738	0.189	0.77712232	12
soy_OGL_1919	1060	13.194177	0	2001	34.52	10	6.5860491	0.234	0.56218314	20
soy_OGL_3718	1400	7.065599	2.5714285	4817	32.57	9	8.9217615	0.16500001	0.82625324	27
soy_OGL_3996	1194	11.197123	14.572865	2171	29.56	10	5.0183692	0.18799999	0.82554638	15
soy_OGL_951	1300	13.818732	11.076923	2762	33.15	9	6.8384628	0.207	0.744654	21
soy_OGL_1465	1175	9.5639515	12.340425	2001	34.63	6	16.690109	0.21699999	0.92601126	31
soy_OGL_2960	1500	11.810237	5.7333331	1626	36.8	10	20.885221	0.252	0.86741275	21
soy_OGL_5002	1280	26.60531	6.953125	7788	40.85	10	4.1950397	0.255	0.69657183	25
soy_OGL_5387	1327	9.3595705	17.407686	1309	29.84	10	14.462187	0.19400001	0.69969249	19
soy_OGL_6219	1000	9.9893522	18.5	3805	32.4	6	11.533216	0.236	0.87237531	33
soy_OGL_6543	1110	15.158372	16.126125	3585	35.67	7	7.9943948	0.21799999	0.74878937	32
soy_OGL_6644	1300	6.8812695	0	3123	36.3	13	50.045296	0.22	0.98536861	18
soy_OGL_6933	1604	8.8029718	7.3566084	4046	35.09	13	32.128616	0.167	0.90402865	24
soy_OGL_1166	1600	8.8218307	5.375	2112	33.18	13	20.05587	0.125	0.92523682	19
soy_OGL_2508	1200	7.4874678	9.416667	3851	31.66	12	10.996658	0.192	0.83016086	27
soy_OGL_2647	1000	7.4653587	0	1231	37.9	9	29.888224	0.212	0.54208744	29
soy_OGL_3337	1020	13.069633	12.254902	2846	31.17	8	9.4799671	0.222	0.85977787	27
soy_OGL_5588	1400	5.8065071	6.1428571	2071	32.28	12	27.593086	0.14300001	0.6782797	19
soy_OGL_6539	1138	16.765369	9.0509663	4105	35.5	8	9.8061781	0.146	0.74521691	31
soy_OGL_6564	1595	5.9188476	3.3228841	2156	34.54	12	17.7848	0.127	0.77297622	37
soy_OGL_6661	1203	17.215902	0	1025	35.66	13	2.462868	0.20999999	0.003927212	23
soy_OGL_3804	1027	8.2365665	29.795521	4753	31.84	13	55.144451	0.26699999	0.61820602	12
soy_OGL_4918	1235	16.032492	16.518219	1001	37.08	8	32.786858	0.113	0.77869713	24
soy_OGL_4832	1000	17.834297	21.9	1039	29.8	9	11.213829	0.2	0.97935569	15
soy_OGL_2986	1300	12.551965	0	4300	37.46	6	4.717062	0.1	0.81971061	26
soy_OGL_1015	1500	6.0355277	19	5578	31.53	9	7.3424807	0.191	0.81820703	23
soy_OGL_1054	1242	4.5279164	20.772947	1170	29.87	8	11.730541	0.19599999	0.85789609	27
soy_OGL_2528	1492	7.693583	27.74799	1563	27.94	10	8.7188845	0.25799999	0.77506644	10
soy_OGL_3284	1400	2.9900167	21.071428	2707	32.42	10	2.8949852	0.183	0.96724886	23
soy_OGL_3714	1300	6.9130831	18.153847	9222	31.84	10	7.702312	0.20299999	0.8321116	24
soy_OGL_3719	1244	7.0987005	19.292604	2256	29.01	12	6.3841791	0.228	0.82399571	27

soy_OGL_3956	1453	0.89052546	25.739849	5916	30.62	14	5.2749209	0.169	0.98818076	9
soy_OGL_5464	1723	6.4554529	10.795125	1307	30.7	11	8.6415033	0.153	0.89920306	13
soy_OGL_5565	1200	7.8096585	31.166666	3596	27.5	10	9.9675837	0.236	0.71449423	19
soy_OGL_1811	1100	5.8060555	24.454546	2645	29.45	7	5.7046494	0.25799999	0.78311038	21
soy_OGL_5260	1432	10.745309	14.385475	1001	30.65	9	3.1348195	0.154	0.81622726	15
soy_OGL_7	1100	6.2179899	32.363636	2151	31	10	5.2208538	0.186	0.96642423	13
soy_OGL_218	1300	12.026331	25.615385	2239	31.84	10	5.3283558	0.264	0.82370371	26
soy_OGL_264	1636	9.6228313	35.452324	2001	34.29	11	14.869544	0.249	0.88183075	15
soy_OGL_377	1036	11.275837	26.930502	2001	30.69	9	8.542737	0.198	0.79564416	20
soy_OGL_1005	1400	6.542963	35.07143	2836	29.85	10	11.409721	0.25799999	0.79712349	15
soy_OGL_1082	1494	6.4302845	21.41901	2001	33.13	10	25.787382	0.154	0.89833736	15
soy_OGL_1129	1329	2.3948097	28.14146	2001	27.76	14	19.178694	0.204	0.99064499	12
soy_OGL_1159	1466	8.7633495	31.309687	2001	37.44	13	29.523245	0.161	0.94746643	20
soy_OGL_1407	1180	14.723554	31.271187	4784	31.18	11	4.6703668	0.18700001	0.83343357	18
soy_OGL_1476	1571	5.8344817	15.276894	2001	33.35	11	8.6000824	0.189	0.94331288	23
soy_OGL_1483	1343	5.7135592	27.699181	2823	33.28	10	2.0437708	0.184	0.95532173	20
soy_OGL_1485	1074	7.653698	31.191807	1001	31.93	6	6.2856297	0.25299999	0.95963919	20
soy_OGL_1491	1100	7.4780941	32.272728	6933	33.09	12	26.012293	0.214	0.97210664	23
soy_OGL_1496	1700	8.5456972	17	1369	32.58	11	4.8592935	0.222	0.98102236	20
soy_OGL_1677	1500	9.1770983	26.333334	1985	31.4	11	1.4142847	0.17299999	0.71404195	16
soy_OGL_1734	1200	19.55862	33.916668	3175	35.41	11	8.926178	0.208	0.86630273	13
soy_OGL_2444	1300	6.9880362	27	3279	32.46	10	6.7665086	0.17299999	0.96919233	13
soy_OGL_2456	1774	9.9290686	17.361895	1007	32.46	13	15.074607	0.19599999	0.93796593	15
soy_OGL_2461	1200	6.3500705	29.166666	2331	28.66	11	24.930519	0.23199999	0.92797554	15
soy_OGL_2574	1200	5.1065083	35.916668	1300	30.16	12	2.2242792	0.193	0.67689162	18
soy_OGL_2577	1744	4.9172516	23.165138	2001	37.61	10	3.1794512	0.18099999	0.6756838	18
soy_OGL_2913	1443	10.078434	22.869022	2798	35.68	8	12.170823	0.12	0.97281522	26
soy_OGL_2963	1219	12.075033	26.168991	1263	31.41	11	18.941345	0.21600001	0.86038482	19
soy_OGL_3204	1613	8.2018318	17.48295	2001	34.4	9	5.5541368	0.197	0.69303393	36
soy_OGL_3227	1100	7.2186852	17.272728	1001	33.18	8	6.5541153	0.18099999	0.71773088	41
soy_OGL_3287	1506	3.1094046	28.353254	1711	35.19	9	10.635258	0.252	0.96425349	23

soy_OGL_3600	1100	4.7033892	39.272728	3794	32.09	10	12.964001	0.22499999	0.86543036	24
soy_OGL_3647	1664	4.3527098	21.57452	2508	32.93	9	13.887196	0.233	0.93781996	26
soy_OGL_3664	1625	4.1581578	33.846153	3374	32.18	17	16.131607	0.20999999	0.98111051	13
soy_OGL_3676	1588	6.1510382	32.430729	1001	32.11	13	27.038797	0.154	0.94085407	12
soy_OGL_3696	1621	7.5635667	25.41641	2001	34.85	10	6.1276422	0.25	0.88725913	19
soy_OGL_3723	1144	7.0879893	37.062939	1001	35.75	11	6.569644	0.20100001	0.81688839	26
soy_OGL_4504	1200	8.7601175	29	2052	36.41	12	5.3049798	0.149	0.74271965	31
soy_OGL_4800	1328	12.748341	32.379517	1144	35.09	11	2.7864258	0.155	0.92255533	19
soy_OGL_4802	1400	5.6626678	34.07143	2392	31.07	14	3.6203778	0.29800001	0.93405676	15
soy_OGL_4833	1429	17.834297	26.941917	5481	34.63	11	8.2695618	0.16500001	0.98013812	15
soy_OGL_4876	1100	4.184063	29.818182	3598	30.36	12	4.7164745	0.19400001	0.93085903	25
soy_OGL_4880	1500	3.9014754	32.799999	3938	38.53	14	3.8072455	0.186	0.92482245	19
soy_OGL_4896	1145	9.0506868	34.585152	1001	33.97	11	13.416374	0.18000001	0.89965421	15
soy_OGL_4911	1497	14.910236	30.06012	1001	34.6	12	18.128496	0.161	0.78224021	21
soy_OGL_4943	1667	9.4054356	18.116377	1001	37.97	8	10.114618	0.132	0.75708878	37
soy_OGL_4989	1078	8.6126404	32.560295	2731	30.33	9	3.250526	0.266	0.7055071	26
soy_OGL_5457	1122	6.9202266	38.324421	1562	30.65	12	8.5473814	0.192	0.91184974	17
soy_OGL_5549	1400	7.1524053	30	1100	31.85	13	11.855951	0.204	0.75257474	15
soy_OGL_5589	1435	6.0190163	24.947735	1001	31.14	9	24.153839	0.245	0.67057335	22
soy_OGL_5790	1300	14.27938	33.307693	5893	36.76	5	15.903885	0.37599999	0.85047323	40
soy_OGL_6283	1300	6.8549829	26.846153	1519	36.84	9	8.2519484	0.20200001	0.94028854	29
soy_OGL_6725	2200	8.1198025	18.40909	1672	35.09	12	6.5976377	0.153	0.70939291	10
soy_OGL_2140	1200	6.6979451	19.166666	2361	32.5	11	10.620339	0.175	0.86750919	31
soy_OGL_2454	1200	7.5181608	25	1984	28.83	12	12.027554	0.20200001	0.94098949	15
soy_OGL_3983	1579	4.8896408	18.682711	1001	28.49	13	22.919279	0.155	0.88861841	12
soy_OGL_2714	1000	4.0992632	29.9	2970	28	10	4.3808403	0.222	0.44725525	24
soy_OGL_3962	1300	8.0179386	29.076923	4857	29.07	8	12.10102	0.205	0.97001541	9
soy_OGL_4449	2058	3.2397017	16.277939	1034	32.65	10	9.6343508	0.094999999	0.6515457	13
soy_OGL_355	1025	4.0336118	31.219513	2356	33.46	6	2.5685842	0.236	0.837152	29
soy_OGL_927	1000	11.929564	35.5	3410	31.7	8	3.4833732	0.24600001	0.69988316	24
soy_OGL_1256	1000	11.230193	35.900002	1600	27.8	9	8.51404	0.222	0.71150875	19

soy_OGL_1413	1100	16.339678	39.090908	3488	33.45	7	7.4281936	0.26499999	0.84325087	20
soy_OGL_1741	1050	3.8039601	34.857143	3377	32.57	10	7.7685757	0.207	0.98747504	13
soy_OGL_1792	1302	5.5180402	32.94931	3030	29.26	10	11.215698	0.15899999	0.82879537	11
soy_OGL_2549	1200	3.6582618	36.333332	4501	33.91	11	4.0255795	0.214	0.72761536	22
soy_OGL_3176	1000	11.598832	27	6372	31.7	10	4.4895511	0.22499999	0.64847958	22
soy_OGL_3528	1900	1.9912556	23.157894	3108	34.26	13	12.521164	0.090999998	0.7603997	12
soy_OGL_3824	1813	7.7698202	16.602316	1001	36.34	8	14.156557	0.176	0.55436856	27
soy_OGL_4707	1300	9.078599	29.692308	4323	36.84	11	2.7525873	0.163	0.59908497	33
soy_OGL_4838	1263	5.7022271	26.761679	5128	30	10	14.03543	0.178	0.990116	8
soy_OGL_4839	1100	5.6178126	35.363636	4721	32.63	10	5.2450509	0.199	0.98914361	9
soy_OGL_6272	1100	5.5629621	37.454544	4095	36.81	10	12.760016	0.134	0.92957801	26
soy_OGL_6484	1300	8.5538664	26.76923	1258	32.46	11	9.0119047	0.16599999	0.64501548	18
soy_OGL_3276	1264	1.907052	31.803797	5904	29.58	9	31.662285	0.20900001	0.98883873	14
soy_OGL_3487	1200	5.426621	30.25	2304	29	9	18.006123	0.20900001	0.65184808	21
soy_OGL_3993	1167	11.197123	30.077122	4598	30.33	7	13.403285	0.241	0.82933515	14
soy_OGL_5015	1300	6.9104013	23.692308	2360	31.46	8	8.2807903	0.198	0.67327935	23
soy_OGL_2589	1000	4.7247066	34.700001	3455	28.8	12	12.620179	0.20200001	0.64329022	15
soy_OGL_6793	1500	8.9071083	15.266666	3618	35.93	9	1.4747676	0.093999997	0.77954233	24
soy_OGL_256	1069	12.798174	39.195511	1001	30.96	14	18.711962	0.177	0.86996341	21
soy_OGL_761	1386	4.6026144	29.36508	1001	26.55	12	15.982697	0.17200001	0.9725368	7
soy_OGL_1135	1400	5.9197373	12.785714	1008	32.92	12	1.132512	0.139	0.97881579	25
soy_OGL_1162	1223	8.7535009	27.800491	2171	26.9	13	14.437702	0.18700001	0.93596661	13
soy_OGL_1181	1165	4.3006682	23.862661	4507	28.66	14	11.181979	0.15899999	0.90033925	29
soy_OGL_2134	1491	8.1029568	18.376928	2974	31.12	13	5.6525106	0.13	0.88189489	23
soy_OGL_2905	1560	13.152136	18.910257	1001	31.73	16	3.1047127	0.142	0.98121262	24
soy_OGL_2936	1277	10.919902	15.896633	2001	31.63	8	5.2454028	0.146	0.92751163	19
soy_OGL_3694	1100	7.5635667	35.909092	1448	34.09	15	7.3063464	0.125	0.89152789	18
soy_OGL_3920	1173	9.3006687	30.093777	1170	30.26	10	5.1956143	0.162	0.79778767	20
soy_OGL_4604	1745	5.7093301	12.550143	2001	33.98	12	6.8016148	0.081	0.88210815	10
soy_OGL_6247	1086	7.2568383	20.073666	4025	34.34	9	2.2729661	0.152	0.9047786	26
soy_OGL_6607	1481	8.5314484	13.301823	2001	30.45	13	7.5978522	0.148	0.87190628	17

soy_OGL_6917	1300	8.8029718	24.76923	2412	30.92	11	4.1475959	0.146	0.89316255	23
soy_OGL_193	1300	8.3450031	14.307693	3636	31.69	7	5.0911403	0.107	0.80124694	20
soy_OGL_3799	1387	1.1583297	23.503965	2001	28.4	12	10.722028	0.15800001	0.64491415	14
soy_OGL_4584	1265	1.4350497	18.33992	1001	30.67	7	5.9922099	0.155	0.83764035	18
soy_OGL_197	1313	10.74993	25.590252	1001	35.41	8	6.7512412	0.111	0.80596012	21
soy_OGL_6483	1200	8.5538664	31.5	2858	31.25	11	9.0119047	0.15099999	0.64495909	18
soy_OGL_314	1300	12.282213	29.384615	3485	36.61	14	12.165944	0.088	0.93183786	16
soy_OGL_410	1329	11.870942	31.828442	1221	32.43	14	18.060057	0.11	0.73310232	13
soy_OGL_1438	1091	8.1389084	23.373053	4504	33.18	9	29.941973	0.113	0.89542478	26
soy_OGL_3336	1000	13.069633	23.6	1346	33.9	8	9.4799671	0.13	0.8598479	27
soy_OGL_5021	1082	8.8939037	27.818853	1001	33.73	10	11.233791	0.13500001	0.66846687	26
soy_OGL_5534	1090	11.696812	23.761467	2476	33.85	8	6.1653848	0.12899999	0.78649461	26
soy_OGL_6643	1200	6.8812695	30.75	1027	34.08	8	4.3342295	0.11	0.98372513	18
soy_OGL_4113	1176	10.062737	19.132652	2968	32.05	8	3.1292629	0.149	0.78693146	17
soy_OGL_305	1300	9.2237349	13.615385	4297	31.46	12	4.8681974	0.226	0.9535045	10
soy_OGL_791	1200	8.4274712	11.333333	1976	31.75	8	3.932632	0.229	0.8764531	22
soy_OGL_1065	1900	4.5279164	0	2771	39.36	7	5.5126562	0.20999999	0.86545181	24
soy_OGL_1475	1100	5.8344817	0	3179	38	11	8.6000824	0.296	0.94320923	25
soy_OGL_1851	1115	4.8108158	20.179373	3216	31.39	8	7.4539757	0.229	0.73125327	27
soy_OGL_2448	1000	7.4119039	22.6	4009	29.6	9	12.817232	0.26899999	0.9593147	14
soy_OGL_2555	1100	3.5880075	33	3554	30	8	21.579374	0.32699999	0.7196154	22
soy_OGL_2560	1200	5.5703273	22.583334	2458	30.91	10	6.1119142	0.204	0.70598954	18
soy_OGL_3546	1319	8.9636507	3.2600455	4044	34.42	12	2.9371023	0.234	0.80313063	24
soy_OGL_3927	1800	8.1360826	0	1808	44.33	6	26.604071	0.43399999	0.84512883	21
soy_OGL_4988	1100	8.6126404	11.090909	2891	34.09	9	1.9241153	0.21699999	0.70574933	27
soy_OGL_7012	1016	6.3987536	18.799213	3168	30.9	11	16.545746	0.287	0.98586094	12
soy_OGL_605	1189	6.3866854	21.36249	2538	31.62	9	10.01146	0.322	0.67427677	14
soy_OGL_2399	1000	11.483459	0	2487	36.9	9	8.7448454	0.26300001	0.68632108	15
soy_OGL_6396	1077	6.8150654	23.58403	3127	39.46	9	13.487434	0.49399999	0.46728703	12
soy_OGL_1	1200	5.6447883	21.166666	1946	28.08	12	5.744885	0.20999999	0.98169696	11
soy_OGL_326	1241	11.160845	5.7211924	2578	33.03	11	3.8590367	0.20900001	0.88907921	18

soy_OGL_352	1176	3.5052428	13.010204	2523	30.52	8	6.8790965	0.20100001	0.84455514	29
soy_OGL_1522	1078	6.1372461	0	1001	35.52	8	7.4847178	0.212	0.90541786	37
soy_OGL_1692	1386	6.2621088	0	1001	34.55	11	12.471795	0.184	0.80626595	24
soy_OGL_2109	1134	6.7726569	9.435626	1174	30.86	12	7.3908148	0.241	0.95036185	13
soy_OGL_2503	1196	7.4874678	11.87291	2001	32.77	10	5.5139952	0.20999999	0.83779722	21
soy_OGL_2868	1001	5.7699661	18.581419	1714	26.87	12	8.187376	0.25	0.79374707	18
soy_OGL_2928	1500	7.8788042	0	3634	36	10	5.3508592	0.13699999	0.94649786	19
soy_OGL_4541	1300	5.1131511	8.9230766	3443	31.61	11	7.1182885	0.197	0.78277391	26
soy_OGL_4841	1034	5.557663	10.541586	2260	32.49	12	13.716799	0.226	0.98418713	13
soy_OGL_4859	1100	5.903389	18.636364	3929	31.45	8	3.7823892	0.19400001	0.95224023	19
soy_OGL_5462	1328	6.4554529	0	2001	34.03	14	4.0297756	0.229	0.90388125	12
soy_OGL_6973	1000	4.5740175	0	5146	36.2	9	6.2816501	0.20900001	0.94184047	32
soy_OGL_249	1464	12.616118	17.554646	2289	37.77	13	5.8262506	0.175	0.86520725	19
soy_OGL_651	1300	5.5061193	0	4627	41.53	8	2.4758072	0.19	0.75984401	30
soy_OGL_687	1200	11.121198	18	1007	34	8	8.4118338	0.191	0.80827296	21
soy_OGL_764	1322	3.7208717	16.187595	2001	33.66	12	36.08263	0.20200001	0.98001194	7
soy_OGL_1031	1368	6.3006811	35.672516	1001	40.49	10	9.6499834	0.46200001	0.83161205	28
soy_OGL_1081	1212	8.4925194	39.10891	2001	34.73	14	5.2158365	0.26800001	0.89575332	14
soy_OGL_1097	1000	8.3014231	30.9	2758	30.4	11	4.8634062	0.271	0.93260372	18
soy_OGL_1170	1600	8.7739639	4.75	1642	40.12	7	9.5627394	0.229	0.91156578	27
soy_OGL_1173	1612	8.4058905	22.084368	2001	37.46	9	9.3531704	0.287	0.90889019	26
soy_OGL_1219	1172	6.7576227	28.924915	2173	30.71	13	37.990582	0.214	0.80730385	21
soy_OGL_1546	1236	7.6185937	30.825243	1001	35.76	8	9.4041891	0.39500001	0.8690455	33
soy_OGL_1668	1086	9.1770983	11.786372	1016	36.27	13	11.162999	0.273	0.69931877	12
soy_OGL_1695	1140	6.8353257	22.280703	2466	34.56	9	3.169317	0.205	0.81044441	26
soy_OGL_1731	1291	23.1719	18.048025	2300	36.48	12	7.7043509	0.31200001	0.8586666	18
soy_OGL_1748	1100	13.638608	8.909091	2772	35.9	12	18.105524	0.39399999	0.97997725	16
soy_OGL_1751	1500	13.638608	24.799999	4309	38.8	11	7.1323061	0.25	0.97469807	18
soy_OGL_1862	1000	5.4766021	24	2066	43.9	8	3.135761	0.40700001	0.72135389	34
soy_OGL_2151	1000	6.5589557	0	1269	43.2	10	22.390087	0.31600001	0.85294497	32
soy_OGL_2168	1000	8.3187399	33.400002	2808	34.4	8	19.192303	0.39399999	0.83044034	28

soy_OGL_2179	1035	8.9299202	20.869566	4948	41.44	9	11.669174	0.28200001	0.80627364	25
soy_OGL_2221	1200	3.8589771	10	3423	38.16	9	3.9038873	0.189	0.74312842	25
soy_OGL_2465	2100	5.3914428	0	1015	43	10	15.121598	0.28400001	0.9168182	21
soy_OGL_2593	1062	7.7565408	29.190207	2546	29.37	12	13.338039	0.211	0.63545805	17
soy_OGL_2738	1000	6.8346286	27.1	1175	45.9	9	3.5682023	0.479	0.40669581	18
soy_OGL_3000	1000	8.7826014	0	4225	42.5	7	9.9407654	0.29100001	0.79275745	24
soy_OGL_3165	1007	10.987015	16.881826	1001	35.35	10	3.6752775	0.24600001	0.61472607	16
soy_OGL_3355	2100	11.131104	0	1732	42.85	6	14.171261	0.25400001	0.82445163	17
soy_OGL_3361	1000	13.791044	9.3999996	3331	43.2	10	4.8050876	0.292	0.80774653	14
soy_OGL_3599	1600	4.7033892	13.875	2478	34.5	10	16.911081	0.236	0.86418074	24
soy_OGL_3652	1301	2.0692353	39.200615	2736	44.04	10	10.37935	0.26300001	0.95120633	17
soy_OGL_3670	1200	5.1030955	24.666666	1269	34.16	12	18.436405	0.199	0.96266097	12
soy_OGL_3735	1000	9.0400381	24	4606	35.7	10	9.613905	0.20999999	0.79005152	26
soy_OGL_3745	1200	7.8206534	17.416666	6888	35	10	6.1006684	0.19	0.77716309	26
soy_OGL_3959	1100	0.89052546	37.18182	2606	33	12	3.6662087	0.19499999	0.98039234	9
soy_OGL_4102	1029	12.218921	23.420797	1001	30.02	9	5.8359866	0.24600001	0.68927604	20
soy_OGL_4149	1132	12.139669	17.491165	2906	33.21	10	4.6472626	0.191	0.87292928	25
soy_OGL_4569	1035	4.667098	31.111111	3333	37.68	9	3.3282983	0.38600001	0.82190591	23
soy_OGL_4671	1009	10.891823	24.479683	2022	40.83	7	23.888765	0.29100001	0.65158135	36
soy_OGL_4817	1065	12.994103	21.12676	2001	40.65	8	6.817811	0.40799999	0.95993125	16
soy_OGL_5189	1131	12.841619	0	1788	41.9	7	22.535049	0.23899999	0.94295406	19
soy_OGL_5416	1111	11.581077	24.752476	2020	31.32	12	17.048847	0.221	0.94447404	6
soy_OGL_5445	1189	5.0694704	25.735912	1214	32.88	9	2.8753231	0.227	0.94925714	15
soy_OGL_5468	1300	5.9574423	31.384615	1177	41.46	10	18.746777	0.32300001	0.88146746	24
soy_OGL_5500	1000	4.4117389	9.3000002	4670	35.9	10	11.680937	0.25400001	0.84690803	28
soy_OGL_5580	1151	5.9725876	22.067768	3403	30.66	11	11.834027	0.226	0.68712646	20
soy_OGL_5851	1036	6.2637763	39.864864	2001	31.46	13	14.237758	0.252	0.96485394	8
soy_OGL_6171	1300	10.119716	0	1053	44.76	7	15.184947	0.31299999	0.81308037	16
soy_OGL_6478	1389	9.90658	16.918646	1169	38.94	7	4.3660746	0.361	0.63665879	17
soy_OGL_6501	1206	8.8186426	0	3786	45.77	8	2.7572544	0.31900001	0.68559903	26
soy_OGL_6581	1000	5.2729778	0	3099	42.2	9	16.620815	0.324	0.78569162	33

soy_OGL_6605	1170	8.5314484	20	2555	39.91	9	28.194931	0.229	0.86826313	16
soy_OGL_6619	1162	8.7494211	22.71945	3067	35.11	12	5.8433433	0.25099999	0.94761449	11
soy_OGL_6903	1213	7.0806479	4.7815332	2398	41.63	8	4.7884359	0.35800001	0.87194932	24
soy_OGL_3	1628	5.6447883	13.452088	1001	32.98	12	5.7463531	0.127	0.98025453	11
soy_OGL_258	1000	11.080333	8	2555	34	10	5.7467842	0.245	0.87270206	18
soy_OGL_375	1239	11.080396	13.882163	1001	33.73	9	8.0077686	0.175	0.79820269	18
soy_OGL_735	1064	9.5748711	17.199247	1001	32.33	12	9.5553827	0.204	0.88675737	11
soy_OGL_762	1074	4.3378634	5.9590316	2001	40.68	12	6.8428798	0.243	0.9752081	6
soy_OGL_1180	1013	4.3006682	15.103653	2207	31.49	13	11.854368	0.23199999	0.90044677	29
soy_OGL_1739	1200	15.988809	0	2157	38.83	12	10.669778	0.176	0.87143683	11
soy_OGL_2118	1163	7.0475831	26.99914	2526	31.81	13	9.1705208	0.177	0.92463475	14
soy_OGL_2421	1300	11.967738	9.8461542	2473	37.92	8	2.2041049	0.12800001	0.71658164	28
soy_OGL_2877	1600	4.2962294	8.0625	3544	36.5	11	9.8585176	0.121	0.82057595	14
soy_OGL_3323	1077	11.138845	21.169916	2385	33.33	11	6.2332606	0.18700001	0.88345623	22
soy_OGL_3666	1329	4.1581578	17.381491	2001	31.67	12	17.44483	0.18099999	0.97911161	14
soy_OGL_3668	1611	4.1581578	14.587213	2220	32.15	14	6.8571367	0.14	0.97687507	14
soy_OGL_3737	1041	9.7512617	11.815562	2001	31.89	15	11.135215	0.244	0.78612143	22
soy_OGL_4544	1316	6.9025164	0	3628	36.39	12	3.3901925	0.186	0.7869516	32
soy_OGL_4591	1304	4.07375	0	1001	38.72	13	36.259483	0.206	0.9591043	13
soy_OGL_5252	1305	11.726306	2.8352489	1688	35.7	8	7.2177005	0.176	0.85947531	23
soy_OGL_5318	1218	11.453777	5.0082102	1001	34.89	10	3.5872161	0.16	0.67101222	26
soy_OGL_5397	1226	9.4848547	21.288744	1001	34.17	12	6.8356376	0.15700001	0.71387345	19
soy_OGL_5460	1272	6.9202266	16.273584	2553	32.31	10	26.466839	0.15800001	0.91008919	17
soy_OGL_5606	1200	3.8285015	8.916667	1807	34.08	12	10.480185	0.204	0.6403563	29
soy_OGL_5890	1000	10.038893	12.2	2425	36.4	8	16.84602	0.18099999	0.88575	38
soy_OGL_6529	1000	8.7852011	0	2868	40.4	14	17.278425	0.228	0.73041779	21
soy_OGL_6530	1400	8.7852011	13.5	1368	31.42	14	17.278425	0.17299999	0.73045915	21
soy_OGL_6532	1165	10.313567	25.579399	3089	30.64	16	11.366461	0.189	0.73269445	19
soy_OGL_6587	1000	4.9233418	17.700001	2415	33.7	10	24.704937	0.178	0.7971285	31
soy_OGL_7009	1100	7.8198791	21.09091	2054	32	11	12.594508	0.186	0.97771895	11
soy_OGL_4573	1149	5.7964573	6.0052218	2001	38.12	7	11.951467	0.16599999	0.82618099	22

soy_OGL_3698	1600	7.5635667	12.625	7702	35	9	11.967902	0.16	0.87934333	13
soy_OGL_4454	1423	4.9273844	2.6704147	5236	38.86	12	4.9654565	0.14300001	0.6697638	11
soy_OGL_5	1000	6.3666444	34.400002	3180	31.8	9	29.657707	0.26199999	0.97146058	13
soy_OGL_624	1300	2.9936664	35.46154	3127	44.07	7	3.0009742	0.347	0.70391941	22
soy_OGL_693	1161	11.121198	29.112833	1001	38.58	8	7.9458938	0.17299999	0.81310511	20
soy_OGL_1744	1000	3.8039601	33.200001	2798	38.9	9	24.11062	0.252	0.98211688	16
soy_OGL_1843	1235	5.552063	33.279354	1001	35.7	10	42.675961	0.178	0.7381531	26
soy_OGL_4292	1033	4.9876347	24.007744	1001	42.01	11	5.5107322	0.27900001	0.3862114	25
soy_OGL_5406	1600	9.4738331	16.625	1776	36.93	10	10.134604	0.088	0.74586785	14
soy_OGL_6503	1700	8.8186426	3.2941177	4093	38.52	8	0.41364676	0.082999997	0.68744588	24
soy_OGL_2972	1000	11.973789	17.5	2759	40.1	9	8.3711128	0.127	0.84718722	24
soy_OGL_3443	1137	7.5834217	28.583994	1001	32.54	15	23.640272	0.168	0.5556553	12
soy_OGL_4373	1017	9.312314	9.1445427	2001	36.18	8	7.4432034	0.153	0.52447462	26
soy_OGL_5328	1400	7.7459235	3.6428571	2925	37.85	10	3.6535888	0.111	0.65034145	19
soy_OGL_5560	1668	8.1122494	0	1352	38.96	7	4.7071018	0.068000004	0.72062069	18
soy_OGL_45	1007	10.496729	11.22145	1863	36.94	6	7.9258327	0.138	0.87116927	32
soy_OGL_1126	1376	2.5821292	18.168604	2001	35.9	10	13.232954	0.112	0.98491538	15
soy_OGL_2576	1310	4.9172516	18.931297	1001	33.58	10	3.1794512	0.119	0.67575896	18
soy_OGL_2888	1400	8.9753227	18.857143	1342	37.28	10	8.7312098	0.098999999	0.86744314	21
soy_OGL_4900	1000	9.0506868	22.5	5290	33.7	9	5.4457316	0.162	0.89442039	17
soy_OGL_5976	1400	7.2017879	16.928572	1030	32.92	10	11.571778	0.112	0.62901533	15
soy_OGL_1917	1500	4.4789438	17	2634	29.8	9	17.351849	0.185	0.56568831	17
soy_OGL_3918	1000	9.3006687	24.9	5054	29.6	5	9.0677586	0.221	0.79599744	22
soy_OGL_5341	1125	14.08873	0	2136	38.57	4	16.643496	0.33500001	0.53086585	9
soy_OGL_604	1314	7.0646491	27.092846	2420	28.91	8	3.3526294	0.183	0.67156947	14
soy_OGL_1013	1200	6.0355277	32.833332	7655	31.91	6	13.410166	0.294	0.81403762	19
soy_OGL_5600	1224	4.509737	21.078432	1001	29.73	7	8.9869328	0.183	0.64980841	21
soy_OGL_1640	1497	4.9139419	19.505678	2001	28.99	10	4.7296419	0.139	0.5764842	14
soy_OGL_2397	1369	7.888226	0	1001	40.46	8	10.84018	0.324	0.63245529	8
soy_OGL_6001	1041	3.3781426	0	1001	40.82	6	6.8082323	0.29699999	0.54359996	16
soy_OGL_1280	1161	3.5235167	18.346252	2001	36.86	4	0.93278968	0.242	0.66534621	24

soy_OGL_4289	1568	5.4090037	15.369898	2001	36.03	7	4.3275843	0.197	0.38276285	27
soy_OGL_4297	1100	4.904017	10.909091	2953	39.09	7	6.6400352	0.24699999	0.39398122	26
soy_OGL_1806	1652	4.1940126	0	2734	40.13	6	5.9037504	0.075000003	0.78503573	20
soy_OGL_5422	1400	11.129184	10.285714	2134	27.35	13	5.9495854	0.16500001	0.97202128	13
soy_OGL_5502	1235	5.1489553	15.708502	1001	26.63	12	5.9042754	0.17900001	0.84106195	21
soy_OGL_6223	1000	11.1694	0	1517	32.6	11	4.4697652	0.21600001	0.87465751	27
soy_OGL_1099	1336	8.7746096	0	3203	34.28	13	34.938721	0.139	0.93514979	18
soy_OGL_4672	1000	10.891823	0	3423	38.6	8	19.985018	0.13500001	0.65079087	35
soy_OGL_1032	1408	6.3006811	0	1001	32.74	12	6.8929653	0.15000001	0.83286268	27
soy_OGL_3205	1056	5.7394161	0	1001	31.06	10	4.6948175	0.17900001	0.69486958	36
soy_OGL_3992	1442	11.197123	3.6754508	2001	29.33	14	7.3253236	0.138	0.83459473	12
soy_OGL_6782	1000	11.863941	0	1568	31.2	11	9.1993723	0.208	0.76895648	19
soy_OGL_4490	1000	7.2240438	0	5556	33.4	10	15.315961	0.14399999	0.72478515	29
soy_OGL_6531	1047	10.313567	0	1604	29.6	15	11.135835	0.214	0.73211676	19
soy_OGL_4977	1008	11.98569	0	1018	31.94	9	5.8820705	0.168	0.71863449	17
soy_OGL_974	1000	13.568718	4.3000002	2654	33.6	7	0.83586955	0.16599999	0.76364702	36
soy_OGL_4940	1000	9.3127365	11.2	6045	35.1	10	17.037771	0.114	0.75867885	37
soy_OGL_6300	1089	8.9406195	9.6418734	2016	31.86	10	16.153822	0.17900001	0.95057511	18
soy_OGL_1167	1003	8.8485327	3.4895315	1765	33.89	7	20.118813	0.12899999	0.91955233	22
soy_OGL_2875	1139	7.7406311	4.3898158	5079	32.48	10	15.948177	0.13500001	0.81787312	14
soy_OGL_1564	1121	10.696995	18.911686	4175	34.7	12	47.569935	0.092	0.82232141	25
soy_OGL_4905	1200	9.0506868	14.083333	4529	31.5	12	27.935453	0.139	0.884094	9
soy_OGL_3673	1037	6.1510382	24.879459	3004	25.45	11	6.3381081	0.193	0.94339055	13
soy_OGL_6276	1226	5.2486868	15.008157	1524	29.93	10	7.1459785	0.15700001	0.9318881	26
soy_OGL_363	1300	7.5258417	0	1005	34.69	7	5.3888817	0.14300001	0.82595497	28
soy_OGL_366	1122	7.2482986	0	1001	32.79	13	6.7712941	0.227	0.82148683	22
soy_OGL_1078	1516	7.9827704	0	2001	32.38	14	10.990029	0.153	0.89150882	15
soy_OGL_2114	1300	6.8356886	0	1068	34.07	10	5.252419	0.16500001	0.93655962	15
soy_OGL_2634	1300	7.9126515	0	1890	35.07	11	5.9082398	0.15800001	0.56559443	22
soy_OGL_6940	1032	10.270773	11.24031	2532	30.32	11	4.9588733	0.215	0.90919161	18
soy_OGL_187	1344	5.266325	6.0267859	1001	33.7	11	20.607441	0.142	0.79128289	12

soy_OGL_325	1100	11.160845	0	1378	34.81	11	3.8590367	0.183	0.88913965	18
soy_OGL_3188	1000	8.1508684	0	3578	38.6	10	7.9743629	0.178	0.66787308	23
soy_OGL_5329	1161	7.7459235	0	2975	39.7	11	4.9912586	0.156	0.64890856	18
soy_OGL_5867	1200	9.8030567	0	2026	36.5	12	6.0033016	0.162	0.92308164	28
soy_OGL_6263	1250	4.9055071	0	1001	41.12	8	7.4388008	0.102	0.92094636	26
soy_OGL_6642	1000	6.8812695	0	3447	38.2	8	11.855694	0.182	0.98293531	19
soy_OGL_6827	1100	6.5125389	0	2476	40.09	8	15.405775	0.13500001	0.80950111	35
soy_OGL_1074	1000	7.9827704	0	4774	37.5	10	23.985182	0.183	0.88351935	13
soy_OGL_2630	1368	7.9126515	0	2582	36.18	9	5.818224	0.112	0.56662697	25
soy_OGL_1109	1294	6.0702662	9.8918085	1649	30.37	14	11.051649	0.18000001	0.94699204	17
soy_OGL_1111	1596	5.3702755	4.3859649	1547	36.09	10	3.8661773	0.093000002	0.95364404	10
soy_OGL_3665	1050	4.1581578	12.476191	2001	30.19	13	16.218006	0.19400001	0.97978109	13
soy_OGL_3811	1189	8.2365665	6.1396132	1001	31.79	13	7.5013604	0.16599999	0.59703863	9
soy_OGL_5160	1200	7.2901845	2.3333333	2001	33	8	4.7789049	0.14300001	0.79880327	22
soy_OGL_6598	1351	3.883358	0	2001	35.23	10	12.442206	0.12800001	0.80844307	14
soy_OGL_1068	1100	4.5279164	0	1575	33.45	9	3.7651041	0.141	0.86764902	23
soy_OGL_257	1485	11.080333	0	2001	39.79	11	5.2288685	0.079999998	0.87244153	18
soy_OGL_1212	1100	6.7576227	24	1741	32.18	14	8.3634357	0.156	0.82020617	25
soy_OGL_1462	1092	9.1846943	0	2001	37.27	9	10.279806	0.119	0.92402762	31
soy_OGL_1507	1276	6.1372461	0	2358	38	10	10.095404	0.107	0.9311012	19
soy_OGL_1537	1013	7.7790313	0	1001	40.86	10	10.387392	0.115	0.88279086	38
soy_OGL_4788	1321	13.341439	2.1196063	4494	37.01	11	3.5822015	0.102	0.90352523	12
soy_OGL_4842	1197	6.4237089	12.030075	1364	34.25	11	9.0887232	0.122	0.97792953	15
soy_OGL_5447	1287	5.0694704	14.685315	1001	38.85	11	3.1913702	0.085000001	0.94802296	15
soy_OGL_5906	1000	7.6130018	16.700001	2893	35.2	10	8.6323776	0.145	0.86462247	32
soy_OGL_6267	1300	7.0510011	9.7692308	1076	39.38	13	4.3712845	0.1	0.92465019	28
soy_OGL_6795	1437	8.7524481	7.9331942	1292	34.02	11	1.6788955	0.092	0.78420335	21
soy_OGL_2	1007	5.6447883	2.979146	4400	36.84	13	5.278522	0.168	0.98099393	11
soy_OGL_1738	1100	15.988809	0	3457	40.9	12	10.669778	0.114	0.87138832	11
soy_OGL_6779	1051	10.637803	3.8058991	1001	34.53	16	10.175757	0.171	0.76616222	13
soy_OGL_6998	1000	5.2629671	0	2360	41	10	10.253155	0.107	0.95615411	22

soy_OGL_751	1200	5.8384724	13.25	2530	31.25	8	14.867681	0.15700001	0.9389081	11
soy_OGL_323	1061	10.951405	16.211123	2001	38.64	10	8.6107292	0.106	0.89682156	16
soy_OGL_344	1067	9.9017172	20.993439	4068	36.17	11	32.596199	0.101	0.85295498	26
soy_OGL_740	1043	8.9459286	22.53116	2055	31.16	9	18.278177	0.138	0.90776652	11
soy_OGL_3683	1165	7.5635667	18.62661	1345	36.3	10	15.073077	0.105	0.90506589	15
soy_OGL_5317	1200	12.163104	12.666667	1092	35.58	9	3.9574203	0.101	0.67212802	26
soy_OGL_5322	1018	11.453777	25.83497	2001	35.46	12	14.132495	0.115	0.66322452	25
soy_OGL_408	1016	9.5747099	0	2001	40.15	11	8.7823944	0.117	0.73635137	14
soy_OGL_1660	1000	8.7383938	7.4000001	2285	39.4	12	14.365769	0.118	0.61811084	17
soy_OGL_78	1100	9.6598225	0	4902	37.18	5	15.03484	0.121	0.8004303	26
soy_OGL_2419	1000	11.967738	0	4729	34.7	5	3.1359632	0.132	0.71470129	28
soy_OGL_4965	1000	10.245035	0	4827	32.4	9	6.0729322	0.142	0.73698175	16
soy_OGL_182	1100	5.00559	0	2072	37.72	8	5.2826042	0.133	0.77720559	14
soy_OGL_2216	1000	6.146626	3.5999999	3129	33.2	6	1.0916889	0.131	0.75171101	25
soy_OGL_873	2336	1.0942405	5.0513697	6757	31.29	4	3.5799215	0.15899999	0.59256136	6
soy_OGL_5348	2100	2.9911871	5.7619047	2789	30.38	5	3.8919523	0.112	0.48067588	13
soy_OGL_3815	1900	7.7295065	13.368421	8370	33.15	8	8.1365385	0.16500001	0.56779826	16
soy_OGL_4120	1600	7.7928329	1.75	10935	35.25	3	0.005968305	0.093999997	0.79854077	26
soy_OGL_5684	1400	9.2884445	25.071428	1332	27.07	5	2.4302669	0.221	0.46093488	14
soy_OGL_4310	1297	3.4580755	16.268311	1135	28.45	7	3.2572432	0.16500001	0.40896955	23
soy_OGL_586	1700	1.2381235	5.8235292	6154	29.47	1	1.6640171	0.12899999	0.59897333	7
soy_OGL_1295	1100	0.3178266	19.727272	37082	34	1	3.4559839	0.124	0.48543131	3
soy_OGL_4037	1400	6.9868879	34	2243	24	5	11.180912	0.266	0.44943076	2
soy_OGL_5691	1300	2.4935195	24.307692	5287	26.92	5	4.1028051	0.186	0.41244444	14
soy_OGL_6069	2100	0.49320355	16.761906	6640	31.61	6	9.3747625	0.205	0.036510203	14
soy_OGL_6075	1800	1.3030386	16	15576	30.66	4	4.4355297	0.071000002	0.008841545	3
soy_OGL_6107	1500	0.40301201	16.933332	6766	26.46	3	1.1165984	0.17399999	0.67653191	8
soy_OGL_6124	1749	2.099159	9.4339619	27671	34.76	2	0.14236361	0.18099999	0.73332489	13
soy_OGL_6130	1935	1.449016	3.3591731	10114	32.91	3	2.9582314	0.138	0.75263834	9
soy_OGL_6408	1100	6.8150654	22	14961	29.36	5	2.1947012	0.198	0.49377877	9
soy_OGL_6696	1600	7.2336855	24.75	3503	27.37	6	3.9759839	0.154	0.03812905	6

soy_OGL_4767	1200	5.5016065	17	6349	27.91	4	2.9567723	0.167	0.81225514	5
soy_OGL_5999	1302	3.0450165	15.360983	4808	28.26	5	0.13399482	0.154	0.55501014	19
soy_OGL_2371	1200	1.0815198	18	24319	29.75	3	0.14301617	0.102	0.088032112	5
soy_OGL_3116	1222	5.6704493	19.067102	13788	27.9	5	0.22968972	0.183	0.51833487	12
soy_OGL_5344	1000	2.1644964	20.299999	19349	27.3	2	0.27184433	0.152	0.50684756	6
soy_OGL_6081	1320	1.2300193	25.90909	29492	32.57	2	17.659643	0.114	0.070019737	3
soy_OGL_6374	1000	3.3670716	22.700001	35700	31.9	1	0.001751572	0.119	0.42500001	1
soy_OGL_6062	1300	2.0422838	17.384615	2946	26.61	3	8.6049013	0.142	0.054010205	11
soy_OGL_6490	1130	8.9400244	22.743362	5720	28.84	5	7.3325543	0.18700001	0.65759563	17
soy_OGL_5640	1021	9.2479429	14.593535	14998	31.83	4	2.8148227	0.122	0.54028273	17
soy_OGL_5965	1000	7.5982332	22.9	2465	26.5	7	6.3752666	0.19599999	0.66347957	14
soy_OGL_6142	1554	4.9215565	9.2020588	2001	29.79	5	4.415329	0.104	0.77041745	16
soy_OGL_2859	1200	5.5548873	18.083334	5956	27.66	8	6.9590759	0.17299999	0.71482193	10
soy_OGL_874	1200	1.0942405	20.333334	13893	27.25	4	3.5799215	0.122	0.59276712	6
soy_OGL_2765	1446	3.4072301	19.7787	2089	28.97	4	13.881188	0.075000003	0.32857344	12
soy_OGL_118	1500	0.55841309	10	7477	31.73	2	14.491967	0.366	0.52453995	4
soy_OGL_1312	1700	2.0239863	0	7039	30.76	6	1.6502854	0.171	0.59658229	10
soy_OGL_2761	1434	4.497745	3.2775452	1001	31.86	5	11.007262	0.191	0.33136144	12
soy_OGL_4012	1000	7.0667925	8.8999996	12665	33	4	5.9975424	0.338	0.70399618	15
soy_OGL_4766	1300	5.1086917	18.76923	3572	30	3	20.754265	0.289	0.80970466	6
soy_OGL_5685	1450	9.2884445	2.5517242	3903	33.72	6	6.9866042	0.244	0.44938505	8
soy_OGL_5690	1500	2.4935195	0	3887	31.06	4	1.0342195	0.23999999	0.41380459	14
soy_OGL_452	1200	3.3224196	0	3349	29.33	4	3.7089946	0.206	0.58786488	12
soy_OGL_3415	1200	0.44054028	0	2252	27.75	3	8.3811512	0.23100001	0.53928572	6
soy_OGL_3429	1280	3.4495571	0	1738	31.17	7	15.962694	0.182	0.50983483	7
soy_OGL_4193	1312	4.947145	17.378048	1077	30.41	7	11.812413	0.215	0.20663153	20
soy_OGL_4254	1539	9.2218924	18.97336	1492	29.95	8	11.622464	0.222	0.31116799	10
soy_OGL_2014	1200	3.2330246	0	11148	33.33	4	5.3407445	0.226	0.38024676	9
soy_OGL_2366	2272	8.1184855	3.3450704	6801	36.17	5	2.7939754	0.16599999	0.11955174	10
soy_OGL_2372	1400	1.5388894	14.5	13963	29.78	2	5.1729226	0.14	0.068045869	3
soy_OGL_2781	1340	2.5931845	18.134329	11830	33.13	4	17.769964	0.248	0.23532584	10

soy_OGL_2809	1500	1.2017028	0	23712	34.86	1	2.7027426	0.199	0.36120084	5
soy_OGL_3878	1435	1.2656252	0	2763	31.14	5	8.0981112	0.186	0.2222088	7
soy_OGL_4044	1300	0.43234766	5.8461537	15006	30.69	2	2.2522616	0.17399999	0.40888077	15
soy_OGL_4205	1000	3.197732	22.200001	7479	28.5	5	11.685421	0.236	0.22135265	17
soy_OGL_4740	1043	1.3662759	0	23586	35.66	4	0.43826443	0.33000001	0.11564425	5
soy_OGL_4742	1000	0.54586262	0	15545	31.2	3	4.4792137	0.257	0.3410522	2
soy_OGL_6052	1300	2.2715514	0	10518	34.61	2	5.6450248	0.2	0.16757143	6
soy_OGL_6055	1700	1.8384589	15.176471	8733	30	2	6.6789274	0.21600001	0.14305101	6
soy_OGL_6085	1129	0.40784842	3.4543843	24756	34.54	2	2.1651914	0.22	0.41778553	3
soy_OGL_6388	1189	2.1314628	10.344828	17246	31.87	1	1.4752691	0.121	0.36032829	6
soy_OGL_6391	1500	4.8115296	10.266666	4634	29.66	3	5.6715841	0.156	0.36960164	6
soy_OGL_6706	1000	0.14302784	0	22561	35	2	3.0458267	0.28999999	0.49579689	6
soy_OGL_575	1529	1.7942995	0	3186	29.36	5	5.3792286	0.139	0.16753471	1
soy_OGL_865	1094	5.4632983	11.700183	3078	30.25	4	18.141113	0.206	0.54374218	5
soy_OGL_2042	1200	1.6522079	2.3333333	4722	27.83	4	0.19824664	0.205	0.46616554	9
soy_OGL_2817	1400	0.18303733	9.5	4705	27.21	4	2.3832035	0.178	0.47455674	2
soy_OGL_3891	1058	0.8433677	22.117203	3330	24.95	4	9.5550089	0.219	0.57285088	6
soy_OGL_4033	1298	1.2838418	9.5531588	2001	27.73	6	16.285486	0.183	0.55433464	3
soy_OGL_4197	1066	3.415179	0	9668	32.55	4	0.034008622	0.17200001	0.21211208	19
soy_OGL_4745	1173	1.305691	0	3403	28.13	4	4.9381843	0.221	0.38690889	5
soy_OGL_5069	1000	4.6671739	0	21249	33.6	3	0.40835661	0.14300001	0.55103654	5
soy_OGL_5071	1394	2.1815977	11.119081	5753	27.18	4	3.6873653	0.148	0.54107589	4
soy_OGL_5093	1000	1.3434016	5.0999999	22529	35.3	1	13.632154	0.082000002	0.11381201	1
soy_OGL_5359	1400	2.9911871	0	4045	32.64	3	13.986319	0.13699999	0.50556844	11
soy_OGL_5707	1200	0.030896906	5.25	6645	29.91	2	1.7317685	0.178	0.24531035	2
soy_OGL_6044	1293	1.461244	0	20038	33.33	3	5.6597161	0.061999999	0.20242892	10
soy_OGL_2362	1161	9.6849852	12.919897	1378	29.97	7	17.068718	0.17900001	0.12934862	8
soy_OGL_5055	1300	6.5904026	0	8964	36.15	4	11.274491	0.133	0.6049974	11
soy_OGL_5108	1171	8.890192	8.7105036	2001	31.34	3	11.03127	0.15000001	0.29339838	8
soy_OGL_6054	1500	1.8251891	11.733334	10316	34.26	1	25.699793	0.029999999	0.15398979	6
soy_OGL_4309	1000	3.4580755	20.6	2276	26.3	8	9.3970079	0.205	0.40859985	23

soy_OGL_1326	1959	0.24154867	24.093925	10261	37.46	7	0.5732339	0.27000001	0.62933475	13
soy_OGL_117	1400	0.55841309	21.714285	4356	28.78	2	14.491967	0.153	0.52441025	4
soy_OGL_135	1951	0.20161225	11.686315	8343	31.21	4	5.7600536	0.147	0.62194407	5
soy_OGL_1297	1460	0.3178266	32.876713	30853	35.34	1	3.4559839	0.25299999	0.48565665	3
soy_OGL_1316	1812	0.24154867	13.852098	9526	33.05	3	0.32865816	0.138	0.61780417	14
soy_OGL_1631	1172	3.0774791	27.21843	25032	33.02	3	4.5560207	0.23999999	0.49607831	8
soy_OGL_2052	1776	3.2522252	14.076576	6412	30.63	6	3.7713294	0.081	0.49673864	9
soy_OGL_2378	1179	0.77947766	26.293468	2027	25.27	2	10.15065	0.23899999	0.5579955	2
soy_OGL_3103	1500	1.1479118	26.066668	3636	29.6	5	1.4350877	0.184	0.42493522	5
soy_OGL_3896	1354	0.99678105	18.906942	1303	26.44	3	0.8829391	0.17900001	0.59604621	6
soy_OGL_4758	1347	0.84740651	23.682257	6650	26.8	3	0.37984896	0.213	0.74048263	5
soy_OGL_5123	1119	1.0946937	30.920465	3788	25.29	4	5.5481458	0.24699999	0.41547206	8
soy_OGL_5352	1194	2.9911871	29.480738	10246	28.14	7	3.3538368	0.237	0.49139866	14
soy_OGL_6030	1248	2.5894165	25	11785	31.16	4	2.3842518	0.192	0.36880878	12
soy_OGL_6032	2619	0.25243905	2.978236	8144	37.68	5	0.66960675	0.15800001	0.36036259	9
soy_OGL_6710	1219	0.14302784	33.634125	14980	29.61	6	0.19302216	0.192	0.51446342	2
soy_OGL_172	1200	1.4454956	18.416666	13157	30.58	2	5.7018776	0.115	0.74090451	3
soy_OGL_838	1783	4.8925047	8.3006172	10833	34.82	6	7.6754203	0.046	0.65266228	16
soy_OGL_2026	1300	2.5144458	31.23077	2297	29	3	2.6617048	0.169	0.31186688	3
soy_OGL_2056	1200	3.071409	23.083334	5260	29.66	3	11.486713	0.169	0.56394762	11
soy_OGL_2334	1400	8.9873266	30	4243	30.42	3	5.2179418	0.222	0.33288532	11
soy_OGL_2769	1526	2.8268042	22.542595	4443	31.32	5	8.34902	0.185	0.32201883	13
soy_OGL_2779	1352	0.58232224	28.254438	1001	27.36	9	2.9994814	0.199	0.25042972	7
soy_OGL_4059	1417	1.328638	35.497532	2330	32.03	3	3.4912271	0.206	0.32225946	2
soy_OGL_5680	1300	9.2884445	25.23077	4050	30	5	3.9808526	0.208	0.46545976	14
soy_OGL_6714	1346	2.7221162	25.185736	3792	32.91	1	2.604495	0.162	0.65630072	8
soy_OGL_2776	1447	6.7741928	16.862474	7392	31.51	5	5.9992394	0.077	0.27300134	3
soy_OGL_4728	1019	4.8687081	27.772326	2792	26.59	6	3.5661631	0.199	0.54063928	10
soy_OGL_1642	1400	4.9992714	18.071428	4622	29	9	1.5393933	0.132	0.58039331	16
soy_OGL_3413	1300	2.0739	24.23077	2754	28.76	4	0.90955061	0.134	0.60028112	5
soy_OGL_573	1283	5.1880841	24.395947	1001	27.2	8	6.6053429	0.147	0.29032508	9

soy_OGL_582	1256	0.57824314	25.159235	6482	29.93	3	11.167197	0.068000004	0.57900679	4
soy_OGL_2365	1500	5.1381469	16.133333	2129	30.33	7	6.4716816	0.072999999	0.12469266	8
soy_OGL_3430	1420	3.2008245	24.225351	2001	26.97	8	7.3111596	0.117	0.51637173	8
soy_OGL_4738	1332	1.3662759	20.195196	6957	31.68	3	2.9796147	0.068999998	0.14043137	10
soy_OGL_4781	1100	3.6792157	26	8676	27.81	6	8.0773363	0.153	0.88165462	9
soy_OGL_5413	1326	4.7039185	25.565611	2728	27.97	5	12.065036	0.126	0.82973415	4
soy_OGL_6705	1400	0.14302784	20.5	3563	32.78	2	0.025140388	0.064999998	0.49445003	6
soy_OGL_2433	1100	0.78866917	18.90909	11420	37.09	5	3.6619811	0.32100001	0.74999702	8
soy_OGL_2072	1000	3.5357072	22.200001	2282	26.4	5	0.27462721	0.219	0.65458179	12
soy_OGL_4028	1000	0.4967483	9.1999998	1322	28.3	3	2.7892387	0.242	0.63703078	7
soy_OGL_6016	1300	1.8578844	15	1827	26.84	7	1.4189835	0.215	0.45666838	3
soy_OGL_1998	1500	6.4805918	15.333333	4341	34.33	6	8.7124557	0.23999999	0.445737	17
soy_OGL_5994	1058	0.28763628	27.221172	3096	30.15	7	1.8126264	0.233	0.56875902	12
soy_OGL_113	1000	0.25185886	0	8568	40.9	5	3.6891508	0.26499999	0.497861	3
soy_OGL_114	1100	0.39723444	34	8110	31	1	4.5759964	0.252	0.50756961	4
soy_OGL_137	1000	0.98707271	2.8	11648	32.4	3	1.1761322	0.245	0.63138306	7
soy_OGL_446	1500	5.6306467	0	17133	39.93	2	0.61232048	0.104	0.60493243	12
soy_OGL_596	1000	0.5085156	0	18962	42	2	3.6889629	0.193	0.64071405	8
soy_OGL_1609	1026	0.27222601	21.832359	6154	26.99	1	0.19307427	0.20299999	0.41651785	1
soy_OGL_1612	1200	1.1756582	0	15242	41.91	2	0.068626605	0.22499999	0.33913043	4
soy_OGL_1633	1100	3.0774791	0	11928	39.54	4	8.5009146	0.236	0.50594461	6
soy_OGL_2017	1300	2.1202712	34.23077	4525	31.53	4	1.2226309	0.31099999	0.36453897	6
soy_OGL_2020	1549	1.1950978	0	9823	34.79	4	1.2725915	0.18799999	0.34454545	6
soy_OGL_2021	1000	1.1950978	24.1	5851	32.1	4	1.2725915	0.24600001	0.34438962	6
soy_OGL_2024	1170	1.3061663	0	6532	36.41	4	1.0441139	0.207	0.3284578	6
soy_OGL_2083	1035	2.1464672	15.458938	12154	33.14	6	8.5657616	0.21799999	0.71106344	5
soy_OGL_2348	1565	2.8688939	2.5559106	1806	32.2	4	2.5783103	0.178	0.22697082	8
soy_OGL_2374	1300	1.1965841	0	28828	38.15	2	0.11454418	0.106	0.1115372	1
soy_OGL_2783	1100	2.5931845	9.636364	4358	30.63	6	7.8973269	0.228	0.23395455	10
soy_OGL_2815	1100	0.37861791	8	2256	34.36	3	3.6707091	0.28	0.41530314	6
soy_OGL_3062	1000	3.8372588	17.5	18816	39.7	1	0.26694459	0.20999999	0.31600001	1

soy_OGL_3081	1345	0.30723089	20.594795	2001	31.07	2	12.312259	0.18799999	0.25065175	8
soy_OGL_3420	1551	0.42184711	9.8001289	6492	39.52	2	2.2397165	0.36700001	0.012857143	1
soy_OGL_4026	1500	0.4967483	10.933333	5101	30	3	4.531208	0.22	0.64379233	7
soy_OGL_4754	1166	0.28445095	17.838764	2371	34.73	2	3.6809552	0.22	0.55431449	3
soy_OGL_5074	1261	0.16888668	14.195084	27592	33.78	2	1.3422467	0.14300001	0.50914359	2
soy_OGL_5092	1400	1.092412	0	16451	39.07	2	5.9780822	0.134	0.12948042	2
soy_OGL_5096	1000	0.67571795	0	7270	32.2	4	2.0907872	0.37400001	0.068497404	6
soy_OGL_5101	1300	6.1076021	7.3846154	2370	31.3	3	0.000415085	0.17900001	0.149821	3
soy_OGL_5103	1277	1.7257677	15.740016	3792	32.49	4	0.28134465	0.191	0.18883522	3
soy_OGL_5714	1700	0.97552228	0	13780	37.23	4	3.180768	0.119	0.32415721	1
soy_OGL_6018	1263	1.718382	15.835313	5662	29.92	2	0.71125728	0.18099999	0.4068847	12
soy_OGL_6026	1400	1.5537344	4.0714288	2056	33.21	4	0.74820036	0.192	0.38334185	15
soy_OGL_6047	1100	1.461244	17.90909	3021	32.18	2	5.0487928	0.175	0.19729592	9
soy_OGL_6058	1200	0.82387042	0	17731	41.16	1	0.55265409	0.17200001	0.081280611	4
soy_OGL_6065	1200	2.2850323	0	13211	40.75	3	9.2035656	0.122	0.0517551	11
soy_OGL_6080	1500	1.2300193	26.133333	4492	35.93	1	0.93724853	0.27900001	0.06942603	3
soy_OGL_6082	1092	1.5192883	15.567765	16225	33.79	3	0.024011277	0.235	0.08320237	2
soy_OGL_6100	1336	0.477795	0	14242	37.12	1	0.81927806	0.32300001	0.66266048	13
soy_OGL_6376	1000	0.64646894	24.5	1591	34.2	1	0.000969824	0.26899999	0.076628201	1
soy_OGL_6381	1232	2.4318435	7.9545455	1234	33.84	2	5.1449666	0.18799999	0.24972202	2
soy_OGL_6390	1300	2.1314628	16.461538	5104	33.23	2	1.7552081	0.127	0.36221525	5
soy_OGL_519	1277	2.3637695	5.8731403	2001	32.49	4	5.0272951	0.167	0.42601022	14
soy_OGL_1626	1138	2.8390529	0	2001	34.88	1	11.110225	0.189	0.47767717	7
soy_OGL_2030	1500	0.99519539	0	6111	34.33	2	10.61917	0.068999998	0.2667987	2
soy_OGL_2047	1210	1.2741382	14.628099	2001	29	3	0.001358077	0.17299999	0.48588178	11
soy_OGL_3071	1456	1.0271347	0	1001	31.73	6	0.58744925	0.153	0.20639874	8
soy_OGL_3091	1279	0.6157763	15.1681	11704	35.18	2	0.74965876	0.068999998	0.34152523	7
soy_OGL_3882	1200	0.023634408	0	4901	32.25	1	0.006973176	0.16599999	0.079905577	1
soy_OGL_4065	1000	0.90285671	0	11437	36	6	0.68014628	0.189	0.5114584	17
soy_OGL_4165	1300	0.7456544	13.923077	1677	30.46	4	6.3089485	0.16	0.214959	3
soy_OGL_5048	1077	6.5904026	5.6638813	2365	33.42	2	5.3573589	0.204	0.61946535	8

soy_OGL_5061	1000	3.1510634	0	8312	32.5	5	8.0112991	0.215	0.58358222	3
soy_OGL_5075	1078	2.9883757	0	1001	37.66	2	0.048508465	0.189	0.4610261	2
soy_OGL_5090	1400	1.4403361	3.5	2361	35.14	1	5.4210734	0.097000003	0.15197128	1
soy_OGL_6089	1000	0.69722927	0	6145	35.8	2	5.961226	0.21600001	0.55825078	6
soy_OGL_6091	1100	0.69722927	6.818182	12110	34.18	2	5.961226	0.152	0.55879462	6
soy_OGL_574	1200	0.015745375	3.9166667	3341	44	4	4.3675389	0.192	0.010657658	1
soy_OGL_2032	1362	1.7172174	22.246696	8093	32.15	3	21.232882	0.167	0.3001065	3
soy_OGL_2373	1321	2.2550869	0	1001	40.19	5	10.06756	0.16	0.055476099	2
soy_OGL_2778	1100	0.728338	19	1631	31.54	7	7.4194317	0.23800001	0.25334615	4
soy_OGL_3876	1389	2.5121698	21.454283	1060	35.56	4	5.2481794	0.206	0.22760086	5
soy_OGL_3886	1200	0.027143367	24.833334	2432	33.41	4	6.0680461	0.20200001	0.39806661	8
soy_OGL_4729	1193	4.8687081	23.637888	5992	31.43	5	3.2369969	0.185	0.54041874	10
soy_OGL_5723	1601	0.11220059	19.42536	1001	37.35	3	13.408423	0.228	0.51702607	2
soy_OGL_6071	1298	1.2072753	28.043144	3706	33.66	2	5.9450364	0.13	0.013642959	5
soy_OGL_6125	1129	2.099159	24.712135	24966	40.21	3	0.11022708	0.23800001	0.73340386	13
soy_OGL_2028	1000	0.84385622	0	20123	40.8	1	30.472464	0.059999999	0.28555843	1
soy_OGL_3104	1131	1.1479118	22.369585	2573	30.06	4	15.048862	0.13500001	0.43294472	4
soy_OGL_5066	1400	5.2891674	0	4760	37.85	5	1.9739037	0.141	0.56504703	6
soy_OGL_6068	1000	1.6618187	0	9142	40	3	24.153093	0.14300001	0.042709183	12
soy_OGL_3419	1326	0.38842908	17.797888	2386	22.02	9	6.4923463	0.169	0.52619696	6
soy_OGL_4262	1149	2.3084447	23.672758	2001	24.28	6	6.1241779	0.153	0.33492392	12
soy_OGL_2011	1016	4.4198856	0	2867	31.39	4	10.224638	0.186	0.38438591	10
soy_OGL_6117	1100	2.2216065	12	2081	27.18	3	0.73669559	0.15800001	0.72675735	13
soy_OGL_1652	1300	8.6515789	0	8948	33	8	4.3491969	0.090999998	0.60230827	19
soy_OGL_3471	1062	8.2846069	0	5797	32.76	4	1.9134001	0.13600001	0.63283294	26
soy_OGL_4305	1300	4.4642582	0	4391	32.38	8	4.356883	0.111	0.40024331	26
soy_OGL_146	1300	3.6264029	0	12410	32.84	5	2.4536507	0.102	0.67420578	12
soy_OGL_170	1200	2.0941939	9.833333	6613	27.75	3	0.088223323	0.149	0.72946376	9
soy_OGL_3885	1000	0.027143367	5.6999998	19198	30	3	3.2220836	0.090000004	0.38638157	8
soy_OGL_4750	1549	1.3206984	1.8076178	1431	28.46	5	2.9404655	0.114	0.40466917	5
soy_OGL_6694	1600	7.2336855	0	1911	30.81	6	3.9451084	0.063000001	0.037327457	6

soy_OGL_3881	1104	3.3834631	0	1001	30.97	4	6.9910631	0.11	0.1929279	3
soy_OGL_5706	1000	0.31566539	0	7775	29.1	3	3.0889552	0.114	0.25559005	2
soy_OGL_5642	1400	9.2479429	0	4119	33.28	4	5.4106827	0.092	0.53986591	17
soy_OGL_451	1182	4.6825724	20.558376	3896	29.01	5	2.9671957	0.113	0.58830714	13
soy_OGL_130	1000	1.5132793	0	6401	37.2	2	0.88605857	0.124	0.59695905	9
soy_OGL_152	1239	4.8982654	0	4278	35.91	1	0.15238471	0.103	0.68448925	13
soy_OGL_2040	1300	0.94065005	2.8461537	1574	33.76	2	14.193683	0.093000002	0.36670446	7
soy_OGL_5076	1200	1.9288176	0	2741	36.41	1	1.5730382	0.097999997	0.45995823	3
soy_OGL_6104	1083	0.42877111	0	2298	34.62	2	0.47203743	0.138	0.6696263	11
soy_OGL_6129	1100	1.3637165	4.3636365	6086	32.81	5	2.024009	0.162	0.74672264	6
soy_OGL_6038	1500	0.96124917	0	2118	39.6	4	9.6470222	0.050999999	0.26041836	2
soy_OGL_2048	1113	2.9409354	0	2895	33.24	3	2.9748011	0.132	0.48962238	11
soy_OGL_2827	1200	2.0155141	0	3178	30.91	4	3.0324292	0.138	0.58784044	5
soy_OGL_3895	1100	0.99678105	0	8854	35.54	3	0.8829391	0.096000001	0.59557462	6
soy_OGL_5722	1000	4.7354045	5.5	6130	35.1	1	0.035494115	0.097999997	0.48133597	7
soy_OGL_6037	1100	1.5279608	18.818182	6424	31.81	2	0.23171447	0.068000004	0.30795917	3
soy_OGL_136	1100	0.98707271	0	8948	32.63	3	1.1761322	0.088	0.6313144	7
soy_OGL_584	1000	0.87742698	0	8510	31.4	5	4.5062675	0.12899999	0.59259349	9
soy_OGL_587	1000	1.3118454	0	2603	32.3	1	0.15962952	0.125	0.60126048	7
soy_OGL_3092	1000	0.6157763	7.5	7000	30.7	5	15.069901	0.112	0.34447089	7
soy_OGL_3106	1059	1.1353548	0	4688	32.38	4	4.3316379	0.117	0.46714368	3
soy_OGL_4060	1000	0.13326561	4.6999998	4242	31.6	4	3.8728414	0.131	0.12707308	1
soy_OGL_5072	1100	2.1815977	0	3497	31.36	3	0.12916583	0.125	0.53562665	3
soy_OGL_5112	1000	3.8103819	0	5398	31.5	6	1.7200029	0.118	0.34186888	11
soy_OGL_145	1000	3.6625237	18.6	2915	30.7	4	5.0200315	0.138	0.67224723	12
soy_OGL_4070	1004	5.8943801	6.5737052	5866	34.86	4	2.7261918	0.112	0.52037114	18
soy_OGL_4748	1600	1.3206984	0	5135	37.5	4	5.1554308	0.003	0.39219961	7
soy_OGL_5732	1051	0.27211389	12.369172	5628	35.39	3	11.827112	0.105	0.64326429	8
soy_OGL_6719	1200	2.7221162	0	9268	38.83	1	6.7336202	0.039999999	0.6660111	10
soy_OGL_5357	1200	2.9911871	0	8031	36.41	5	10.296455	0.048	0.49580759	14
soy_OGL_6384	1000	1.4019195	0	3192	38.1	2	3.9759934	0.061999999	0.2824806	3

soy_OGL_5475	1093	4.9895315	30.283623	4776	31.38	7	35.889202	0.147	0.86957085	28
soy_OGL_1995	1091	6.3444653	31.347387	1001	27.95	10	25.927839	0.20999999	0.45108441	19
soy_OGL_2567	1452	7.0306044	21.00551	3265	30.37	10	35.889072	0.12	0.69066781	20
soy_OGL_2988	1200	10.917853	18.166666	9124	33.66	7	15.636501	0.097999997	0.8129319	27
soy_OGL_5653	1200	7.9065285	24.083334	2379	28.66	10	24.290611	0.132	0.51537162	20
soy_OGL_3806	1700	8.2365665	6.5882354	1510	38.76	9	56.725891	0.155	0.61207724	12
soy_OGL_2186	1088	10.96957	11.121324	6825	35.84	5	12.632515	0.096000001	0.79350054	30
soy_OGL_6244	1400	5.7421308	21	4954	31.92	6	5.6032743	0.138	0.90093982	19
soy_OGL_90	1038	7.4370308	27.938343	1001	36.51	5	4.7828898	0.17299999	0.77434546	27
soy_OGL_1682	1100	9.1770983	36.727272	4372	31.63	10	8.4272614	0.19	0.72553104	16
soy_OGL_1978	1147	9.7761993	30.078466	1001	32.51	10	10.978649	0.169	0.47860888	25
soy_OGL_3998	1152	11.197123	26.649305	5617	33.33	9	10.767996	0.154	0.82392305	16
soy_OGL_4498	1000	8.7435341	32.599998	3392	37.3	5	23.646412	0.2	0.73761213	35
soy_OGL_5389	1400	9.3595705	29.5	3311	35.5	9	15.551739	0.155	0.70007366	19
soy_OGL_2302	1400	5.7557502	24.5	1123	33.5	10	2.5569127	0.13500001	0.58184403	16
soy_OGL_2601	1127	3.365438	35.936115	1446	30.16	10	24.525871	0.20200001	0.62274033	14
soy_OGL_2704	1200	3.3485649	32.25	1432	28.91	10	4.7229114	0.175	0.45686364	24
soy_OGL_2744	2000	5.5999656	14.75	3539	34.15	11	11.667296	0.108	0.39640209	20
soy_OGL_3839	1400	7.1014504	33.642857	3881	32.28	8	9.2016029	0.23899999	0.5343262	21
soy_OGL_4187	1524	6.9757385	26.115486	1898	32.28	13	13.913801	0.124	0.19416821	20
soy_OGL_5927	1000	28.940582	37.900002	2902	40.5	5	4.2328305	0.082000002	0.75337243	15
soy_OGL_1867	1000	5.0498676	32.099998	2141	35.9	5	14.265493	0.14	0.71424025	28
soy_OGL_4186	1400	6.9757385	36.5	3049	31.57	14	13.33756	0.14	0.19340725	19
soy_OGL_5572	1068	8.6886683	30.524345	4855	33.61	7	7.5166168	0.134	0.70115066	22
soy_OGL_5969	1500	7.5982332	39.799999	2862	36.73	6	10.82803	0.222	0.6602245	16
soy_OGL_1072	1000	7.9827704	35.900002	3924	35.3	10	10.165655	0.125	0.88004768	15
soy_OGL_1393	1100	6.9438424	23.636364	2249	36	5	3.9326344	0.122	0.80986869	33
soy_OGL_2559	1200	5.2298207	39.666668	1566	31.25	15	41.93774	0.104	0.70829022	17
soy_OGL_3183	1000	12.003224	28.700001	1299	30.4	8	11.887067	0.138	0.65749717	22
soy_OGL_3249	1100	9.1212559	38	1086	36	10	21.348293	0.102	0.74280447	24
soy_OGL_3277	1000	1.907052	36.5	3004	31.3	9	31.662285	0.14399999	0.9887051	14

soy_OGL_5273	1000	7.5360255	34	4518	32.3	12	33.546188	0.146	0.7847988	17
soy_OGL_6228	1200	8.562501	28.5	1031	35.08	11	41.449989	0.079999998	0.88124055	18
soy_OGL_4448	1070	5.3789964	33.644859	2001	31.12	11	4.3659368	0.13500001	0.64706784	14
soy_OGL_6242	1010	5.4170856	26.633663	1001	31.28	5	5.9789271	0.14300001	0.90061927	19
soy_OGL_1847	1000	5.552063	35.200001	6330	32.9	10	30.180906	0.114	0.73628247	26
soy_OGL_2720	1063	6.366055	34.524929	1001	31.51	10	13.903862	0.115	0.43386713	21
soy_OGL_4228	1218	4.0722065	31.691298	2087	31.85	12	17.832321	0.101	0.26739028	30
soy_OGL_6891	1200	7.0806479	25.75	1791	37.58	5	57.758587	0.17399999	0.86629277	25
soy_OGL_3044	1100	12.289925	34.272728	2216	33.45	7	1.2276733	0.25	0.673783	11
soy_OGL_3184	1148	10.778469	14.02439	6963	36.49	10	23.796827	0.116	0.66173261	23
soy_OGL_3688	1000	7.5635667	25	4070	34.8	7	9.0628195	0.146	0.90199143	15
soy_OGL_3681	1018	6.1510382	32.318272	3823	34.87	7	18.807613	0.132	0.93335623	11
soy_OGL_5379	1000	8.9067116	26.700001	2686	39.3	9	8.4556255	0.097999997	0.67759967	13
soy_OGL_4090	1300	12.218921	23.461538	5258	30.69	8	8.3381214	0.20999999	0.64516228	12
soy_OGL_4318	1349	2.6951132	25.50037	2079	28.68	8	25.781862	0.171	0.4240593	22
soy_OGL_5149	1400	8.7838383	15.928572	2761	30.92	4	2.8828597	0.14399999	0.77075356	20
soy_OGL_5760	1400	14.102677	18.5	5082	30.71	7	5.0145154	0.14300001	0.7731806	13
soy_OGL_6648	1500	13.28592	14.866667	6535	31.66	6	2.3051341	0.13699999	0.76949638	12
soy_OGL_4218	1200	4.8260355	22	3827	30.33	8	19.396837	0.189	0.25863665	32
soy_OGL_4314	1095	2.3265874	37.168949	2882	25.11	10	28.628353	0.22499999	0.41588771	19
soy_OGL_3802	1300	8.0413237	24.538462	5124	28.69	7	26.375441	0.191	0.62417597	12
soy_OGL_6678	1489	8.8698769	15.648086	1001	32.63	6	0.3265526	0.15000001	0.016640438	28
soy_OGL_1975	1100	11.715036	29.818182	7126	31.18	5	4.7570877	0.233	0.48499352	27
soy_OGL_6165	1300	6.4251461	27.538462	8102	32.3	6	37.154495	0.178	0.8031559	18
soy_OGL_6469	1100	5.7027311	27.90909	8843	27.72	7	19.716688	0.131	0.60892594	11
soy_OGL_2005	1500	5.0966048	28.133333	1445	31.73	4	47.936932	0.048999999	0.4362857	11
soy_OGL_3369	1100	11.584485	26.90909	9150	29.18	8	27.428143	0.102	0.77928108	10
soy_OGL_3083	1150	0.30723089	34	3584	29.65	2	55.348843	0.057	0.2572585	9
soy_OGL_6663	1111	12.137495	22.412241	1679	29.52	9	4.1667647	0.24699999	0.006320986	25
soy_OGL_550	1200	18.677822	2.4166667	6509	37.91	8	8.705574	0.206	0.33512613	17
soy_OGL_2552	1400	3.931226	13.142858	6267	32.57	9	31.086432	0.114	0.72088462	22

soy_OGL_528	1421	11.005226	15.974666	1001	30.11	7	8.6256666	0.147	0.38622427	11
soy_OGL_2754	1563	7.8969092	21.113243	6415	30.13	11	23.04159	0.17399999	0.36412588	8
soy_OGL_4184	1167	8.7795687	23.050556	5280	29.99	10	6.873323	0.183	0.18800052	19
soy_OGL_1982	1000	9.5797806	0	2106	41.4	4	49.224926	0.199	0.47635713	25
soy_OGL_6657	1289	15.964157	18.541506	1001	33.66	7	6.3346801	0.147	0.1687928	19
soy_OGL_3880	1000	1.4084551	2.8	7307	40.8	8	80.576248	0.207	0.20524463	5
soy_OGL_2606	1200	7.2494159	31.25	3580	29	9	2.6460655	0.19599999	0.60404193	14
soy_OGL_2702	1522	3.3123655	22.207621	2452	33.96	7	10.073252	0.161	0.46450001	21
soy_OGL_2952	1071	9.0759773	26.890757	9671	31.18	4	8.4233713	0.249	0.88617146	16
soy_OGL_4610	1400	6.7095437	27.785715	5754	32.92	7	3.045388	0.171	0.83352286	8
soy_OGL_570	1091	5.1880841	38.863426	2001	26.03	13	9.3539095	0.249	0.29605243	12
soy_OGL_4188	1400	5.4690461	21.5	1170	30.71	11	9.4516296	0.15000001	0.19895479	20
soy_OGL_5998	1870	3.0450165	23.582888	2172	39.19	7	0.17699665	0.197	0.55625361	19
soy_OGL_6356	1233	5.3133087	32.603405	4011	32.27	4	1.1067978	0.16	0.86804253	10
soy_OGL_1622	1000	1.5494736	35.900002	7149	31.4	5	6.073246	0.12899999	0.41454932	7
soy_OGL_2016	1000	3.4557509	32.799999	8829	30.7	4	3.3257394	0.132	0.37857142	10
soy_OGL_3089	1000	1.3628819	37.099998	2852	29	3	16.117872	0.145	0.29162791	5
soy_OGL_3901	1200	9.3006687	21.416666	14743	35.5	3	14.430862	0.13600001	0.7588225	13
soy_OGL_4020	1009	7.0667925	30.921705	11490	32.11	3	2.2070997	0.17399999	0.69582659	16
soy_OGL_4052	1005	0.29615524	38.805969	8482	33.03	5	1.6782029	0.13699999	0.3896654	13
soy_OGL_4071	1046	5.8943801	28.011473	6999	34.03	4	2.7261918	0.178	0.52045375	18
soy_OGL_4208	1400	3.107893	28.285715	2914	27.42	11	17.104668	0.15099999	0.2372068	13
soy_OGL_5097	1050	3.6329696	34.952381	13832	34.38	3	0.8635394	0.116	0.07308998	6
soy_OGL_6051	1300	2.2715514	30	1318	32.46	3	4.4625711	0.103	0.16804081	6
soy_OGL_6389	1094	2.1314628	33.180988	3910	33.45	2	1.7552081	0.126	0.36217034	5
soy_OGL_6409	1300	6.8150654	28.846153	13361	35.76	5	2.1947012	0.141	0.4938314	9
soy_OGL_3395	1100	4.2915759	20.09091	7288	33.18	5	3.1401823	0.138	0.69695389	18
soy_OGL_3426	1200	2.36814	30.75	4952	28.33	10	5.7736464	0.16599999	0.50649589	6
soy_OGL_460	1252	3.9802828	36.661343	1154	34.02	5	17.539118	0.20299999	0.55652469	19
soy_OGL_1687	1470	9.1770983	26.32653	3231	33.87	8	29.928612	0.097000003	0.73879933	9
soy_OGL_2394	1400	7.888226	36	1904	35.78	8	4.357058	0.15700001	0.62814265	10

soy_OGL_2597	1200	3.365438	35	2650	30.66	8	28.147635	0.145	0.62771326	16
soy_OGL_3519	1200	1.9912556	38.833332	7510	33.16	7	9.4584799	0.21699999	0.74821448	17
soy_OGL_3864	1400	9.8148384	31.642857	3186	33	7	10.763212	0.24600001	0.25802147	21
soy_OGL_4083	1189	7.4914689	35.323803	2001	28.17	7	18.137709	0.178	0.56939638	12
soy_OGL_4226	1200	4.0722065	39.166668	3188	35.08	9	25.866713	0.163	0.26483539	30
soy_OGL_5647	1214	8.8125191	31.21911	4346	35.83	6	9.3715401	0.13699999	0.53604925	17
soy_OGL_6399	1300	6.8150654	37.846153	2070	35.15	7	14.941936	0.149	0.47098023	12
soy_OGL_6466	1300	5.5870967	32.76923	3042	32.46	9	5.2720952	0.13600001	0.60420603	16
soy_OGL_2335	1900	8.9873266	17.421053	1141	36.84	4	6.2002711	0.094999999	0.33241743	11
soy_OGL_3088	1800	1.2103244	27.777779	5345	35.94	7	6.9922061	0.026000001	0.28778306	5
soy_OGL_3386	1200	5.6634336	27.166666	10544	40.75	4	4.7871318	0.043000001	0.71012443	17
soy_OGL_3409	2100	2.4898665	24.666666	4012	38.14	3	19.103653	0.12	0.61250693	5
soy_OGL_3434	1058	7.1049542	35.066162	2392	31.56	4	8.6184397	0.213	0.54061925	12
soy_OGL_4307	1400	3.4580755	25.428572	5740	35.64	8	9.3970079	0.079999998	0.40827599	23
soy_OGL_4374	1009	6.5817218	35.282459	8572	35.57	5	25.257736	0.116	0.52713984	25
soy_OGL_6690	1400	6.1426415	33.285713	5331	33.92	9	17.748732	0.138	0.025744503	17
soy_OGL_2329	1300	8.2941523	20.538462	1466	33.38	5	2.4319007	0.11	0.51683486	14
soy_OGL_2301	1300	6.2270303	17.538462	1406	30.76	7	4.9788089	0.123	0.58544034	16
soy_OGL_5992	1000	0.28763628	38	10342	32.5	6	1.0639614	0.114	0.56925511	11
soy_OGL_5366	1200	8.8820086	17.333334	5640	31.58	7	2.5822415	0.11	0.61966449	15
soy_OGL_1338	1500	2.2828174	21.866667	6980	31.66	8	7.2052855	0.096000001	0.70413554	10
soy_OGL_2771	1100	0.64794296	33.727272	5462	30.63	7	2.3828759	0.097999997	0.3071993	6
soy_OGL_4031	1128	0.4967483	31.028368	5903	29.69	7	9.5697088	0.116	0.63547969	7
soy_OGL_4168	1000	1.2871063	39.5	5141	31	1	7.3999209	0.083999999	0.16752681	1
soy_OGL_5152	1100	4.1436477	22.181818	11135	32.09	4	3.7551308	0.115	0.77379334	19
soy_OGL_5713	1200	0.88965857	31.75	10309	36.25	1	0.39395815	0	0.27441451	1
soy_OGL_1281	1061	3.5235167	29.594723	1747	31.76	5	0.74623173	0.119	0.66507894	21
soy_OGL_2080	1346	1.6845587	39.895988	1659	34.02	8	60.273689	0.034000002	0.70396543	8
soy_OGL_4722	1000	5.8001513	29.9	1266	33.2	6	3.4519484	0.123	0.56529415	23
soy_OGL_2338	1100	11.063083	27	2857	30.63	6	2.3017642	0.119	0.32119265	12
soy_OGL_2591	1100	4.8519325	26.818182	10997	33.09	8	12.876298	0.085000001	0.64014333	19

soy_OGL_4274	1089	5.724844	29.752066	1796	29.47	7	7.7076349	0.146	0.36062908	19
soy_OGL_5414	1095	4.7039185	32.328766	4516	31.5	3	18.060522	0.088	0.83064318	4
soy_OGL_5678	1200	9.7722187	28.5	2084	30	5	6.002212	0.125	0.47071648	13
soy_OGL_4264	1400	2.6787946	29.071428	2475	31	10	10.912324	0.257	0.34008276	15
soy_OGL_6404	1100	6.8150654	24.454546	1150	30.45	7	3.8562994	0.236	0.47733238	16
soy_OGL_4087	1170	7.4914689	9.6581192	1001	32.99	5	16.549639	0.207	0.57503408	11
soy_OGL_5995	1472	0.28763628	23.913044	1519	33.55	7	1.8126264	0.168	0.56867856	12
soy_OGL_623	1800	2.9936664	0	4535	38.11	7	6.1957598	0.056000002	0.70296645	21
soy_OGL_1577	1000	8.3843002	14.4	8841	38.8	6	24.339819	0.19400001	0.79372025	25
soy_OGL_1638	1500	4.9139419	21.866667	2249	37.93	6	4.3526478	0.234	0.57001996	11
soy_OGL_3445	1200	7.2829056	18.5	5198	32.33	12	27.129391	0.185	0.56930649	11
soy_OGL_3464	1000	7.6505504	32.299999	4590	36.8	6	19.756832	0.27700001	0.6241501	19
soy_OGL_4271	1552	5.2203422	31.121134	5054	42.52	7	4.6838021	0.31200001	0.35411704	21
soy_OGL_6475	1100	8.1601791	28	2133	36.9	6	3.2367179	0.198	0.6334545	17
soy_OGL_265	1200	6.2561297	3	7758	41.5	6	9.9848576	0.090999998	0.88635314	18
soy_OGL_4233	1126	4.5469155	0	3076	38.98	7	14.361069	0.14300001	0.27252924	29
soy_OGL_2053	1261	1.6451907	21.173672	1001	34.97	4	17.808405	0.198	0.55808669	10
soy_OGL_2071	1341	4.3679075	23.34079	1474	36.39	3	2.1961107	0.171	0.64281249	11
soy_OGL_2367	1210	5.8270121	10.330579	2001	39.91	2	0.35439047	0.2	0.11565138	10
soy_OGL_2816	1500	0.18303733	32.200001	2025	35.53	4	0.24846426	0.15800001	0.463943	2
soy_OGL_4032	1300	0.4967483	18.538462	10294	37.15	5	13.611153	0.117	0.62611157	7
soy_OGL_4062	1075	0.41162741	35.348839	7119	33.3	5	8.8907537	0.18700001	0.06165427	3
soy_OGL_4167	1300	1.4769267	29	4904	37.76	2	1.3663538	0.088	0.20774132	3
soy_OGL_5117	1400	5.8165097	26.357143	3149	34.14	4	14.901487	0.19599999	0.37199453	11
soy_OGL_6127	1000	1.5205039	34.099998	8665	34.5	2	2.9032104	0.23	0.74194682	12
soy_OGL_448	1193	5.2086315	0	2001	41.49	4	7.634007	0.141	0.60112613	13
soy_OGL_5729	1200	1.3011107	18.75	3212	38.08	3	3.9451611	0.097000003	0.62341034	5
soy_OGL_6064	1000	2.0422838	12.6	2611	39.3	4	6.9026737	0.121	0.052306123	11
soy_OGL_2526	1000	7.693583	38.5	4120	31.5	7	18.394766	0.23899999	0.78260839	5
soy_OGL_6405	1000	6.8150654	14.7	3196	38.1	8	39.383381	0.205	0.4781861	16
soy_OGL_121	1600	0.78663576	36.6875	2581	35.5	3	73.187958	0.191	0.56101149	6

soy_OGL_541	1018	10.749329	24.852652	5547	39.19	6	5.4183969	0.214	0.36031333	18
soy_OGL_2436	1506	0.78866917	34.063744	13750	40.9	5	7.5610828	0.211	0.75405812	6
soy_OGL_2717	1000	4.0992632	18.299999	7081	39.1	7	7.3302622	0.139	0.44568881	24
soy_OGL_3101	1100	1.1479118	33.272728	1708	38.18	6	1.5711184	0.199	0.40860975	6
soy_OGL_4397	1000	8.2008438	24.9	6589	39.5	5	2.9729493	0.15899999	0.55994993	22
soy_OGL_6689	1100	6.1426415	32	1083	35.09	7	22.27211	0.121	0.025286138	17
soy_OGL_2697	1237	8.1054287	21.665319	3439	35.81	9	7.176785	0.12	0.4729183	19
soy_OGL_4776	1200	6.7159791	23.583334	2313	33.91	4	4.1469378	0.131	0.85301006	9
soy_OGL_456	1100	3.3159945	28.545454	4781	38.27	7	4.7494693	0.107	0.57713062	12
soy_OGL_3848	1014	7.4157596	20.611441	1001	34.31	5	8.7360783	0.141	0.29329613	11
soy_OGL_3439	1497	7.5834217	11.155644	3013	33.6	11	8.6020422	0.097000003	0.55308962	12
soy_OGL_2000	1026	7.0577431	18.518518	10671	34.5	4	2.5105858	0.094999999	0.44316074	15
soy_OGL_5334	1000	18.828636	27.9	3371	34.8	7	19.812536	0.086999997	0.56415242	8
soy_OGL_2731	1083	7.717042	19.944599	2073	31.94	4	11.385121	0.112	0.40986714	19
soy_OGL_2789	1200	6.0796947	24.833334	4557	33.83	5	11.82972	0.064000003	0.21467832	8
soy_OGL_2869	1100	5.5274458	23.636364	5525	34.81	9	4.2722106	0.096000001	0.79801482	18
soy_OGL_6645	1124	4.0469542	28.736654	2940	35.76	8	8.8325615	0.086000003	0.9909113	13
soy_OGL_2322	1100	11.537634	4.2727275	1089	31.63	7	5.4367285	0.138	0.52252752	15
soy_OGL_5381	1100	9.3595705	0	9356	36.45	4	10.568127	0.063000001	0.6865623	14
soy_OGL_4295	1000	3.9414778	14.5	4989	30.5	10	32.912186	0.116	0.3903873	23
soy_OGL_852	1066	4.7059131	16.979362	1914	32.73	6	43.03051	0.083999999	0.59839845	15
soy_OGL_5183	1000	12.31167	0	13028	37.6	4	15.027229	0.078000002	0.92048389	19
soy_OGL_5977	1063	6.5187864	22.389463	2001	29.06	7	12.477116	0.13699999	0.62554592	14
soy_OGL_4979	1000	11.98569	0	2639	39.5	5	1.4021957	0.139	0.71718276	21
soy_OGL_607	1089	7.0958691	10.835629	1402	32.41	7	11.678254	0.14300001	0.6829226	16
soy_OGL_4974	1099	10.245035	0	4451	38.03	7	11.392615	0.112	0.72887993	16
soy_OGL_5005	1276	10.049834	0	4558	37.46	8	3.8124893	0.083999999	0.69067103	16
soy_OGL_5233	1000	9.6439486	6.1999998	5078	37.7	5	8.5155277	0.104	0.91138417	22
soy_OGL_5431	1178	4.0297146	18.505941	2001	34.55	7	17.606289	0.114	0.97902769	5
soy_OGL_622	1100	2.9936664	0	3361	40.81	8	6.1067214	0.066	0.70292485	21
soy_OGL_506	1000	4.4821186	10.3	3197	32.7	7	7.1511703	0.126	0.46037838	23

soy_OGL_602	1200	5.8804049	18.333334	2826	31.41	5	8.2982149	0.11	0.66166931	8
soy_OGL_844	1000	5.9970145	13.8	3147	33.7	5	3.9663272	0.121	0.64036721	15
soy_OGL_1630	1128	3.0774791	21.897163	1158	31.29	7	13.621281	0.126	0.49375501	9
soy_OGL_3053	1273	0.13881704	0	1001	42.1	3	9.3992996	0.039999999	0.59061539	5
soy_OGL_501	1000	4.4821186	15.9	1060	37	7	2.522342	0.13	0.46832883	24
soy_OGL_2384	1338	7.888226	0	3966	38.78	8	3.3241808	0.059999999	0.60006762	13
soy_OGL_2401	1300	11.483459	0	4968	39.53	6	15.698646	0.063000001	0.68782002	16
soy_OGL_3019	1200	11.978103	0	6608	41.66	6	17.651766	0.041000001	0.7547915	22
soy_OGL_5957	1400	9.0571718	0	1103	39.85	4	15.920022	0.046999998	0.69086224	17
soy_OGL_5360	1708	9.3808632	3.1030445	1001	38.34	3	6.1386256	0	0.58873755	5
soy_OGL_594	1100	0.50659025	0	5225	41.18	5	35.101582	0.021	0.63398772	7
soy_OGL_5920	1000	8.3593283	0	8478	40.2	5	11.821296	0.052000001	0.83415818	15
soy_OGL_5956	1000	9.0571718	0	2603	40.7	4	15.920022	0.074000001	0.69093877	17
soy_OGL_2115	1200	6.8356886	17	1187	25	10	4.4560003	0.178	0.93619722	15
soy_OGL_5199	1591	3.4622521	11.187932	2977	27.27	10	8.0608807	0.094999999	0.98509145	13
soy_OGL_2525	1100	7.7435093	28.636364	5037	21.72	13	2.1359754	0.206	0.78799301	5
soy_OGL_1512	1260	6.1372461	9.9206352	5038	29.44	7	6.2125831	0.090999998	0.92185259	22
soy_OGL_6305	1207	5.4021316	9.6934547	2001	25.18	9	5.1129079	0.101	0.98451066	9
soy_OGL_2514	1385	7.4874678	0	2001	30.61	9	0.55344528	0.068000004	0.82365435	25
soy_OGL_3986	1400	4.8896408	8.2857141	2665	25.14	14	3.9750774	0.027000001	0.88263464	11
soy_OGL_5509	1038	5.4987149	13.969172	2001	23.31	10	2.8456898	0.068000004	0.82562691	16
soy_OGL_4	1183	5.6447883	3.6348267	2001	26.54	11	6.251996	0.164	0.98017681	11
soy_OGL_1105	1448	5.1525106	0	1001	30.8	12	5.5651851	0.112	0.94108093	20
soy_OGL_3626	1127	3.8479979	0	4175	31.41	11	3.9420722	0.149	0.91832018	27
soy_OGL_1813	1083	5.8060555	9.4182825	1001	28.62	7	6.7997284	0.132	0.78216231	23
soy_OGL_1123	1100	2.3138869	0	3555	27.9	9	9.0121927	0.118	0.98166221	15
soy_OGL_327	1017	5.030407	9.3411999	2758	27.33	10	3.5970862	0.13600001	0.88900822	18
soy_OGL_1027	1000	6.3006811	0	2938	30.7	9	2.6209931	0.118	0.82828748	30
soy_OGL_2476	1216	4.7351184	0	3749	29.35	10	6.3287444	0.081	0.90266025	25
soy_OGL_3756	1000	6.4369183	0	1753	28.8	11	8.1181574	0.141	0.75505149	20
soy_OGL_5207	1038	6.245574	0	2001	28.13	10	5.9616418	0.092	0.96658534	20

soy_OGL_6196	1200	6.3268976	0	2083	29.33	13	4.4146981	0.114	0.8552171	16
soy_OGL_765	1014	4.2022138	15.285996	1846	23.57	11	5.1809421	0.13699999	0.98404491	7
soy_OGL_1124	1000	2.5821292	0	2138	29.2	9	8.4202681	0.13	0.98407274	15
soy_OGL_1128	1000	3.0311241	0	4484	27.8	11	10.497891	0.12	0.98653805	15
soy_OGL_1202	1025	6.7576227	0	2001	29.56	8	3.7838805	0.079999998	0.83121932	23
soy_OGL_3272	1000	5.2893763	0	3344	26.9	12	8.4192686	0.117	0.85832822	14
soy_OGL_3278	1100	1.1170077	0	1492	31.18	7	16.169323	0.071000002	0.97901845	21
soy_OGL_4598	1155	6.5523405	0	2096	28.39	11	16.647259	0.119	0.91559118	9
soy_OGL_4599	1014	6.5523405	10.749507	2358	26.72	10	9.2286224	0.119	0.91356224	11
soy_OGL_5512	1300	5.0622344	6.2307692	2390	29.15	10	5.8616896	0.081	0.81943297	18
soy_OGL_6352	1000	5.8339896	0	2729	29.2	8	2.0757606	0.079000004	0.88589787	22
soy_OGL_7011	1100	7.1566463	0	1157	27.81	9	6.2346964	0	0.98274142	11
soy_OGL_3988	1282	5.4523196	2.2620904	2248	26.67	12	9.343112	0	0.87394297	11
soy_OGL_3978	1300	1.8111591	4.0769229	2361	25.3	17	2.7935047	0.163	0.90203846	12
soy_OGL_1878	1127	5.170598	0	2499	31.67	10	5.1067872	0.13	0.70667535	21
soy_OGL_3653	1039	1.9542303	0	4476	30.89	10	15.281493	0.12800001	0.95372492	14
soy_OGL_4601	1200	5.2704782	0	3008	28.83	16	8.9018068	0.111	0.90692157	9
soy_OGL_5452	1012	5.0694704	5.237154	1001	28.06	12	5.3344097	0.13600001	0.92646742	12
soy_OGL_1121	1328	2.2730639	0	2001	31.47	9	7.5355978	0.079000004	0.98028392	15
soy_OGL_3658	1000	4.1581578	13.9	1017	27.5	8	4.226171	0.13500001	0.99226183	12
soy_OGL_445	1300	5.4366574	16	1326	26.15	10	10.787103	0.131	0.61077476	10
soy_OGL_2098	1115	2.4134915	13.004484	3310	25.38	8	1.3315576	0.104	0.78462136	14
soy_OGL_620	1000	2.9936664	14	1001	25.2	8	5.0374351	0.104	0.70222485	21
soy_OGL_4583	1200	1.4350497	10	3766	27.41	8	5.2837291	0.071999997	0.83754534	18
soy_OGL_4592	1000	5.2460666	11.6	4870	26.1	9	10.329822	0.089000002	0.95351636	13
soy_OGL_4457	1300	5.0366921	2.8461537	1602	30.07	11	14.980851	0.118	0.67816961	11
soy_OGL_4602	1300	5.1728916	0	2744	30	9	10.347064	0.1	0.89118302	9
soy_OGL_4606	1177	7.6084938	4.2480884	2027	28.29	9	9.7728977	0.119	0.86949825	7
soy_OGL_2535	1078	7.129993	0	2608	31.63	8	11.751297	0.132	0.75588536	12
soy_OGL_3444	1057	7.4322267	0	2879	29.13	10	5.3042855	0.132	0.55845869	11
soy_OGL_6463	1057	5.1859083	0	3613	30.36	9	2.2665029	0.12	0.58900452	21

soy_OGL_1798	1100	5.5180402	0	2475	27.81	9	6.7496748	0.112	0.81384093	9
soy_OGL_2077	1000	1.1110874	0	2803	27	8	3.8257167	0.13600001	0.68264985	9
soy_OGL_4846	1300	6.5432658	0	3072	31	7	4.1558948	0.037	0.9758172	13
soy_OGL_7016	1077	6.6724973	0	2103	30.26	7	10.260416	0.108	0.99099612	9
soy_OGL_4415	1300	5.6794109	0	2892	30.61	12	2.7268114	0.097000003	0.5904755	13
soy_OGL_2518	1167	7.5373769	35.561268	2001	31.1	15	7.8069844	0.132	0.81710953	18
soy_OGL_2947	1591	10.47059	18.478945	1001	34.88	11	5.8982325	0.055	0.90105253	15
soy_OGL_994	1100	7.9917173	16.90909	1079	28.09	10	5.7088308	0.164	0.77629948	30
soy_OGL_5448	1170	5.0694704	22.478632	2126	25.04	13	21.401491	0.15899999	0.94698083	16
soy_OGL_6997	1347	5.2629671	13.066072	1400	27.98	9	4.9964638	0.107	0.95564049	22
soy_OGL_3615	1175	5.2820034	22.297873	1001	23.57	14	15.562062	0.16	0.89665616	13
soy_OGL_1876	1400	5.170598	6.5714288	3429	30.42	11	7.1982799	0.075999998	0.70824999	21
soy_OGL_6781	1188	11.863941	15.23569	1101	27.77	9	6.3198204	0.147	0.76869798	19
soy_OGL_4952	1100	8.947258	11.454545	2625	32.36	9	10.809357	0.093000002	0.75359267	34
soy_OGL_1714	1134	8.4408894	8.7301588	2001	29.89	11	7.0031433	0.12899999	0.82911021	35
soy_OGL_3212	1322	7.9806147	6.732224	2109	30.4	12	6.4476118	0.094999999	0.70003802	37
soy_OGL_3552	1100	8.9050951	18.181818	3770	28	9	3.1234105	0.124	0.80841893	22
soy_OGL_3818	1500	7.7295065	8.8000002	2147	29.73	12	10.490335	0.075999998	0.56445491	21
soy_OGL_1480	1100	5.5293665	18.363636	3922	28.9	7	14.98117	0.13699999	0.94879591	20
soy_OGL_5268	1024	8.0089588	17.675781	1647	27.44	8	6.1049094	0.141	0.79763412	20
soy_OGL_6623	1100	9.2474756	15	1778	29.27	6	4.8814683	0.121	0.95245332	15
soy_OGL_324	1300	10.951405	15.615385	3513	30.38	9	7.4612322	0.085000001	0.89569819	16
soy_OGL_5847	1000	9.6763773	26	4567	28.7	8	21.237579	0.13500001	0.97908294	20
soy_OGL_6915	1200	8.8029718	14.5	7123	30.83	10	5.6880126	0.106	0.89265859	21
soy_OGL_1587	1031	6.6485653	19.786615	2351	27.93	9	17.208748	0.13600001	0.7705577	16
soy_OGL_2627	1000	8.794776	22.200001	6518	27.9	12	1.6578146	0.121	0.57570982	24
soy_OGL_4562	1082	8.4823227	14.879852	4785	30.22	8	6.2451515	0.11	0.80596793	26
soy_OGL_914	1100	6.3260517	17.363636	1609	27.27	10	9.7425737	0.117	0.68300653	26
soy_OGL_1669	1094	9.1770983	19.561243	2001	25.13	13	13.537057	0.126	0.69983619	12
soy_OGL_2881	1100	7.0442643	17.818182	2551	23.72	15	1.7031596	0.113	0.84848291	17
soy_OGL_6248	1500	7.2568383	2	4428	32.26	9	1.9875386	0.029999999	0.90514332	27

soy_OGL_6291	1100	6.0841422	16.363636	2055	26.72	10	5.6806564	0.097999997	0.94724208	22
soy_OGL_6733	1626	5.9758563	0	1001	30.44	11	14.939007	0.023	0.7208851	19
soy_OGL_741	1159	8.9459286	20.2761	2157	24.15	11	8.7504339	0.107	0.9114725	11
soy_OGL_7013	1192	7.0298228	11.157718	2390	24.83	13	13.359934	0	0.98795497	11
soy_OGL_406	1054	7.8340631	16.888046	2130	26.94	14	14.291978	0.116	0.74302012	22
soy_OGL_5211	1119	7.1378236	16.443253	2001	27.34	10	8.6277866	0.117	0.9608171	27
soy_OGL_6194	1098	6.2678766	19.489983	2001	25.59	9	5.6787629	0.115	0.84944862	18
soy_OGL_739	1503	9.1148996	10.711909	1001	28.67	8	6.4393706	0.064999998	0.90737295	12
soy_OGL_1088	1100	7.5212369	15.727273	1712	28	8	13.12507	0.109	0.91170472	11
soy_OGL_1690	1043	3.0398238	20.325983	2262	25.59	9	18.410624	0.127	0.80410725	21
soy_OGL_53	1059	9.9992008	10.481586	3663	31.53	8	13.066521	0.082000002	0.85183638	28
soy_OGL_1842	1078	5.552063	21.057514	2734	28.1	10	19.704119	0.090999998	0.73882794	24
soy_OGL_3930	1000	8.2275667	17.299999	2924	28.1	8	11.241423	0.12	0.84785622	24
soy_OGL_4942	1216	9.3127365	12.5	1001	34.12	9	22.3855	0.044	0.75783026	38
soy_OGL_3475	1200	7.0972891	13.333333	1238	29.83	10	17.97382	0.026000001	0.64057767	30
soy_OGL_4925	1200	14.560184	7.6666665	3138	34	7	8.7943621	0.030999999	0.76998693	33
soy_OGL_1010	1253	7.2566323	3.3519554	2001	30.4	9	11.806088	0	0.81028056	21
soy_OGL_2479	1383	6.1731362	0	1001	31.16	13	6.7163239	0.13	0.89425582	23
soy_OGL_5861	1066	9.3926363	0	2604	33.48	7	4.9707103	0.132	0.93367523	23
soy_OGL_6232	1000	11.124028	2.9000001	1863	30.8	10	8.7083693	0.147	0.88911313	19
soy_OGL_3362	1468	13.791044	5.3814712	1995	31.74	10	5.6554308	0.079999998	0.80685401	14
soy_OGL_4491	1266	7.953218	0	2001	34.75	8	14.377826	0.086999997	0.72734421	30
soy_OGL_5288	1061	17.586075	12.723845	1001	31.38	10	5.7014422	0.126	0.73697799	22
soy_OGL_1151	1000	5.8387361	0	2645	33.5	9	26.886911	0.132	0.96006143	28
soy_OGL_2912	1000	10.078434	0	2047	35	6	15.085391	0.106	0.9731915	26
soy_OGL_3313	1006	13.943912	5.2683897	2001	30.41	9	6.2724428	0.125	0.90842831	19
soy_OGL_3532	1000	8.9636507	0	2879	32.3	11	23.233994	0.138	0.78966826	21
soy_OGL_3821	1110	7.7295065	8.1081085	2159	30.81	12	14.54731	0.119	0.56239015	23
soy_OGL_4518	1108	8.9862776	0	1442	33.21	8	7.9312878	0.093999997	0.75395203	37
soy_OGL_5567	1188	7.5257554	9.848485	2001	29.62	10	5.2591677	0.111	0.71087021	18
soy_OGL_5862	1200	9.3926363	3.1666667	4204	33.5	6	3.6816833	0.088	0.93358672	23

soy_OGL_2188	1151	10.96957	2.5195482	2007	34.31	6	11.183036	0.102	0.79134864	30
soy_OGL_1846	1000	5.552063	8.6999998	4830	32.2	10	30.180906	0.121	0.73633116	26
soy_OGL_2450	1200	8.1517172	3.6666667	3056	32.66	8	26.763371	0.089000002	0.95185316	14
soy_OGL_787	1370	7.4971967	0	1001	29.92	9	5.9180937	0.037999999	0.89410937	17
soy_OGL_1086	1053	7.4506559	4.8433046	2697	27.25	14	6.7799845	0.118	0.90957391	12
soy_OGL_3617	1300	5.4662189	0	3052	29.76	11	12.076207	0.074000001	0.90422958	21
soy_OGL_3689	1179	7.5635667	0	1246	29.43	13	5.8742623	0.059	0.89960873	16
soy_OGL_4423	1000	9.7329044	0	2782	31.8	11	5.5951505	0.078000002	0.61133862	24
soy_OGL_4570	1109	5.6887312	0	1441	30.47	11	5.3143191	0.074000001	0.82308477	23
soy_OGL_4586	1031	4.07375	0	2001	29.77	12	28.663088	0.089000002	0.97342485	12
soy_OGL_4815	1100	6.1591496	7	2495	28.27	12	17.13553	0.093999997	0.95391828	18
soy_OGL_5210	1000	7.1378236	0	2854	31.2	8	11.24736	0.107	0.96254879	26
soy_OGL_5214	1100	7.9554181	0	1577	31.54	6	5.1270323	0.061999999	0.95294511	26
soy_OGL_5547	1100	7.121428	7.3636365	1260	26.45	13	7.3554635	0.103	0.75745595	13
soy_OGL_6183	1128	5.2827721	0	1262	27.3	12	6.2682233	0	0.83132082	15
soy_OGL_6585	1100	4.8956351	0	4444	33	10	4.935101	0.081	0.78926444	34
soy_OGL_6632	1121	8.3712139	3.8358607	2865	28.99	10	5.6697946	0.086999997	0.96967816	24
soy_OGL_3011	1262	6.5628276	0	2001	30.98	9	10.604451	0.067000002	0.7735548	23
soy_OGL_3293	1000	5.0341988	0	3775	29.7	10	15.962563	0.008	0.9559862	26
soy_OGL_277	1000	6.375752	0	1797	30.7	11	4.3874183	0.032000002	0.90212804	27
soy_OGL_1011	1087	6.8298855	15.823367	1386	28.05	11	27.118805	0.103	0.81273723	20
soy_OGL_1138	1245	5.6738558	0	1001	31.72	10	12.517944	0.048	0.97678506	25
soy_OGL_1406	1000	14.723554	0	2862	31.3	11	5.5311065	0.115	0.83261496	18
soy_OGL_1536	1000	7.5677972	0	2017	33.9	9	6.9632969	0.055	0.8828631	38
soy_OGL_1552	1000	8.9413004	0	4043	35.1	10	15.233479	0.072999999	0.85412502	29
soy_OGL_2896	1000	8.9753227	0	3677	29.2	12	10.069893	0	0.8866201	13
soy_OGL_189	1015	7.8639984	0	1558	29.35	11	5.4138069	0.029999999	0.79649782	12
soy_OGL_1018	1200	6.0355277	0	1783	31.33	9	9.8099995	0	0.81961995	24
soy_OGL_2850	1000	5.5548873	0	2543	33	8	11.034592	0.075999998	0.6851368	29
soy_OGL_5542	1000	7.2413769	9.1999998	1327	26.8	9	9.5752869	0.096000001	0.76747894	18
soy_OGL_5563	1221	7.787199	0	2186	30.54	10	8.9710941	0.026000001	0.71824056	20

soy_OGL_649	1000	8.1819096	0	2136	30.8	8	2.8823094	0.006	0.75808358	30
soy_OGL_6318	1032	12.685363	0	2303	29.45	8	1.0791311	0	0.94329226	15
soy_OGL_1446	1048	10.671152	0	2001	33.39	7	9.1899281	0	0.90714896	29
soy_OGL_2520	1023	7.5373769	0	6231	30.59	14	10.398708	0.007	0.81667399	18
soy_OGL_6317	1000	13.656694	0	2024	32.3	8	2.001693	0.041000001	0.94390213	15
soy_OGL_3675	1100	6.1510382	3.3636363	2164	30.36	10	21.052967	0	0.94270384	13
soy_OGL_3764	1021	10.661443	0	1001	31.34	9	12.464992	0.079000004	0.74138963	18
soy_OGL_3820	1054	7.7295065	0	1197	31.78	11	15.855034	0.071000002	0.56245065	23
soy_OGL_4605	1485	5.7093301	17.710438	1001	28.61	12	5.9015331	0.097999997	0.87653661	8
soy_OGL_5501	1062	4.4117389	21.280603	3003	27.96	11	5.7607298	0.13600001	0.84240615	22
soy_OGL_43	1000	10.198316	20	2798	30.8	8	4.8643594	0.133	0.87690908	31
soy_OGL_750	1000	5.2482963	30.299999	3148	29.2	13	1.9931269	0.14399999	0.93431294	15
soy_OGL_1052	1126	4.5279164	19.271759	1001	30.99	11	5.5941772	0.14	0.8570928	27
soy_OGL_1211	1000	6.7576227	24	1363	28.7	11	16.606298	0.14	0.82273686	27
soy_OGL_1712	1048	8.4408894	19.847328	2001	34.73	11	8.4678297	0.121	0.82653368	35
soy_OGL_4893	1391	9.0506868	21.926672	2001	27.67	13	4.4237795	0.117	0.90528029	12
soy_OGL_5852	1564	8.4169607	20.332481	1325	34.14	13	7.848505	0.057	0.95458859	15
soy_OGL_2455	1055	7.5181608	22.369669	3136	28.53	12	12.027554	0.12899999	0.94091356	15
soy_OGL_3305	1000	14.710406	20.799999	3104	31.9	11	4.4157495	0.11	0.91933638	17
soy_OGL_1510	1286	6.1372461	16.096422	2001	31.41	9	14.3956	0.092	0.92432225	21
soy_OGL_1657	1100	8.8195906	21.545454	1384	28.81	10	6.6370978	0.12	0.6067996	21
soy_OGL_2563	1402	5.5083914	19.044222	1001	33.23	12	8.032053	0.077	0.70293355	18
soy_OGL_2900	1022	13.152136	23.581213	1001	33.85	9	16.117895	0.096000001	0.98491341	20
soy_OGL_3271	1100	5.2893763	26.363636	2826	28.9	12	10.345975	0.113	0.85699165	14
soy_OGL_3605	1100	4.2983022	29.272728	2026	29.36	11	2.8360915	0.116	0.87802285	18
soy_OGL_4447	1100	5.3659263	31.636364	1709	26.9	12	2.7421849	0.133	0.64517653	14
soy_OGL_4806	1000	5.6626678	32.099998	1346	28	10	3.4644935	0.132	0.93572778	14
soy_OGL_4830	1713	17.834297	13.543491	2252	37.88	10	14.798489	0	0.97853154	15
soy_OGL_5434	1147	4.0297146	31.037489	2001	29.11	11	24.44693	0.12800001	0.97368783	7
soy_OGL_5546	1120	7.2413769	38.392857	3979	30.26	16	13.827795	0.112	0.76188815	14
soy_OGL_3618	1064	5.6561656	23.778196	5099	29.04	8	9.0199022	0.122	0.90571046	22

soy_OGL_1117	1100	3.6042941	20.90909	2208	27.63	12	4.5015988	0.133	0.97613758	15
soy_OGL_700	1100	10.265951	22.272728	1838	28.09	14	5.9475279	0.093999997	0.82383609	19
soy_OGL_1059	1066	4.5279164	24.953096	1001	28.14	15	10.58745	0.086999997	0.86132663	27
soy_OGL_1184	1107	4.3006682	22.673893	1217	29.26	11	8.1135759	0.104	0.89711374	28
soy_OGL_3624	1000	3.9820173	24.6	1146	29.9	11	6.6992178	0.119	0.91643202	24
soy_OGL_3980	1022	5.9596634	23.581213	1001	26.32	12	4.8085289	0.115	0.89309913	14
soy_OGL_1125	1100	2.5821292	26.545454	1716	26.54	9	8.4202681	0.12800001	0.98417366	15
soy_OGL_2884	1079	7.0442643	9.4531975	3489	27.98	12	3.6073871	0	0.84941208	16
soy_OGL_3260	1073	5.2893763	22.367195	2781	27.02	10	4.6444116	0.121	0.83969408	19
soy_OGL_340	1200	9.9017172	19.5	1621	32.25	9	10.129355	0.072999999	0.86081982	27
soy_OGL_4849	1100	6.3080449	27.818182	1401	28.54	10	15.042856	0.107	0.97167885	17
soy_OGL_4855	1003	6.8892426	30.00997	2930	27.41	11	5.2540402	0.12800001	0.95921409	14
soy_OGL_995	1109	6.1700201	13.61587	1924	30.02	12	10.232059	0	0.78143746	25
soy_OGL_1533	1111	7.5794353	3.420342	2925	36	5	3.3002264	0.029999999	0.88586903	38
soy_OGL_1776	1076	5.2867265	21.282528	1001	30.57	8	3.6068027	0.090000004	0.89771509	23
soy_OGL_4419	1100	6.5623188	29.90909	1010	27.9	15	10.982924	0.071000002	0.60321796	19
soy_OGL_4593	1000	5.2460666	14.8	2171	28.6	12	10.949891	0	0.95007187	13
soy_OGL_5451	1000	5.0694704	24.200001	1255	29.9	11	3.5194166	0.098999999	0.92823374	13
soy_OGL_3262	1197	5.2893763	6.0985799	5006	32.49	11	3.3503406	0.082999997	0.84153843	19
soy_OGL_4542	1142	5.1131511	0	1001	33.36	11	7.1182885	0.101	0.78286541	26
soy_OGL_2558	1100	5.4913468	4.2727275	1930	33	11	9.0112743	0.132	0.71059787	17
soy_OGL_2587	1000	1.6719028	0	1025	33.3	12	13.705764	0.14300001	0.64887065	15
soy_OGL_2878	1026	4.2962294	0	4110	32.94	11	9.8585176	0.118	0.8207857	16
soy_OGL_1504	1200	8.5456972	15.666667	1018	33.08	9	6.4033203	0.103	0.98764962	16
soy_OGL_4878	1300	3.7867911	11.538462	3418	32.46	12	6.4816704	0.115	0.92725062	23
soy_OGL_1502	1000	8.5456972	10.8	1425	34.9	8	7.715251	0.125	0.98647088	17
soy_OGL_2604	1400	6.5441737	3	2028	35.14	15	12.806851	0.079999998	0.61173779	16
soy_OGL_2924	1200	8.2135067	0	2306	32.66	14	2.3951175	0.117	0.95866811	23
soy_OGL_3822	1021	7.5490041	0	1001	34.76	18	13.214281	0.112	0.55790466	23
soy_OGL_4004	1100	11.197123	0	3311	39.9	12	3.2280686	0.078000002	0.80704618	15
soy_OGL_4852	1000	7.6953392	22.700001	2610	31.2	15	5.1717582	0.139	0.9629817	15

soy_OGL_5435	1200	4.0297146	19.916666	1314	30.5	11	10.018218	0.104	0.96980077	12
soy_OGL_5541	1300	7.2413769	0	1122	35.38	11	8.3077745	0.072999999	0.7678774	19
soy_OGL_6218	1000	8.06742	0	3717	36.4	10	16.60523	0.097000003	0.87058228	30
soy_OGL_6624	1200	9.2474756	0	2392	37.83	11	9.3725719	0.085000001	0.95482641	16
soy_OGL_1791	1100	5.5180402	16.636364	1069	28.54	9	8.5699787	0.124	0.83016235	9
soy_OGL_5558	1358	7.472156	4.6391754	1001	32.4	9	5.7930717	0.096000001	0.73027968	16
soy_OGL_5975	1058	9.9497595	14.744802	2875	30.71	11	8.6409616	0.13699999	0.63510203	17
soy_OGL_1038	1104	8.4023438	0	3575	37.68	9	26.04953	0.081	0.83832872	27
soy_OGL_1234	1057	9.0944204	16.177862	1001	31.78	9	14.784658	0.097000003	0.76037282	23
soy_OGL_4418	1046	6.6752057	10.516253	2224	37.09	12	5.5848293	0.081	0.59904158	18
soy_OGL_4787	1000	13.341439	20.799999	2961	32.1	10	3.5762384	0.111	0.90332788	12
soy_OGL_6282	1033	5.7888355	3.9690223	4147	37.36	7	9.8850412	0.07	0.93730932	28
soy_OGL_3961	1100	8.0179386	0	3129	38.27	8	11.975069	0.077	0.97126538	9
soy_OGL_754	1100	5.2869329	0	2842	30.36	12	11.399844	0.061000001	0.94672948	12
soy_OGL_1743	1200	3.8039601	0	1819	32.08	13	5.7499733	0.103	0.98675972	14
soy_OGL_3989	1071	4.3140473	17.927172	1914	25.39	14	8.7340107	0.113	0.87050432	8
soy_OGL_4804	1100	5.6626678	6.909091	4862	30.36	15	3.4201603	0.096000001	0.93444669	14
soy_OGL_4874	1028	4.0852547	8.0739298	1995	29.57	12	6.6143007	0.085000001	0.93171966	27
soy_OGL_5463	1220	6.4554529	0	1001	29.75	15	3.8709495	0.11	0.90372336	12
soy_OGL_6324	1070	6.7954488	0	2001	31.49	9	4.0916629	0.089000002	0.92475724	19
soy_OGL_387	1100	7.7681108	0	2709	34.9	11	3.5890367	0.078000002	0.77377927	26
soy_OGL_420	1000	13.982355	0	3175	37.1	13	3.235137	0.055	0.70507658	20
soy_OGL_1077	1000	7.9827704	11.6	1455	30.7	13	16.111982	0.114	0.88983691	16
soy_OGL_1495	1180	8.5456972	4.1525426	2001	32.79	9	5.2240887	0.059999999	0.98040032	20
soy_OGL_2101	1200	4.9611359	0	1057	31.08	15	19.190214	0.056000002	0.98066056	6
soy_OGL_2208	1000	6.1444073	7.6999998	2642	32	11	9.0992565	0.109	0.75948626	28
soy_OGL_2959	1000	11.454642	11.2	4590	31.4	13	2.3004606	0.074000001	0.87102979	20
soy_OGL_3619	1000	5.0325108	0	2015	30.2	14	10.580534	0	0.91060865	20
soy_OGL_4124	1066	9.6362591	7.3170733	1010	33.02	13	9.3964949	0	0.80886906	28
soy_OGL_4597	1174	4.5745411	28.279387	1001	32.62	17	6.9650517	0.083999999	0.93202132	12
soy_OGL_5430	1000	5.8905592	0	1562	40.1	14	4.0776339	0	0.99682248	8

soy_OGL_6631	1000	8.3712139	0	2382	34	11	5.6558657	0.017999999	0.96925318	24
soy_OGL_7018	1022	4.8958359	18.395304	1001	29.74	15	12.006363	0.131	0.99540359	7
soy_OGL_2863	1200	5.7699661	0	2412	33	10	6.1850662	0.074000001	0.78034377	14
soy_OGL_5433	1000	4.0297146	3.5	7325	31.9	12	13.344413	0.092	0.97808045	7
soy_OGL_5461	1041	6.4554529	16.23439	7052	30.16	12	3.2912657	0.109	0.90458745	12
soy_OGL_1557	1000	9.3490543	0	4598	35	9	6.7765508	0	0.84207141	25
soy_OGL_3534	1000	8.9636507	4.5999999	1174	34.4	11	20.742655	0	0.79211909	23
soy_OGL_3613	1208	5.4494624	6.9536424	2144	32.36	12	26.338915	0.013	0.89262086	14
soy_OGL_5581	1132	5.9725876	0	2352	36.04	14	9.8794641	0	0.68565518	20
soy_OGL_6552	1200	13.347547	0	1134	37.25	8	5.138762	0	0.75883508	33
soy_OGL_6766	1022	7.5721488	0	1001	35.12	9	1.2482015	0.071000002	0.74702877	23
soy_OGL_4451	1211	3.4002233	19.983484	2001	28.73	13	10.046446	0.086999997	0.6597842	10
soy_OGL_1226	1100	9.0944204	3.4545455	4722	31.27	8	11.217484	0.113	0.76954389	20
soy_OGL_5271	1400	7.4900575	0	2500	33.14	7	13.351365	0.067000002	0.79003656	20
soy_OGL_6359	1089	5.9217067	0	2751	30.76	10	25.323818	0.12	0.85062176	4
soy_OGL_4851	1100	7.0726852	0	4770	29.72	8	8.1826735	0	0.96532637	17
soy_OGL_4446	1100	5.4720469	11.545455	3304	31.9	11	3.2202053	0.12	0.6447717	13
soy_OGL_6144	1007	4.9215565	0	2126	35.94	7	7.9049125	0.111	0.77152783	16
soy_OGL_6599	1000	3.883358	0	4652	33.4	10	12.442206	0.11	0.80854279	14
soy_OGL_699	1100	10.568119	0	3049	35.63	7	6.3320332	0.082999997	0.82035679	17
soy_OGL_5551	1300	7.1524053	11.230769	9682	31.07	8	2.2372785	0.082000002	0.74930269	18
soy_OGL_450	1000	4.6825724	17.799999	3203	26.3	4	1.7504002	0.13500001	0.5887748	13
soy_OGL_2027	1500	2.5324562	16.533333	2044	26	7	6.3093967	0.079999998	0.30204871	2
soy_OGL_5077	1000	0.43851015	16.4	7476	24.8	2	5.4043751	0.107	0.4479295	2
soy_OGL_6095	1325	0.54288405	0	21613	32.22	4	1.8975407	0	0.65218985	8
soy_OGL_1332	1100	4.6044507	19.363636	2549	27.36	4	9.986455	0.103	0.68496782	10
soy_OGL_2775	1579	7.2343197	19.759342	1001	26.47	11	9.27353	0.092	0.28313985	6
soy_OGL_2735	1088	6.8346286	17.371323	1710	26.1	7	2.8939235	0.12899999	0.40796155	18
soy_OGL_6159	1009	7.8820863	9.2170467	1813	28.04	5	1.2645833	0.097000003	0.79484397	18
soy_OGL_6467	1014	5.5870967	20.216963	2117	25.04	9	4.0897059	0.105	0.60493135	15
soy_OGL_5144	1100	4.3852158	14.454545	2193	26	5	5.5778108	0.082999997	0.74117166	21

soy_OGL_2060	1098	2.3059373	9.7449913	16502	29.32	2	1.031481	0	0.57854593	11
soy_OGL_1913	1200	2.9864438	12	2870	26.75	10	7.5416217	0	0.61141235	12
soy_OGL_6728	1172	7.3430734	14.846416	2001	28.66	4	2.0485077	0.041999999	0.71415466	14
soy_OGL_5375	1095	6.2914834	20.913242	2116	24.01	6	4.8974667	0.126	0.63972646	13
soy_OGL_148	1024	7.3133149	0	5188	29.98	5	4.5678024	0.13699999	0.67686886	11
soy_OGL_2044	1000	2.5458627	0	4286	28.4	8	8.6608562	0.125	0.47350246	11
soy_OGL_4611	1278	6.7095437	0	8370	29.42	8	3.0957539	0.097000003	0.83269459	8
soy_OGL_6017	1098	1.8960881	0	1638	25.95	7	6.9088621	0.141	0.45010215	3
soy_OGL_1892	1100	9.4963474	0	2930	32.45	6	4.0851679	0.097000003	0.66535717	15
soy_OGL_2070	1000	4.3679075	0	4715	28.4	4	2.4900041	0.118	0.64265597	11
soy_OGL_2813	1100	0.37861791	11.090909	1101	26.36	3	1.5661993	0.104	0.41200787	6
soy_OGL_5696	1160	1.1854842	0	1001	28.53	5	3.9784093	0.123	0.39826438	15
soy_OGL_6057	1067	1.0384094	0	3862	27.55	5	1.6172503	0.101	0.10733674	2
soy_OGL_6103	1000	0.477795	0	7892	28.2	4	2.1915698	0.104	0.66439652	11
soy_OGL_6112	1117	1.5760107	0	3282	27.48	5	12.577241	0.115	0.71177214	3
soy_OGL_6368	1027	2.5912349	0	1001	29.01	2	7.5501709	0.12800001	0.64898002	6
soy_OGL_6382	1053	1.4697928	0	1756	28.39	3	0.068795972	0.131	0.27251047	3
soy_OGL_578	1000	0.46867135	0	24794	31.4	1	1.0436537	0.033	0.35382411	1
soy_OGL_2352	1000	2.8688939	0	1362	26.2	10	0.36916527	0.12800001	0.2190734	9
soy_OGL_1880	1000	4.2531829	9.6999998	5282	25.9	11	10.098972	0.075000003	0.69106168	8
soy_OGL_5331	1100	6.8539505	0	3213	28.18	10	2.5293972	0	0.63813412	13
soy_OGL_6727	1100	7.5409741	0	2883	30.18	7	2.8464355	0.086000003	0.71368545	14
soy_OGL_161	1002	3.8654892	0	7557	29.34	4	0.96058947	0.068000004	0.70709854	10
soy_OGL_579	1069	0.084886439	0	2562	27.4	1	0.9587912	0.071999997	0.48208889	2
soy_OGL_2049	1000	2.9409354	0	4589	30.9	3	2.9748011	0.011	0.49131289	11
soy_OGL_4768	1200	6.7980485	0	1227	29.91	3	2.1454339	0.046999998	0.83128703	8
soy_OGL_5988	1000	1.6204541	9.5	6355	28	6	7.0407257	0.083999999	0.59559184	13
soy_OGL_151	1200	4.8982654	0	4973	32.16	3	7.0430737	0.030999999	0.68412548	13
soy_OGL_2099	1000	9.64013	0	5268	29.8	8	2.9616265	0	0.79498154	5
soy_OGL_2300	1212	6.7678699	4.0429044	1020	31.1	4	0.11322137	0	0.59259576	15
soy_OGL_4325	1199	2.6155119	0	2001	30.52	6	3.7792008	0	0.43805885	19

soy_OGL_601	1011	5.8804049	0	3542	28.28	6	8.790885	0	0.66120148	8
soy_OGL_2078	1591	1.1110874	13.890635	2001	28.4	8	3.8257167	0.072999999	0.68308067	9
soy_OGL_6106	1058	0.46364269	21.550095	4178	25.33	5	2.9861679	0.12800001	0.67286378	12
soy_OGL_176	1200	2.1532793	18.583334	6312	29.75	4	0.047363445	0.067000002	0.76861107	12
soy_OGL_3056	1000	5.589066	28.200001	3236	26.3	3	4.6132493	0.13	0.52431065	2
soy_OGL_4327	1236	2.6155119	14.563107	2863	30.82	6	2.3745637	0.092	0.43930015	19
soy_OGL_6379	1300	0.32445011	24.846153	4222	27.92	6	2.0309567	0.048	0.22556703	2
soy_OGL_4027	1000	0.4967483	26	2223	24.9	5	4.6936874	0.106	0.64170003	7
soy_OGL_6079	1100	1.2300193	21.545454	4496	26.09	1	0.93724853	0	0.069138676	3
soy_OGL_2787	1066	4.2231936	22.983114	2179	26.92	8	3.2117417	0.068000004	0.21957462	11
soy_OGL_6369	1167	2.3242586	15.766924	6500	30.67	4	3.6572742	0.048	0.64291066	7
soy_OGL_5137	1000	0.96030283	4.9000001	2778	30.3	6	4.976438	0.13600001	0.70191848	12
soy_OGL_4270	1122	4.2217674	0	3249	32.35	11	4.4469466	0.109	0.34837943	18
soy_OGL_1884	1073	4.6904893	14.72507	7086	28.23	10	4.241643	0.124	0.68640345	9
soy_OGL_6077	1000	1.768098	19.9	9107	29.5	2	8.4533157	0.050999999	0.027139669	1
soy_OGL_128	1162	1.3806362	0	9061	32.96	5	3.5342636	0.071999997	0.59464288	9
soy_OGL_4036	1000	1.2838418	8.5	6507	30.7	3	1.1181407	0.078000002	0.52056921	1
soy_OGL_6108	1000	0.21696903	18.1	8407	28.9	6	2.6281276	0.104	0.68040764	8
soy_OGL_3096	1200	0.6157763	18.333334	4155	28.25	5	12.612445	0.079000004	0.3567996	7
soy_OGL_143	1200	1.6926541	0	3558	32.5	5	18.153097	0.074000001	0.66169167	5
soy_OGL_2822	1300	2.0155141	10.692307	6511	33.84	3	10.035489	0	0.54740816	7
soy_OGL_4166	1200	1.4769267	0	3304	37.83	2	1.3663538	0	0.20784858	3
soy_OGL_2079	1029	1.2481024	14.188533	1001	26.53	7	9.4542227	0.124	0.68722796	10
soy_OGL_1294	1000	4.637219	17.299999	2666	26.9	11	4.2340012	0.12899999	0.63053071	5
soy_OGL_3518	1127	1.9912556	5.4126	1283	30.43	6	9.4247637	0.033	0.74799955	17
soy_OGL_514	1202	2.5546122	0	1001	31.19	6	0.99594408	0.055	0.44343233	17
soy_OGL_585	1017	1.0318911	0	4981	31.46	5	6.1709328	0.052999999	0.59529513	9
soy_OGL_1634	1000	0.71848589	9.3999996	12515	32	2	6.1450109	0	0.5270915	2
soy_OGL_2018	1000	1.6336222	13.8	6818	30.4	1	0.0053136	0.045000002	0.36273053	4
soy_OGL_2770	1171	0.64794296	0	1001	28.18	7	2.3733718	0	0.30767584	6
soy_OGL_3108	1041	3.0439923	0	1304	29.68	6	3.2408457	0.090999998	0.48384169	5

soy_OGL_4749	1200	1.3206984	0	2683	29.58	5	2.9404655	0.034000002	0.40433931	5
soy_OGL_5100	1000	2.0037358	0	9267	32.7	8	1.3546424	0	0.10478493	5
soy_OGL_6702	1000	0.53584969	0	1033	30.3	5	4.0033474	0.050000001	0.12862684	1
soy_OGL_6709	1127	0.14302784	11.446318	4021	30.16	3	3.4536695	0.048999999	0.51237196	3
soy_OGL_144	1213	1.6926541	0	6374	35.44	4	1.2539581	0	0.66468507	7
soy_OGL_866	1180	1.0942405	2.3728814	2001	32.79	7	4.2089787	0	0.57002908	5
soy_OGL_2794	1100	2.9072554	0	2046	34.09	6	5.5989199	0	0.18855245	5
soy_OGL_3403	1000	2.5044255	0	4297	31.1	6	9.1436205	0	0.6687327	7
soy_OGL_3416	1000	0.44054028	0	1152	32.4	3	8.3811512	0	0.539235	6
soy_OGL_4744	1100	1.305691	0	2940	37.09	2	3.5528748	0	0.38461265	5
soy_OGL_6072	1000	1.2072753	20.1	5702	30.1	2	5.9450364	0	0.012663265	5
soy_OGL_4563	1072	8.1862221	29.944031	2001	34.23	9	10.909743	0.102	0.80881846	26
soy_OGL_3450	1046	10.103625	28.011473	5053	26.38	7	13.410707	0.134	0.58815223	12
soy_OGL_2237	1102	7.3392978	27.22323	1647	29.31	7	2.5588644	0.132	0.69300002	16
soy_OGL_5067	1000	5.2891674	37.5	2597	28.6	6	4.9006371	0.123	0.56153786	7
soy_OGL_6078	1237	21.697058	28.779305	3433	36.37	4	1.5721381	0.005	0.046778176	1
soy_OGL_3168	1197	11.522215	24.310778	2451	28.65	9	15.804436	0.118	0.62852198	15
soy_OGL_3368	1200	11.584485	28.583334	1224	29.25	7	30.5828	0.082000002	0.78103226	10
soy_OGL_1002	1434	7.2732038	16.039051	3301	29.56	11	22.482008	0.039000001	0.79427183	15
soy_OGL_2202	1016	8.5738249	11.318897	1001	32.48	8	13.825203	0	0.76972622	32
soy_OGL_3928	1200	8.1360826	12.5	1056	32.58	7	19.357901	0	0.84671223	24
soy_OGL_3364	1051	12.993029	22.549952	2370	33.2	8	36.082726	0	0.79980868	14
soy_OGL_5596	1174	4.4148474	21.379898	1914	28.1	10	37.224129	0	0.65550673	18
soy_OGL_5284	1200	16.654408	0	3531	37.41	6	4.4658694	0.039999999	0.74535978	20
soy_OGL_4002	1023	11.197123	16.520039	1942	31.57	11	40.550243	0.061999999	0.81128758	17
soy_OGL_1354	1200	11.526744	0	2517	31.83	9	6.1403975	0	0.755687	15
soy_OGL_4790	1000	13.341439	0	2709	32.6	8	8.788312	0	0.91055715	14
soy_OGL_950	1011	13.818732	5.3412461	3344	33.43	8	3.3284454	0	0.74314851	18
soy_OGL_5314	1240	18.329891	0	1749	37.33	4	3.4199481	0	0.67805487	29
soy_OGL_2443	1000	6.9880362	29	3259	33.6	10	6.7274404	0.086000003	0.96944404	12
soy_OGL_3957	1200	0.89052546	36.25	3816	32.58	13	5.6244783	0.071000002	0.98809999	9

soy_OGL_3982	1417	4.8896408	22.300634	2605	36.2	12	17.094622	0.026000001	0.8886801	12
soy_OGL_6193	1155	6.6425095	23.376623	2380	31.25	9	7.7466416	0.088	0.8490355	17
soy_OGL_6776	1052	10.114168	26.425856	3653	31.84	12	9.8901253	0.108	0.76374435	13
soy_OGL_6885	1000	6.5062184	21.700001	3677	32.9	9	10.999313	0.1	0.85968453	21
soy_OGL_7017	1000	6.6724973	39.599998	1027	36.2	12	14.353896	0.061999999	0.99318391	9
soy_OGL_746	1050	7.9587779	23.047619	1256	31.33	6	4.0615807	0.11	0.91920209	13
soy_OGL_785	1000	7.8119359	26.299999	2253	32.7	5	6.6157389	0.106	0.9011094	20
soy_OGL_1085	1063	6.1470599	30.573847	4248	30.57	9	8.4983454	0.103	0.90260571	15
soy_OGL_2453	1300	7.4458432	11.923077	7919	32.84	9	18.21773	0.071000002	0.94660139	15
soy_OGL_4153	1000	9.8956871	22.5	9478	32.5	8	9.7893705	0.106	0.89067864	21
soy_OGL_2580	1000	3.9058185	27.5	1441	30	11	13.895232	0.11	0.66584265	15
soy_OGL_3372	1010	13.207669	28.118813	2001	33.66	6	17.280615	0.082000002	0.76863682	17
soy_OGL_4837	1400	5.7022271	30.785715	3376	34.5	9	24.640301	0.027000001	0.99080157	6
soy_OGL_5916	1200	8.4431925	15.583333	6252	34.66	7	4.1640239	0.043000001	0.8443163	22
soy_OGL_367	1400	7.2482986	26.214285	2337	37.71	13	6.3123527	0	0.82106757	22
soy_OGL_916	1400	6.3260517	17.928572	1181	36.35	9	10.825082	0	0.68352264	27
soy_OGL_1116	1308	4.3241005	18.883793	1001	36.62	9	11.975992	0.015	0.9730463	16
soy_OGL_1800	1073	9.4984035	25.535881	5375	28.05	14	9.3508472	0.074000001	0.80565584	8
soy_OGL_3610	1100	5.3962822	30	2355	33.72	12	29.945431	0.046999998	0.88849241	17
soy_OGL_3707	1054	7.8270955	21.062618	1001	29.79	11	8.4879274	0	0.84088415	20
soy_OGL_4469	1100	7.0369272	19.818182	4693	32	12	16.110952	0	0.7025739	24
soy_OGL_6497	1000	8.8186426	20.799999	1657	32.8	9	0.88735545	0	0.68183458	28
soy_OGL_2592	1200	5.162776	20.166666	2151	29.08	10	11.487336	0.077	0.63855594	18
soy_OGL_2855	1000	5.5548873	34.099998	1328	36.1	12	2.5379655	0	0.70848149	11
soy_OGL_2420	1059	11.967738	16.902739	1407	35.31	5	3.1785007	0.035	0.71506661	28
soy_OGL_4406	1077	8.6647367	30.176416	1695	35.28	9	30.239738	0.002	0.57217139	23
soy_OGL_395	1100	9.5874052	9.363636	3342	36.18	6	6.4867473	0.066	0.76402253	24
soy_OGL_3837	1200	7.0545988	23.25	3194	37.58	12	41.907196	0.023	0.5355708	22
soy_OGL_3441	1000	7.5834217	33.400002	6268	34.3	14	22.107468	0.081	0.55547822	12
soy_OGL_1689	1176	3.0398238	17.17687	1001	36.13	10	17.71719	0.004	0.80405629	21
soy_OGL_4595	1100	5.2460666	15.363636	4897	33.36	11	10.200455	0.032000002	0.942451	15

soy_OGL_6177	1134	8.6720114	13.932981	1827	31.92	12	9.6100864	0	0.82228047	14
soy_OGL_12	1000	10.026835	0	3029	35.3	8	10.881158	0	0.94580001	18
soy_OGL_364	1071	7.5258417	0	5959	36.78	7	5.3888817	0	0.82560039	28
soy_OGL_4459	1073	5.4048753	0	1001	36.9	12	14.314117	0	0.68291259	13
soy_OGL_4973	1049	10.245035	5.815062	3008	36.89	9	10.310915	0.039000001	0.72966939	18
soy_OGL_5598	1307	4.5567188	9.9464426	2001	34.5	10	4.2039037	0	0.65397316	18
soy_OGL_3156	1213	8.8903952	12.036274	1048	29.92	7	4.0613441	0.097999997	0.60073936	19
soy_OGL_2740	1000	5.9830751	22.200001	3649	25	13	18.252216	0.13600001	0.40000001	18
soy_OGL_3270	1047	5.2893763	18.720152	4549	28.93	7	21.567369	0.097000003	0.85057139	16
soy_OGL_1653	1100	9.0782251	14	7648	29.81	7	2.6960566	0.1	0.60236889	19
soy_OGL_2339	1100	11.044018	20.727272	1134	27.81	6	2.3017642	0.111	0.32064679	12
soy_OGL_3472	1500	8.2846069	5.2666669	4197	35	4	1.9134001	0	0.63287306	25
soy_OGL_5657	1000	6.3537583	25.700001	3064	27.5	6	7.0583987	0.118	0.50760537	19
soy_OGL_4311	1353	2.3265874	9.6082783	2534	30.37	6	20.723942	0.061000001	0.41313362	24
soy_OGL_4408	1100	8.6647367	24.181818	5786	29.81	9	13.96318	0.1	0.57498389	22
soy_OGL_495	1000	5.067452	25.5	4367	29.3	6	19.600311	0.083999999	0.47689641	24
soy_OGL_4229	1000	4.0722065	17.1	4304	30.5	10	21.35421	0.079999998	0.26816532	32
soy_OGL_5745	1200	13.020522	17.833334	2452	30.08	6	10.894938	0.079999998	0.70709223	15
soy_OGL_3865	1127	9.8148384	17.923691	2407	30.34	6	15.829026	0.072999999	0.25646782	20
soy_OGL_5106	1000	8.7867098	24.5	2921	26.5	7	1.3568596	0.097999997	0.28898218	8
soy_OGL_3258	1200	5.2893763	7.4166665	1402	28.83	6	17.719536	0	0.83077192	17
soy_OGL_2344	1198	7.3284101	14.524207	1001	27.37	9	14.035109	0.022	0.2951422	8
soy_OGL_4014	1110	7.0667925	13.243243	2930	29	3	7.6479712	0	0.70223463	15
soy_OGL_4398	1100	8.2008438	6.2727275	8089	32.27	5	2.9729493	0	0.56000274	22
soy_OGL_1960	1114	6.5777268	13.913824	2209	28.99	6	9.4972534	0	0.49664935	25
soy_OGL_1662	1400	8.7383938	7.2857141	3755	30.71	8	5.6860275	0.061999999	0.62384731	13
soy_OGL_1866	1100	5.0498676	0	3241	34.45	5	14.265493	0.085000001	0.71427596	28
soy_OGL_379	1012	7.3968039	10.27668	2031	30.83	3	7.3726082	0.098999999	0.78913462	20
soy_OGL_3792	1000	3.1278274	13.6	2621	28.8	8	27.600634	0.113	0.65579826	10
soy_OGL_4211	1021	3.5955544	24.877571	3174	26.73	11	28.145926	0.108	0.24283104	16
soy_OGL_1356	1000	10.431696	5.5	7169	29.8	9	8.7797747	0.063000001	0.75927329	13

soy_OGL_2649	1100	7.4653587	0	4374	31.81	10	5.8213129	0.022	0.53948599	28
soy_OGL_2741	1100	5.9830751	11.727273	2353	27.27	13	14.803272	0.064000003	0.39942658	19
soy_OGL_4106	1000	12.218921	0	2137	31.9	6	2.7802658	0.039999999	0.69724375	19
soy_OGL_4384	1000	6.3989863	0	2596	34.7	10	36.293129	0.041000001	0.53754503	21
soy_OGL_5923	1077	8.3593283	5.7567315	2001	32.03	6	22.838839	0.075000003	0.83174098	15
soy_OGL_4334	1105	5.7800207	0	1229	31.04	8	5.3064528	0	0.45447266	21
soy_OGL_4757	1100	0.84740651	15.090909	3104	30.45	1	30.818483	0	0.7367081	5
soy_OGL_2097	1019	2.4134915	25.024534	1231	29.24	6	6.3490191	0.111	0.78069544	17
soy_OGL_2245	1600	2.4539056	12.25	1999	33.18	7	9.2535172	0.017999999	0.67848623	15
soy_OGL_4331	1225	6.1024008	16.244898	4188	29.87	8	4.2601452	0.089000002	0.44638017	20
soy_OGL_95	1087	10.343252	22.447102	7469	33.3	8	6.6642113	0.081	0.76439393	19
soy_OGL_569	1017	5.1880841	35.201572	2145	30.48	12	7.4330277	0.102	0.29657131	12
soy_OGL_572	1649	5.1880841	18.73863	1001	32.2	12	12.138191	0.012	0.29482213	12
soy_OGL_1606	1122	5.281703	29.500891	1001	32.08	5	4.373529	0.090999998	0.68039882	14
soy_OGL_4234	1073	4.5469155	30.195713	3183	34.94	8	15.782213	0.021	0.27293846	29
soy_OGL_6470	1000	5.050159	35.900002	4307	34.5	9	16.248323	0.075999998	0.61073118	11
soy_OGL_439	1200	6.6230578	26.083334	7581	38.16	7	2.4276423	0	0.66214865	14
soy_OGL_444	1053	3.7117856	33.143398	3738	28.86	7	12.468649	0.088	0.61951876	7
soy_OGL_567	1100	5.1880841	27.636364	3943	29.45	11	2.9672434	0.111	0.29692793	12
soy_OGL_3428	1077	3.4495571	38.625813	1001	29.34	6	17.038574	0.082999997	0.50971574	7
soy_OGL_5682	1202	9.2884445	20.715475	2159	29.78	6	2.0456254	0.059999999	0.46200383	14
soy_OGL_4261	1200	2.6054327	19	8059	31.41	4	6.7386851	0	0.33176848	13
soy_OGL_2307	1000	9.1589794	27.5	3839	28.4	9	5.223248	0.090999998	0.56283027	17
soy_OGL_2644	1200	7.4653587	18.583334	4506	36.16	6	6.1071692	0	0.54781121	26
soy_OGL_6028	1134	1.5537344	24.514992	8685	34.3	5	2.2369802	0.005	0.38246429	15
soy_OGL_481	1101	5.5857544	17.892824	1001	29.88	8	4.8894353	0	0.52421165	19
soy_OGL_1087	1000	7.5212369	21.1	2912	28.4	8	13.12507	0	0.91167301	11
soy_OGL_1334	1100	3.0309455	31.363636	1673	31.36	7	19.267431	0	0.69489342	11
soy_OGL_1883	1052	4.6904893	27.281368	3186	29.37	10	4.9506712	0.057999998	0.68653077	9
soy_OGL_1896	1049	9.4963474	15.919924	1001	29.64	9	5.9370546	0.013	0.65373868	14
soy_OGL_3406	1000	2.5044255	29.299999	1497	30.3	10	3.24791	0.022	0.65435022	9

soy_OGL_4323	1119	2.1383734	31.814119	1015	31.36	8	4.6630073	0.041999999	0.43622202	18
soy_OGL_5429	1103	6.0296702	22.212149	1265	29.73	5	4.6953516	0.050000001	0.98253691	11
soy_OGL_162	1100	3.7334805	20.454546	2664	32.27	5	12.720572	0	0.70927072	10
soy_OGL_1985	1100	9.6599522	16.818182	6453	34.9	7	9.981041	0	0.46945781	19
soy_OGL_2041	1000	0.71943778	37.799999	2302	34.2	3	4.2689471	0	0.37116921	7
soy_OGL_3035	1000	7.153666	28.5	4286	33.1	2	0.10158782	0	0.71202129	6
soy_OGL_3432	1100	3.4753761	20.90909	2281	29.45	8	9.2227039	0	0.5268448	9
soy_OGL_4025	1100	7.0667925	25.454546	2170	32	5	8.7926273	0.043000001	0.68134999	10
soy_OGL_4266	1000	3.4015584	25.4	4496	30.7	5	3.5985482	0.018999999	0.34334934	16
soy_OGL_5362	1000	8.8681479	25.299999	4250	32.8	6	7.921792	0	0.60222	11
soy_OGL_6111	1003	0.25847596	37.487537	2065	32.5	4	11.47816	0	0.68654186	5
soy_OGL_1357	1100	10.431696	0	2368	34.63	7	9.0831108	0.082999997	0.75999129	13
soy_OGL_6459	1040	5.8666077	13.75	1001	30.38	8	3.8819923	0.112	0.58582658	22
soy_OGL_6883	1400	4.5204587	0	2559	34.92	7	6.6311531	0.045000002	0.85471636	15
soy_OGL_1592	1042	5.281703	0	6662	33.68	8	13.74927	0.094999999	0.7183333	12
soy_OGL_5380	1000	8.9067116	0	2812	38.2	8	8.6423025	0.055	0.67914313	14
soy_OGL_1627	1100	3.0774791	18.454546	1166	31.18	1	16.430616	0.075000003	0.48261878	7
soy_OGL_442	1100	3.0958874	22.545454	4542	29.72	9	9.1333189	0.088	0.62219822	7
soy_OGL_1314	1400	2.0239863	0	2727	37.85	3	11.52931	0	0.60102099	13
soy_OGL_6380	1000	0.1485212	21.799999	4003	35.2	3	0.32607284	0.043000001	0.23102407	3
soy_OGL_6150	1000	4.9855185	22.799999	7154	34	8	18.346344	0.086000003	0.78451341	16
soy_OGL_1641	1063	4.9992714	0	3324	38.28	9	3.6076064	0.045000002	0.57949585	16
soy_OGL_2297	1158	9.808919	7.4265976	4314	36.01	9	18.405722	0.033	0.60279816	22
soy_OGL_2733	1200	7.717042	13.833333	3237	36	6	8.8036394	0.015	0.4090105	18
soy_OGL_2785	1000	3.0612319	23.1	2033	38.3	10	3.1734426	0.037	0.2277063	12
soy_OGL_4163	1131	0.61671168	18.21397	2486	36.87	3	17.320709	0	0.43464789	2
soy_OGL_4180	1000	18.090168	14.5	3878	39.6	5	7.5692778	0	0.17851406	15
soy_OGL_2246	1275	3.7894936	4.4705882	1001	31.92	8	6.811368	0	0.66642314	18
soy_OGL_2856	1100	5.5548873	0	3328	38.72	11	2.6755137	0	0.70859259	11
soy_OGL_4115	1000	8.1381798	2.9000001	3235	33.1	9	3.7095339	0	0.79094946	17
soy_OGL_6151	1100	4.9855185	0	1001	34.09	8	19.710842	0	0.7849884	16

soy_OGL_1885	1008	4.6904893	9.8214283	5639	32.73	10	6.8699603	0.077	0.68544453	9
soy_OGL_124	1042	4.7504425	6.1420345	8398	36.37	5	1.5182137	0	0.5643239	6
soy_OGL_141	1200	2.8892014	0	4121	38	5	10.410838	0	0.64749628	4
soy_OGL_2780	1016	2.5453448	20.669291	2128	32.48	5	1.2524463	0	0.24516784	8
soy_OGL_3084	1143	1.6525757	18.372704	2001	31.58	7	4.8543453	0.017999999	0.26306733	9
soy_OGL_3875	1140	2.5121698	23.947369	1001	32.36	5	0.69764072	0.021	0.22952789	6
soy_OGL_4338	1000	5.0690784	0	7179	34.5	9	14.914173	0.01	0.4619492	19
soy_OGL_5332	1000	6.2109938	8.1000004	1971	32.2	4	6.6747708	0.037	0.57695735	6
soy_OGL_6014	1010	1.5527503	20.09901	1048	30.69	5	5.2135324	0	0.49155101	7
soy_OGL_1802	1000	3.2149055	20.799999	3717	34.9	10	8.1887703	0	0.79145455	14
soy_OGL_1911	1000	9.2646599	18.700001	3915	33.5	11	7.4736209	0.028000001	0.6143344	12
soy_OGL_3093	1104	0.6157763	23.460144	1267	32.06	5	15.069901	0.032000002	0.34548154	7
soy_OGL_4202	1000	3.713707	25.1	4745	36.4	8	8.7749338	0	0.21674494	19
soy_OGL_4255	1000	9.2218924	24	2135	32.7	9	10.72535	0	0.311986	10
soy_OGL_5716	1000	7.9770703	0	2016	39.4	3	0.89941299	0	0.45568067	7
soy_OGL_6809	1000	6.2792668	10.6	7418	37.9	5	4.1205931	0	0.79695368	20

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WHAT IS CLAIMED IS:

1. A recombinant sequence, said recombinant sequence comprising:

a nongenic soybean genomic sequence of at least 1 Kb, said nongenic sequence being hypomethylated, targetable, located proximal to a genic region within a soybean genome, and exemplifying evidence of recombination; and

an DNA of interest, wherein the DNA of interest is inserted into said nongenic sequence.

2. The recombinant sequence of claim 1, wherein said nongenic sequence comprises the following characterstics:

a. the level of methylation of said nongenic sequence is 1% or less;

b. said nongenic sequence shares less than 40% sequence identity with any other sequence contained in the soybean genome;

c. said nongenic sequence is located within a 40 Kb region of a known or predicted expressive soybean coding sequence; and

d. said nongenic sequence exhibits a recombination frequency within the soybean genome of greater than 0.01574 cM/Mb.

3. The recombinant sequence of claim 1 or 2, wherein said nongenic sequence comprises a maximum length of 5.73 Kb.

4. The recombinant sequence of claim 1 or 3, wherein said nongenic sequence comprises 1% or less nucleotide methylation.

5. The recombinant sequence of any one of claims 1 to , wherein said nongenic sequence is 1 Kb to 5.73 Kb in length and contains no methylated cytosine residues.

6. The recombinant sequence of any one of claims 1, 3 to 5, wherein said nongenic sequence does not align with greater than 40% sequence identity to any other sequence within the soybean genome.

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7. The recombinant sequence of any one of claims 1, 3 to 6, wherein said nongenic sequence exemplifies evidence of recombination at a recombination frequency of greater than 0.01574 cM/Mb.

8. The recombinant sequence of any one of claims 1, 3 to 7, wherein a 40 Kb region of native soybean genome comprising said nongenic sequence also comprises at least one known or predicted soybean coding sequence, or a sequence comprising a 2 Kb upstream and/or 1 Kb downstream sequence of a known soybean gene.

9. The recombinant sequence of claim 8, wherein said known or predicted soybean coding sequence expresses a soybean protein.

10. The recombinant sequence of any one of claims 1 to 9, wherein said nongenic sequence does not contain a methylated polynucleotide.

11. The recombinant sequence of any one of claims 1 to 10, wherein one end of said nongenic sequence is within 40 Kb of an expressed endogenous gene.

12. The recombinant sequence of any one of claims 1 to 11, wherein said DNA of interest comprises an analytical domain.

13. The recombinant sequence of any one of claims 1 to 12, wherein said DNA of interest does not encode a peptide.

14. The recombinant sequence of any one of claims 1 to 12, wherein said DNA of interest encodes a peptide.

15. The recombinant sequence of any one of claims 1 to 14, 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.

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16. The recombinant sequence of claim 1, wherein said recombinant sequence comprises the following characteristics:

a. said nongenic sequence contains less than 1% DNA methylation;

b. said nongenic sequence exhibits a 0.01574 to 83.52 cM/Mb recombination frequency within the soybean genome;

c. said nongenic sequence exhibits a 0 to 0.494 level of nucleosome occupancy of the soybean genome;

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

e. said nongenic sequence has a relative location value from 0 to 0.99682 ratio of genomic distance from a soybean chromosomal centromere;

f. said nongenic sequence has a guanine/cytosine percent content range of 14.36 to 45.9%;

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

h. said nongenic sequence is located in a 1 Mb region of soybean genomic sequence that comprises one or more additional nongenic sequences.

17. A soybean plant, soybean plant part, or soybean plant cell comprising a recombinant sequence of any one of claims 1-16.

18. The soybean plant, soybean plant part, or soybean plant cell of claim 17, wherein said known or predicted soybean coding sequence expresses at a level ranging from 0.000415 to 872.7198.

19. The recombinant sequence of any one of claims 1 to 16, wherein said DNA of interest and/or said nongenic sequence are modified during insertion of said DNA of interest into said nongenic sequence.

20. A method of making a transgenic plant cell comprising a DNA of interest targeted to one nongenic soybean genomic sequence, the method comprising:

a. selecting an optimal nongenic soybean genomic locus;

b. introducing a site specific nuclease into a plant cell, wherein the site specific nuclease cleaves said nongenic soybean genomic sequence;

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

d. targeting the DNA of interest into said nongenic locus, wherein the cleavage of said nongenic sequence facilitates integration of the polynucleotide sequence into said nongenic locus; and

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

21. The method of making a transgenic plant cell of claim 20, wherein said DNA of interest comprises an analytical domain.

22. The method of making a transgenic plant cell of claim 20 or 21, wherein said DNA of interest does not encode a peptide.

23. The method of making a transgenic plant cell of claim 20 or 21, wherein said DNA of interest encodes a peptide.

24. The method of making a transgenic plant cell of any one of claims 20 to 23, wherein said DNA of interest comprises a gene expression cassette comprising a transgene.

25. The method of making a transgenic plant cell of any one of claims 20 to 24, 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.

26. The method of making a transgenic plant cell of any one of claims 20 to 25, wherein said DNA of interest is integrated within said nongenic locus via a homology directed repair integration method.

27. The method of making a transgenic plant cell of any one of claims 20 to 25, wherein said DNA of interest is integrated within said nongenic locus via a non-homologous end joining integration method.

28. The method of making a transgenic plant cell of any one of claims 20 to 27, wherein said selected nongenic locus comprises the following characteristics:

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a. said nongenic locus has less than 1% DNA methylation within the sequence;

b. said nongenic locus exhibits a 0.001574 to 83.52 cM/Mb rate of recombination within the soybean genome;

c. said nongenic locus exhibits a 0 to 0.494 level of nucleosome occupancy of the soybean genome;

d. said nongenic locus shares less than 40% sequence identity with any other 1 Kb sequence contained in the soybean genome;

e. said nongenic locus has a relative location value from 0 to 0.99682 ratio of genomic distance from a soybean chromosomal centromere;

f. said nongenic locus has a guanine/cytosine percent content range of 14.36 to 45.9%;

g. said nongenic locus is located proximally to an genic sequence; and,

h. a 1 Mb region of soybean genomic sequence comprising said nongenic locus comprises at least one second nongenic sequence.

29. The method of making a transgenic plant cell of claim 28, wherein said nongenic locus is at least 1 Kb in length.

30. The method of making a transgenic plant cell of claim 28 or 29, wherein a known or predicted soybean coding sequence, or a sequence comprising a 2 Kb upstream and 1 Kb downstream region of a known gene, is located within 40 Kb of said nongenic locus.

31. The method of making a transgenic plant cell of any one of claims 20 to 27, wherein said DNA of interest and/or said nongenic locus are modified during said integration of the polynucleotide sequence into said nongenic locus of step (d).

32. A purified nongenic soybean genomic sequence of at least 1Kb, said nongenic sequence being hypomethylated, targetable, located proximal to a genic region within a soybean genome, and exemplifying evidence of recombination.

33. The purified sequence of claim 32, wherein said nongenic sequence comprises the following characterstics:

a. the level of methylation of said nongenic sequence is 1% or less;

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b. said nongenic sequence shares less than 40% sequence identity with any other sequence contained in the soybean genome;

c. said nongenic sequence is located within a 40 Kb region of a known or predicted expressive soybean coding sequence; and

d. said nongenic sequence exhibits a recombination frequency within the soybean genome of greater than 0.01574 cM/Mb.

34. The purified sequence of claim 32 or 33, wherein said nongenic sequence comprises a maximum length of 5.73 Kb.

35. The purified sequence of claim 32 or 34, wherein said sequence comprises the following characteristics:

a. said nongenic sequence contains less than 1% DNA methylation in its native location;

b. said nongenic sequence, in its native location, exhibits a 0.01574 to 83.52 cM/Mb recombination frequency within the soybean genome;

c. said nongenic sequence exhibits a 0 to 0.494 level of nucleosome occupancy of the soybean genome, in its native location;

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

e. said nongenic sequence has a relative location value from 0 to 0.99682 ratio of genomic distance from a soybean chromosomal centromere in its native location;

f. said nongenic sequence has a guanine/cytosine percent content range of 14.36 to 45.9%;

g. said nongenic sequence is located within 40 Kb of a known or predicted soybean coding sequence, or a sequence comprising a 2 Kb upstream and 1 Kb downstream region of a known gene in its native location; and,

h. said nongenic sequence is located in a 1 Mb region of soybean genomic sequence that comprises one or more additional nongenic sequences in its native location.

36. A vector comprising the purified sequence according to any one of claims 32 to 35.

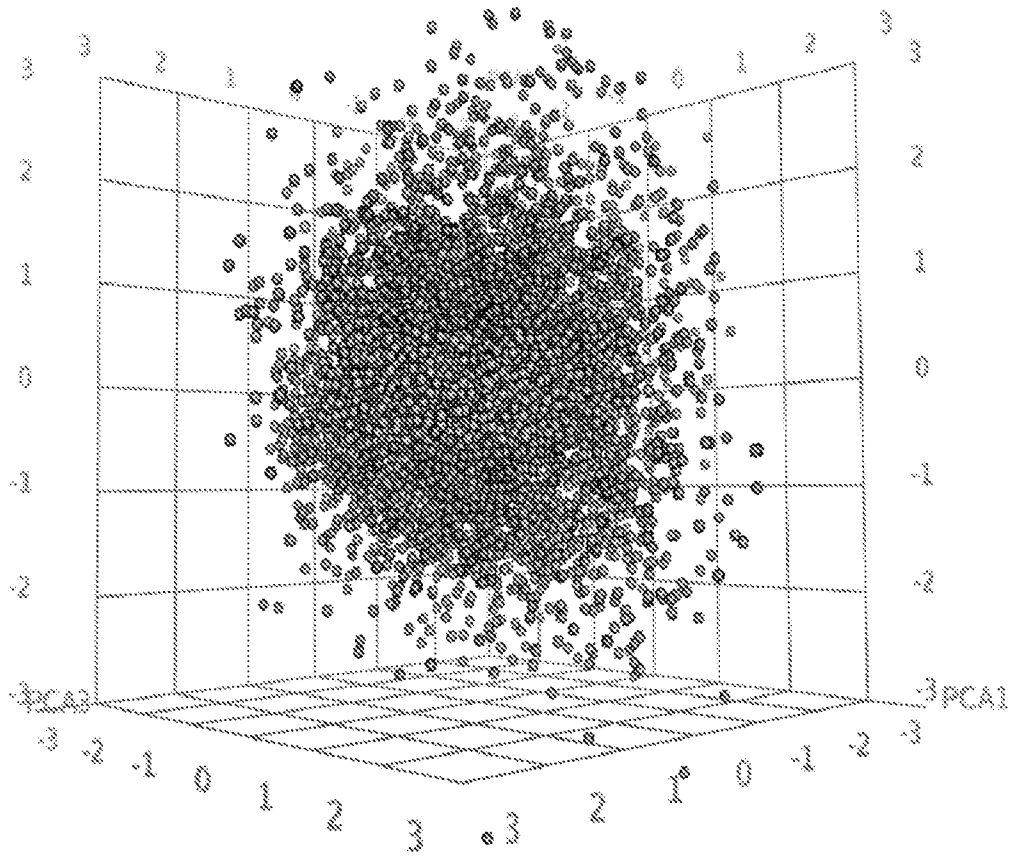


Fig. 1

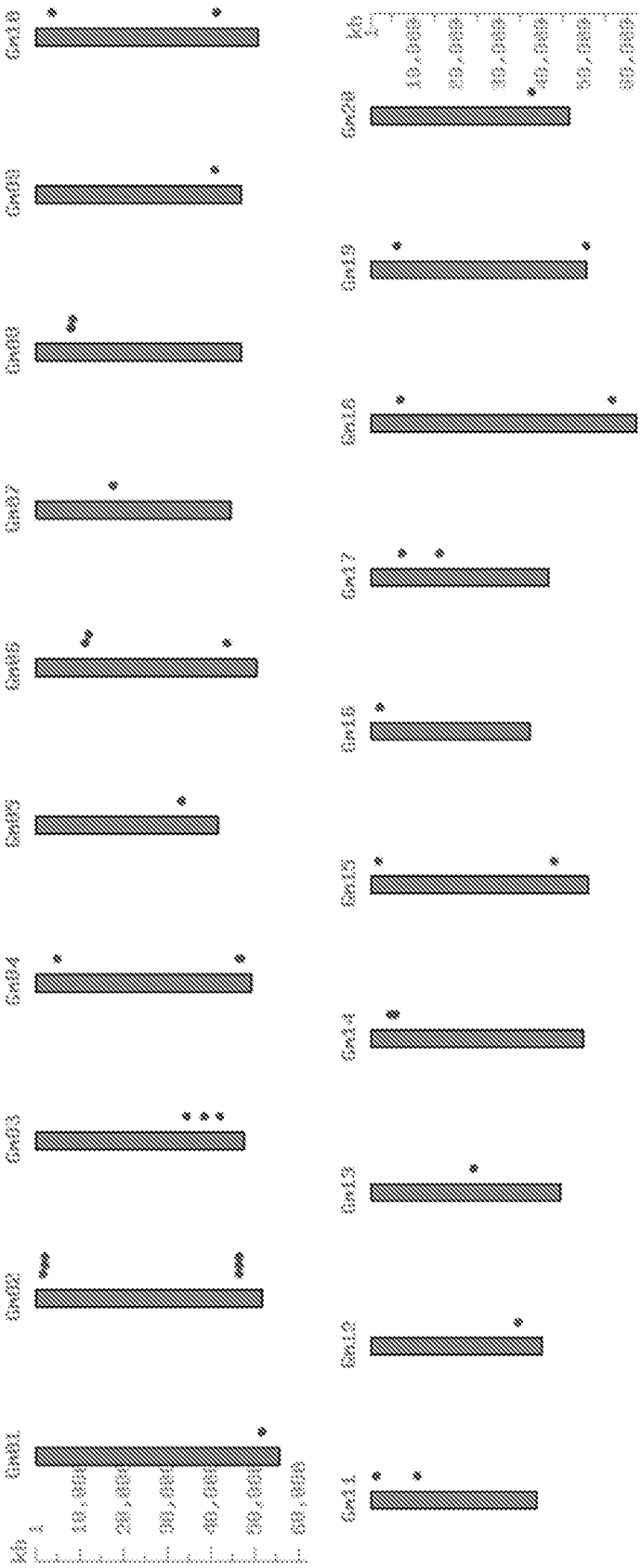


Fig. 2

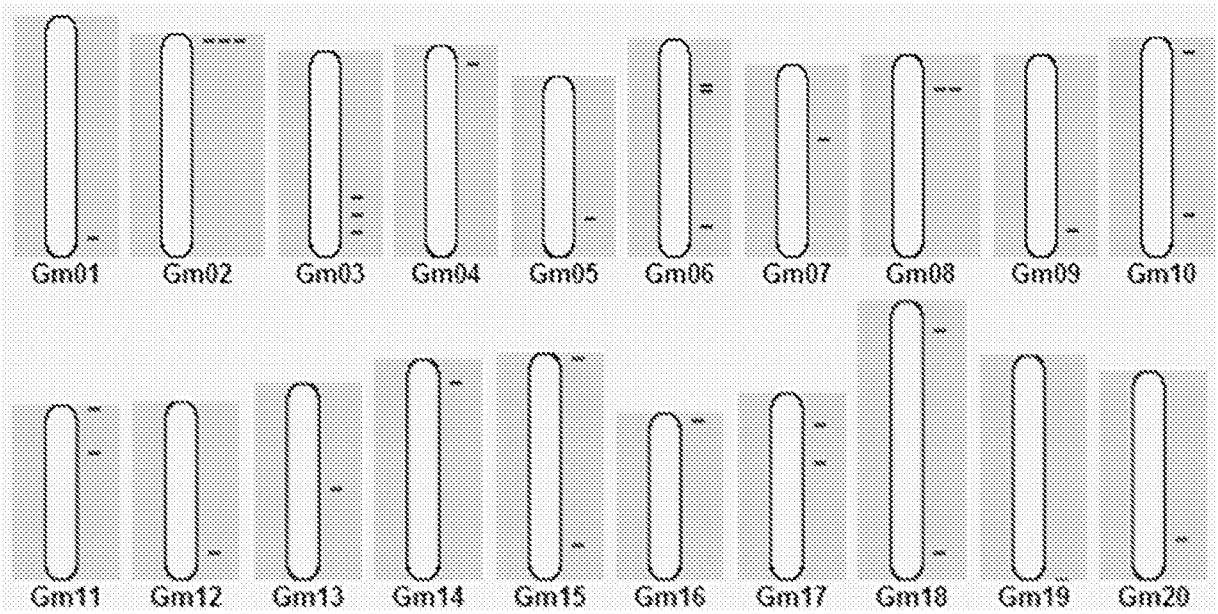

Gm01
Gm02
Gm03
Gm04
Gm05
Gm06
Gm07
Gm08
Gm09
Gm10
Gm11
Gm12
Gm13
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Gm17
Gm18
Gm19
Gm20

Fig. 3

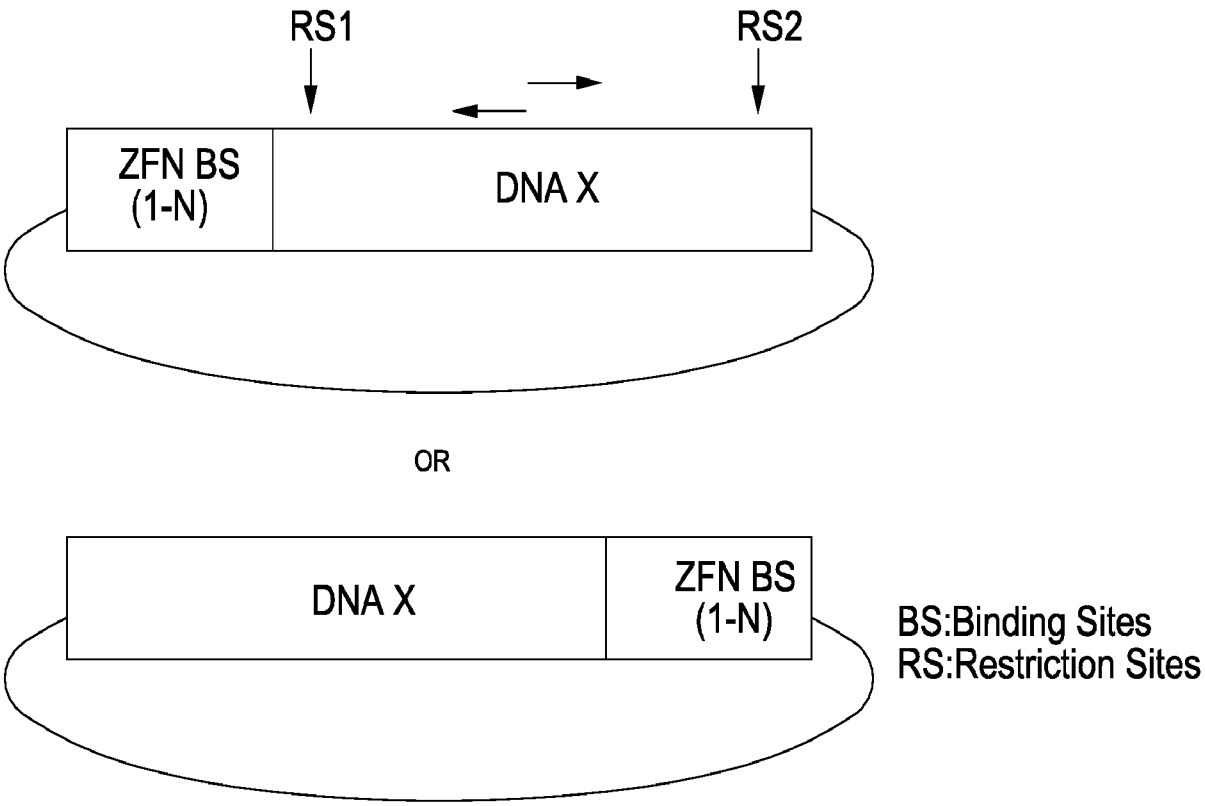

RS1
RS2
ZFN BS
(1-N)
DNA X
OR
DNA X
ZFN BS
(1-N)
BS:Binding Sites
RS:Restriction Sites

Fig. 4

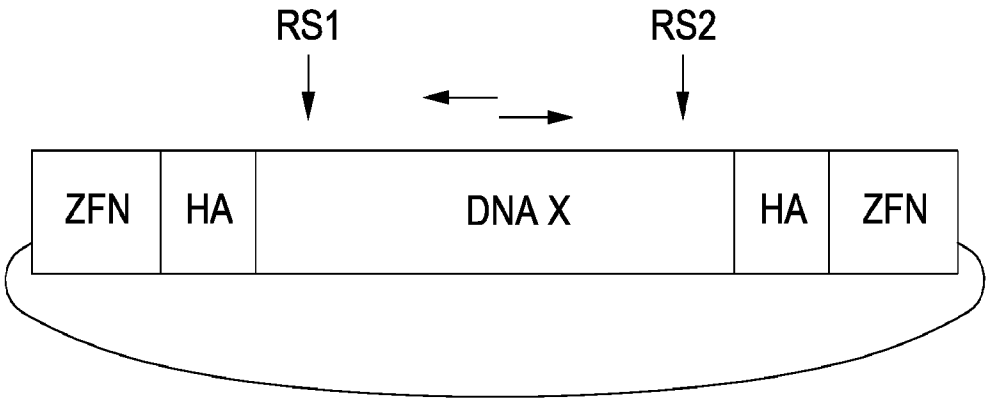

RS1
RS2
ZFN
HA
DNA X
HA
ZFN

Fig. 5

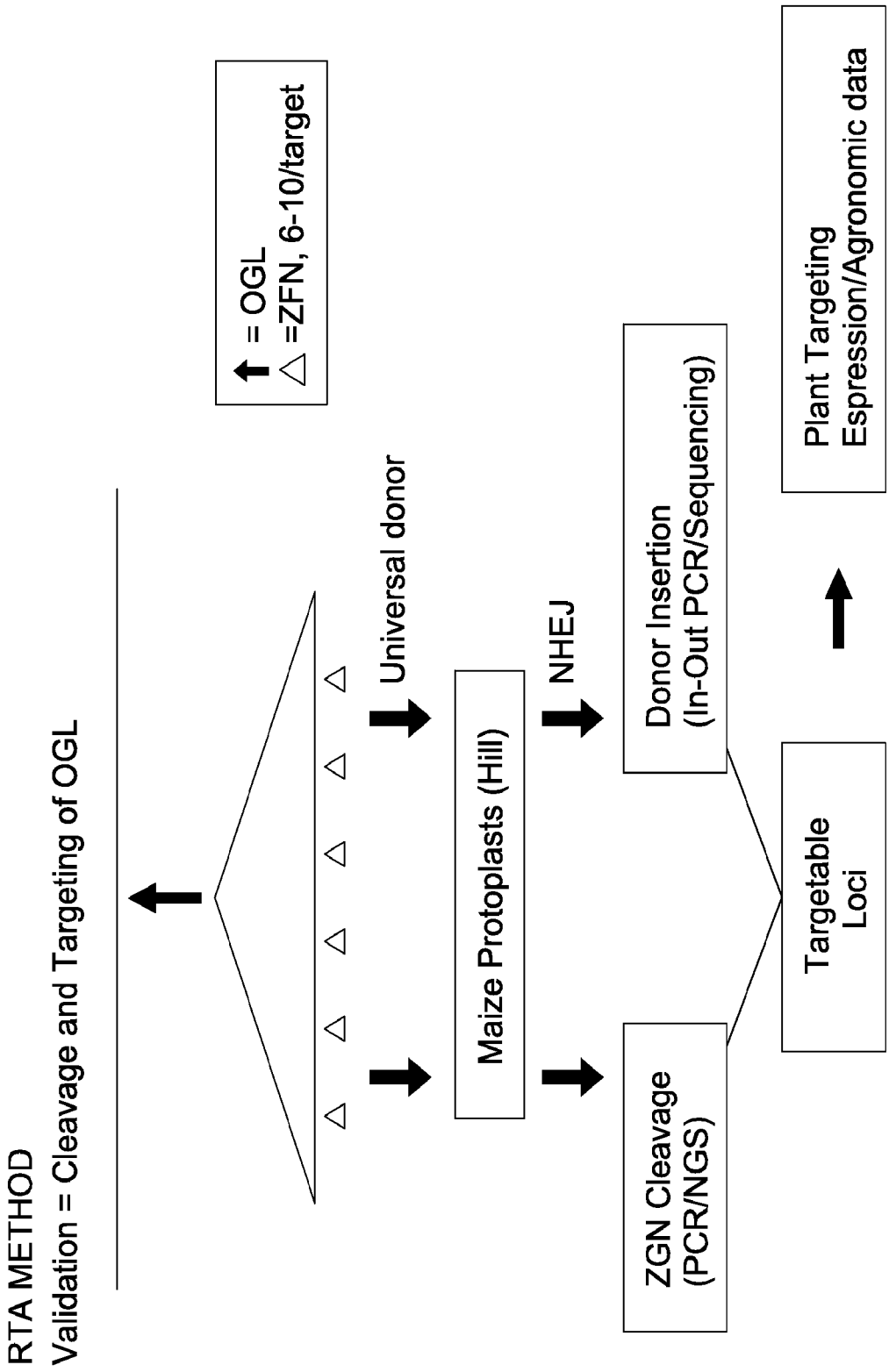

RTA METHOD
Validation = Cleavage and Targeting of OGL
= OGL
△ =ZFN, 6-10/target
Universal donor
Maize Protoplasts (Hill)
NHEJ
Donor Insertion
(In-Out PCR/Sequencing)
ZGN Cleavage
(PCR/NGS)
Targetable
Loci
Plant Targeting
Espression/Agronomic data

Fig. 6

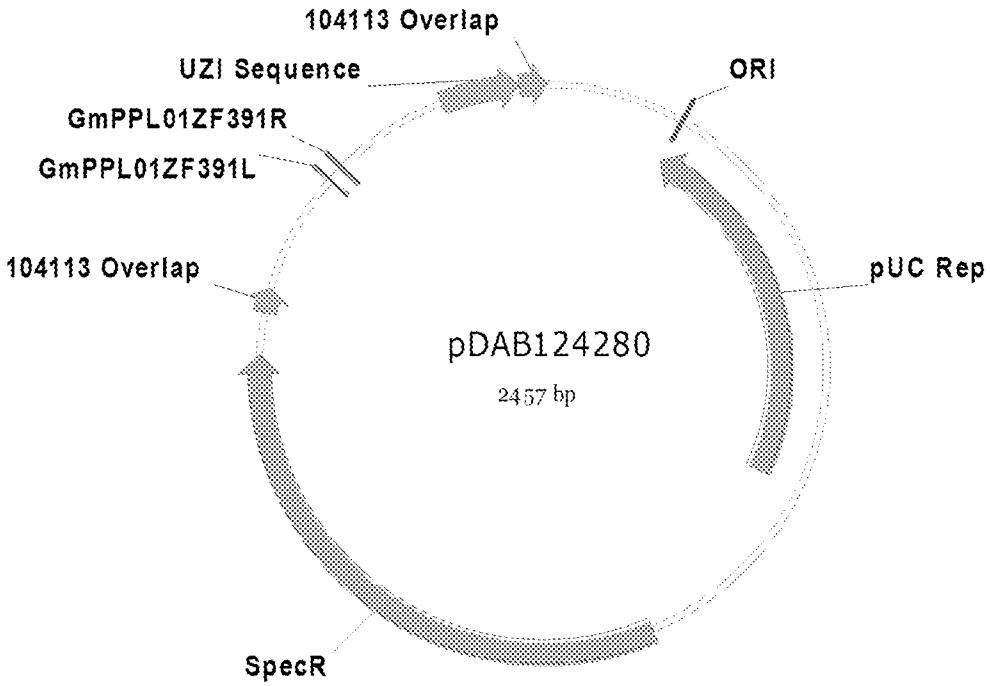

104113 Overlap
UZI Sequence
GmPPL01ZF391R
GmPPL01ZF391L
104113 Overlap
SpecR
ORI
pUC Rep
pDAB124280
2457 bp

Fig. 7

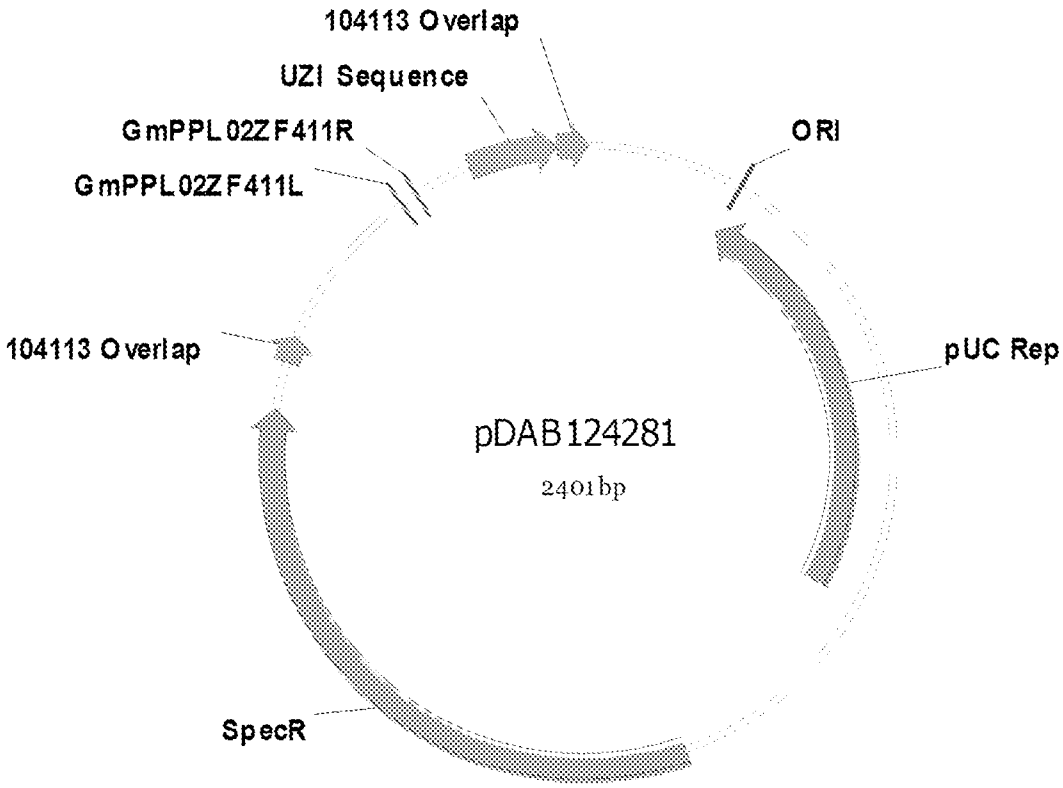

104113 Overlap
UZI Sequence
GmPPL02ZF411R
GmPPL02ZF411L
ORI
104113 Overlap
pUC Rep
pDAB124281
2401bp
SpecR

Fig. 8

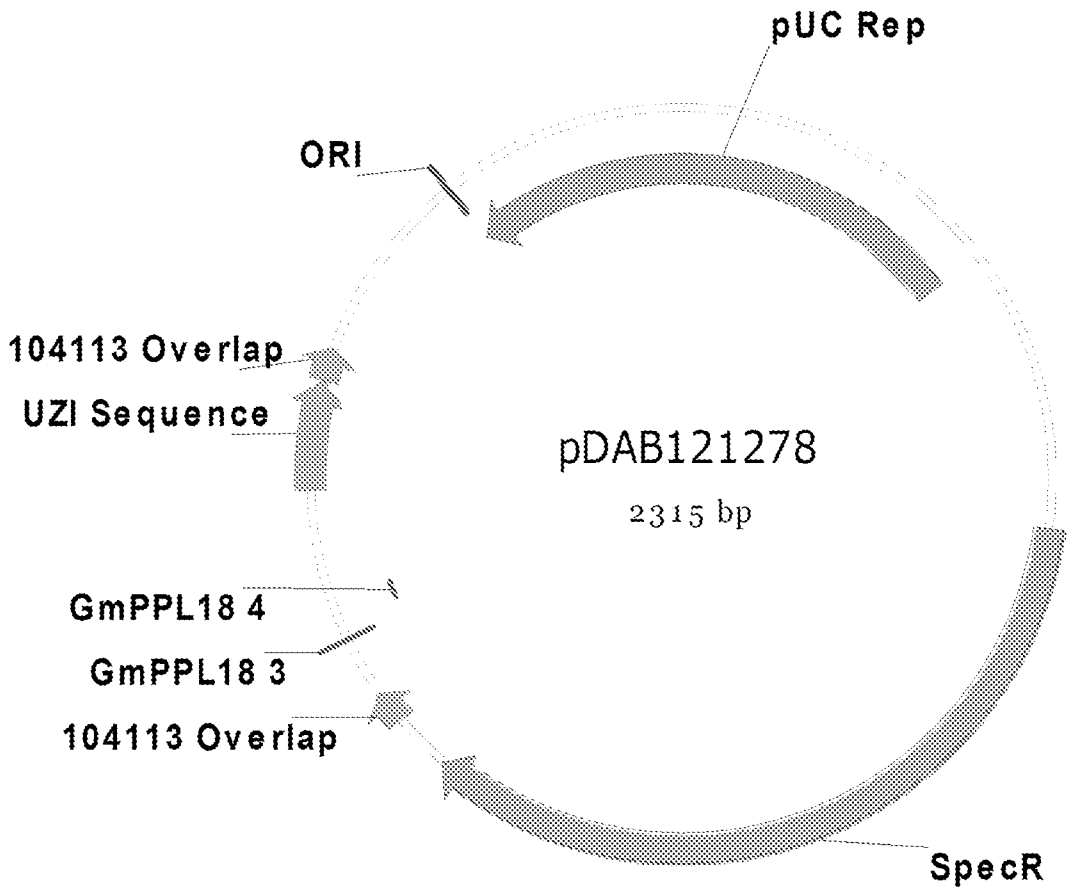

pUC Rep
ORI
104113 Overlap
UZI Sequence
pDAB121278
2315 bp
GmPPL18 4
GmPPL18 3
104113 Overlap
SpecR

Fig. 9

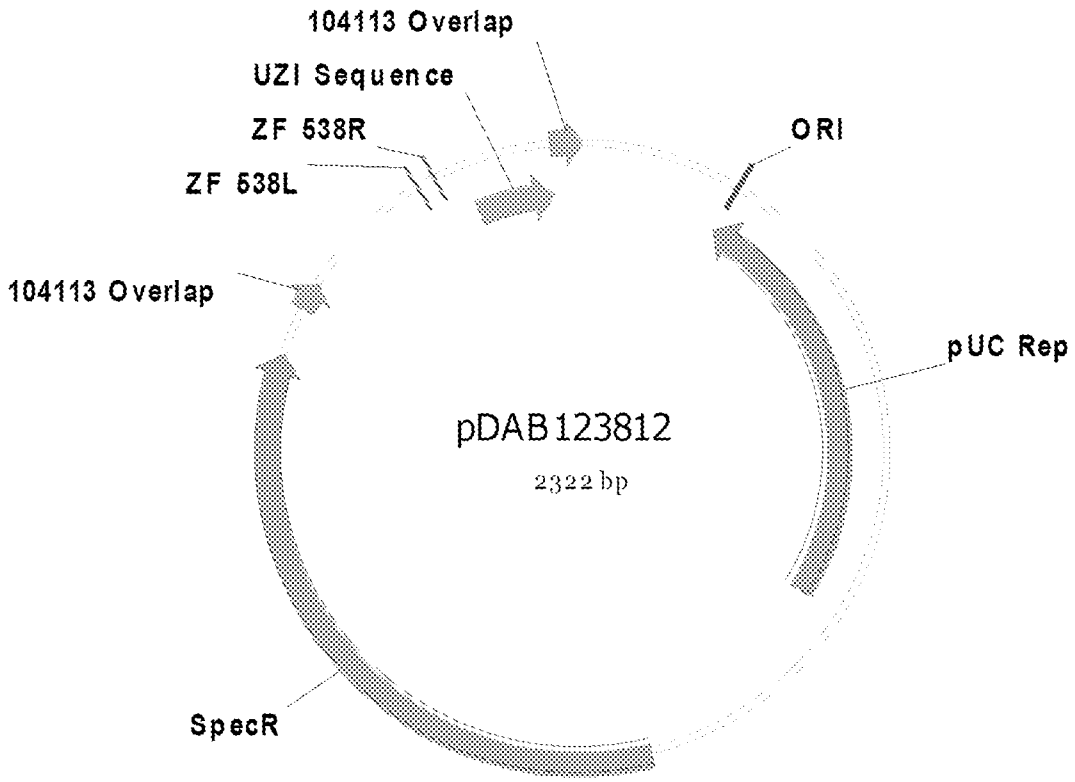

104113 Overlap
UZI Sequence
ZF 538R
ZF 538L
ORI
104113 Overlap
pUC Rep
pDAB123812
2322 bp
SpecR

Fig. 10

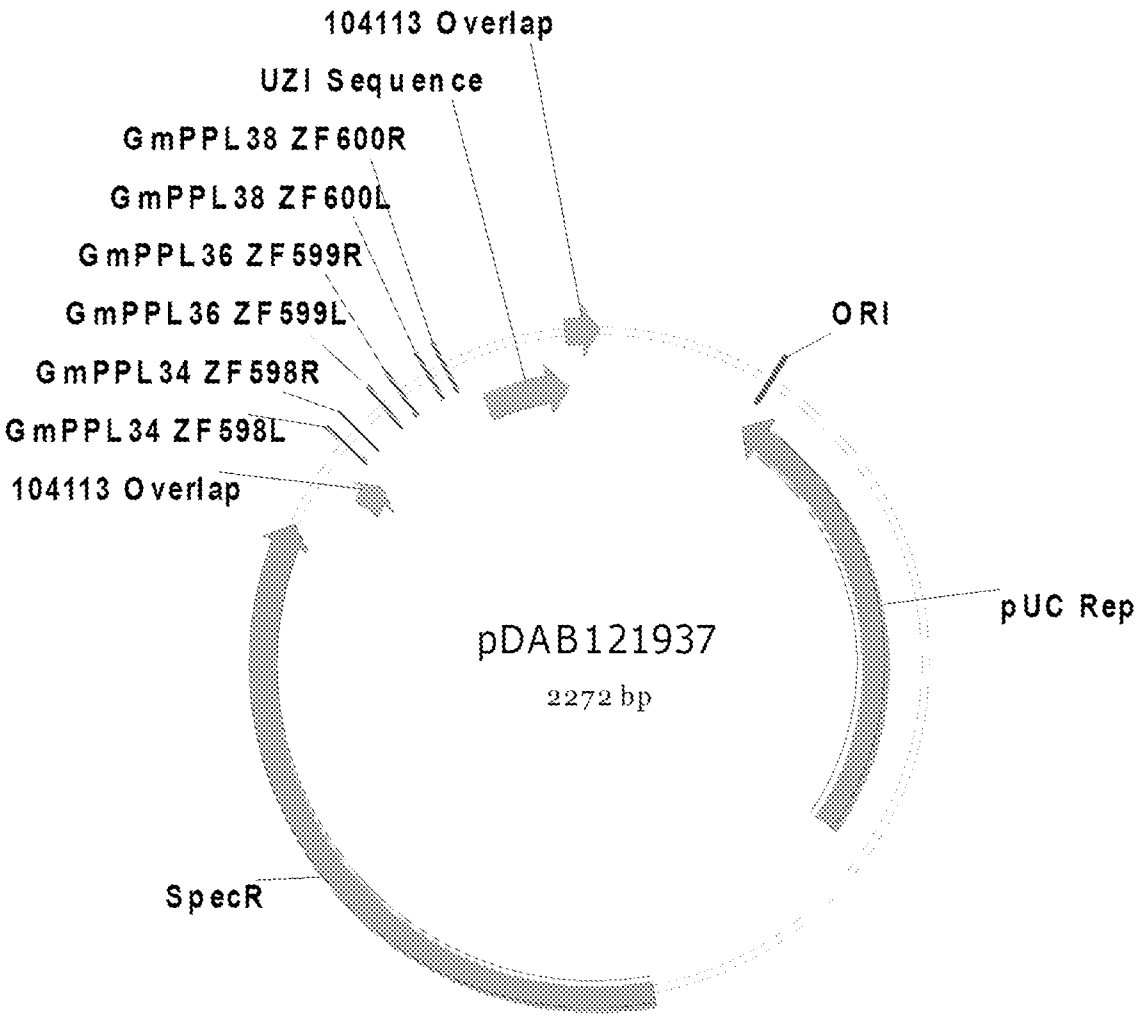

104113 Overlap
UZI Sequence
GmPPL38 ZF600R
GmPPL38 ZF600L
GmPPL36 ZF599R
GmPPL36 ZF599L
GmPPL34 ZF598R
GmPPL34 ZF598L
104113 Overlap
ORI
pUC Rep
SpecR
pDAB121937
2272 bp

Fig. 11

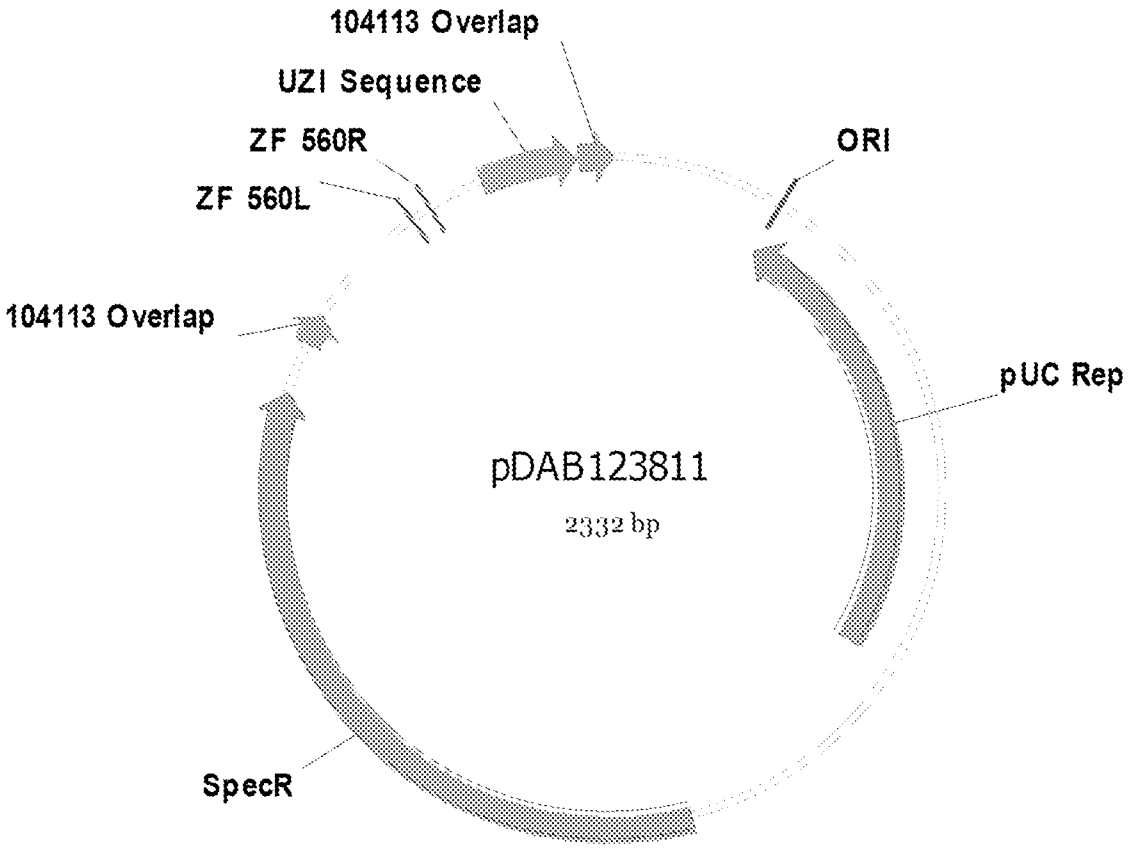

104113 Overlap
UZI Sequence
ZF 560R
ZF 560L
ORI
104113 Overlap
pUC Rep
pDAB123811
2332 bp
SpecR

Fig. 12

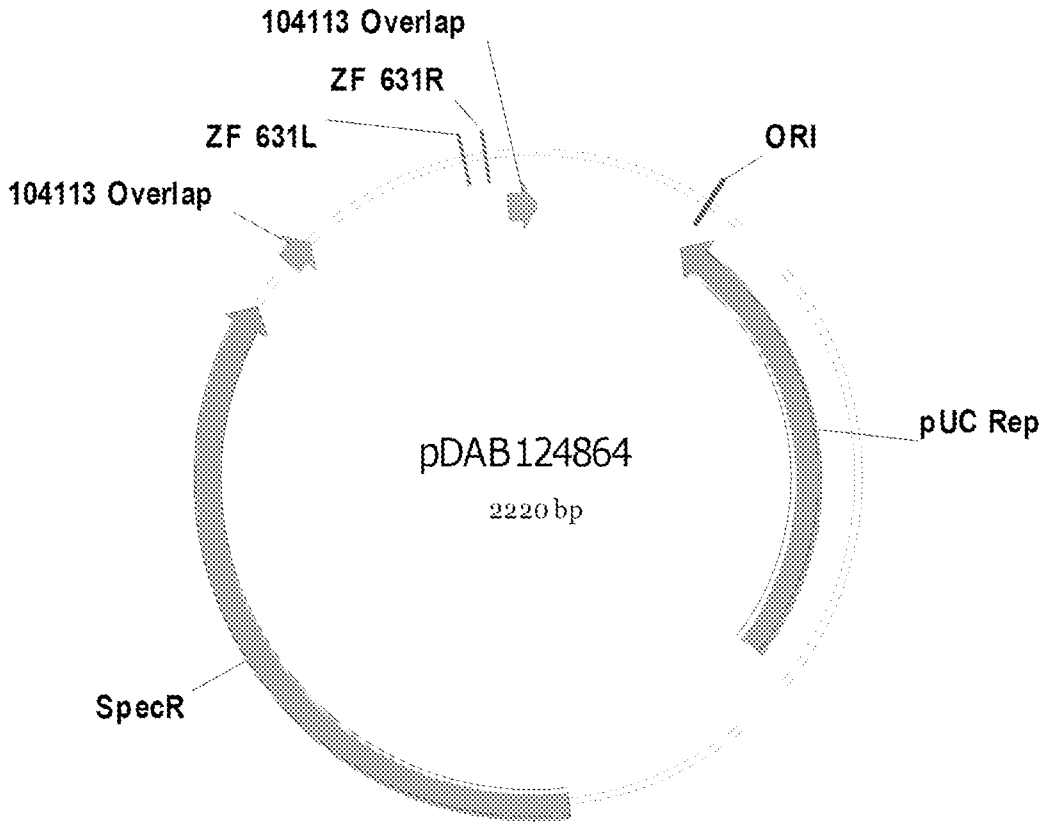

104113 Overlap
ZF 631R
ZF 631L
104113 Overlap
ORI
pUC Rep
pDAB124864
2220 bp
SpecR

Fig. 13

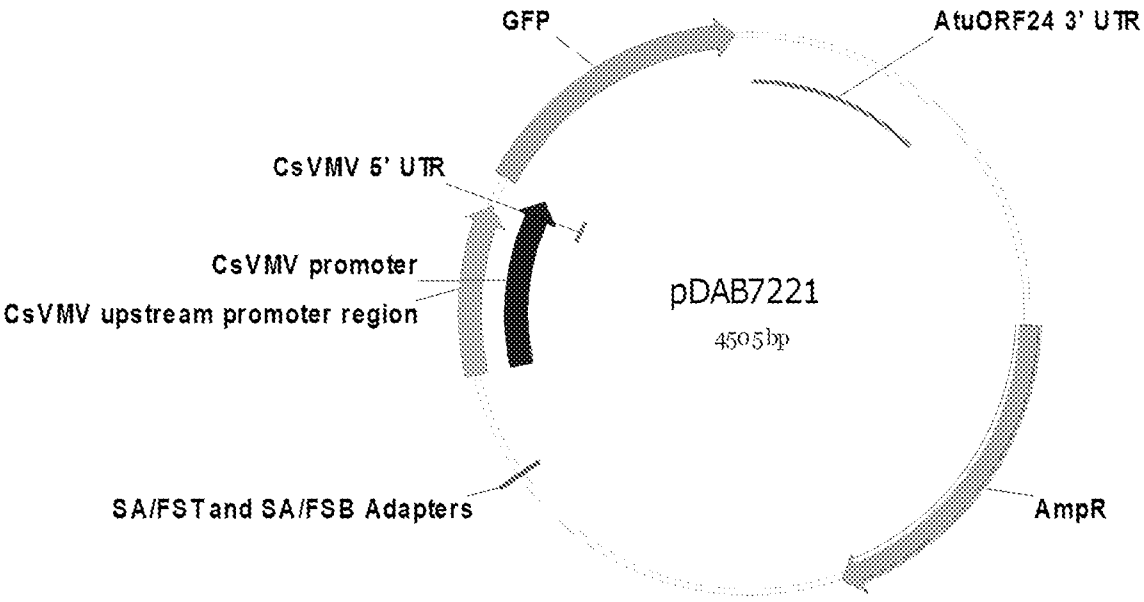

GFP
AtuORF24 3' UTR
CsVMV 5' UTR
CsVMV promoter
CsVMV upstream promoter region
pDAB7221
4505bp
SA/FST and SA/FSB Adapters
AmpR

Fig. 14

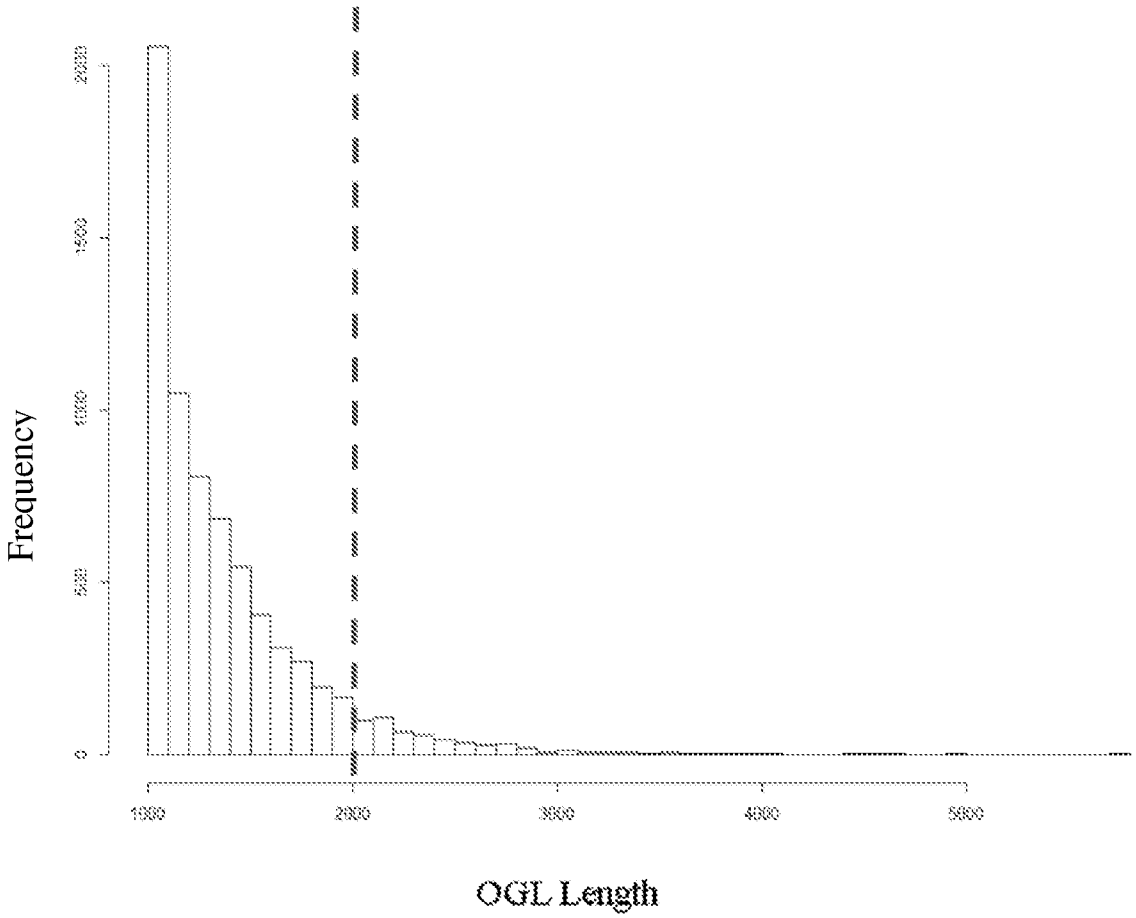


Fig. 15A

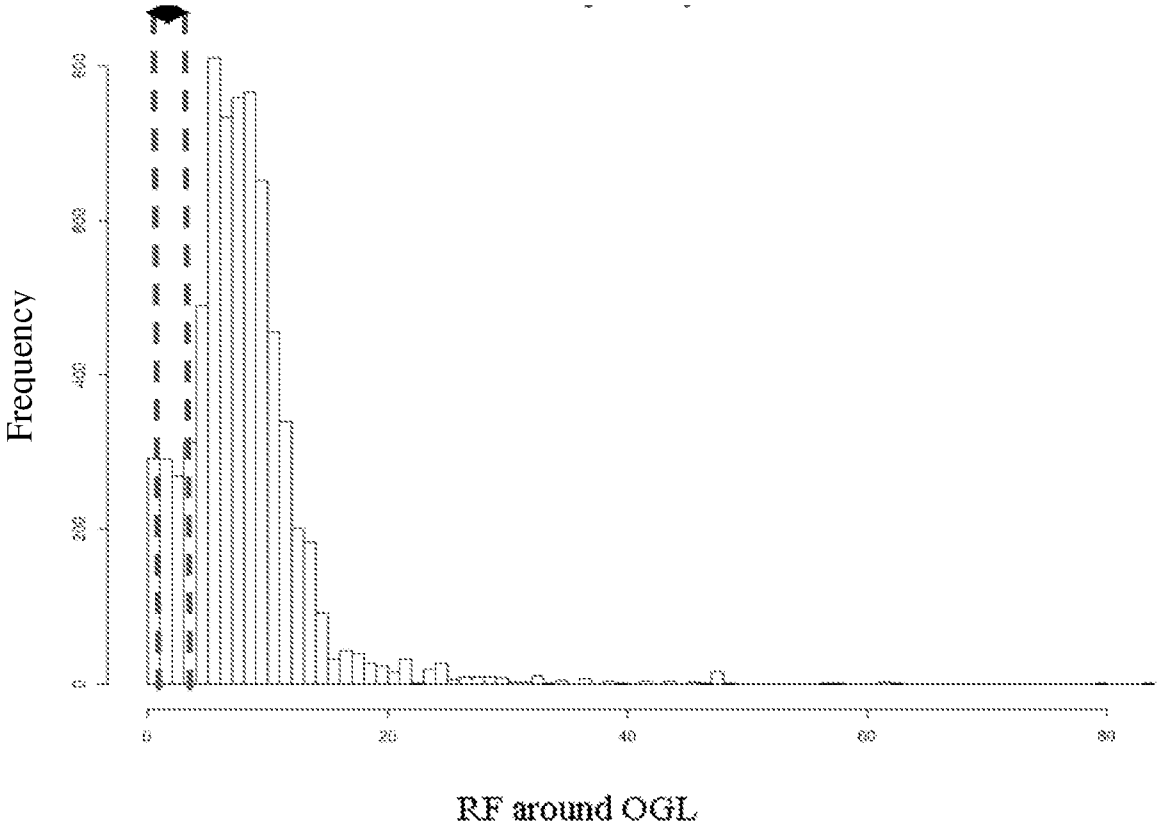


Fig. 15B

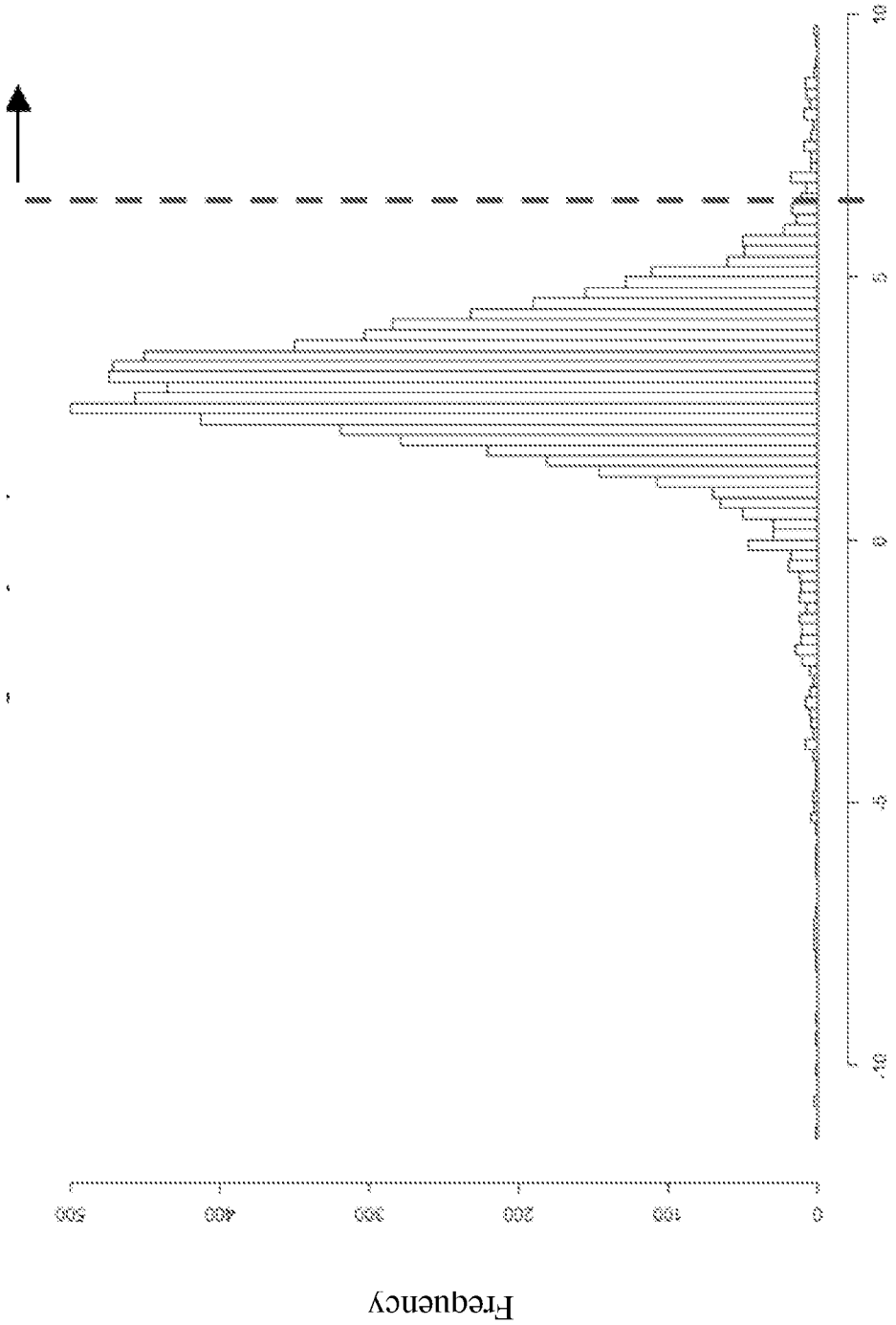

Frequency
0
100
200
300
400
500
10
5
0
-5
-10
Log2 expression around OGL

Fig. 15C

To whom it may concern,

Gene Sequence is available from IP Australia upon request.

Gene Sequence has been placed on the Y Drive.