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Title:

Identification of molecular variants of the nonrestoring *restorer-of-fertility 1* allele in sugar beet (*Beta vulgaris* L.)

Authors:

Takashi Ohgami¹, Daisuke Uchiyama¹, Sachiyo Ue¹, Rika Yui-Kurino¹, Yu Yoshida¹, Yoko Kamei¹, Yosuke Kuroda², Kazunori Taguchi², Tomohiko Kubo¹

Affiliations:

¹Research Faculty of Agriculture, Hokkaido University, N-9, W-9, Kita-Ku, Sapporo 060-8589, Japan

²Hokkaido Agricultural Research Center, National Agriculture and Food Research Organization, Memuro 082-0081, Japan

Correspondence to:

Tomohiko Kubo, tomohiko@abs.agr.hokudai.ac.jp, tel/fax +81-11-706-2484

Conflict of interest:

The authors declare that there is no conflict of interest.

Author contribution:

TK designed this study; YKu, KT and TK developed plant materials; TO, DU, SU, RYK, YY, YKa and TK performed the experiments and analyzed the data; TK wrote the manuscript.

Key Message:

Only three variants of nonrestoring alleles for sugar beet *Rf1* were found from the US maintainer lines which were the selections from a broad range of genetic resources.

Abstract

Cytoplasmic male sterility is widely used for hybrid breeding of sugar beets. Specific genotypes with a nonsterility-inducing cytoplasm and a nonrestoring allele of *restorer-of-fertility* gene (*rf*) are called maintainers. The infrequent occurrence of the maintainer genotype evokes the need to diagnose *rf* alleles.

Molecular analysis of *Rf1*, one of the sugar beet *Rf*s, revealed a high level of nucleotide sequence diversity, but three variants were tightly associated with maintainer selection in Japan. The question was raised whether this small number of variants would be seen in cases where a wider range of genetic resources was used for maintainer selection. Fifty-seven accessions registered as maintainers in the USDA germplasm collection were characterized in this study. Mitochondrial DNA types (mitotypes) of 551 plants were diagnosed based on minisatellite polymorphism. A mitotype associated with sterility-inducing (S) cytoplasm was identified in 58 plants, indicating S-cytoplasm contamination. The organization of *rf1* was investigated by two PCR markers and DNA gel blot analysis. Eight haplotypes were found among the US maintainers, but subsequently two haplotypes were judged as restoring alleles after a test cross and another haplotype was not inherited by the progeny. Nucleotide sequences of *rf1* regions in the remaining five haplotypes were compared, and despite the sequence diversity of the gene-flanking regions, the gene-coding regions were identified to be three types. Therefore, there are three *rf1* variants in US maintainers, the same number as in the Japanese sugar beet germplasm collection. The implications of having a small repertoire of *rf1* variants are discussed.

Key words

cytoplasmic male sterility, F1 hybrid, genetic resources, marker-assisted selection, nuclear-mitochondrial interaction, *Rf* gene

Introduction

Cytoplasmic male sterility (CMS) is the inability of plants to produce functional pollen (Schnable and Wise 1998). Genetic models to explain CMS expression postulate the interaction of male-sterility inducing cytoplasm (S) and alleles of a nuclear *restorer-of-fertility* gene (*Rf*) that together affect pollen development. Under this genetic model, CMS is expressed when a plant has the genotype S-*rf**rf*, where *rf* denotes the nonrestoring allele of *Rf*. Plants shed functional pollen grains with the other genotypes such as N-*rf**rf*, where N denotes a non-male-sterility inducing cytoplasm, or S-*Rf*_, where *Rf* denotes a restoring allele.

CMS is a prerequisite for hybrid seed production in some crop species (Budar et al. 2006) providing the ideal seed parent; the seeds set on CMS plants are exclusively hybrids as CMS plants cannot self-pollinate. On the other hand, CMS lines cannot be maintained or propagated by selfing. For this purpose, a specific line with the same nuclear genotype as the CMS line but with the N cytoplasm to secure pollen production is necessary. Plant lines with this genotype (i.e. N-*rf**rf*) are called maintainer lines, and the *rf* allele is sometimes called a maintainer allele.

Maintainer lines are highly valuable in some crop species because of the infrequent occurrence of the maintainer genotype. For example, the frequency of the maintainer genotype in sugar beet is 3-5% on average (Bosemark 2006). Large scale screening for maintainer lines is laborious because the *Rf/rf* genotype is known only by conducting test crosses using the CMS line as a tester. Consequently, the efficiency of maintainer line selection is very low and a major rate-limiting process for sugar beet breeding. The introduction of DNA marker assisted selection (MAS) would facilitate more efficient maintainer line selection.

As molecular studies on the genetic factors involved in sugar beet CMS have progressed, the level of molecular diversity of cytoplasm and *Rf* genes has been found to be greater than expected. In *Beta vulgaris*, there are more than ten cytoplasm types that can be distinguished by their mitochondrial DNA organization (Cuguen et al. 1994). Mitochondrial DNA types (mitotypes) can be discriminated by length polymorphism of four mitochondrial minisatellite loci that are composed of tandem arrays of nucleotide sequence units (30-66 base pairs) (Nishizawa et al. 2000; Nishizawa et al. 2007). In Japanese and Chinese sugar beet lines, two mitotypes were identified from N cytoplasm plants, whereas one mitotype was identified from S cytoplasm plants on the basis of mitochondrial minisatellite polymorphism (Cheng et al. 2009).

According to Owen (the discoverer of sugar beet CMS), there are two *Rf*s for sugar beet CMS (Owen 1945). The two *Rf*s, termed *X* and *Z* by Owen, have been genetically mapped on chromosomes 3 and 4, respectively (Pillen et al. 1993; Hjerdin-Panagopoulos et al. 2002; Honma et al. 2014). A strong allele of *X* was found in a Japanese sugar beet line and was named *Rf1* (Hagihara et al. 2005). Nucleotide sequence analysis of the *Rf1* locus revealed a gene cluster composed of four copies of genes encoding a protein resembling yeast OMA1, which is involved in the quality control of mitochondrial inner-membrane proteins (Matsuhira et al. 2012). Hereafter, we refer to such sugar beet genes resembling yeast *Oma1* as *Oma1*-like genes. One of the four *Oma1*-like gene copies, *bvORF20*, restored partial pollen fertility to CMS sugar beet when expressed as a transgene (Matsuhira et al. 2012). Additionally, the protein product of *bvORF20* was shown to bind to a 39-kDa mitochondrial protein that is encoded by S mitochondria (Kitazaki et al. 2015). Expression of *bvORF20* is predominant in immature anthers, and, concomitant with its expression, the amount of a protein complex that includes the 39-kDa protein is reduced (Kitazaki et al. 2015). Detailed analysis of an *rf1* allele of a Japanese maintainer line revealed a solitary *Oma1*-like gene instead of clustered copies (this solitary gene is named *bvORF20L*) (Matsuhira et al. 2012). The protein product of *bvORF20L* is incapable of binding to the 39-kDa mitochondrial protein (Kitazaki et al. 2015).

Investigation of the molecular organization of the *Rf1* in Japanese sugar beet lines revealed that the *Rf1* locus has multiple molecular variants and only a few variants are associated with maintainer selection (Moritani et al. 2013; Taguchi et al. 2014). This finding suggests that, although the entire molecular

diversity of sugar beet *Rfl* is unknown, the repertoire of molecular variants associated with maintainer alleles is small. Thus, a better approach for MAS of a maintainer line is tagging the maintainer allele for selection, instead of purging the restoring allele. MAS for one of the identified molecular variants was conducted, and the maintainer genotype was enriched from breeding materials (Moritani et al. 2013).

There are three identified molecular variants associated with Japanese maintainer lines: one occurs predominantly and the others are less frequent (Taguchi et al. 2014). However, it is too early to conclude that only three *rfl* maintainer-allele variants exist in the entire sugar beet gene pool because the genetic diversity of the Japanese sugar beet population is small (Taguchi et al. 2006). Hence, a small number of maintainer-allele variants might merely reflect this small genetic diversity. To examine this possibility, we investigated maintainer lines that were selected from a population whose genetic diversity is larger than that of Japanese sugar beet.

Since the discovery of sugar beet CMS by Owen, the United States (US) has continued hybrid breeding of sugar beet using a number of European cultivars and wild beets (sources of disease resistance) (Lewellen 1992), from which US maintainer lines were selected (Hecker and Helmerick 1985). Moreover, the total genetic diversity in the US germplasm pool has remained constant since the 1920s (McGrath et al. 1999). Therefore, the US maintainer lines have likely been selected from a more diverse population than the population used in Japan. As such, additional molecular variants of the maintainer allele, if any, might be expected in the US maintainer lines. To test this hypothesis, we examined the mitotypes and *rfl* organization of maintainer lines obtained from the US Department of Agriculture (USDA). Surprisingly, from the viewpoint of amino acid sequences encoded by *Oma1*-like genes, the repertoire of molecular variants of the maintainer allele is the same as that of the Japanese sugar beet accessions, suggesting that the number of maintainer-allele variants in sugar beet is constant and that MAS for these maintainer-allele variants is possible.

Materials and methods

Plant materials and male fertility phenotyping

US sugar beet accessions used in this study are listed in Table 1. These accessions were retrieved as follows: first, Germplasm Resources Information Network (http://www.ars-grin.gov/npgs/acc/acc_queries.html) was searched using ‘O-type’ (the sugar beet terminology for maintainer genotype is O-type, after Owen) as a query word, then diploid accessions were selected. The fifty-seven accessions listed in Table 1 include three accessions originating from the Soviet Union, one from Poland, and the remaining accessions are from California (22 accessions), Colorado (16),

Maryland (8), Michigan (4), and Utah (4) as described at the website. NK-219mm-O is a Japanese maintainer line developed by the Hokkaido Agricultural Research Center (HARC), National Agriculture and Food Research Organization (NARO), Japan (Moritani et al. 2013). Seeds were sown in a greenhouse and plants were grown in an experimental field at Hokkaido University. Sugar beet roots were kept in a cold room (4°C) of HARC/NARO at Memuro during the winter for vernalization. Test crosses were done using TA-33BB-CMS, an annual CMS line developed by HARC/NARO (Moritani et al. 2013), as the seed parent. Inflorescences of TA-33BB-CMS plants were covered with paper bags before anthesis. Following the flowering of bag-enclosed plants, the edge of the bag was cut and the male-sterile flowers were pollinated with pollen from a single parental plant, then the bag was resealed. Self-pollination was accomplished by covering individual plants with paper bags. Male fertility was determined by visual inspection of anther color and morphology for more than three different days, and classified into fertile-, partially-fertile-, and completely sterile classes according to Onodera et al. (2015). Fisher's exact test was used at the website of Gunma University (<http://aoki2.si.gunma-u.ac.jp/exact/fisher/getpar.html>).

Isolation of total cellular DNA

Fully expanded green leaves were powdered in liquid nitrogen and used for DNA isolation according to the procedure of Doyle and Doyle (1990). If necessary, sample DNAs were purified by CsCl continuous density gradient centrifugation (Sambrook et al. 1989).

DNA markers

Details about DNA markers for mitochondrial minisatellites were described in Nishizawa et al. (2000) except for TR-1 amplification, in which the primer nucleotide sequences are 5'-AGAACTTCGATAGGCGAGAGG-3' and 5'-TTCCAATTACTCTACCCCGCT-3'. PCR products of TR-1 and TR-3 from a single plant were mixed and electrophoresed in 5% polyacrylamide gels. Nucleotide sequences of oligonucleotide primers and protocols for *orf129*-, *s17*-, and 20L-int PCR markers are detailed in Cheng et al. (2011), Taguchi et al. (2014), and Moritani et al. (2013), respectively. PCR products of *s17* were digested with restriction endonucleases *HindIII* and *HapII* (Takara Bio, Ohtsu, Japan). If necessary, PCR products of 20L-int were digested with *HindIII* (Takara Bio).

DNA gel blot hybridization

About 1 µg of total cellular DNA was digested with *Hind*III (Takara Bio). DNA fragments were separated by electrophoresis using a 1.0% agarose gel. Following electrophoresis, the gel was soaked in a NaOH solution to denature the DNA fragments and then neutralized according to the procedure described in Sambrook et al. (1989). Capillary blotting onto Biodyne B Nylon Membrane (Pall, Port Washington, NY) was done according to the manufacturer's instruction manual. Hybridization probes were prepared as detailed in Matsuhira et al. (2012), and labeled with the AlkPhos Direct Labeling and Detection System (GE Healthcare UK Ltd, Amersham Place England). Hybridization signals were detected on X-ray film according to the manufacturer's protocol.

Genome library construction and screening

A genomic library was constructed using total cellular DNA as described in Sambrook et al. (1989). Briefly, sample DNA was partially digested with restriction endonuclease *Sau*3AI (Takara Bio) to generate ~20-kbp DNA fragments that were then size-fractionated by centrifugation on 10-40% sucrose continuous density gradients. Fractions containing 16-23-kbp DNA fragments were collected and the fragments were ligated to λ DASH II (Agilent Technologies, Santa Clara, CA), a replacement-type λ phage vector. Concatenated DNA was packaged *in vitro* using Gigapack III Gold (Agilent Technologies) to form phage particles that were then infected with *E. coli* strain P2392. Recombinant phage plaques (~1 x 10⁶ in total) were transferred onto Hybond N+ membranes (GE Healthcare). Probes were labeled using the ECL Direct Nucleic Acid Labeling and Detection System (GE Healthcare), and plaque hybridization was conducted according to the manufacturer's instructions. Phage DNA was isolated by the liquid culture method (Sambrook et al. 1989).

Primer walking and nucleotide sequencing

PCR products for nucleotide sequencing were amplified with PrimeSTAR GXL DNA Polymerase (Takara Bio), a high fidelity DNA polymerase. PCR products were cloned into the pBluescript II plasmid vector or subjected to direct sequencing. Nucleotide sequences were determined by using an ABI3130 Genetic Analyzer (Life Technologies, Carlsbad, CA). Sequence data were assembled using Sequencher software (ver. 4.0) (Gene Codes Corporation, Ann Arbor, MI). Homology searching was done at the website of the National Center for Biotechnology Information (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>). Nucleotide and amino-acid sequences were aligned using ClustalW at the National Institute of Genetics, Japan (<http://clustalw.ddbj.nig.ac.jp/index.php?lang=ja>). Nucleotide sequences were deposited in DDBJ/EMBL/GenBank under accession numbers LC085626, LC085627, LC685268, and LC085629.

Results

Mitotypes of US maintainer lines

A brief description of mitochondrial minisatellites in beet is necessary before presenting the results of this study. Sugar beet mitotypes are characterized based on the organization of four mitochondrial minisatellites, TR-1 to TR-4 (Cheng et al. 2009). The number of repeated sequence units (30-66 base pairs) in the four loci is characteristic of each mitotype. For example, if a plant has thirteen repeated-sequence units in TR-1, three in TR-2, three in TR-3, and three in TR-4, these numbers are coded as [13, 3, 3, 3] and the mitotype of this plant is min18 (Cheng et al. 2009). In sugar beet, min18, min09 ([6, 3, 3, 3]), and min04 ([4, 3, 2, 4]) have been reported and correspond to Normal-1-, Normal-2- (both are subclasses of N cytoplasm), and S cytoplasms, respectively (Cheng et al. 2009). Therefore, not all of the minisatellites have to be investigated to distinguish these three cytoplasms. We selected TR-1 and TR3 for mitotype identification.

In this study, we determined the mitotypes of a total of 551 plants from 57 accessions listed in Table 1. TR-1 and TR-3 from all 551 plants were PCR amplified. The expected size of TR-1 is 698, 474, and 410 bp and the expected size of TR-3 is 442, 442 and 376 bp for Normal-1, Normal-2, and S, respectively. Hence, if mixed PCR products of TR-1 and TR-3 from a plant were electrophoresed, specific band patterns corresponding to either Normal-1, Normal-2, or S would be evident on the gel. Fig. 1 shows the band patterns of these mitotypes. Plants used in this study were classified into Normal-1, Normal-2, or S, except for some plants from accessions PI 411128 and PI 633934, from which an unexpected band pattern emerged (Fig. 1). We PCR amplified all four minisatellites from these plants, and the resultant PCR products were sequenced to determine the unit number of each of the mitochondrial minisatellites. Our results showed that the code of unit numbers was [5, 3, 2, 3], corresponding to min06 (Cheng et al. 2011). Mitotype min06 can be further subdivided into two groups according to the presence or absence of *orf129*, a mitochondrial gene that is associated with a wild beet-derived CMS (a different cytoplasm from sugar beet S) (Yamamoto et al. 2008). Therefore, DNA samples of the min06 plants of PI 411128 and PI 633934 were subjected to PCR amplification targeting *orf129*, but no amplicon was observed. Thus, the mitotype was identified as min06/*-orf129*, which has been found from other cultivated beets (Cheng et al. 2011). No CMS has been associated with min06/*-orf129* as far as we know. All PI 411128- and PI 633934 plants in question were min06/*-orf129* according to their mitochondrial minisatellite pattern and the presence/absence of the *orf129* sequence.

In summary, of the 551 plants listed in Table 1, there were 272 Normal-1 and 191 Normal-2 plants. We found 30 plants of min06/*-orf129*. The remaining 58 plants have the S cytoplasm. Plants from accessions PI

486361, PI 636335, and PI 636336 have the S cytoplasm exclusively.

Rfl organization of US maintainer lines

Rfl organization was investigated using two PCR markers, s17 and 20L-int (Taguchi et al. 2014; Moritani et al. 2013). The former is a cleaved-amplified-polymorphic-sequence marker that targets the intergenic region between the *Oma1*-like gene and *bvORF17*, the downstream gene encoding ribosomal protein L13 of cytosolic 60S ribosomes (Taguchi et al. 2014). Types 1 to 5 are known as s17 marker types (Taguchi et al. 2014). The 20L-int targets the first intron of the *Oma1*-like genes that can be divided into L- and S-classes (Moritani et al. 2013). Because the number of *Oma1*-like gene copies in a plant is unpredictable in most cases, the 20L-int only denotes the intronic composition. For example, emergence of both L-class and S-class signal bands may result from copies of the *Oma1*-like gene cluster having both L-class and S-class introns or from the *Oma1*-like genes being heterozygous, one with an L-class intron and the other with an S-class intron (Moritani et al. 2013). Combining s17 and 20L-int, the marker type of a plant can be identified, such as 44L, a notation indicating that the plant is homozygous for type 4 of s17, and the plant's intronic composition is an L-class intron (Taguchi et al. 2014).

The s17/20L-int marker types of the 551 plants are listed in Table 1 and summarized in Table 2. We found a total of thirteen s17/20L-int marker types. The most frequent marker type was 44L, followed by 55LS and 55S (Table 2). The s17/20L-int marker type was homogeneous in 24 accessions, of which eleven accessions are exclusively 44L, seven are 55S, five are 55LS, and one is 55L. Each of the remaining 33 accessions is heterogeneous in terms of the s17/20L-int marker type.

We next examined the copy number and organization of the *Oma1*-like genes in each of the s17/20L-int marker types by DNA gel blot analysis to identify molecular variants. The probe was a 3' untranslated region (UTR) of the *Oma1*-like genes, a nucleotide sequence that is conserved among *Oma1*-like genes (Moritani et al. 2013). We selected 59 representative plants to cover almost all the s17/20L-int marker types of each origin. Plants of accessions PI 486361, PI 636335 and PI 636336 were excluded from this analysis and further study because all of these accessions have S cytoplasm (see Table 1), suggesting contamination of the restoring allele.

Examples of the DNA gel blot analysis are shown in Fig. 2. The results of a total of 59 plants are shown in Table S1 and summarized in Table 3. We found some cases where plants of the same s17/20L-int marker type differed in the signal pattern on the DNA gel blot. For example, although plants of both PI 518644 and PI 411128 are 55LS in terms of their s17/20L-int marker type, the former yielded 7.9, 5.9 and 2.1-kbp bands on the blot, whereas the latter yielded 7.2, 5.9 and 1.9-kbp bands (Table 3). In contrast, some

plants whose s17/20L-int marker type varied have the same signal pattern (e.g., see 44L and 55L in Table 3).

Combining the s17/20L-int marker type with the signal pattern on the DNA gel blot, the 59 plants were classified into 16 types (Table 3). We resolved these 16 types into the combinations of DNA-marker haplotypes (combination of s17/20L-int type and signal band pattern on the DNA gel blot) as described below.

All 44L plants had a 5.9-kbp band on the blot. This s17/20L-int marker type and hybridization pattern are the same as TK-81mm-O, a Japanese maintainer line whose entire *rfl* region had been sequenced in the previous study (Moritani et al. 2013). TK-81mm-O *rfl* has a solitary *Oma1*-like gene with an L-class intron (Moritani et al. 2013). The *rfl* sequence of TK-81mm-O is classified as a type 4 of s17, the L class of 20L-int, and has a 5.9-kbp signal band on the gel blot, hereafter referred to as DNA-marker haplotype 4L-5.9. Given this, the genotype of the 44L plants in Table 3 is homozygous for 4L-5.9 (i.e. 4L-5.9/4L-5.9).

Plants of 33S, 55L and 55S (except for PI 486358) in Table 3 appear to be homozygous at the *rfl* locus according to their s17 type, and a solitary *Oma1*-like gene copy is expected in their DNA-marker haplotypes according to their hybridization pattern. We postulate three DNA marker haplotypes, 3S-5.4, 5L-5.9 and 5S-5.9, and the genotypes of the 33S, 55L and 55S plants are 3S-5.4/3S-5.4, 5L-5.9/5L-5.9, and 5S-5.9/5S-5.9, respectively.

The genotypes of 34LS plants having 5.9- and 5.4-kbp signal bands on the blots from PI 615522 are considered heterozygotes of 3S-5.4 and 4L-5.9. Also, the putative genotype of 45LS plants having an 5.9-kbp band from PI 558514 and PI 634210 is 4L-5.9/5L-5.9. It is necessary to postulate a 4S-5.9 haplotype to explain the 44LS plant of PI 411128, although no 4S-5.9/4S-5.9 homozygous plants were found.

Two 55S plants from PI 486358 had 5.9- and 7.2-kbp bands on the blot (Table S1). In our experience, the 5.9-kbp band, which covers the conserved intergenic region of the *Oma1*-like gene and the *bvORF17*, was present in almost all the plants (Matsuhira et al. 2012; Moritani et al. 2013). On the other hand, the 7.2-kbp band was auxiliary to the 5.9-kbp band, and we found no plants having only the 7.2-kbp band. Hence, we propose a DNA-marker haplotype of 5S-7.2+5.9 that may have a gene cluster of two *Oma1*-like gene copies. Given this DNA-marker haplotype, 55S plants from PI 486358 are homozygous for 5S-7.2+5.9. Plants of 45LS from PI 486358 and PI 607897 are 4L-5.9/5S-7.2+5.9, and a plant of 35S from PI 610319 is 3S-5.4/5S-7.2+5.9.

We also propose the DNA-marker haplotype of 5LS-7.2+5.9+1.9 for some PI 411128 plants, and 5LS-7.9+5.9+2.1 for some PI 590720 plants. Altogether, a combination of eight DNA-marker haplotypes can explain all 16 proposed genotypes listed in Table 3.

Genetic function of eight DNA-marker haplotypes

We identified eight DNA-marker haplotypes, 3S-5.4, 4L-5.9, 4S-5.9, 5S-5.9, 5S-7.2+5.9, 5LS-7.2+5.9+1.9, 5LS-7.9+5.9+2.1, and 5L-5.9, as possible molecular variants of the nonrestoring allele but needed to show that these haplotypes could act as nonrestoring alleles. We selected 19 plants having these DNA-marker haplotypes, induced flowering and found that all 19 plants were male fertile. We subsequently conducted test crosses with annual CMS sugar beets whose DNA-marker haplotype is 4L-5.9/4L-5.9 to determine the male fertility of the F1 progeny (Table S2).

Table 4 summarizes the results of the test cross in which DNA-marker haplotypes were inferred by s17/20L-int. For example, we obtained a total of 20 F1 plants that inherited 3S-5.4 from five crosses, and all 20 F1 plants were completely male sterile (Table 4). Similarly, F1 plants that inherited 4L-5.9, 5L-5.9, 5LS-7.9+5.9+2.1, or 5S-5.9 from pollen parents were completely male sterile (Table 4). Therefore, these five DNA-marker haplotypes correspond to nonrestoring alleles.

On the other hand, a total of 42 F1 plants with the haplotype 5S-7.2+5.9 could have their fertility restored (i.e. either fertile or partially fertile). Linkage between 5S-7.2+5.9 and fertility restoration was examined in the F1 progeny in which plant ID 12-72, a 4L-5.9/5S-7.2+5.9 heterozygous plant, was used as the pollen parent (Table S2). In the F1 progeny (22 plants), twelve plants that inherited the 4L-5.9 from 12-72 were male sterile and ten plants that inherited the 5S-7.2+5.9 had restored fertility. A null hypothesis that the 5S-7.2+5.9 is independent of fertility restoration was rejected (Fisher's exact test; $p=1.55 \times 10^{-6}$). Therefore, 5S-7.2+5.9 is associated with the restoring allele.

The pollen fertility phenotype of F1 plants with a 5LS-7.2+5.9+1.9 haplotype segregated (four restored plants and one male sterile plant) (Table 4). We selfed two of the fertility restored F1 plants (ID 14-171 and 14-177) to generate F2 plants. We used s17 to follow the 5LS-7.2+5.9+1.9 haplotype. Male fertility and DNA-marker genotypes of the F2 progeny are shown in Table 5. In the F2 population derived from 14-171, all eight plants with a 4L-5.9/4L-5.9 genotype were male sterile, whereas the fertility of all seven plants with the 5LS-7.2+5.9+1.9/5LS-7.2+5.9+1.9 genotype was restored. In the heterozygous plants, the phenotype segregated as 17 restored plants and 4 male sterile plants. These results can be explained given that fertility restoration by 5LS-7.2+5.9+1.9 occurs in a semi-dominant manner. A null hypothesis that the 5LS-7.2+5.9+1.9 is independent of fertility restoration was rejected (Fisher's exact test; $p=1.51 \times 10^{-5}$). Results from the F2 population derived from 14-177 were similar to those of 14-171 (Fisher's exact test; $p=3.48 \times 10^{-7}$) (Table 5). However, the emergence of an exceptional fertility-restored plant with a putative 4L-5.9/4L-5.9 genotype is puzzling. Because the degree of fertility restoration in this plant is low

(partially fertile), another weak fertility restorer gene may exist in this plant.

The function of 4S-5.9 is unknown because none of the 14 F1 plants inherited 4S-5.9 (Table S2), which precluded the further study of this DNA-marker haplotype.

Nucleotide sequences of molecular variants of the nonrestoring allele

Five DNA-marker haplotypes were found to correspond to the nonrestoring allele, but detailed organization is known only for 4L-5.9 (TK-81mm-O *rfl*). To compare the *Oma1*-like gene copies among the five DNA-marker haplotypes, we determined the nucleotide sequences of the *rfl* region of the remaining four DNA-marker haplotypes.

Plants homozygous for the 3S-5.4, 5L-5.9, and 5S-5.9 DNA-marker haplotypes were selected from PI 615522, PI 590774, and PI 590689, respectively, and their *rfl* regions were PCR amplified and sequenced. We obtained ~12-kbp sequences from each of the 3S-5.4, 5L-5.9, and 5S-5.9 plants. These sequences are fairly well conserved with that of 4L-5.9, enabling us to determine exon/intron boundaries of the *Oma1*-like genes (Fig. S1). A multiple alignment of the nucleotide sequences is shown in Fig. S1 and schematically illustrated in Fig. 3. The gene-coding region for the *Oma1*-like gene in 5L-5.9 is identical to that of 4L-5.9 and has the potential to encode a 434 amino-acid polypeptide (Fig. S2). Hence the open reading frame (ORF) in 5L-5.9 is named *bvORF20L*, the same as that of 4L-5.9 (Matsuhira et al. 2012). On the other hand, the gene-coding region in 3S-5.4 potentially encodes a 429 amino-acid residue polypeptide that is similar but not identical to *bvORF20L* (Figs. S1 and S2) and is named *bvORF20L_S*. Homology between *bvORF20L* and *bvORF20L_S* is 89% at the amino-acid sequence level. Surprisingly, *bvORF20L_S* is perfectly conserved in 5S-5.9 (Figs. S1 and S2, schematically shown in Fig. 3). Therefore, from the viewpoint of the coding region, four out of the five DNA-marker haplotypes encode either *bvORF20L* or *bvORF20L_S*.

The non-coding regions of 3S-5.4, 4L-5.9, 5L-5.9, and 5S-5.9 were also compared (Fig. 3 and Fig. S1). The four DNA-marker haplotypes were 98-99% homologous in the upstream region of the *Oma1*-like gene and 93-99% homologous in the downstream region. Among the upstream regions, 4L-5.9 and 5L-5.9 were 99% homologous and 3S-5.4 and 5S-5.9 were 99% homologous; both were the best scores. Among the downstream regions, homology between 5L-5.9 and 5S-5.9 gave the best score (99%).

We determined the nucleotide sequence of the *rfl* region from the Japanese maintainer line NK-219mm-O, which is homozygous at 5LS-7.9+5.9+2.1 (Moritani et al. 2013; Taguchi et al. 2014). We first screened our NK-219mm-O genomic library using the same probe as that used in the DNA gel blot analysis. Two recombinant phage clones were obtained and their inserts were sequenced; however, the nucleotide sequences of these two phage clones did not overlap, necessitating PCR amplification to fill the

gap and primer walking to reveal the entire *rfl* region of NK-219mm-O. Finally, a 31733-bp continuous sequence was obtained (Fig. 4).

Coding regions for the *Oma1*-like genes were identified by homology searches. We found three coding regions arranged in tandem (Fig. 4), a result consistent with the DNA gel blot analysis (Moritani et al. 2013; see the pattern of PI 590720 in Fig. 2 of this study). Their deduced amino-acid sequences differ from each other and differ from that of *bvORF20L*, *bvORF20L_S* or any of the four copies of *Oma1*-like genes in NK-198, a Japanese restorer line (Fig. S2). These newly identified ORFs are, hence, named *bvORF20L₂₁₉₋₁*, *bvORF20L₂₁₉₋₂*, and *bvORF20L₂₁₉₋₃* (Fig. 4). The *bvORF20L₂₁₉₋₁* sequence has a premature stop codon in its second exon (Fig. 4), resulting in a truncated translation product (Fig. S2). The amino acid sequences of *bvORF20L₂₁₉₋₂* and *bvORF20L₂₁₉₋₃* are 427 and 432 residues in length, respectively, sizes comparable to those of other *Oma1*-like genes (Fig. S2). Further comparison of *rfl/Rfl* organization will be presented in another report.

We next examined whether the *bvORF20L₂₁₉₋₁/bvORF20L₂₁₉₋₂/bvORF20L₂₁₉₋₃* sequences are preserved in the US maintainers with the 5LS-7.9+5.9+2.1 DNA-marker haplotype. The intronic composition of *bvORF20L₂₁₉₋₁/bvORF20L₂₁₉₋₂/bvORF20L₂₁₉₋₃* is one S-class intron and two L-class introns, of which one L-class intron has a recognition site for *HindIII* (Fig. S3). As such, gel electrophoresis of *HindIII* digests of the 20L-int-PCR products from NK-219mm-O exhibit the signal band pattern shown in Fig. 4. We tested whether the same band patterns are obtained from US maintainers having the DNA marker haplotype 5LS-7.9+5.9+2.1. Eight plants from different accessions were subjected to this analysis, of which seven were homozygous for 5LS-7.9+5.9+2.1 and one was homozygous for 5LS-7.2+5.9+1.9. The seven 5LS-7.9+5.9+2.1 plants gave the same signal band pattern as that of NK-219mm-O, whereas the band pattern of the 5LS-7.2+5.9+1.9 plant was distinctive (Fig. 4).

Discussion

Analysis of 57 US maintainer lines revealed five DNA-marker haplotypes corresponding to the nonrestoring allele. Another two DNA-marker haplotypes (5S-7.2+5.9 and 5S-7.2+5.9+1.9) are considered to be restoring alleles in this study, but we cannot exclude the possibility that they may act as nonrestoring alleles in different environmental conditions than those of this study.

Of the fifty-seven US maintainers, seven accessions exclusively have S cytoplasm or are contaminated with a restoring allele. Besides these, fifty accessions are considered to be maintainer lines or near-maintainer lines (for accessions that are mixtures of N- and S cytoplasms but are not contaminated with a restoring allele). Among these 50 accessions, 20 are homogeneous for both cytoplasm and

DNA-marker haplotype, and the remaining are heterogeneous for cytoplasm or DNA-marker haplotype, or both. According to Hecker and Helmerick (1985), US sugar beet breeders frequently synthesize heterogeneous maintainer populations from which to extract new lines, one of the potential explanations for the genetic heterogeneity observed in this study.

Considering the broad range of genetic backgrounds of US sugar beet germplasm (McGrath et al. 1999), it is possible that the five DNA-marker haplotypes represent nearly all the molecular variants of the nonrestoring allele in sugar beet. As Lewellen pointed out (1992), genetic diversity of sugar beet is low compared to other outcrossing crops because sugar beets originated from a limited range of fodder beet types. Although we think it likely that there are additional maintainer-allele variants in the entire *B. vulgaris* gene pool, only a small repertoire of maintainer-allele variants may have been introduced into ancestral sugar beet populations.

DNA-marker haplotypes of the nonrestoring allele in Japanese sugar beets are 4L-5.9, 3S-5.4, and 5LS-7.9+5.9+2.1, of which the first haplotype predominates (Moritani et al. 2013; Taguchi et al. 2014). The 4L-5.9 haplotype is also the most frequently occurring DNA-marker haplotype among US sugar beets (Table 2). We noticed that two 4L-5.9-containing accessions, PI 590811 and PI 663878, are selections from annual beets that were developed by Munerati, an Italian sugar beet geneticist. Abegg (1936) noted that Munerati's annual beets were selected from European commercial varieties. PI 372277, a Polish maintainer line, also has the 4L-5.9 haplotype (Table 3). European open-pollinated varieties that were introduced into Japan contain type 4 of s17 (Taguchi et al. 2014). Therefore, it is likely that 4L-5.9 is derived from old European varieties. Investigating the frequency of 4L-5.9 in various worldwide *B. vulgaris* populations would better define the dissemination of this DNA-marker haplotype.

Kleinwanzleben E (also known as Klein E) is an old European variety that greatly contributed to the initial sugar beet breeding conducted in the US (Lewellen 1992). PI 633934 is registered as a selection from Klein E. Although no 4L-5.9 was found in any of sixteen PI 633934 plants, 3S-5.4 and 5LS-7.9+5.9+2.1 were identified from this accession, suggesting that 3S-5.4 and 5LS-7.9+5.9+2.1 are also derived from a European variety.

No 5L-5.9 or 5S-5.9 plant has been found among Japanese maintainer lines to date (Moritani et al. 2013; Taguchi et al. 2014). The origin of these two DNA-marker haplotypes may be European varieties that were not introduced into Japan. Another possibility is that, as wide crosses including wild beets (*B. vulgaris* ssp. *maritima*) were conducted to improve disease resistance in the US (Lewellen 1992), 5L-5.9 or 5S-5.9 (or both) may be derived from wild beets. On the other hand, given that the frequency of the maintainer genotype in wild beet is generally low (Touzet 2012), wild beet is less likely the source of the maintainer

allele. We also think it possible that 5L-5.9 and 5S-5.9 may have emerged in US breeding lines as a result of chromosomal crossing over and/or mutational accumulation, but this hypothesis needs further study.

Origins of the fifty US accessions of maintainer or near-maintainer lines are California, Colorado, Maryland, Michigan, Utah, and Poland. We compared the frequencies of DNA-marker haplotypes among all points of origin. As types 3 and 4 of s17 tag 4L-5.9 and 3S-5.4, respectively (see Table 3), we calculated the allelic frequencies of types 3 and 4 (Table 6). In the US, the total allelic frequencies of types 3 and 4 are 0.05 and 0.45, respectively, whereas the figures are 0.06 and 0.75, respectively, in Japan. Thus, the frequency of type 4 greatly differs between the US and Japan. This result is partly due to the presence of unique DNA-marker haplotypes (5L-5.9 and 5S-5.9) in the US and the differential frequency of 5LS-7.9+5.9+2.1. In addition, it is conspicuous that the frequency of type 4 in Californian maintainer lines is very low compared to the other states and countries (Table 6).

The Californian maintainer lines are the most divergent group in terms of the repertoire of maintainer-allele variants, including four out of the five DNA-marker haplotypes (Table 1). Moreover, in the US, type 3 of s17 is found only from the Californian lines (Table 6). The 3S-5.4 was likely present in Klein E, a genetic resource that was repeatedly selected in the US (Lewellen 1992). Hence, the absence of type 3 from the maintainer lines other than those of California origin is puzzling. The 5S-5.9, *bvORF20L_S*-encoding variant as 3S-5.4, was found in accessions from Colorado and Utah. However, neither 3S-5.4 nor 5S-5.9 was found in accessions from Maryland or Michigan. In Japan, 3S-5.4 was found in two old maintainer lines but not from recently selected maintainer lines (Moritani et al. 2013; Taguchi et al. 2014). One possibility is that *bvORF20L_S* has some pleiotropic effect on sugar beet breeding or local adaptation or is linked to genes having such effects. Another possibility is that the loss of *bvORF20L_S* occurred by chance (i.e. genetic drift). Further study is necessary to investigate these possibilities.

Constituent *Oma1*-like gene copy of the five DNA-marker haplotypes is *bvORF20L*, *bvORF20L_S*, or *bvORF20L₂₁₉₋₁*/*bvORF20L₂₁₉₋₂*/*bvORF20L₂₁₉₋₃* (a tandem gene cluster found in NK-219mm-O). In spite of the sequence diversity in noncoding regions surrounding *bvORF20L*, the *bvORF20L*-coding regions are perfectly conserved between different DNA-marker haplotypes (compare 4L-5.9 and 5L-5.9). This degree of sequence conservation is also the case for *bvORF20L_S* (compare 3S-5.4 and 5S-5.9). This reminds us of the absence of sequence polymorphism in *bvORF20L* copies among the 21 Japanese maintainer lines (Moritani et al. 2013). Both *bvORF20L* and *bvORF20L_S* are apparently functional genes in terms of the absence of nonsense mutations. Transcripts of *bvORF20L* have been detected (Kitazaki et al. 2015). Altogether, it seems unlikely that *bvORF20L* and *bvORF20L_S* are amorphic, but they might have some function that is different from fertility restoration. This notion can be applied to *bvORF20L₂₁₉₋₁*/*bvORF20L₂₁₉₋₂*/*bvORF20L₂₁₉₋₃*, in which only *bvORF20L₂₁₉₋₁* seems to be a pseudogene.

The molecular function of *bvORF20L*, *bvORF20L_S*, and *bvORF20L₂₁₉₋₁*/*bvORF20L₂₁₉₋₂*/*bvORF20L₂₁₉₋₃* clearly needs additional investigation.

In conclusion, molecular variants of a maintainer allele in both US and Japan encode *bvORF20L*, *bvORF20L_S*, or *bvORF20L₂₁₉₋₁*/*bvORF20L₂₁₉₋₂*/*bvORF20L₂₁₉₋₃*. The origin of these variants can be traced to old European varieties that were introduced in the initial stage of sugar beet breeding. Because the nucleotide sequences of the coding regions are conserved among maintainer accessions, it is possible to select maintainer alleles through MAS. On the other hand, a fundamental issue remains whether this repertoire of variants is sufficient for the future and whether there should be some concern for potential genetic vulnerability. This issue is difficult to approach, but long-term monitoring of maintainer lines and a careful investigation of the organizational diversity of *rfl* may be necessary.

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- 538

539 Table 1 Mitotypes and marker types of plants used in this study

Accession	Mitotype	Type of s17/20L-int	No. of plants	Origin
PI 372277	Normal-2	44L	12	Poland
PI 411128	min06/-orf129	44L	7	Soviet Union
	min06/-orf129	44LS	1	
	min06/-orf129	45L	2	
	min06/-orf129	45LS	6	
	min06/-orf129	55S	1	
	S	44L	1	
	S	55LS	1	
PI 486358	Normal-1	44L	4	Soviet Union
	Normal-1	45LS	4	
	Normal-1	55S	2	
	S	44L	8	
	S	45LS	3	
PI 486361	S	11S	4	Soviet Union
	S	15S	2	
	S	45LS	2	
	S	55S	2	
PI 512298	Normal-1	55S	8	California
PI 518644	Normal-1	44L	4	Colorado
	Normal-1	55L	1	
	Normal-1	55LS	2	
	Normal-2	55LS	1	
PI 558514	Normal-1	44L	2	Colorado
	Normal-1	45L	2	
	Normal-1	45LS	6	
	Normal-1	55LS	1	
	Normal-1	55S	1	
	S	45LS	1	
PI 558515	Normal-2	55LS	6	Colorado
PI 560130	Normal-2	55LS	6	California
	S	35LS	2	
	S	55LS	1	
PI 564757	Normal-2	44L	5	California
PI 564758	Normal-1	44L	1	California
	Normal-2	44L	8	
	Normal-2	45LS	5	

PI 564759	Normal-2	44L	10	California
PI 574625	Normal-1	44L	9	Colorado
PI 590645	Normal-2	55LS	8	California
PI 590647	Normal-1	55LS	10	California
PI 590672	Normal-1	44L	2	Maryland
PI 590686	Normal-2	45LS	3	California
	Normal-2	55LS	5	
PI 590687	Normal-2	44L	1	California
	Normal-2	45LS	2	
	Normal-2	55LS	8	
PI 590689	Normal-1	55S	6	Utah
PI 590694	Normal-1	44L	3	Maryland
	S	44L	1	
PI 590697	Normal-1	44L	12	Maryland
	Normal-1	45LS	1	
	Normal-1	55LS	1	
	Owen	44L	2	
PI 590714	Normal-2	44L	4	California
	Normal-2	55LS	5	
PI 590720	Normal-2	44L	2	Michigan
	Normal-2	55LS	4	Michigan
PI 590767	Normal-2	44L	2	Colorado
	Normal-2	45LS	1	
	Normal-2	55LS	1	
PI 590771	Normal-1	44L	4	Maryland
	Normal-1	45LS	4	
PI 590772	Normal-1	44L	8	Maryland
	Normal-1	45L	3	
	Normal-1	55L	3	
PI 590773	Normal-1	44L	3	Maryland
	Normal-1	55LS	2	
PI 590774	Normal-1	55L	8	Maryland
	Normal-1	55LS	6	
PI 590775	Normal-1	44L	14	Maryland
	Normal-1	45LS	1	
PI 590811	Normal-1	44L	3	Utah
PI 590813	Normal-2	55LS	13	California
PI 590815	Normal-1	55LS	7	California

	Normal-1	55S	3	
PI 590821	Normal-2	44L	3	Colorado
	Normal-2	45LS	1	
	Normal-2	55S	2	
PI 590823	Normal-1	44L	13	Colorado
PI 590839	Normal-2	55S	3	Utah
PI 590841	Normal-2	44L	14	Utah
PI 590845	Normal-1	55S	3	Colorado
PI 590847	Normal-2	55LS	10	California
	S	55LS	1	
PI 590849	Normal-2	44L	3	California
	Normal-2	45LS	2	
	Normal-2	55LS	4	
PI 590851	Normal-2	55S	9	California
PI 590867	Normal-1	33S	6	California
	Normal-1	35LS	5	
	Normal-1	55LS	4	
PI 590869	Normal-1	44L	6	California
	Normal-1	45LS	2	
PI 590871	Normal-1	45L	7	Colorado
	Normal-1	45LS	1	
	Normal-2	44L	1	
PI 594910	Normal-1	55S	14	Colorado
	S	55S	1	
PI 607897	Normal-1	44L	4	Michigan
	Normal-1	45LS	3	
PI 610319	Normal-2	35S	1	California
	Normal-2	55LS	6	
	Normal-2	55S	6	
PI 615522	Normal-1	33S	8	California
	Normal-1	34LS	3	
PI 632251	Normal-1	55S	14	Colorado
PI 633934	min06/-orf129	35LS	3	California
	min06/-orf129	55LS	10	
	Normal-2	35LS	1	
	Normal-2	55LS	2	
PI 634018	Normal-2	44L	1	Colorado
	Normal-2	55S	1	

	S	44L	1	
	S	45LS	4	
	S	55LS	1	
	S	55S	1	
PI 634210	Normal-2	44L	2	Colorado
	Normal-2	45LS	3	
PI 634217	Normal-1	45LS	2	California
	Normal-1	55LS	7	
	Normal-2	45LS	1	
	Normal-2	55LS	2	
PI 636335	S	55LS	6	Colorado
	S	55S	9	
PI 636336	S	45LS	1	Colorado
	S	55S	3	
PI 663878	Normal-1	44L	11	California
W6 17112	Normal-1	44L	6	Michigan
	Normal-2	44L	2	
W6 17122	Normal-1	55L	1	Colorado

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543 Table 2 Number of plants and accessions of each marker type

Type of s17/20L-int	No. of plants	No. of accessions
44L	199	32
55LS	141	25
55S	89	17
45LS	59	20
45L	14	5
33S	14	2
55L	13	4
35LS	11	4
11S	4	1
34LS	3	1
15S	2	1
35S	1	1
44LS	1	1

544

545 Table 3 Summary of DNA gel blot analysis and possible DNA-marker genotypes

Type of s17/20L-in t	Signal bands (kbp)			Possible DNA-marker genotype	Accessions
33S		5.4		3S-5.4/3S-5.4	PI 615522
34LS		5.9	5.4	3S-5.4/4L-5.9	PI 615522
35LS	7.9	5.9	5.4 2.1	3S-5.4/5LS -7.9+5.9+2.1	PI 590867, PI 633934
35S	7.2	5.9	5.4	3S-5.4/5S-7.2+5.9	PI 610319
44L		5.9		4L-5.9/4L-5.9	PI 372277, PI 411128, PI 486358, PI 564757, PI 564758, PI 590694, PI 590697, PI 590821, PI 590823, PI 590841, PI 607897, W6 17112
44LS		5.9		4L-5.9/4S-5.9	PI 411128
45L		5.9		4L-5.9/5L-5.9	PI 558514, PI 590871, PI 590772, PI 411128
45LS	7.9	5.9	2.1	4L-5.9/5LS-7.9+5.9+2.1	PI 564758, PI 590771, PI 590775, PI 634217
45LS	7.2	5.9		4L-5.9/5S-7.2+5.9	PI 486358, PI 607897
45LS		5.9		4L-5.9/5S-5.9	PI 558514, PI 634210
45LS	7.2	5.9	1.9	4L-5.9/5LS-7.2+5.9+1.9	PI 411128
55L		5.9		5L-5.9/5L-5.9	PI 518644, PI 590772, PI 590774, W6 17122
55LS	7.9	5.9	2.1	5LS-7.9+5.9+2.1/5LS-7.9+5.9 +2.1	PI 518644, PI 558515, PI 590720, PI 590773, PI 590774, PI 590847, PI 634217
55LS	7.2	5.9	1.9	5LS-7.2+5.9+1.9/5LS-7.2+5.9 +1.9	PI 411128
55S	7.2	5.9		5S-7.2+5.9/5S-7.2+5.9	PI 486358
55S		5.9		5S-5.9/5S-5.9	PI 512298, PI 590689, PI 590839, PI 594910, PI 610319, PI 632251

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548 Table 4 Summary of male fertility in F1 progeny

Transmitted DNA-marker haplotype from the pollen parent	No. of test crosses	No. of fertility restored ^a plants	No. of male sterile plants	Total no. of plants
3S-5.4	5	0	20	20
4L-5.9	7	0	52	52
5L-5.9	3	0	12	12
5LS -7.9+5.9+2.1	4	0	27	27
5LS -7.2+5.9+1.9	1	4	1	5
5S-5.9	2	0	8	8
5S-7.2+5.9	4	42	0	42

549 ^aSum of fertile and partially fertile plants

550

551

552 Table 5 Summary of male fertility of F2 progeny derived from plant ID 14-171 and 14-177

a) 14-171 self pollination

DNA-marker genotype	No. of plants		
	Fertility restored ^a	Sterile	Total
4L-5.9/4L-5.9	0	8	8
4L-5.9/5LS-7.2+5.9+1.9	17	4	21
5LS-7.2+5.9+1.9/5LS-7.2+5.9+1.9	7	0	7
Total	24	12	36

b) 14-177 self pollination

DNA-marker genotype	No. of plants		
	Fertility restored ^a	Sterile	Total
4L-5.9/4L-5.9	1	13	14
4L-5.9/5LS-7.2+5.9+1.9	22	9	31
5LS-7.2+5.9+1.9/5LS-7.2+5.9+1.9	12	0	12
Total	35	22	57

^aSum of fertile and partially fertile plants

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556 Table 6 Allelic frequencies of types 3 and 4 of s17 in maintainer lines of the US, Poland and Japan

		No. of maintainer lines	Frequency of s17 type			
			Type 3	Type 4	Others	Total
Origin						
US	California	21	0.10	0.27	0.63	1.00
	Colorado	14	0	0.44	0.56	1.00
	Maryland	8	0	0.69	0.31	1.00
	Michigan	2	0	0.71	0.29	1.00
	Utah	4	0	0.65	0.35	1.00
	US total	49	0.05	0.45	0.50	1.00
Poland		1	0	1.00	0	1.00
Japan ^a		22	0.06	0.75	0.19	1.00

557 ^aData from Moritani et al. (2013) and Taguchi et al. (2014)

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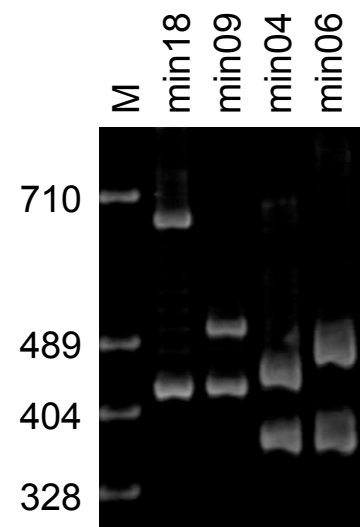
Figure legends

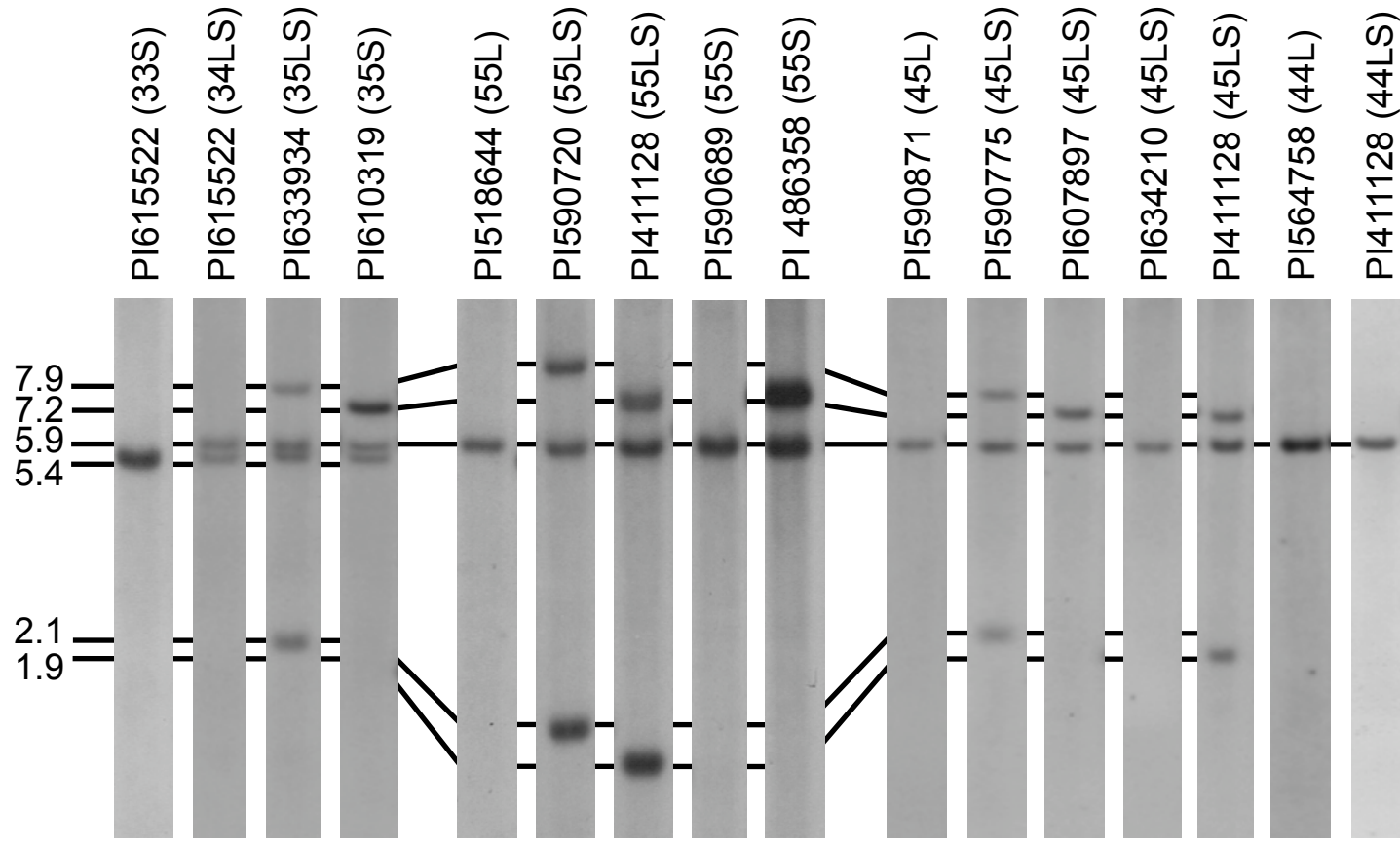
Fig. 1 Gel electrophoresis of mixed PCR products (one amplified from mitochondrial TR-1 and the other from TR-3) in a 5% polyacrylamide gel. The DNA from representative plants with min18, min09, min04, and min06/-orf129, respectively, were used as templates. M denotes size marker. Sizes of the marker bands (in bp) are shown on the left

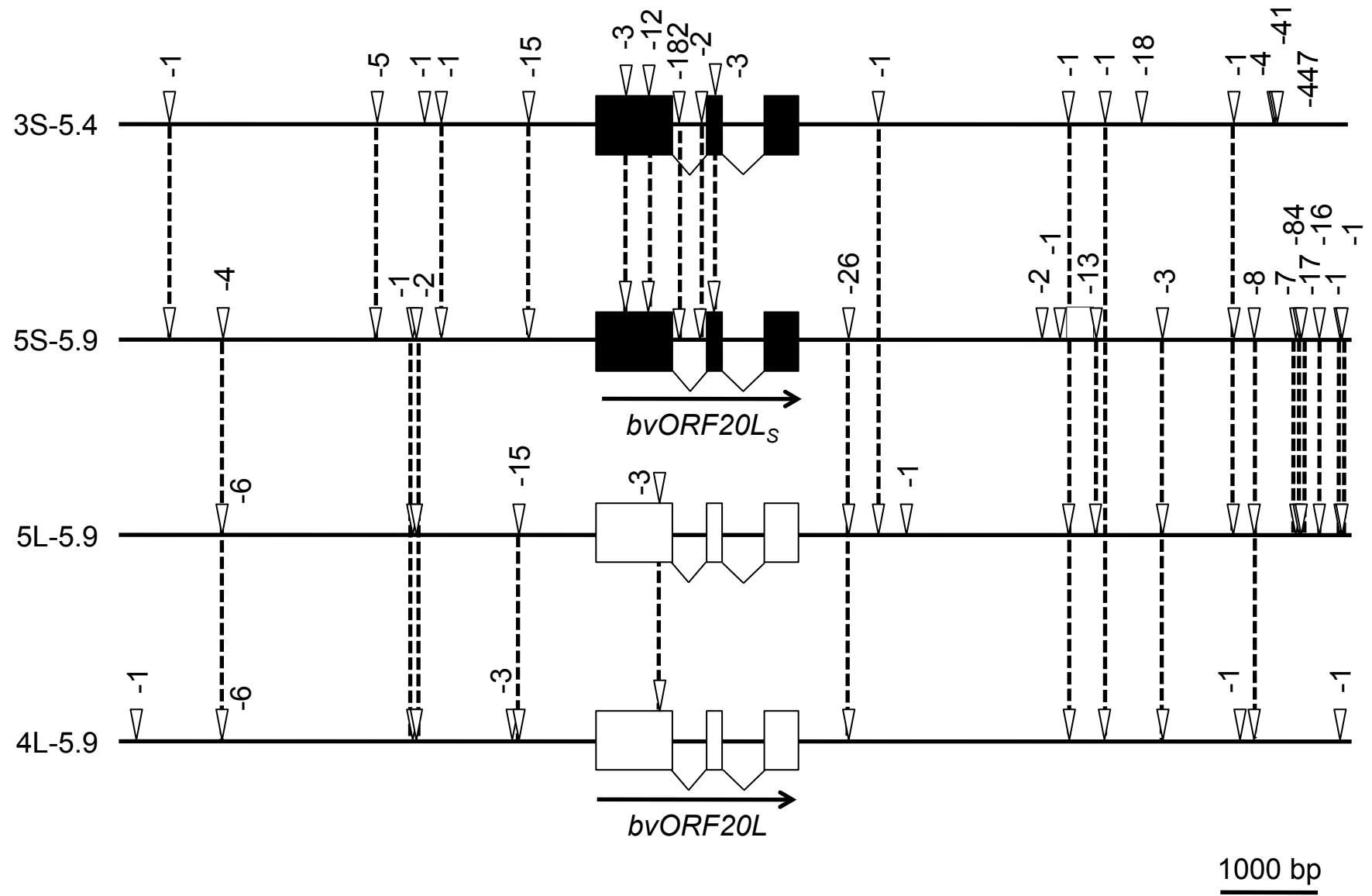
Fig. 2 Signal bands on the blots of *Hind*III-digested total cellular DNA electrophoresed in 1% agarose gels. Blots were hybridized with the 3' UTR of an *Oma1*-like gene from the sugar beet *Rfl* locus (Moritani et al. 2013). Names of accessions and their s17/20L-int marker types (in parenthesis) are shown above the blots. Size markers (in kbp) are shown on the left

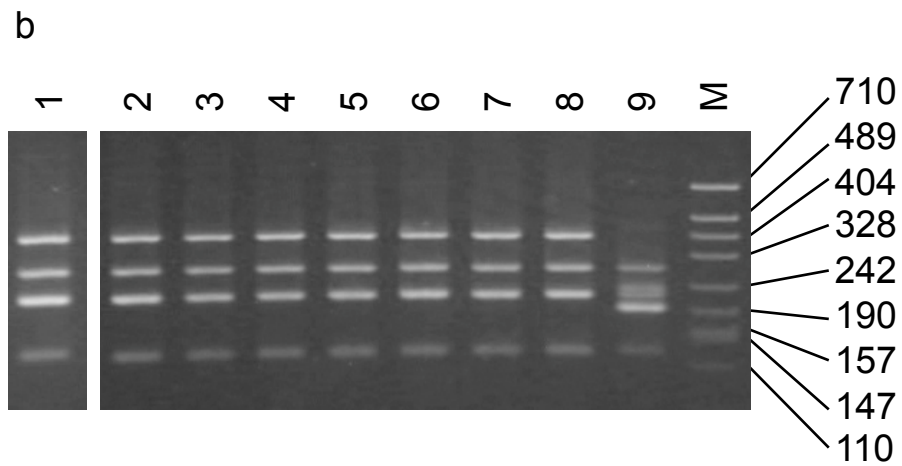
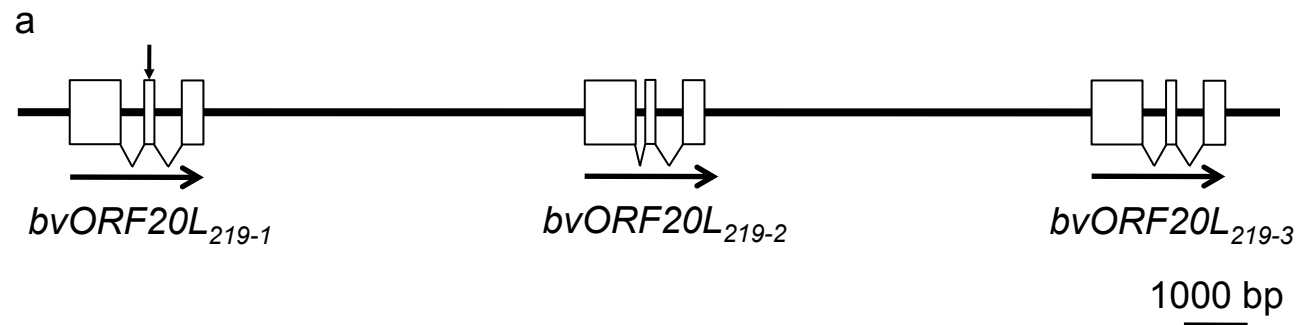
Fig. 3 Organization of *rfl* regions of plants with 3S-5.4, 5S-5.9, 5L-5.9, and 4L-5.9 DNA-marker haplotypes. Exons of *bvORF20L_S* are indicated by filled boxes and those of *bvORF20L* are indicated by open boxes. Wedges indicate introns. Transcriptional directions are from left to right (shown by arrows). Triangles denote deletions, and dashed lines show the occurrence of similar deletions. A scale bar is shown on the lower right

Fig. 4 Organization of the *rfl* region in NK-219mm-O and preservation of 20L-int nucleotide sequences in US maintainer lines with the DNA-marker haplotype of 5LS-7.9+5.9+2.1. **Panel a** Organization of the *rfl* region of NK-219mm-O. Open boxes and wedges indicate exons and introns, respectively. The direction of transcription is shown by horizontal arrows. The position of a premature stop codon in *bvORF20L₂₁₉₋₁* is depicted by a vertical arrow. A scale bar is shown on the lower right. **Panel b** Images of gel electrophoresis of *Hind*III digests of 20L-int PCR products in 3% agarose gels. Size markers (in bp) are shown on the right (lane M). Plants of NK-219mm-O (lane 1), PI 518644 (lane 2), PI 558515 (lane 3), PI 590720 (lane 4), PI 590773 (lane 5), PI 590774 (lane 6), PI 590847 (lane 7), and PI 634217 (lane 8) are homozygous accessions of 5LS-7.9+5.9+2.1, and the plant representing accession PI 411128 (lane 9) is homozygous for 5LS-7.2+5.9+1.9









5S-5.9	TGCATTTGATGATTTGAATGTGTTGGTTATTGTCCTTCAAGCTTAAATGTGCCTATATTAA	60
3S-5.4	TGCATTTGATGATTTGAATGTGTTGGTTATTGTCCTTCAAGCTTAAATGTGCCTATATTAA	60
4L-5.9	TGCATTTGATGATTTGAATGTGTTGGTTATTGTCCTTCAAGCTTAAATGTGCCTATATTAA	60
5L-5.9	TGCATTTGATGATTTGAATGTGTTGGTTATTGTCCTTCAAGCTTAAATGTGCCTATATTAA	60

5S-5.9	TACAACCTTTTTTTAAGGTATATTTGTACATGATTTTCATTTCTTAACTAGTATTTGGGTTT	120
3S-5.4	TACAACCTTTTTTTAAGGTATATTTGTACATGATTTTCATTTCTTAACTAGTATTTGGGTTT	120
4L-5.9	TACAACCTTTTTTTAAGGTATATTTGTACATGATTTTCATTTCTTAACTAGTATTTGGGTTT	120
5L-5.9	TACAACCTTTTTTTAAGGTATATTTGTACATGATTTTCATTTCTTAACTAGTATTTGGGTTT	120

5S-5.9	GGGTGTTGTCCCGGGATAGTATTGTTTTCTGAATTTGATATGCATTTTTTCTTTTCATTT	180
3S-5.4	GGGTGTTGTCCCGGGATAGTATTGTTTTCTGAATTTGATATGCATTTTTTCTTTTCATTT	180
4L-5.9	GGGTGTTGTCCCGGGATAGTATTGTTTTCTGAATTTGATATGCATTTTTTCTTTTCATTT	179
5L-5.9	GGGTGTTGTCCCGGGATAGTATTGTTTTCTGAATTTGATATGCATTTTTTCTTTTCATTT	180
	***** ** *	
5S-5.9	CCATTAATAATATACTCCCTCCGTCCCAAAATATAGTTTCCATTTCCATTTTGGGTGTCCC	240
3S-5.4	CCATTAATAATATACTCCCTCCGTCCCAAAATATAGTTTCCATTTCCATTTTGGGTGTCCC	240
4L-5.9	CCATTAATAATATACTCCCTCCGTCCCAAAATATAGTTTCCATTTCCATTTTGGGTGTCCC	239
5L-5.9	CCATTAATAATATACTCCCTCCGTCCCAAAATATAGTTTCCATTTCCATTTTGGGTGTCCC	240

5S-5.9	AAAATATAGTTCCCATATCCCATTTCCATATTTAGTTCACGTTTTTTTCGTAATTTGTCT	300
3S-5.4	AAAATATAGTTCCCATATCCCATTTCCATATTTAGTTCACGTTTTTTTCGTAATTTGTCT	300
4L-5.9	AAAATATAGTTCCCATATCCCATTTCCATATTTAGTTCACGTTTTTTTCGTAATTTGTCT	299
5L-5.9	AAAATATAGTTCCCATATCCCATTTCCATATTTAGTTCACGTTTTTTTCGTAATTTGTCT	300

5S-5.9	AGAAAAACCGTGTCCCCTCATTTATTTGCTTCTTGAATTTTGGTTTTTCCTTTGTTTATT	360
3S-5.4	AGAAAAACCGTGTCCCCTCATTTATTTGCTTCTTGAATTTTGGTTTTTCCTTTGTTTATT	360
4L-5.9	AGAAAAACCGTGTCCCCTCATTTATTTGCTTCTTGAATTTTGGTTTTTCCTTTGTTTATT	359
5L-5.9	AGAAAAACCGTGTCCCCTCATTTATTTGCTTCTTGAATTTTGGTTTTTCCTTTGTTTATT	360

5S-5.9	CAACCAAAATGTTACAATTAATGCTCTTCCACCAATTATTCTCCACTCTTTCCTCTAAAA	420
3S-5.4	CAACCAAAATGTTACAATTAATGCTCTTCCACCAATTATTCTCCACTCTTTCCTCTAAAA	420
4L-5.9	CAACCAAAATGTTACAATTAATGCTCTTCCACCAATTATTCTCCACTCTTTCCTCTAAAA	419
5L-5.9	CAACCAAAATGTTACAATTAATGCTCTTCCACCAATTATTCTCCACTCTTTCCTCTAAAA	420

5S-5.9	TCATCTTTTCCCATACAACATTTATTTAAATAAACAAAAAATCATTACTATTTCATCTTAT	480
3S-5.4	TCATCTTTTCCCATACAACATTTATTTAAATAAACAAAAAATCATTACTATTTCATCTTAT	480
4L-5.9	TCATCTTTTCCCATACAACATTTATTTAAATAAACAAAAAATCATTACTATTTCATCTTAT	479
5L-5.9	TCATCTTTTCCCATACAACATTTATTTAAATAAACAAAAAATCATTACTATTTCATCTTAT	480

5S-5.9	ATTCTACTTACATAAAATTACCGTGAAAAAAGGGAAATGGGAACATATATTTTGGGACGGAG	540
3S-5.4	ATTCTACTTACATAAAATTACCGTGAAAAAAGGGAAATGGGAACATATATTTTGGGACGGAG	540
4L-5.9	ATTCTACTTACATAAAATTACCGTGAAAAAAGGGAAATGGGAACATATATTTTGGGACGGAG	539
5L-5.9	ATTCTACTTACATAAAATTACCGTGAAAAAAGGGAAATGGGAACATATATTTTGGGACGGAG	540

5S-5.9	GGAGTATTAAGTAAAACTC-AACATTTAAACCATACAAATATAATAATATGGGAGACTTAA	599
3S-5.4	GGAGTATTAAGTAAAACTC-AACATTTAAACCATACAAATATAATAATATGGGAGACTTAA	599
4L-5.9	GGAGTATTAAGTAAAACTCCTAACATTTAAACCATACAAATATAATAATATGGGAGACTTAA	599
5L-5.9	GGAGTATTAAGTAAAACTCTAACATTTAAACCATACAAATATAATAATATGGGAGACTTAA	600

5S-5.9	AGCATGATTAAAAAGTTGGTTGAGATGGTAATTGTGTCATGTATAATAACAAGAGACTACA	659
3S-5.4	AGCATGATTAAAAAGTTGGTTGAGATGGTAATTGTGTCATGTATAATAACAAGAGACTACA	659
4L-5.9	AGCATGATTAAAAAGTTGGTTGAGATGGTAATTGTGTCATGTATAATAACAAGAGACTACA	659
5L-5.9	AGCATGATTAAAAAGTTGGTTGAGATGGTAATTGTGTCATGTATAATAACAAGAGACTACA	660

5S-5.9	AGTTCAAATCTTGTTGCAAGCTTATTTTACTTTTGTTAATTGACATGAGATATATACACA	719
3S-5.4	AGTTCAAATCTTGTTGCAAGCTTATTTTACTTTTGTTAATTGACATGAGATATATACACA	719
4L-5.9	GGTTCAAATCTTGTTGCAAGCTTATTTTACTTTTGTTAATTGACATGAGATATATACACA	719
5L-5.9	GGTTCAAATCTTGTTGCAAGCTTATTTTACTTTTGTTAATTGACATGAGATATATACACA	720

3S-5.4&5S-5.9	MAWYRNSRFVYNALKLNLRSKTFGTIPTPRVHSNSSLFYNQST-KCSGLFSGSAKSGYFN	59
4L-5.9&5L-5.9	MAWYRNSRFVYNALKLNLRSKTFGTIPTPRVHSNSSLFYNQST-KCSGLFSGSAKSGYFN	59
NK219_1	MAWYRNSRFVYNALKLNLRSKTFGTIPTPRVHSNSSLFYNQST-KCSGLFSGSAKSGYFN	59
NK219_2	MAWYRNSRFVYNALKLNLRSKTFGTIPTPRVHSNSSLFYNQST-KCSGLFSGSAKSGYFN	59
NK219_3	MAWYRNSRFVYNALKLNLRSKTFGTIPTPRVHSNSSLFYNQST-KCSGLFSGSAKSGYFN	59
NK198_ORF18/21	MAWYRNSRFVYNALKLNLRSKTFGTIPTPRVHSNSSLFYNQSTNKCSGLFSGSAKSGYFN	60
NK198_ORF19	MAWYRNSRFVYNALKLNLRSKTFGTIPTPRVHSNSSLFYNQSTNKCSGLFSGSAKSGYFN	60
NK198_ORF20	MAWYRNSRFVYNALKLNLRSKTFGTIPTPRVHSNSSLFYNQSTNKCSGLFSGSAKSGYFN	60
3S-5.4&5S-5.9	GFKHHQEISSFSGFARRNYHGDKTEVSVESWLEKLLLGIA-LMLSTGIFAYRHVHPVVVP	118
4L-5.9&5L-5.9	GFKHHQEISSFSGFARRNYHGVKTEVSVFEFRVEKLLLGIALIISHSGMIAFFYLHPVVVP	119
NK219_1	GFKHHQEISSFSGFARRNYHGDKTEESVESWLEKLLLGIA-LILSTGIFAYRHVHPVVVP	118
NK219_2	GFKHHQEISSFSGFARRNYHGDKTEVSVESWLEKLLL-----LALILIAAYRHVHPVVVP	113
NK219_3	GFKHHQEISSFSGFARRNYHGVKTEVSVFEFRVKGLLLGIAIIILHSGMTAFLYLHPVVVP	119
NK198_ORF18/21	GFKHHQEISSFSGFARRNYHGDKTEVSVESWLEKFLVPIG-LILTFGILGYPHVHPVVVP	119
NK198_ORF19	GFKHHQEISSFSGFARRNYHGDKTEVSAESLLEKLLL----LAVAILIAAYRHVHPVVVP	116
NK198_ORF20	GFKHHQEISSFSGFARRNYHGDKTEVSVESWLEKFLVPIG-LILTFGILGYPHVHPVVVP	119
3S-5.4&5S-5.9	YTGRKHYVLISTTDENEKGEVEKRKIQPATHPDTRVRSIFQHILESLEIREINHHELELE	178
4L-5.9&5L-5.9	YTGRKHYVILSTTHENENGEFEKRKIQPATHPDTERVRSIFQHILESLEIREINHHELELE	179
NK219_1	YTGRKHYVLISTTDENEKGEVEKRKIQPATHPDTRVRSIFQHILESLEIREINHHELELE	178
NK219_2	YTGRKHYVLMSTTRENEIGEVEKRKIQPATHPDTRVRSIFQHILESLEIREINHHELELE	173
NK219_3	YTGRKHYVILSTTHENENGEFEKRKIQPATHPDTERVRSIFQHILESLEIREINHHELELE	179
NK198_ORF18/21	YTGRKHYVLMSTTRENEIGEVEKRKIQPATHPDTRVRSIFQHILESLEIREINHHELELE	179
NK198_ORF19	YTGRKHYVLMSTTRENEIGEVEKRKIQPATHPDTERVRSIFQHIIESLEIREINHHELELE	176
NK198_ORF20	YTGRKHYVLMSTTRENEIGEVEKRKIQPATHPDTRVRSIFQHILESLEIREINHHELELE	179
3S-5.4&5S-5.9	----RDETFKEITIWKEETVDDKDSRKKHSGAKITTNHLEGLNWEIFVVDKPLVESSCLF	234
4L-5.9&5L-5.9	LELERDETFKEKTIWKEETDHDKDSRKKHSGAKITTNH-EGMNWEIFVVDKPWVESSCIF	238
NK219_1	----RDETFKEITIWKEETIDDKDSRKKHSGAKITTNHLEGLNWEIFVVDKPLVESSYLY	234
NK219_2	LELERDETLKENTIWKEETVDDKDSRKKHSGAKITTNHLEGLNWEIFVVDKPLVESSYLF	233
NK219_3	LELERDETFKEKTIWKEETDHDKDSRKKHSGAKITTNH-EGMNWEIFVVDKPWVESSCIF	238
NK198_ORF18/21	LE--RDETFKEKTIWKEETVDDKDSRKKHSGAKITTNHLEGMNWEIFVVDKPLVESSYLL	237
NK198_ORF19	----RDETFKEKTIWKEETVDDKDSRKKHSGAKITTNHLEGLNWEIFVVDKPLVESSCLF	232
NK198_ORF20	----RDETFKEKTIWKEETVDDKDSRKKHSGAKITTNHLEGMNWEIFVVDKPLVESSYLL	235
3S-5.4&5S-5.9	GGKIVVYTGLLNHCNSDAELATIIAHQVGHAVARHQAEDRTAFFWWSMS-LYVIIFEVLF	293
4L-5.9&5L-5.9	GGKIVVYTGLLNHCISDAELATIIAHQVGHAVARHEAHTTLLWSILLVIYMTIFQYLF	298
NK219_1	GGKIVVYTGLLNHCNSDAELATIIAHQVGHAVARHEAEDWTIL---S-SGSY-----	282
NK219_2	GGKIVVYTGLLNHCNSDAELATIIAHQVGHAVARHQAENRTAFFWWSMS-LYVIIFEVLF	292
NK219_3	GGKIVVYTGLLNHCISDAELATIIAHQVGHAVARHEAHTTLLWSILLVIYMTIFQILF	298
NK198_ORF18/21	GGKIVVYTGLLNHCNSDAELATIIAHQVGHAVARHEAEDSTAFFWLLIS-LNVILFKILF	296
NK198_ORF19	DGKIVVYTGLLNHFNSDAELATIIAHQVGHAVARHEAHTALFWSMLGFYVTLFEILF	292
NK198_ORF20	GGKIVVYTGLLNHCNSDAELATIIAHQVGHAVARHEAEDSTAFFWLLIS-LNVILFKILF	294
3S-5.4&5S-5.9	TARKFANARSKLLLRHPLLQKVWKIIQARFHQLLPRTTLHLGFLGLSSLVFILYFGRKEI	353
4L-5.9&5L-5.9	TAPEFANAISKLLSRHPLLQKVWKIIQARFHQLLPRTTLHLGFLGLSSLVFILYFGRKEI	358
NK219_1	-----	282
NK219_2	TARKFANARSKLLLRHPLLQKVWKIIQAR-APQLLPRTICLSLVGLFSSVFILYFGRKEI	351
NK219_3	TAPEFANAISKLLSRHPLLQKLWKIIQATAHLLPRT--ALGVVGLFSLVFILYFGRKEI	356
NK198_ORF18/21	TEPESANARSKLLLRHPLLQKVWKIIQAR-APQLLPRTICLSLVGLFSSVFILYFGRKEI	355
NK198_ORF19	TAPEFANARSKLLLRHPLLQKVWKIIQARFHQLLPRTTLRLGFVGLSSLVFILYFGRKEI	352
NK198_ORF20	TEPESANARSKLLLRHPLLQKVWKIIQAR-APQLLPRTICLSLVGLFSSVFILYFGRKEI	353
3S-5.4&5S-5.9	EADHIGVLLMASAGYDPRVAPQVYDKLAKPLGDWNCCLATHPFARMRAKLLARADVMKEAD	413
4L-5.9&5L-5.9	EADHIGVLLMASAGYDPRVAPQVYDKLAKPLGDWNCCLATHPFARMRAKLLARADVMKEAD	418
NK219_1	-----	282
NK219_2	EADHIGVLLMASAGYDPRVAPQVYDKLAKPLGDWNCCLATHPFARMRAKLLARADVMKEAD	411
NK219_3	EADHIGVLLMASAGYNPRVAPQAYDKLAKPLGDWNCCLATHPFARMRAKLLARADVMKEAD	416
NK198_ORF18/21	EADHIGVLLMASAGYDPRVAPQVYDKLAKPLGDWNCCLATHPFARMRAKLLARADVMKEAD	415
NK198_ORF19	EADHIGVLLMASAGYDPRVAPQVYDKLAKPLGDWNCCLATHPFARMRAKLLARADVMKEAD	412
NK198_ORF20	EADHIGVLLMASAGYDPRVAPQVYDKLAKPLGDWNCCLATHPFARMRAKLLARADVMKEAD	413

3S-5.4&5S-5.9	KIYNEVVAGRAIQGLQ	429
4L-5.9&5L-5.9	KIYNEVVAGRAIQGLQ	434
NK219_1	-----	282
NK219_2	KIYNEVVAGRAIQGLQ	427
NK219_3	KIYNEVVAGRAIQGLQ	432
NK198_ORF18/21	KIYNEVVAGRAIQGLQ	431
NK198_ORF19	KIYNEVVAGRAIQGLQ	428
NK198_ORF20	KIYNEVVAGRAIQGLQ	429

Fig. S2 Alignment of the deduced amino acid sequences encoded by *Oma1*-like genes in the sugar beet *Rf1* loci of several lines. Dashes are incorporated for maximum matching. Abbreviations indicate: 3S-5.4&5S-5.9, bvORF20L_S; 4L-5.9&5L-5.9, bvORF20; NK219_1, bvORF20L₂₁₉₋₁; NK219_2, bvORF20L₂₁₉₋₂; NK219_3, bvORF20L₂₁₉₋₃; NK198_ORF18/21, bvORF18 and bvORF21 (the two amino acid sequences are identical); NK198_ORF19, bvORF19; and NK198_ORF20, bvORF20 (for bvORF18-bvORF20, see Matsuhira et al. 2012).

5S-5.9	TTGGACAAATCTACTGAAGTAACAGAGGTGCCACGTGGTGGGTATACATTGTCACGCACA	779
3S-5.4	TTGGACAAATCTACTGAAGTAACAGAGGTGCCACGTGGTGGGTATACATTGTCACGCACA	779
4L-5.9	TTGGACAAATCTACTGAAGTAACAGAGGTGCCACGTGGCGGGTATACATTGTCACGCACA	779
5L-5.9	TTGGACAAATCTACTGAAGTAACAGAGGTGCCACGTGGCGGGTATACATTGTCACGCACA	780

5S-5.9	CCTTTAAATATATTTGTATAGATGAACTAGAACTGTTTTCTTCTAATAATAAAGAACGAT	839
3S-5.4	CCTTTAAATATATTTGTATAGATGAACTAGAACTGTTTTCTTCTAATAATAAAGAACGAT	839
4L-5.9	CCTTTAAATATATTTGTATAGATGAACTAGAACTGTTTTCTTCTAATAATAAAGAACGAT	839
5L-5.9	CCTTTAAATATATTTGTATAGATGAACTAGAACTGTTTTCTTCTAATAATAAAGAACGAT	840

5S-5.9	AAGGATGAAGTTTATTAACAGATGGTCTGTAGAAAATGTGATTGCTTCAACTTTGTAAG	899
3S-5.4	AAGGATGAAGTTTATTAACAGATGGTCTGTAGAAAATGTGATTGCTTCAACTTTGTAAG	899
4L-5.9	AATGATGAAGTTTATTAACAAATGGTATGTAGAAAATGTGATTGCTTCAACTTTGTAAG	899
5L-5.9	AATGATGAAGTTTATTAACAAATGGTATGTAGAAAATGTGATTGCTTCAACTTTGTAAG	900
	** *****	
5S-5.9	GTAAAATCATGGCAATTAAGCTTTTAGGCGAGGAAAATTAAGATCATGAATATTATTTAAT	959
3S-5.4	GTAAAATCATGGCAATTAAGCTTTTAGGCGAGGAAAATTAAGATCATGAATATTATTTAAT	959
4L-5.9	GTAAAATCATGGCAATTAAGCTTTTAGGCGAGGAAAATTAAGATCATGAGTATCATTTAAT	959
5L-5.9	GTAAAATCATGGCAATTAAGCTTTTAGGCGAGGAAAATTAAGATCATGAGTATCATTTAAT	960

5S-5.9	TTGTAAACTCTTTGTATATCTATCATTTTGTGTGCTTATAGTATGCACCATTTTCCTATGT	1019
3S-5.4	TTGTAAACTCTTTGTATATCTATCATTTTGTGTGCTTATAGTATGCACCATTTTCCTATGT	1019
4L-5.9	TTGTAAACTCTTTGTATATCTATCATTTTGTGTGCTTATAGTATGCACCATTTTCCTATGT	1019
5L-5.9	TTGTAAACTCTTTGTATATCTATCATTTTGTGTGCTTATAGTATGCACCATTTTCCTATGT	1020

5S-5.9	CTTCAAAGCCTCAAAGGAATACTCCATTTCTTTTTTTTTTTTTTTTTTTT---GGTCAAG	1075
3S-5.4	CTTCAAAGCCTCAAAGGAATACTCCATTTCTTTTTTTTTTTTTTTTTTTTTTTTGGTCAAG	1079
4L-5.9	CTTCAAAGCCTCAAAGGAATACTCCATTTCTTTTCTTTTTTTTTTTTTT-----GGTCAAG	1073
5L-5.9	CTTCAAAGCCTCAAAGGAATACTCCATTTCTTTTCTTTTTTTTTTTTTT-----GGTCAAG	1074

5S-5.9	TGGTGATTGGTGAAGTCCCTAGAACCGTGCATTTTGAGTAAAAAAATTAACGAAACAGGT	1135
3S-5.4	TGGTGATTGGTGAAGTCCCTAGAACCGTGCATTTTGAGTAAAAAAATTAACGAAACAGGT	1139
4L-5.9	TGGTGATTGGTGAAGTCCCTAGAACCGTGCATTTTGAGTAAAAAAATTAACGAAACAGGT	1133
5L-5.9	TGGTGATTGGTGAAGTCCCTAGAACCGTGCATTTTGAGTAAAAAAATTAACGAAACAGGT	1134

5S-5.9	TGAAACTTTTTATTTGTAAATCATATAAAAATTTTGTGTCATCAGTCAAAAGTAACAGAG	1195
3S-5.4	TGAAACTTTTTATTTGTAAATCATATAAAAATTTTGTGTCATCAGTCAAAAGTAACAGAG	1199
4L-5.9	TGAAACTTTTTACTTTGTAAATCATATAAAAATTTTGTGTCATCAGTCAAAAGTGACAGAG	1193
5L-5.9	TGAAACTTTTTACTTTGTAAATCATATAAAAATTTTGTGTCATCAGTCAAAAGTGACAGAG	1194

5S-5.9	GGTGCAAATTCGCGAATTACTTCCTCATATACCTTGATGTACCGTTGATATGGTACACTC	1255
3S-5.4	GGTGCAAATTCGCGAATTACTTCCTCATATACCTTGATGTACCGTTGATATGGTACACTC	1259
4L-5.9	GGTGCAAATTCGCGAATTACTTCCTCATATACCTTGATGTACCGTTGATATGGTACACTC	1253
5L-5.9	GGTGCAAATTCGCGAATTACTTCCTCATATACCTTGATGTACCGTTGATATGGTACACTC	1254

5S-5.9	AATACTAATTTATGTTTCATTTGCTTATTTGAAATTTTCTTATTTTGTTTCATTTCAATGAT	1315
3S-5.4	AATACTAATTTATGTTTCATTTGCTTATTTGAAATTTTCTTATTTTGTTTCATTTCAATGAT	1319
4L-5.9	AATACTAATTTATGTTTCATTTGCTTATTTGAAATTTTCTTATTTTGTTTCATTTCAATGAT	1313
5L-5.9	AATACTAATTTATGTTTCATTTGCTTATTTGAAATTTTCTTATTTTGTTTCATTTCAATGAT	1314

5S-5.9	TTCAAATAAATAATAGGCAAAAAAATAGCCTTTAAATGTATCATGCTCGCAACATTTAGG	1375
3S-5.4	TTCAAATAAATAATAGGCAAAAAAATAGCCTTTAAATGTATCATGCTCGCAACATTTAGG	1379
4L-5.9	TTCAAATAAATAATAGGCAAAAAAATAGCCTTTAAATGTATCATGCTCGCAACATTTAGG	1373
5L-5.9	TTCAAATAAATAATAGGCAAAAAAATAGCCTTTAAATGTATCATGCTCGCAACATTTAGG	1374

5S-5.9	TATATGATAAAATTTATACAAATTTTAATGAAAAAAAATGTTGAAACAAAAATTTAAGC	1435
3S-5.4	TATATGATAAAATTTATACAAATTTTAATGAAAAAAAATGTTGAAACAAAAATTTAAGC	1439
4L-5.9	TATATGATAAAATTTATACAAATTTTAATGAAAAAAAATGTTGAAACAAAAATTTAAGC	1433
5L-5.9	TATATGATAAAATTTATACAAATTTTAATGAAAAAAAATGTTGAAACAAAAATTTAAGC	1434

5S-5.9	TAAGCTAAAGTTGACTTTTAAAGCTCTCTCCTTTTATGATGCAACAAAGATTTTGTTTTAG	1495
3S-5.4	TAAGCTAAAGTTGACTTTTAAAGCTCTCTCCTTTTATGATGCAACAAAGATTTTGTTTTAG	1499
4L-5.9	TAAGCTAAAGTTGACTTTTAAAGCTCTCTCCTTTTCTGATGCAACAAAGATTTTGTTTTAG	1493
5L-5.9	TAAGCTAAAGTTGACTTTTAAAGCTCTCTCCTTTTCTGATGCAACAAAGATTTTGTTTTAG	1494

5S-5.9	CACTAGCTACTTTTTCTATCCCCATAAAATTCGCCATTTGTTTTCTCAAACCTCAAATTTTC	1555
3S-5.4	CACTAGCTACTTTTTCTATCCCCATAAAATTCGCCATTTGTTTTCTCAAACCTCAAATTTTC	1559
4L-5.9	CACTAGCTACTTTTTCTATCCCCATAAAATTCGCCATTTGTTTTCTCAAACCTCAAATTTTC	1553
5L-5.9	CACTAGCTACTTTTTCTATCCCCATAAAATTCGCCATTTGTTTTCTCAAACCTCAAATTTTC	1554

5S-5.9	ATCAATTTTGTATTATGTTTTTTCACCATGTAAGAAAATATCTTATCATGTGTTTTTCGTA	1615
3S-5.4	ATCAATTTTGTATTATGTTTTTTCACCATGTAAGAAAATATCTTATCATGTGTTTTTCGTA	1619
4L-5.9	ATCAATTTTGTATTATGTTTTTTCACCATGTAAGAAAATATCTTATCATGTGTTTTTCGTA	1613
5L-5.9	ATCAATTTTGTATTATGTTTTTTCACCATGTAAGAAAATATCTTATCATGTGTTTTTCGTA	1614

5S-5.9	ATCGAGGAAACCCATATAGGAAACTGCTTATAAAGCTAGTGAATCAACGAAATATCAACA	1675
3S-5.4	ATCGAGGAAACCCATATAGGAAACTGCTTATAAAGCTAGTGAATCAACGAAATATCAACA	1679
4L-5.9	ATCGAGGAAACCCATATAGGAAACTGCTTATAAAGCTAGTGAATCAACGAAATATCAACA	1673
5L-5.9	ATCGAGGAAACCCATATAGGAAACTGCTTATAAAGCTAGTGAATCAACGAAATATCAACA	1674

5S-5.9	GGAAAATCACATTGTTCATAGGAAACTCCTATAACATTTGCATACATTGTAGGTCATTG	1735
3S-5.4	GGAAAATCACATTGTTCATAGGAAACTCCTATAACATTTGCATACATTGTAGGTCATTG	1739
4L-5.9	GGAAAATCACATTGTTCATAGGAAACTCCTATAACATTTGCATACATTGTAGGTCATTG	1733
5L-5.9	GGAAAATCACATTGTTCATAGGAAACTCCTATAACATTTGCATACATTGTAGGTCATTG	1734

5S-5.9	TTGCACTTTATTCCTCGGCCCTCGTATATTGATATTAAGTGTATTTTAATCTACGTTTT	1795
3S-5.4	TTGCACTTTATTCCTCGGCCCTCGTATATTGATATTAAGTGTATTTTAATCTACGTTTT	1799
4L-5.9	TTGCACTTTATTCCTCGGCCCTCGTATATTGATATTAAGTGTATTTTAATCTACGTTTT	1793
5L-5.9	TTGCACTTTATTCCTCGGCCCTCGTATATTGATATTAAGTGTATTTTAATCTACGTTTT	1794

5S-5.9	TTTCTATTGCAACAATTACTACTTTGGATAATTTTACATCTATTGCAACAATTCATTTT	1855
3S-5.4	TTTCTATTGCAACAATTACTACTTTGGATAATTTTACATCTATTGCAACAATTCATTTT	1859
4L-5.9	TTTCTATTGCAACAATTACTACTTTGGATAATTTTACATCTATTGCAACAATTCATTTT	1853
5L-5.9	TTTCTATTGCAACAATTACTACTTTGGATAATTTTACATCTATTGCAACAATTCATTTT	1854

5S-5.9	TGGTATAAAAAGCAACATTTTCAAGACAAAGCATGGATTATGCACTAGGGTACCATTTCATA	1915
3S-5.4	TGGTATAAAAAGCAACATTTTCAAGACAAAGCATGGATTATGCACTAGGGTACCATTTCATA	1919
4L-5.9	TGGTATAAAAAGCAACATTTTCAAGACAAAGCATGGATTATGCACTAGGGTACCATTTCATA	1913
5L-5.9	TGGTATAAAAAGCAACATTTTCAAGACAAAGCATGGATTATGCACTAGGGTACCATTTCATA	1914

5S-5.9	TAGAAGAATATGATTTTTTTTCAACAACCTTTTCAAGATAAAAAAAGCACACAATATAAAA	1975
3S-5.4	TAGAAGAATATGATTTTTTTTCAACAACCTTTTCAAGATAAAAAAAGCACACAATATAAAA	1979
4L-5.9	TAGAAGAATATGATTTTTTTTCAACAACCTTTTCAAGATAAAAAAAGCACACAATATAAAA	1973
5L-5.9	TAGAAGAATATGATTTTTTTTCAACAACCTTTTCAAGATAAAAAAAGCACACAATATAAAA	1974

5S-5.9	TTAAAGAACATGTAAGAGTGCGTTTTTATTCAACTTATTGGCCCTGAACTTATTGGACCTT	2035
3S-5.4	TTAAAGAACATGTAAGAGTGCGTTTTTATTCAACTTATTGGCCCTGAACTTATTGGACCTT	2039
4L-5.9	TTAAAGAACATGTAAGAGTGCGTTTTTATTCAACTTATTGGCCCTGAACTTATTGGACCTT	2033
5L-5.9	TTAAAGAACATGTAAGAGTGCGTTTTTATTCAACTTATTGGCCCTGAACTTATTGGACCTT	2034

5S-5.9	ATCTGAACTGAATTTATTGAACCTGAACTGAACTTATTGGAACCTATTAAACCTGATTGG	2095
3S-5.4	ATCTGAACTGAATTTATTGAACCTGAACTGAACTTATTGGAACCTATTAAACCTGATTGG	2099
4L-5.9	ATCTGAACTGAATTTATTGAACCTGAACTGAACTTATTGGAACCTATTAAACCTGATTGG	2093
5L-5.9	ATCTGAACTGAATTTATTGAACCTGAACTGAACTTATTGGAACCTATTAAACCTGATTGG	2094

5S-5.9	ACCTGATTCAACTTATTGGACCTGATTAAACCTGATTGGAACCTATTGGAACCTATTGAC	2155
3S-5.4	ACCTGATTCAACTTATTGGACCTGATTAAACCTGATTGGAACCTATTGGAACCTATTGAC	2159
4L-5.9	ACCTGATTCAACTTATTGGACCTGATTAAACCTGATTGGAACCTATTGGAACCTATTGAC	2153
5L-5.9	ACCTGATTCAACTTATTGGACCTGATTAAACCTGATTGGAACCTATTGGAACCTATTGAC	2154

5S-5.9	CTTATTGAAACCTATTAGACCTTATTGGCCCTGATTGAAACCTATTAGACCTTATTGGAC	2215
3S-5.4	CTTATTGAAACCTATTAGACCTTATTGGCCCTGATTGAAACCTATTAGACCTTATTGGAC	2219
4L-5.9	CTTATTGAAACCTATTAGACCTTATTGGCCCTGATTGAAACCTATTAGACCTTATTGGAC	2213
5L-5.9	CTTATTGAAACCTATTAGACCTTATTGGCCCTGATTGAAACCTATTAGACCTTATTGGAC	2214

5S-5.9	CTGATTGAAACCTATTAGACCTTATTGGACCTTATTCGACAAAAACATTGACCATGAATA	2275
3S-5.4	CTGATTGAAACCTATTAGACCTTATTGGACCTTATTCGACAAAAACATTGACCATGAATA	2279
4L-5.9	CTGATTGAAACCTATTAGACCTTATTGGACCTTATTCGACAAAAACATTGACCATGAATA	2273
5L-5.9	CTGATTGAAACCTATTAGACCTTATTGGACCTTATTCGACAAAAACATTGACCATGAATA	2274

5S-5.9	ACATAAATATTACCACTAACGTAATACTACCCCTCAAAATTTTTTATGGAGTAATAATT	2335
3S-5.4	ACATAAATATTACCACTAACGTAATACTACCCCTCAAAATTTTTTATGGAGTAATAATT	2339
4L-5.9	ACATAAATATTACCACTAACGTAATACTACCCCTCAAAATTTTTTATGGAGTAATAATT	2333
5L-5.9	ACATAAATATTACCACTAACGTAATACTACCCCTCAAAATTTTTTATGGAGTAATAATT	2334

5S-5.9	ATTATAATTCGTCCTTTAAAAATAATGATTATTAATTATCTCTTATGATAATTAATTTAA	2395
3S-5.4	ATTATAATTCGTCCTTTAAAAATAATGATTATTAATTATCTCTTATGATAATTAATTTAA	2399
4L-5.9	ATTATAATTCGTCCTTTAAAAATAATGATTATTAATTATCTCTTATGATAATTAATTTAA	2393
5L-5.9	ATTATAATTCGTCCTTTAAAAATAATGATTATTAATTATCTCTTATGATAATTAATTTAA	2394

5S-5.9	TAAAAAAATTTACTATTTATATATTTGCCTATACATAACTTTCACCACTAATATGTTTTG	2455
3S-5.4	TAAAAAAATTTACTATTTATATATTTGCCTATACATAACTTTCACCACTAATATGTTTTG	2459
4L-5.9	TAAAAAAATTTACTATTTATATATTTGCCTATACATAACTTTCACCACTAATATGTTTTG	2453
5L-5.9	TAAAAAAATTTACTATTTATATATTTGCCTATACATAACTTTCACCACTAATATGTTTTG	2454

5S-5.9	ATTTTATAAAACACTAGTAGAAAATCAAAAGTTAATTAACATTTATTGCTAACAAAGTTAA	2515
3S-5.4	ATTTTATAAAACACTAGTAGAAAATCAAAAGTTAATTAACATTTATTGCTAACAAAGTTAA	2519
4L-5.9	ATTTTATAAAACACTAGTAGAAAATCAAAAGTTAATTAACATTTATTGCTAACAAAGTTAA	2513
5L-5.9	ATTTTATAAAACACTAGTAGAAAATCAAAAGTTAATTAACATTTATTGCTAACAAAGTTAA	2514

5S-5.9	AATTGACACATATAAAAAATTAACATTTATTGAAGAGGGTGATGTAGAAGATGAAGAAAG	2575
3S-5.4	AATTGACACATATAAAAAATTAACATTTATTGAAGAGGGTGATGTAGAAGATGAAGAAAG	2579
4L-5.9	AATTGACACATATAAAAAATTAACATTTATTGAAGAGGGTGATGTAGAAGATGAAGAAAG	2573
5L-5.9	AATTGACACATATAAAAAATTAACATTTATTGAAGAGGGTGATGTAGAAGATGAAGAAAG	2574

5S-5.9	ATACCCCGATGAAGAAAGATACTCTAGTGATGATAATGAAGCAATCAATTGACAACAATT	2635
3S-5.4	ATACCCCGATGAAGAAAGATACTCTAGTGATGATAATGAAGCAATCAATTGACAACAATT	2639
4L-5.9	ATACCCCGATGAAGAAAGATACTCTAGTGATGATAATGAAGCAATCAATTGACAACAATT	2633
5L-5.9	ATACCCCGATGAAGAAAGATACTCTAGTGATGATAATGAAGCAATCAATTGACAACAATT	2634

5S-5.9	ATGTCTTTCATTGTTATTA-----GTAACGAAAACATGTTATCTCTAGTTATTTAAAGAC	2690
3S-5.4	ATGTCTTTCATTGTTATTA-----GTAACGAAAACATGTTATCTCTAGTTATTTAAAGAC	2694
4L-5.9	ATGTCTTTCATTGTTATTTATATTAGTAACGAAAACATGTTATCTCTAGTTATTTAAAGAC	2693
5L-5.9	ATGTCTTTCATTGTTATTATATATTAGTAACGAAAACATGTTATCTCTAGTTATTTAAAGAC	2694

5S-5.9	GAATTGCAAATTTATTGTAATTATAATTATTATTATTGTTAACCTTAATTATTTGACC	2750
3S-5.4	GAATTGCAAATTTATTGTAATTATAATTATTATTATTATTGTTAACCTTAATTATTTGACC	2754
4L-5.9	GAATTGCAAATTTATTGTAATTATAATTATTATTATTATTGTTAACCTTAATTATTTGACC	2753
5L-5.9	GAATTGCAAATTTATTGTAATTATAATTATTATTATTATTGTTAACCTTAATTATTTGACC	2754

5S-5.9	ATGATTATAATATTATTTAATAGCAATATGAATAATCAAATAATAGACAATAATACAAGT	2810
3S-5.4	ATGATTATAATATTATTTAATAGCAATATGAATAATCAAATAATAGACAATAATACAAGT	2814
4L-5.9	ATGATTATAATATTATTTAATAGCAATATGAATAATCAAATAATAGACAATAATACAAGT	2813
5L-5.9	ATGATTATAATATTATTTAATAGCAATATGAATAATCAAATAATAGACAATAATACAAGT	2814

5S-5.9	ATAATACTACACATTGTGGTACTTTAATAAAAAATTCTAATAATAACATAATCAGCTAAT	2870
3S-5.4	ATAATACTACACATTGTGGTACTTTAATAAAAAATTCTAATAATAACATAATCAGCTAAT	2874
4L-5.9	ATAATACTACACATTGTGGTACTTTAATAAAAAATTCTAATAATAACATAATCAGCTAAT	2873
5L-5.9	ATAATACTACACATTGTGGTACTTTAATAAAAAATTCTAATAATAACATAATCAGCTAAT	2874

5S-5.9	AGTAATATGAATAATAAAATAATAGACATAATACAGATAAAATAACAAAATAATAGACATA	2930
3S-5.4	AGTAATATGAATAATAAAATAATAGACATAATACAGATAAAATAACAAAATAATAGACATA	2934
4L-5.9	AGTAATATGAATAATAAAATAATAGACATAATACAGATAAAATAACAAAATAATAGACATA	2933
5L-5.9	AGTAATATGAATAATAAAATAATAGACATAATACAGATAAAATAACAAAATAATAGACATA	2934

5S-5.9	ATACAAATAAACAAATAAAGTAATAGACATTAATACAAGTATAATATTATATAATCATTGT	2990
3S-5.4	ATACAAATAAACAAATAAAGTAATAGACATTAATACAAGTATAATATTATATAATCATTGT	2994
4L-5.9	ATACAAATAAACAAATAAAGTAATAGACATTAATACAAGTATAATATTATATAATCATTGT	2993
5L-5.9	ATACAAATAAACAAATAAAGTAATAGACATTAATACAAGTATAATATTATATAATCATTGT	2994

5S-5.9	GGTACTTTAATTAAATTCCTAATAATAACATAATCAACTAATAGTGATATGAAATTATGA	3050
3S-5.4	GGTACTTTAATTAAATTCCTAATAATAACATAATCAACTAATAGTGATATGAAATTATGA	3054
4L-5.9	GGTACTTTAATTAAATTCCTAATAATAACATAATCAACTAATAGTGATATGAAATTATGA	3053
5L-5.9	GGTACTTTAATTAAATTCCTAATAATAACATAATCAACTAATAGTGATATGAAATTATGA	3054

5S-5.9	ATAACAAAATAATGGACAATAATACAAATGTATATTAAACATTGACTATTTGGACCTTAT	3110
3S-5.4	ATAACAAAATAATGGACAATAATACAAATGTATATTAAACATTGACTATTTGGACCTTAT	3114
4L-5.9	ATAACAAAATAATGGACAATAATACAAATGTATATTAAACATTGACTATTTGGACCTTAT	3113
5L-5.9	ATAACAAAATAATGGACAATAATACAAATGTATATTAAACATTGACTATTTGGACCTTAT	3114

5S-5.9	TGGA--CCTTATT-AGACCTGATTGAAACTTATTGGACCTTATTAGACCTGATTGGAAC	3167
3S-5.4	TGGGACCTTTTATTAGACCTGATTCAA-CCTATTGGACCTTATTAGACCTGATTGGAAC	3173
4L-5.9	TGGA--CCTTATT-AGACCTGATTGAAACTTATTGGACCTTATTAGACCTGATTGGAAC	3170
5L-5.9	TGGA--CCTTATT-AGACCTGATTGAAACTTATTGGACCTTATTAGACCTGATTGGAAC	3171
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5S-5.9	TATTGCACCTGATTGAAACTTATTGCACCTGGAACCTTATTGGACCTTATTAGACCTTATT	3227
3S-5.4	TATTGCACCTGATTGAAACTTATTGCACCTGGAACCTTATTGGACCTTATTAGACCTTATT	3233
4L-5.9	TATTGCACCTGATTGAAACTTATTGCACCTGGAACCTTATTGGACCTTATTAGACCTTATT	3230
5L-5.9	TATTGCACCTGATTGAAACTTATTGCACCTGGAACCTTATTGGACCTTATTAGACCTTATT	3231

5S-5.9	GGAAGTTATTGCCCTTATTAGACCTTATTACAACCTATCTGAACTTATTGGACCTGAAAC	3287
3S-5.4	GGAAGTTATTGCCCTTATTAGACCTTATTACAACCTATCTGAACTTATTGGACCTGAAAC	3293
4L-5.9	GGAAGTTATTGCCCTTATTAGACCTTATTACAACCTATCTGAACTTATTGGACCTGAAAC	3290
5L-5.9	GGAAGTTATTGCCCTTATTAGACCTTATTACAACCTATCTGAACTTATTGGACCTGAAAC	3291

5S-5.9	TTAATTTTTTTT-AAGTTGAGCAGAACGCACCCCTAAATCTCCAATTATAAAAATAACATAGG	3346
3S-5.4	TTAATTTTTTTT-AAGTTGAGCAGAACGCACCCCTAAATCTCCAATTATAAAAATAACATAGG	3352
4L-5.9	TTAATTTTTTTTAAAGTTGAGCAGAACGCACCCCTAAATCTCCAATTATAAAAATAACATAGG	3350
5L-5.9	TTAATTTTTTTTAAAGTTGAGCAGAACGCACCCCTAAATCTCCAATTATAAAAATAACATAGG	3351
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5S-5.9	TCGGAATAAAAAAGAAAGTATTGTAAATGAACATTTAGTCTAAATTTAAAGAACCTAACTT	3406
3S-5.4	TCGGAATAAAAAAGAAAGTATTGTAAATGAACATTTAGTCTAAATTTAAAGAACCTAACTT	3412
4L-5.9	TCGGAATAAAAAAGAAAGTATTGTAAATGAACATTTAGTCTAAATTTAAAGAACCTAACTT	3410
5L-5.9	TCGGAATAAAAAAGAAAGTATTGTAAATGAACATTTAGTCTAAATTTAAAGAACCTAACTT	3411

5S-5.9	TTAAATGTAAATTTAAAAAAGGAATCTCGCCAACAACCATTTTTCCTAAAAGGTAAAAACA	3466
3S-5.4	TTAAATGTAAATTTAAAAAAGGAATCTCGCCAACAACCATTTTTCCTAAAAGGTAAAAACA	3472
4L-5.9	TTAAATGTAAATTTAAAAAAGGAATCTCGCCAACAACCATTTTTCCTAAAAGGTAAAAACA	3470
5L-5.9	TTAAATGTAAATTTAAAAAAGGAATCTCGCCAACAACCATTTTTCCTAAAAGGTAAAAACA	3471

5S-5.9	AGTTGCAAGATTTAATGAAACAGATAACAACATTTTTCTTAAATCATAAATTCCTAAAAAT	3526
3S-5.4	AGTTGCAAGATTTAATGAAACAGATAACAACATTTTTCTTAAATCATAAATTCCTAAAAAT	3532
4L-5.9	AGTTGCAAGATTTAATGAAACAGATAACAACATTTTTCTTAAATCATAAATTCCTAAAAAT	3530
5L-5.9	AGTTGCAAGATTTAATGAAACAGATAACAACATTTTTCTTAAATCATAAATTCCTAAAAAT	3531

5S-5.9	ATTAAACCTACATCGTTTAAACAGAGGGTGCACCATCCTTTATGCGTACTTGGATGCATGT	3586
3S-5.4	ATTAAACCTACATCGTTTAAACAGAGGGTGCACCATCCTTTATGCGTACTTGGATGCATGT	3592
4L-5.9	ATTAAACCTACATCGTTTAAACAGAGGGTGCACCATCCTTTATGCGTACTTGGATGCATGT	3590
5L-5.9	ATTAAACCTACATCGTTTAAACAGAGGGTGCACCATCCTTTATGCGTACTTGGATGCATGT	3591

5S-5.9	TCCTATTTGCGCTTTTCCATTCCCTAAAAAACCGAGTCTAAAGCTATTGTTATAATACAC	3646
3S-5.4	TCCTATTTGCGCTTTTCCATTCCCTAAAAAACCGAGTCTAAAGCTATTGTTATAATACAC	3652
4L-5.9	TCCTATTTGCGCTTTTCCATTCCCTAAAAAACCGAGTCTAAAGCTATTGTTATAATACAC	3650
5L-5.9	TCCTATTTGCGCTTTTCCATTCCCTAAAAAACCGAGTCTAAAGCTATTGTTATAATACAC	3651

5S-5.9	TCTAGTAGTCGTCTCAAAAAAAAATAAGGCTTTGCTAAATTACGCCCTAAATTTTCTGG	3706
3S-5.4	TCTAGTAGTCGTCTCAAAAAAAAATAAGGCTTTGCTAAATTACGCCCTAAATTTTCTGG	3712
4L-5.9	TCTAGTAGTCGTCTCAAAAAAAAATAAGGCTTTGCTAAATTACGCCCTAAATTTTCTGG	3710
5L-5.9	TCTAGTAGTCGTCTCAAAAAAAAATAAGGCTTTGCTAAATTACGCCCTAAATTTTCTGG	3711

5S-5.9	TAACGCCCTAAATACGGTATTTTCATACCGTATTTATATACCTGCATTTCTTTCCTCTCT	3766
3S-5.4	TAACGCCCTAAATACGGTATTTTCATACCGTATTTATATACCTGCATTTCTTTCCTCTCT	3772
4L-5.9	TAACGCCCTAAATACGGTATTTTCATACCGTATTTATATACCTGCATTTCTTTCCTCTCT	3770
5L-5.9	TAACGCCCTAAATACGGTATTTTCATACCGTATTTATATACCTGCATTTCTTTCCTCTCT	3771

5S-5.9	TTCCCCTTCACTCACTCACTTTCTCTCTCCTCTCCACCACAACCTGCCACCACACCACCAC	3826
3S-5.4	TTCCCCTTCACTCACTCACTTTCTCTCTCCTCTCCACCACAACCTGCCACCACACCACCAC	3832
4L-5.9	TTCCCCTTCACTCACTCACTTTCTCTCTCCTCTCCACCACAACCTGCCACCACACCACCAC	3830
5L-5.9	TTCCCCTTCACTCACTCACTTTCTCTCTCCTCTCCACCACAACCTGCCACCACACCACCAC	3831

5S-5.9	TACCATATTTCTCTCCAATTTTACACACTTTTGACTCCTATGTCTTCTAACAACATTGTGTC	3886
3S-5.4	TACCATATTTCTCTCCAATTTTACACACTTTTGACTCCTATGTCTTCTAACAACATTGTGTC	3892
4L-5.9	TACCATATTTCTCTCCAATTTTACACACTTTTGACTCCTATGTCTTCTAACAACATTGTGTC	3890
5L-5.9	TACCATATTTCTCTCCAATTTTACACACTTTTGACTCCTATGTCTTCTAACAACATTGTGTC	3891

5S-5.9	GGCACCACCACCACCGACGTACCCCCGACACCCCAACCATCGTCGTATCCCGGCCACCACC	3946
3S-5.4	GGCACCACCACCACCGACGTACCCCCGACACCCCAACCATCGTCGTATCCCGGCCACCACC	3952
4L-5.9	GGCACCACCACCACCGACGTACCCCCGACACCCCAACCATCGTCGTATCCCGGCCACCACC	3950
5L-5.9	GGCACCACCACCACCGACGTACCCCCGACACCCCAACCATCGTCGTATCCCGGCCACCACC	3951

5S-5.9	GCCGTACCCCCGACACACCACCACCATCCCCCTTTTCTCTACTCCGTTTTCTTTATTTTC	4006
3S-5.4	GCCGTACCCCCGACACACCACCACCATCCCCCTTTTCTCTACTCCGTTTTCTTTATTTTC	4012
4L-5.9	GCCGTACCCCCGACACACCACCACCATCCCCCTTTTCTCTACTCCGTTTTCTTTATTTTC	4010
5L-5.9	GCCGTACCCCCGACACACCACCACCATCCCCCTTTTCTCTACTCCGTTTTCTTTATTTTC	4011

5S-5.9	TGATTTTTTTTTTTTAAAAAAAGGGGAGGCGTCCACCATGGACGCCCCACCACCTGGTGGAG	4066
3S-5.4	TGATTTTTTTTTTTTAAAAAAAGGGGAGGCGTCCACCATGGACGCCCCACCACCTGGTGGAG	4072
4L-5.9	TGATTTTTTTTTTTTAAAAAAAGGGGAGGCGTCCACCATGGACGC---ACCACCTGGTGGAG	4067
5L-5.9	TGATTTTTTTTTTTTAAAAAAAGGGGAGGCGTCCACCATGGACGCCCCACCACCTGGTGGAG	4071

5S-5.9	GCGTCCATGGCAGGCGCCTCACCATGTGGTGAAGCGCCTGCCATAGACGCCTCCCCTTTT	4126
3S-5.4	GCGTCCATGGCAGGCGCCTCACCATGTGGTGAAGCGCCTGCCATAGACGCCTCCCCTTTT	4132
4L-5.9	GCGTCCATG-CAGGCGCCTCACCACAT-----ATAGACGCCTCCCCTTTT	4111
5L-5.9	GCGTCCATGGCAGGCGCCTCACCACAT-----ATAGACGCCTCCCCTTTT	4116
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5S-5.9	TTTTTAAAAAAATTTCAAATTACTATTAATGAAGAAACATAGAAGAGGAGGGTGGGTAC	4186
3S-5.4	TTTTTAAAAAAATTTCAAATTACTATTAATGAAGAAACATAGAAGAGGAGGGTGGGTAC	4192
4L-5.9	TTTTTAAAAAAATTTCAAATTACTGTTAATGAAGAAACATAGAAGAGGAGGGTGGGTAC	4171
5L-5.9	TTTTTAAAAAAATTTCAAATTACTGTTAATGAAGAAACATAGAAGAGGAGGGTGGGTAC	4176
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5S-5.9	GACGGTTGTGGTGCGGTGGCAGTGTGTGCGGTGGTGCGGCGCAGTACTGGTGCG-----	4239
3S-5.4	GACGGTTGTGGTGCGGTGGCAGTGTGTGCGGTGGTGCGGCGCAGTACTGGTGCG-----	4245
4L-5.9	GACGGTTGTGGTGCGGTGGCAGTGTGTGCGGTGGTGCGGCGCAGTACTGGTGCGACGGCGA	4231
5L-5.9	GACGGTTGTGGTGCGGTGGCAGTGTGTGCGGTGGTGCGGCGCAGTACTGGTGCGACGGCGA	4236

5S-5.9	-----GCGGTGGTGGTGCAACGGTCCCCAATGGTAATGTGGGAGAAGAGGGGAGAGA	4291
3S-5.4	-----GCGGTGGTGGTGCAACGGTCCCCAATGGTAATGTGGGAGAAGAGGGGAGAGA	4297
4L-5.9	CTGGTGCGGCGGTGGTGGTGCAACGGTCCCCAATGGTAATGTGGGAGAAGAGGGGAGAGA	4291
5L-5.9	CTGGTGCGGCGGTGGTGGTGCAACGGTCCCCAATGGTAATGTGGGAGAAGAGGGGAGAGA	4296

5S-5.9	AGTGAATGTAGAAGGTGGAAAAATATGAAAATGGAAAAATACGTATATTATACGTATTTAG	4351
3S-5.4	AGTGAATGTAGAAGGTGGAAAAATATGAAAATGGAAAAATACGTATATTATACGTATTTAG	4357
4L-5.9	AGTGAATGTAGAAGGTGGAAAAATATGAAAATGGAAAAATACGTATATTATACGTATTTAG	4351
5L-5.9	AGTGAATGTAGAAGGTGGAAAAATATGAAAATGGAAAAATACGTATATTATACGTATTTAG	4356

5S-5.9	GGCGTTAGTAAGATATTCTAGGGCGTCGTTTAGCAAATGAGAAAAAATAATACACTCTAG	4411
3S-5.4	GGCGTTAGTAAGATATTCTAGGGCGTCGTTTAGCAAATGAGAAAAAATAATACACTCTAG	4417
4L-5.9	GGCGTTAGTAAGATATTCTAGGGCGTCGTTTAGCAAATGAGAAAAAATAATACACTCTAG	4411
5L-5.9	GGCGTTAGTAAGATATTCTAGGGCGTCGTTTAGCAAATGAGAAAAAATAATACACTCTAG	4416

5S-5.9	TTGTCGTAGACTCTCAATATGTGTCATTTAGAGACTCGTAACGCATTGACGCACTTACTC	4471
3S-5.4	TTGTCGTAGACTCTCAATATGTGTCATTTAGAGACTCGTAACGCATTGACGCACTTACTC	4477
4L-5.9	TTGTCGTAGACTCTCAATATGTGTCATTTAGAGACTCGTAACGCATTGACGCACTTACTC	4471
5L-5.9	TTGTCGTAGACTCTCAATATGTGTCATTTAGAGACTCGTAACGCATTGACGCACTTACTC	4476

5S-5.9	GGGGTAGAAATATTTTGTTCATTTATTAATGAGAAAATTTTATCCCCTGATCCCAATT	4531
3S-5.4	GGGGTAGAAATATTTTGTTCATTTATTAATGAGAAAATTTTATCCCCTGATCCCAATT	4537
4L-5.9	GGGGTAGAAATATTTTGTTCATTTATTAATGAGAAAATTTTATCCCCTGATCCCAATT	4531
5L-5.9	GGGGTAGAAATATTTTGTTCATTTATTAATGAGAAAATTTTATCCCCTGATCCCAATT	4536

5S-5.9	ATCAAATCAACATCTAAAAATTTAAATGACTAGGTACGTAACGAAAAACGAATGACTCT	4591
3S-5.4	ATCAAATCAACATCTAAAAATTTAAATGACTAGGTACGTAACGAAAAACGAATGACTCT	4597
4L-5.9	ATCAAATCAACATCTAAAAATTTAAATGACTAGGTACGTAACGAAAAACGAATGACTCT	4591
5L-5.9	ATCAAATCAACATCTAAAAATTTAAATGACTAGGTACGTAACGAAAAACGAATGACTCT	4596

5S-5.9	CGATAATAGTACACCCCATTAATCCATTCTTAGTTTGTGTCATAGTTTGTGCGTAGTGC	4651
3S-5.4	CGATAATAGTACACCCCATTAATCCATTCTTAGTTTGTGTCATAGTTTGTGCGTAGTGC	4657
4L-5.9	CGATAATAGTACACCCCATTAATCCATTCTTAGTTTGTGTCATAGTTTGTGCGTAGTGC	4651
5L-5.9	CGATAATAGTACACCCCATTAATCCATTCTTAGTTTGTGTCATAGTTTGTGCGTAGTGC	4656

5S-5.9	ATAGCTGGCTGCAAAAGAAATCTTTTGCACAGAGAAAACCTTTTGCACCTTCGGAATTCAG	4711
3S-5.4	ATAGCTGGCTGCAAAAGAAATCTTTTGCACAGAGAAAACCTTTTGCACCTTCGGAATTCAG	4717
4L-5.9	ATAGCTGGCTGCAAAAGAAATCTTTTGCACAGAGAAAACCTTTTGCACCTTCGGAATTCAG	4711
5L-5.9	ATAGCTGGCTGCAAAAGAAATCTTTTGCACAGAGAAAACCTTTTGCACCTTCGGAATTCAG	4716

5S-5.9	CAGGAATATCATAGCCATTTATGGAAGCAACAACCTCTTGTGACCCATTTTCATCTAAACC	4771
3S-5.4	CAGGAATATCATAGCCATTTATGGAAGCAACAACCTCTTGTGACCCATTTTCATCTAAACC	4777
4L-5.9	CAGGAATATCATAGCCATTTATGGAAGCAACAACCTCTTGTGACCCATTTTCATCTAAACC	4771
5L-5.9	CAGGAATATCATAGCCATTTATGGAAGCAACAACCTCTTGTGACCCATTTTCATCTAAACC	4776

5S-5.9	CTTAATCTCATAAATTTTACATTTTTCAGAATTCAAAAATCACGTAATTTTTTTTTTGGTAT	4831
3S-5.4	CTTAATCTCATAAATTTTACATTTTTCAGAATTCAAAAATCACGTAATTTTTTTTTTGGTAT	4837
4L-5.9	CTTAATCTCATAAATTTTACATTTTTCAGAATTCAAAAATCACGTAATTTTTTTTTTGGTAT	4831
5L-5.9	CTTAATCTCATAAATTTTACATTTTTCAGAATTCAAAAATCACGTAATTTTTTTTTTGGTAT	4836

5S-5.9	GTTACTTGAACCCAGTTCATAACTGACCCGAAATTCAGAATTTGGAGCAAAGTTAGCA	4891
3S-5.4	GTTACTTGAACCCAGTTCATAACTGACCCGAAATTCAGAATTTGGAGCAAAGTTAGCA	4897
4L-5.9	GTTACTTGAACCCAGTTCATAACTGACCCGAAATTCAGAATTTGGAGCAAAGTTAGCA	4891
5L-5.9	GTTACTTGAACCCAGTTCATAACTGACCCGAAATTCAGAATTTGGAGCAAAGTTAGCA	4896

	Exon1	
5S-5.9	CCTTTTGTGTTGTTCAAAAATCATGGCGTGGTACAGAAATTCAGGTTTGTCTACAATGCTT	4951
3S-5.4	CCTTTTGTGTTGTTCAAAAATCATGGCGTGGTACAGAAATTCAGGTTTGTCTACAATGCTT	4957
4L-5.9	CCTTTTGTGTTGTTCAAAAATCATGGCGTGGTACAGAAATTCAGGTTTGTCTACAATGCTT	4951
5L-5.9	CCTTTTGTGTTGTTCAAAAATCATGGCGTGGTACAGAAATTCAGGTTTGTCTACAATGCTT	4956

5S-5.9	TAAAACTCAACTTGC GTTCCAAAACATTTGGTACTATTCCAAC TCCAAGAGTTCATT CGA	5011
3S-5.4	TAAAACTCAACTTGC GTTCCAAAACATTTGGTACTATTCCAAC TCCAAGAGTTCATT CGA	5017
4L-5.9	TAAAACTCAACTTGC GTTCCAAAACATTTGGTACTATTCCAAC TCCAAGAGTTCATT CGA	5011
5L-5.9	TAAAACTCAACTTGC GTTCCAAAACATTTGGTACTATTCCAAC TCCAAGAGTTCATT CGA	5016

5S-5.9	ATTCCTCATCTTTGTTTTACAATCAATCTACTAAGTGTAGTGGGTTATTTGGGTCTGCAA	5071
3S-5.4	ATTCCTCATCTTTGTTTTACAATCAATCTACTAAGTGTAGTGGGTTATTTGGGTCTGCAA	5077
4L-5.9	ATTCCTCATCTTTGTTTTACAATCAATCTACTAAGTGTAGTGGGTTATTTGGGTCTGCAA	5071
5L-5.9	ATTCCTCATCTTTGTTTTACAATCAATCTACTAAGTGTAGTGGGTTATTTGGGTCTGCAA	5076

5S-5.9	AATCTGGGTATTTTAATGGGTTTAAACATCATCAAGAGATTAGCTCTTTCTCTGGTTTTG	5131
3S-5.4	AATCTGGGTATTTTAATGGGTTTAAACATCATCAAGAGATTAGCTCTTTCTCTGGTTTTG	5137
4L-5.9	AATCTGGGTATTTTAATGGGTTTAAACATCATCAAGAGATTAGCTCTTTCTCTGGTTTTG	5131
5L-5.9	AATCTGGGTATTTTAATGGGTTTAAACATCATCAAGAGATTAGCTCTTTCTCTGGTTTTG	5136

5S-5.9	CAAGGAGAAATTATCATGGTGATAAAACCGAAGTAAGTGTGAATCATGGCTGGAAAAAT	5191
3S-5.4	CAAGGAGAAATTATCATGGTGATAAAACCGAAGTAAGTGTGAATCATGGCTGGAAAAAT	5197
4L-5.9	CAAGGAGAACTATCATGGTGTTAAACCGAAGTAAGTGTGAATTCGGGTGGAAAAAT	5191
5L-5.9	CAAGGAGAACTATCATGGTGTTAAACCGAAGTAAGTGTGAATTCGGGTGGAAAAAT	5196
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5S-5.9	TACTTCTTGGAATTGCACTAATG---TTGAGTACTGGTATATTTGCTTACCGTCATGTGC	5248
3S-5.4	TACTTCTTGGAATTGCACTAATG---TTGAGTACTGGTATATTTGCTTACCGTCATGTGC	5254
4L-5.9	TACTTCTTGGAATTGCACTAATAATCTCGCATTTCTGGTATGATTGCTTTCTTTTATTTGC	5251
5L-5.9	TACTTCTTGGAATTGCACTAATAATCTCGCATTTCTGGTATGATTGCTTTCTTTTATTTGC	5256
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5S-5.9	ACCCAGTAGTTGTGCCATATACAGGAAGGAAGCATTATGTGCTTATATCAACAACCTGATG	5308
3S-5.4	ACCCAGTAGTTGTGCCATATACAGGAAGGAAGCATTATGTGCTTATATCAACAACCTGATG	5314
4L-5.9	ACCCAGTAGTTGTGCCATATACAGGAAGGAAGCATTATGTGATTTTGTCAACAACCTCATG	5311
5L-5.9	ACCCAGTAGTTGTGCCATATACAGGAAGGAAGCATTATGTGATTTTGTCAACAACCTCATG	5316
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5S-5.9	AGAATGAAAAGGGGAGAAGTTGAGAAGCGGAAAAATACAACCTGCTACACACCCTGATACTG	5368
3S-5.4	AGAATGAAAAGGGGAGAAGTTGAGAAGCGGAAAAATACAACCTGCTACACACCCTGATACTG	5374
4L-5.9	AGAATGAAAATGGAGAATTTGAGAAGCGGAAAAATACAACCTGCTACACACCCTGATACTG	5371
5L-5.9	AGAATGAAAATGGAGAATTTGAGAAGCGGAAAAATACAACCTGCTACACACCCTGATACTG	5376
	***** *****	
5S-5.9	ATAGGGTTAGGTCAATATTCCAACACATTCCTTGAATCACTGGAAAAGAGAGATTAATCACC	5428
3S-5.4	ATAGGGTTAGGTCAATATTCCAACACATTCCTTGAATCACTGGAAAAGAGAGATTAATCACC	5434
4L-5.9	AGAGGGTTAGGTCTATATTCCAACACATTCCTTGAATCACTGGAAAAGAGAGATTAATCACC	5431
5L-5.9	AGAGGGTTAGGTCTATATTCCAACACATTCCTTGAATCACTGGAAAAGAGAGATTAATCACC	5436
	* *****	
5S-5.9	ATGAACTCGAACTCGAA-----AGAGATGAAACTTTCAAGGAGATAACCATTT	5476
3S-5.4	ATGAACTCGAACTCGAA-----AGAGATGAAACTTTCAAGGAGATAACCATTT	5482
4L-5.9	ATGAACTCGAACTCGAACTCGAAAGAGATGAAACTTTCAAGGAGAAAACCATTT	5491
5L-5.9	ATGAACTCGAACTCGAACTCGAAAGAGATGAAACTTTCAAGGAGAAAACCATTT	5496
	***** *****	
5S-5.9	GGAAGGAGGAGACAGTTGATGATAAAGATAGTAGGAAGAAGCATAGTGGGGCTAAGATAA	5536
3S-5.4	GGAAGGAGGAGACAGTTGATGATAAAGATAGTAGGAAGAAGCATAGTGGGGCTAAGATAA	5542
4L-5.9	GGAAGGAGGAGACAGATCATGATAAAGATAGTAGGAAGAAGCATAGTGGGGCTAAGATAA	5551
5L-5.9	GGAAGGAGGAGACAGATCATGATAAAGATAGTAGGAAGAAGCATAGTGGGGCTAAGATAA	5556
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5S-5.9	CTACTAACCATTGGAAGGGTTGAATTGGGAAATTTTCGTTGTTGATAAACCCTGGTTG	5596
3S-5.4	CTACTAACCATTGGAAGGGTTGAATTGGGAAATTTTCGTTGTTGATAAACCCTGGTTG	5602
4L-5.9	CTACTAACCATT---GAAGGGATGAATTGGGAAATTTTCGTTGTCGATAAACCCTGGTTG	5608
5L-5.9	CTACTAACCATT---GAAGGGATGAATTGGGAAATTTTCGTTGTCGATAAACCCTGGTTG	5613
	***** *****	
5S-5.9	AGTCCAGTTGTTTATTTGGTGGGAAGATTGTTGTTTACACCGGATTGCTCAACCATTGCA	5656
3S-5.4	AGTCCAGTTGTTTATTTGGTGGGAAGATTGTTGTTTACACCGGATTGCTCAACCATTGCA	5662
4L-5.9	AGTCCAGTTGTATATTTGGTGGGAAGATTGTTGTTTACACTGGATTGCTCAACCATTGCA	5668
5L-5.9	AGTCCAGTTGTATATTTGGTGGGAAGATTGTTGTTTACACTGGATTGCTCAACCATTGCA	5673
	***** *****	
	Intron1	
5S-5.9	ACTCTGATGCTGAATTGGCTACAATTATCGCGCATCAGGTATATAAACTATTCCTGGGA	5716
3S-5.4	ACTCTGATGCTGAATTGGCTACAATTATCGCGCATCAGGTATATAAACTATTCCTGGGA	5722
4L-5.9	TCTCTGATGCTGAATTGGCTACAATTATCGCGCATCAGGTATATAAACTATTCCTGGGA	5728
5L-5.9	TCTCTGATGCTGAATTGGCTACAATTATCGCGCATCAGGTATATAAACTATTCCTGGGA	5733
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5S-5.9	CTCCAATTATGTGCTTAAGCTGATGGTTAATAGAA-----	5751
3S-5.4	CTCCAATTATGTGCTTAAGCTGATGGTTAATAGAA-----	5757
4L-5.9	CTCCAACCATCGGCTTAAGCTCATGGTTGATAGAATATAAAATTATTTCTGGGACTCCAA	5788
5L-5.9	CTCCAACCATCGGCTTAAGCTCATGGTTGATAGAATATAAAATTATTTCTGGGACTCCAA	5793
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5S-5.9	-----	
3S-5.4	-----	
4L-5.9	CCAAAAGCTCAGGAATAGCTTTATATTCTATCAGTAGCTTGTAGTAGTTCTTTACTAGAC	5848
5L-5.9	CCAAAAGCTCAGGAATAGCTTTATATTCTATCAGTAGCTTGTAGTAGTTCTTTACTAGAC	5853
5S-5.9	-----	
3S-5.4	-----	
4L-5.9	TGCAGGAATAGATAAATATTTGGTTATCAATATACATGGGTGATTCCGGTTCATATTTAGG	5908
5L-5.9	TGCAGGAATAGATAAATATTTGGTTATCAATATACATGGGTGATTCCGGTTCATATTTAGG	5913
5S-5.9	-----CTATACAAAAAACATGAAAGGA	5773
3S-5.4	-----CTATACAAAAAACATGAAAGGA	5779
4L-5.9	CGTATCAAATGATTTAAGATATTGTATGAAGTTATGAACATACAAAAAACATGAAAGGA	5968
5L-5.9	CGTATCAAATGATTTAAGATATTGTATGAAGTTATGAACATACAAAAAACATGAAAGGA	5973

5S-5.9	ATTATATGAAAAAAA--CTGATGAATTTTAGGTTATCAGATTACATTATGAATGTCATA	5831
3S-5.4	ATTATATGAAAAAAA--CTGATGAATTTTAGGTTATCAGATTACATTATGAATGTCATA	5837
4L-5.9	ATTATATGAAAAAAAACATGATGAATTTTAGGTTATTATATTGCATTATGAATGTCATA	6028
5L-5.9	ATTATATGAAAAAAAACATGATGAATTTTAGGTTATTATATTGCATTATGAATGTCATA	6033
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	Exon2	
5S-5.9	TGTCAATGTGGTGGTATGTATTTGTTAGGTTGGGCATGCTGTGGCTCGACATCAGGCAGA	5891
3S-5.4	TGTCAATGTGGTGGTATGTATTTGTTAGGTTGGGCATGCTGTGGCTCGACATCAGGCAGA	5897
4L-5.9	TGTCAATGTGGTGGTATATATTTGTTAGGTTGGGCATGCTGTGGCTCGACATGAGGCAGA	6088
5L-5.9	TGTCAATGTGGTGGTATATATTTGTTAGGTTGGGCATGCTGTGGCTCGACATGAGGCAGA	6093

5S-5.9	GGATCGGACAGCATTCTTCTGGTGGTCAATGTCCCTC---TACGTGATAATATTTGAAGT	5948
3S-5.4	GGATCGGACAGCATTCTTCTGGTGGTCAATGTCCCTC---TACGTGATAATATTTGAAGT	5954
4L-5.9	GCATTGGACAACATTGTTGTGGTTCGATACGTTAGTGATATACATGACAATATTTCAATA	6148
5L-5.9	GCATTGGACAACATTGTTGTGGTTCGATACGTTAGTGATATACATGACAATATTTCAATA	6153
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5S-5.9	TCTATTTACTGCGCGTAAATTTGCCAATGCAAGATCAAACTACTCTTAAGGCATCCTCT	6008
3S-5.4	TCTATTTACTGCGCGTAAATTTGCCAATGCAAGATCAAACTACTCTTAAGGCATCCTCT	6014
4L-5.9	TCTATTTACTGCGCCTGAATTTGCCAATGCAATATCAAACTACTCTCAAGGCATCCTCT	6208
5L-5.9	TCTATTTACTGCGCCTGAATTTGCCAATGCAATATCAAACTACTCTCAAGGCATCCTCT	6213

	Intron2	
5S-5.9	CTTGCAAAAGTAAGTCTCTTACTCTTAAAATGTTTTCTTGATGATTAACAAACATGTGGT	6068
3S-5.4	CTTGCAAAAGTAAGTCTCTTACTCTTAAAATGTTTTCTTGATGATTAACAAACATGTGGT	6074
4L-5.9	CTTGCAAAAGTAAGTCTCTTACTCTTAAAATGTTTTCTTGATGATTAACAAACATGTGGT	6268
5L-5.9	CTTGCAAAAGTAAGTCTCTTACTCTTAAAATGTTTTCTTGATGATTAACAAACATGTGGT	6273

5S-5.9	ACTGCTACTGCATAACTGTGTTACTGCATCACATATGTTACTGCATAAATTGCAAAACATA	6128
3S-5.4	ACTGCTACTGCATAACTGTGTTACTGCATCACATATGTTACTGCATAAATTGCAAAACATA	6134
4L-5.9	ACTGCTACTGCATAACTGTGTTACTGCATCACATATGTTACTGCATAAATTGCAAAACATA	6328
5L-5.9	ACTGCTACTGCATAACTGTGTTACTGCATCACATATGTTACTGCATAAATTGCAAAACATA	6333

5S-5.9	TCACATTGCCCGGACCTAGTAACTTGTTTCATTTGTCAGCGATTTTCATTTAGACATCCAT	6188
3S-5.4	TCACATTGCCCGGACCTAGTAACTTGTTTCATTTGTCAGCGATTTTCATTTAGACATCCAT	6194
4L-5.9	TCACATTGCCCGGACCTAGTAACTTGTTTCATTTGTCAGCGATTTTCATTTAGACATCCAT	6388
5L-5.9	TCACATTGCCCGGACCTAGTAACTTGTTTCATTTGTCAGCGATTTTCATTTAGACATCCAT	6393

5S-5.9	TTGAAAGCAAGTTAAATTTGTATCAAGTTGTGGAATGGAAAAGTAATAGAACTAAATAGA	6248
3S-5.4	TTGAAAGCAAGTTAAATTTGTATCAAGTTGTGGAATGGAAAAGTAATAGAACTAAATAGA	6254
4L-5.9	TTGAGAGCAAGTTAAATTTGTATCAAGTTGTGGAATGGAAAAGTAATAGAACTAAATAGA	6448
5L-5.9	TTGAGAGCAAGTTAAATTTGTATCAAGTTGTGGAATGGAAAAGTAATAGAACTAAATAGA	6453
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5S-5.9	GAGGTGTGATGCTAACAAAATCTAATCCATTACTGAGTAATGGTTTTGGATCAATATATG	6308
3S-5.4	GAGGTGTGATGCTAACAAAATCTAATCCATTACTGAGTAATGGTTTTGGATCAATATATG	6314
4L-5.9	GAGGTGTGATGCTAACAAAATCTAATCCATTACTGAGTAATGGTTTTGGATCAATATATG	6508
5L-5.9	GAGGTGTGATGCTAACAAAATCTAATCCATTACTGAGTAATGGTTTTGGATCAATATATG	6513

5S-5.9	GATTGCTATATTCACATATTCTATACTTTGCCGCAGATAACATTAAATTGATGTTGTTT	6368
3S-5.4	GATTGCTATATTCACATATTCTATACTTTGCCGCAGATAACATTAAATTGATGTTGTTT	6374
4L-5.9	GATTGCTATATTCACATATTCTATACTTTGCCGCAGATAACATTAAATTGATGTTGTTT	6568
5L-5.9	GATTGCTATATTCACATATTCTATACTTTGCCGCAGATAACATTAAATTGATGTTGTTT	6573

5S-5.9	ATTTACATTTGACACATTTAAATTTGAGTTGTGGACTATAATATATATGCGAGTTAGGTAA	6428
3S-5.4	ATTTACATTTGACACATTTAAATTTGAGTTGTGGACTATAATATATATGCGAGTTAGGTAA	6434
4L-5.9	ATTTACATTTGACACATTTAAATTTGAGTTGTGGACTATAATATATATGCGAGTTAGGTAA	6628
5L-5.9	ATTTACATTTGACACATTTAAATTTGAGTTGTGGACTATAATATATATGCGAGTTAGGTAA	6633

Exon3		
5S-5.9	CATAGAGTGTCAATTTACAGGGTTTGAAGATTATTCAGGCTAGATTTTCATCAATTACTG	6488
3S-5.4	CATAGAGTGTCAATTTACAGGGTTTGAAGATTATTCAGGCTAGATTTTCATCAATTACTG	6494
4L-5.9	CATAGAGTGTCAATTTACAGGGTTTGAAGATTATTCAGGCTAGATTTTCATCAATTACTG	6688
5L-5.9	CATAGAGTGTCAATTTACAGGGTTTGAAGATTATTCAGGCTAGATTTTCATCAATTACTG	6693

5S-5.9	CCACGAACCTACCTTGCACTTTGGGCTTTCTTGGATTGTCTTCCTTGGTGTTTATCTTTAT	6548
3S-5.4	CCACGAACCTACCTTGCACTTTGGGCTTTCTTGGATTGTCTTCCTTGGTGTTTATCTTTAT	6554
4L-5.9	CCACGAACCTACCTTGCACTTTGGGCTTTCTTGGATTGTCTTCCTTGGTGTTTATCTTTAT	6748
5L-5.9	CCACGAACCTACCTTGCACTTTGGGCTTTCTTGGATTGTCTTCCTTGGTGTTTATCTTTAT	6753

5S-5.9	TTTGGTCGGAAGGAAATAGAAGCAGATCACATTGGAGTGCTTCTGATGGCTTCTGCTGGA	6608
3S-5.4	TTTGGTCGGAAGGAAATAGAAGCAGATCACATTGGAGTGCTTCTGATGGCTTCTGCTGGA	6614
4L-5.9	TTTGGTCGGAAGGAAATAGAAGCAGATCACATTGGAGTGCTTCTGATGGCTTCTGCTGGA	6808
5L-5.9	TTTGGTCGGAAGGAAATAGAAGCAGATCACATTGGAGTGCTTCTGATGGCTTCTGCTGGA	6813

5S-5.9	TACGACCCGCGAGTTGCACCTCAAGTATATGACAAGCTTGCAAAGCCACTGGGCGACTGG	6668
3S-5.4	TACGACCCGCGAGTTGCACCTCAAGTATATGACAAGCTTGCAAAGCCACTGGGCGACTGG	6674
4L-5.9	TACGACCCGCGAGTTGCACCTCAAGTATATGACAAGCTTGCAAAGCCACTGGGCGACTGG	6868
5L-5.9	TACGACCCGCGAGTTGCACCTCAAGTATATGACAAGCTTGCAAAGCCACTGGGCGACTGG	6873

5S-5.9	AACTGTTTAGCAACTCATCCATTTGCAAGAATGAGAGCAAAGTTGTTAGCTCGAGCTGAT	6728
3S-5.4	AACTGTTTAGCAACTCATCCATTTGCAAGAATGAGAGCAAAGTTGTTAGCTCGAGCTGAT	6734
4L-5.9	AACTGTTTAGCAACTCATCCATTTGCAAGAATGAGAGCAAAGTTGTTAGCTCGAGCTGAT	6928
5L-5.9	AACTGTTTAGCAACTCATCCATTTGCAAGAATGAGAGCAAAGTTGTTAGCTCGAGCTGAT	6933

5S-5.9	GTTATGAAGGAAGCAGATAAGATATACAATGAAGTTGTAGCAGGACGTGCAATTCAAGGT	6788
3S-5.4	GTTATGAAGGAAGCAGATAAGATATACAATGAAGTTGTAGCAGGACGTGCAATTCAAGGT	6794
4L-5.9	GTTATGAAGGAAGCAGATAAGATATACAATGAAGTTGTAGCAGGACGTGCAATTCAAGGT	6988
5L-5.9	GTTATGAAGGAAGCAGATAAGATATACAATGAAGTTGTAGCAGGACGTGCAATTCAAGGT	6993

Exon3		
5S-5.9	CTTCAGTAACCATTTACCAACCAGCATCTTCTTTTAGCAGCTTCGCCTGTTTATGAATTA	6848
3S-5.4	CTTCAGTAACCATTTACCAACCAGCATCTTCTTTTAGCAGCTTCGCCTGTTTATGAATTA	6854
4L-5.9	CTTCAGTAACCATTTACCAACCAGCATCTTCTTTTAGCAGCTTCGCCTGTTTATGAATTA	7048
5L-5.9	CTTCAGTAACCATTTACCAACCAGCATCTTCTTTTAGCAGCTTCGCCTGTTTATGAATTA	7053

5S-5.9	TGGTAATCAAATTAACAGCTCATGGATCATTATATTGTCGTTATATTTTCGTCTGTTTG	6908
3S-5.4	TGGTAATCAAATTAACAGCTCATGGATCATTATATTGTCGTTATATTTTCGTCTGTTTG	6914
4L-5.9	TGGTAATCAAATTAACAGCTCATGGATCATTATATTGTCGTTATATTTTCATCTGTTTG	7108
5L-5.9	TGGTAATCAAATTAACAGCTCATGGATCATTATATTGTCGTTATATTTTCATCTGTTTG	7113

5S-5.9	ACAAAGTTTAGAGGTTAATTTGAGTTGAAAACCTTGCTATTAGTATGTTATCCTATCCCAC	6968
3S-5.4	ACAAAGTTTAGAGGTTAATTTGAGTTGAAAACCTTGCTATTAGTATGTTATCCTATCCCAC	6974
4L-5.9	ACAAAGTTTAGAGGTTAATTTGAGTTGAAAACCTTGCTATTAGTATGTTATCCTATCCCAC	7168
5L-5.9	ACAAAGTTTAGAGGTTAATTTGAGTTGAAAACCTTGCTATTAGTATGTTATCCTATCCCAC	7173

5S-5.9	TGACCTTGTTAATTCAATCTAATTTAGTTCCTATGTTAATTCAGTCTCTTTTTCTCCTT	7028
3S-5.4	TGACCTTGTTAATTCAATCTAATTTAGTTCCTATGTTAATTCAGTCTCTTTTTCTCCTT	7034
4L-5.9	TGGCCTTGTTAATTCAATCTAATTTAGTTCCTATGTTAATTCAGTCTCTTTTTCTCCTT	7228
5L-5.9	TGACCTTGTTAATTCAATCTAATTTAGTTCCTATGTTAATTCAGTCTCTTTTTCTCCTT	7233
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5S-5.9	TAATAGATCCTCTCTATCCGTTTTCTTTTTCTTTTTGAGAAAAGGAGCATCATAGATA	7088
3S-5.4	TAATAGATCCTCTCTATCCGTTTTCTTTTTCTTTTTGAGAAAAGGAGCATCATAGATA	7094
4L-5.9	TAATAGATCCTCTCTATCCGTTTTCTTTTTCTTTTTGAGAAAAGGAGCATCATAGATA	7288
5L-5.9	TAATAGATCCTCTCTATCCGTTTTCTTTTTCTTTTTGAGAAAAGGAGCATCATAGATA	7293

5S-5.9	AATATAAATCGAAGTCATTACAACTAAACTAGAGCTTCCAATATAAGTCCCTGGAAGTC	7148
3S-5.4	AATATAAATCGAAGTCATTACAACTAAACTAGAGCTTCCAATATAAGTCCCTGGAAGTC	7154
4L-5.9	AATATAAATCGAAGTCATTACAACTAAACTAGAGCTTCCAATATAAGTCCCTGGAAGTC	7348
5L-5.9	AATATAAATCGAAGTCATTACAACTAAACTAGAGCTTCCAATATAAGTCCCTGGAAGTC	7353

5S-5.9	CGAAAGCAATAGTAGTAGATAGCATAGTAGAGATGAGTTTCTCTTTTAGGTAGATAGTAG	7208
3S-5.4	CGAAAGCAATAGTAGTAGATAGCATAGTAGAGATGAGTTTCTCTTTTAGGTAGATAGTAG	7214
4L-5.9	CGAAAGCAATAGTAGTAGATAGCATAGTAGAGATGAGTTTCTCTTTTAGGTAGATAGTAG	7408
5L-5.9	CGAAAGCAATAGTAGTAGATAGCATAGTAGAGATGAGTTTCTCTTTTAGGTAGATAGTAG	7413

5S-5.9	ATAGGAGGATCGATAGATGACCCACCATTGTCGCCGCTTTCGGCGCCACCAACACCAGGG	7268
3S-5.4	ATAGGAGGATCGATAGATGACCCACCATTGTCGCCGCTTTCGGCGCCACCAACACCAGGG	7274
4L-5.9	ATAGGAGGATCGATAGATGACCCACCATTGTCGCCGCTTTCGGCGCCACCAACACCAGGG	7468
5L-5.9	ATAGGAGGATCGATAGATGACCCACCATTGTCGCCGCTTTCGGCGCCACCAACACCAGGG	7473

5S-5.9	GAAGAAGAGCCTCCAATCTGGCCACCACCGGATATAGGAATA-----	7310
3S-5.4	GAAGAAGAGCCTCCAATCTGGCCACCACCGGATATAGGAATACCAAGCATAGTTTGCCA	7334
4L-5.9	GAAGAAGAGCCTCCAATCTGGCCACCACCGGATATAGGAATA-----	7510
5L-5.9	GAAGAAGAGCCTCCAATCTGGCCACCACCGGATATAGGAATA-----	7515

5S-5.9	-----TCAATTCACTCCTTAACGTCCATGGATGTGATTACCCCATGCATGGATAAAC	7362
3S-5.4	CCTGGATATCAATTCACTCCTTAACGTCCATGGATGTGATTACCCCATGCATGGATAAAC	7394
4L-5.9	-----TCAATTCACTCCTTAACGTCCATGGATGTGATTACCCCATGCATGGATAAAC	7562
5L-5.9	-----TCAATTCACTCCTTAACGTCCATGGATGTGATTACCCCATGCATGGATAAAC	7567

5S-5.9	GAGACTGTGATTGGCCCTGCATGTTTTGTTGTGGCAAATGCAATGGCACTTGTTGCCTCA	7422
3S-5.4	GAGACTGTGATTGGCCCTGCATGTTTTGTTGTGGCAAATGCAATGGCACTTGTTGCCTCA	7454
4L-5.9	GAGACTGTGATTGGCCCTGCATGTTTTGTTGTGGCAAATGCAATGGCACTTGTTGCCTCA	7622
5L-5.9	GAGACTGTGATTGGCCCTGCATGTTTTGTTGTGGCAAATGCAATGGCACTTGTTGCCTCA	7627
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5S-5.9	GTAAAATGATTTATGAGTAGACACATGAGATATCTTCCCTTATATTATTGTTTCATTTTGA	7482
3S-5.4	GTAAAATGATTTATGAGTAGACACATGAGATATCTTCCCTTATATTATTGTTTCATTTTGA	7514
4L-5.9	GTAAAATGATTTATGAGTAGACACATGAGATATCTTCCCTTATATTATTGTTTCATTTTGA	7682
5L-5.9	GTAAAATGATTTATGAGTAGACACATGAGATATCTTCCCTTATATTATTGTTTCATTTTGA	7687
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5S-5.9	GTTAGTTATACTCCCTCCTCTTTTTCTTAGTTGCTATATTCCATTTTTGGATACAAAAT	7542
3S-5.4	GTTAGTTATACTCCCTCCTCTTTTTCTTAGTTGCTATATTCCATTTTTGGATACAAAAT	7574
4L-5.9	GTTAGTTATACTCCCTCCTCTTTTTCTTAGTTGCTATATTCCATTTTTGGATACAAAAT	7742
5L-5.9	GTTAGTTATACTCCCTCCTCTTTTTCTTAGTTGCTATATTCCATTTTTGGATACAAAAT	7747

5S-5.9	CACATGAGAATTTTGACTTTCCTTAATTTTATATATGTAAGAAAAAAAAACATAGTATTT	7602
3S-5.4	CACATGAGAATTTTGACTTTCCTTAATTTTATATATGTAAGAAAAAAAA-CATAGTATTT	7633
4L-5.9	CACATGAGAATTTTGACTTTCCTTAATTTTATATATGTAAGAAAAAAAAACATAGTATTT	7802
5L-5.9	CACATGAGAATTTTGACTTTCCTTAATTTTATATATGTAAGAAAAAAAA-CATAGTATTT	7806
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5S-5.9	TATTAGATTTCTCTCAAATGTGTAATTTTCATATATAGTTTTTTTATAATTTTCTCGTAT	7662
3S-5.4	TATTAGATTTCTCTCAAATGTGTAATTTTCATATATAGTTTTTTTATAATTTTCTCGTAT	7693
4L-5.9	TATTAGATTTCTCTCAAATGTGTAATTTTCATATATAGTTTTTTTATAATTTTCTCGTAT	7862
5L-5.9	TATTAGATTTCTCTCAAATGTGTAATTTTCATATATAGTTTTTTTATAATTTTCTCGTAT	7866

5S-5.9	ACATAACTCAACATATTAAGGTTTGAAGTCATGACTGGGAGCAAGAAACCACGCGGGTGG	7722
3S-5.4	ACATAACTCAACATATTAAGGTTTGAAGTCATGACTGGGAGCAAGAAACCACGCGGGTGG	7753
4L-5.9	ACATAACTCAACATATTAAGGTTTGAAGTCATGGCTGCGAGCAAGAAACCACGCGGGTGG	7922
5L-5.9	ACATAACTCAACATATTAAGGTTTGAAGTCATGACTGGGAGCAAGAAACCACGCGGGTGG	7926

5S-5.9	GGCTCACAGCAGCGCCAGCAGGAAGGACGAGTGAAAAATATTAGGGTGAATTAGTGTGGC	7782
3S-5.4	GGCTCACAGCAGCGCCAGCAGGAAGGACGAGTGAAAAATATTAGGGTGAATTAGTGTGGC	7813
4L-5.9	GGCTCACAGCAGCGCCAGCAGGAAGGACGAGTGAAAAATATTAGGGTGAATTAGTGTGGC	7982
5L-5.9	GGCTCACAGCAGCGCCAGCAGGAAGGACGAGTGAAAAATATTAGGGTGAATTAGTGTGGC	7986

5S-5.9	TCTGATACCATGACAAATTGATTAGAGCTTAATGATTTGTGTTACTATTGTTAAACTTAG	7842
3S-5.4	TCTGATACCATGACAAATTGATTAGAGCTTAATGATTTGTGTTACTACTGTTAAACTTAG	7873
4L-5.9	TCTGATACCATGACAAATTGATTAGAGCTTAATGATTTGTGTTACTATTGTTAAACTTAG	8042
5L-5.9	TCTGATACCATGACAAATTGATTAGAGCTTAATGATTTGTGTTACTATTGTTAAACTTAG	8046

5S-5.9	AGTTTATATATATCCTAAGTTTACATCCAAGGCCTTAGGCCCAATATATACAACCTCAACA	7902
3S-5.4	AGTTTATATATATCCTAAGTTTACATCCAAGGCCTTAGGCCCAATATATACAACCTCAACA	7933
4L-5.9	AGTTTATATATATCCTAAGTTTACATCCAAGGCCTTAGGCCCAATATATACAACCTCAACA	8102
5L-5.9	AGTTTATATATATCCTAAGTTTACATCCAAGGCCTTAGGCCCAATATATACAACCTCAACA	8106

5S-5.9	TATATACAAGGTCCAATATGTATTAACAAAATGAAAAATAAAAACATAATGTAGCAACTA	7962
3S-5.4	TATATACAAGGTCCAATATGTATTAACAAAATGAAAAATAAAAACATAATGTAGCAACTA	7993
4L-5.9	TATATACAAGGTCCAATATGTATTAACAAAATGAAAAATAAAAACATAATGTAGCAACTA	8162
5L-5.9	TATATACAAGGTCCAATATGTATTAACAAAATGAAAAATAAAAACATAATGTAGCAACTA	8165

5S-5.9	GCAACTAAAAAAGACGGAGAGAGTATTTAATTTAACAATATAATGATAATTAAATCAGT	8022
3S-5.4	GCAACTAAAAAAGACGGAGAGAGTATTTAAGTTAACAATATAATGATAATTAAATCAGT	8053
4L-5.9	GCAACTAAAAAAGACGGAGAGAGTATTTAAGTTAACAATATAATGATAATTAAATCAGT	8222
5L-5.9	GCAACTAAAAAAGACGGAGAGAGTATTTAATTTAACAATATAATGATAATTAAATCAGT	8225

5S-5.9	GTAAGTATTAGTCAAGATCTAGATTGAAATTACTCTCCGACAACCTCCCCGACCCATTG	8082
3S-5.4	GTAAGTATTAGTCAAGATCTAGATTGAAATTACTCTCCGACGACCTCCCCGACCCATTG	8113
4L-5.9	GTAAGTATTAGTCAAGATCTAGATTGAAATTACTCTCCGACGACCTCCCCGACCCATTG	8282
5L-5.9	GTAAGTATTAGTCAAGATCTAGATTGAAATTACTCTCCGACAACCTCCCCGACCCATTG	8285

5S-5.9	CCTTTATGTAATCAATCATTTATATACAACCTCCGATTCTTTTGATGGCAACTATTTGAAT	8142
3S-5.4	CCTTTATGTAATCAATCATTTATATACAACCTCCGATTCTTTTGATGGCAACTATTTGAAT	8173
4L-5.9	CCTTTATGTAATCAATCATTTATATACAACCTCCGATTCTTTTGATGGCAACTATTTGAAT	8342
5L-5.9	CCTTTATGTAATCAATCATTTATATACAACCTCCGATTCTTTTGATGGCAACTATTTGAAT	8345

5S-5.9	GTTACCTTTTATCAACATGAACTTTAACTATTAATATCTTTATTAATTACTAACATAATT	8202
3S-5.4	GTTACCTTTTATCAACATGAACTTTAACTATTAATATCTTTATTAATTACTAACATAATT	8233
4L-5.9	GTTACCTTTTATCAACATGAACTTTAACTATTAATATCTTTATTAATTACTAACATAATT	8402
5L-5.9	GTTACCTTTTATCAACATGAACTTTAACTATTAATATCTTTATTAATTACTAACATAATT	8405

5S-5.9	TACTACTAATTATAAATGATTTAAATATATACCTTGAGATTAATTTTCCTAACATTTATT	8262
3S-5.4	TACTACTAATTATAAATGATTTAAATATATACCTTGAGATTAATTTTCCTAACATTTATT	8293
4L-5.9	TACTACTAATTATAAATGATTTAAATATATACCTTGAGATTAATTTTCCTAACATTTATT	8462
5L-5.9	TACTACTAATTATAAATGATTTAAATATATACCTTGAGATTAATTTTCCTAACATTTATT	8465

5S-5.9	TACACTCTAACATTTGCTTTTATATTTTATAAAGAAAATGGTGATGGTTAGAAGTATATA	8322
3S-5.4	TACACTCTAACATTTGCTTTTATATTTTATAAAGAAAATGGTGATGGTTAGAAGTATATA	8353
4L-5.9	TACACTCTAACATTTGCTTTTATATTTTATAAAGAAAATGGTGATGGTTAGAAGTATATA	8522
5L-5.9	TACACTCTAACATTTGCTTTTATATTTTATAAAGAAAATGGTGATGGTTAGAAGTATATA	8525

5S-5.9	TATATGAGTAGTTCAATAGTCAAAGCCTTGCAAATTAAAGAAACGGCGGAAGAGTATATT	8382
3S-5.4	TATATGAGTAGTTCAATAGTCAAAGCCTTGCAAATTAAAGAAACGGCGGAAGAGTATATT	8413
4L-5.9	TATATGAGTAGTTCAATAGTCAAAGCCTTGCAAATTAAAGAAACGGCGGAAGAGTATATT	8582
5L-5.9	TATATGAGTAGTTCAATAGTCAAAGCCTTGCAAATTAAAGAAACGGCGGAAGAGTATATT	8585

5S-5.9	GAAAATTTATATTGTCACCTTTTTTAATAGATGAGTCGATGATGGTCTAAAATTGAGGCT	8442
3S-5.4	GAAAATTTATATTGTCACCTTTTTTAATAGATGAGTCGATGATGGTCTAAAATTGAGGCT	8473
4L-5.9	GAAAATTTATATTGTCACCTTTTTTAATAGATGAGTCGATGATGGTCTAAAATTGAGGCT	8642
5L-5.9	GAAAATTTATATTGTCACCTTTTTTAATAGATGAGTCGATGATGGTCTAAAATTGAGGCT	8645

5S-5.9	TCTAATATGCGCTAGCTTAGATTAAAGAGAACAGGAAATTGTTATGACAATTTGCGTAAG	8502
3S-5.4	TCTAATATGCGCTAGCTTAGATTAAAGAGAACAGGAAATTGTTATGACAATTTGCGTAAG	8533
4L-5.9	TCTAATATGCGCTAGCTTAGATTAAAGAGAACAGGAAATTGTTATGACAATTTGCGTAAG	8702
5L-5.9	TCTAATATGCGCTAGCTTAGATTAAAGAGAACAGGAAATTGTTATGACAATTTGCGTAAG	8705

5S-5.9	TTGACTGAGATCATCATGAAGTCGAGTATTAGCAACCTTAGTAATTTATAATTCCTCCGT	8562
3S-5.4	TTGACTGAGATCATCATGAAGTCGAGTATTAGCAACCTTAGTAATTTATAATTCCTCCGT	8593
4L-5.9	TTGACTGAGATCATCATGAAGTCGAGTATTAGCAACCTTAGTAATTTATAATTCCTCCGT	8762
5L-5.9	TTGACTGAGATCATCATGAAGTCGAGTATTAGCAACCTTAGTAATTTATAATTCCTCCGT	8765

5S-5.9	TTCTTTTTTAATTTACTCATTTTATTTTGGGCGAGAATCAAGGAAGAAGTACAAAAGTATG	8622
3S-5.4	TTCTTTTTTAATTTACTCATTTTATTTTGGGCGAGAATCAAGGAAGAAGTACAAAAGTATG	8653
4L-5.9	TTCTTTTTTAATTTACTCATTTTATTTTGGGCGAGAATCAAGGAAGAAGTACAAAAGTATG	8822
5L-5.9	TTCTTTTTTAATTTACTCATTTTATTTTGGGCGAGAATTAAGGAAGAAGTACAAAAGTWTG	8825
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5S-5.9	AGACAAAAACTGAAAAGATAAAGAGAAAAACTGAAAAGTGCAGAGAAATAAAGTAAAAAAG	8682
3S-5.4	AGACAAAAACTGAAAAGATAAAGAGAAAAACTGAAAAGTGCAGAGAAATAAAGTAAAAAAG	8713
4L-5.9	AGACAAAAACTGAAAAGATAAAGAGAAAAACTGAAAAGTGCAGAGAAATAAAGTAAAAAAG	8882
5L-5.9	AGACAAAAACTGAAAAGATAAAGAGAAAAACTGAAAAGTGCAGAGAAATAAAGTAAAAAAG	8885

5S-5.9	TGGGTTAAAAATATTAAAAAGTGGATCACATGGGTAGAAAAGGAGGAGAAAAATAGATGTG	8742
3S-5.4	TGGGTTAAAAATATTAAAAAGTGGATCACATGGGTAGAAAAGGAGGAGAAAAATAAATGTG	8773
4L-5.9	TGGGTTAAAAATATTAAAAAGTGGATCACATGGGTAGAAAAGGAGGAGAAAAATAGATGTG	8942
5L-5.9	TGGGTTAAAAATATTAAAAAGTGGATCACATGGGTAGAAAAGGAGGAGAAAAATAGATGTG	8945
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5S-5.9	ACATGTTACCAAAAAATAGAAAAAGCAGCAGTGTACAGTGTGCAGATTAAAAAGAAACAA	8802
3S-5.4	ACATGTTACCAAAAAATAGAAAAAGCAGCAGTGTACAGTGTGCAGATTAAAAAGAAACAA	8833
4L-5.9	ACATGTTACCAAAAAATAGAAAAAGCAGCAGTGTACAGTGTGCAGATTAAAAAGAAACAA	9002
5L-5.9	ACATGTTACCAAAAAATAGAAAAAGCAGCAGTGTACAGTGTGCAGATTAAAAAGAAACAA	9005

5S-5.9	ACCAAAAAAAAAAATGTATAAATTAAAAAGAAATGGAGGGAGTAATACTTAACACATAAAT	8862
3S-5.4	ACCAAAAAAAAAAATGTATAAATTAAAAAGAAATGGAGGGAGTAATACTTAACACATAAAT	8893
4L-5.9	ACCAAAAAAAAAA-TGTATAAATTAAAAAGAAATGGAGGGAGTAATACTTAACACATAAAT	9061
5L-5.9	ACCAAAAAAAAAAATGTATAAATTAAAAAGAAATGGAGGGAGTAATACTTAACACATAAAT	9065

5S-5.9	ATTGTTTATTAATTGAAGCTCGAGCTTCACCTCAGATACATGATTTTTTAATTTTTTATGAC	8922
3S-5.4	ATTGTTTATTAATTGAAGCTCGAGCTTCACCTCAGATACATGATTTTTTAATTTTTTATGAC	8953
4L-5.9	ATTGTTTACTAATTGAAGCTCGAGCTTCACCTCAGATACATGATTTTTTAATTTTTTATGAC	9121
5L-5.9	ATTGTTTATTAATTGAAGCTCGAGCTTCACCTCAGATACATGATTTTTTAATTTTTTATGAC	9125

5S-5.9	CTATCATAGTAAGTTTGCGGTGCTACTTTGATCCTTCCTTTATGATAAGACACATCCCTT	8982
3S-5.4	CTATCATAGTAAGTTTGCGGTGCTACTTTGATCCTTCCTTTATGATAAGACACATCCCTT	9013
4L-5.9	CTATCATAGTAAGTTTGCGGTGCTACTTTGATCCTTCCTTTATGATAAGACACATCCCTT	9181
5L-5.9	CTATCATAGTAAGTTTGCGGTGCTACTTTGATCCTTCCTTTATGATAAGACACATCCCTT	9185

5S-5.9	TATTCTCTAAGAGAATCACTTAAATTTATAAGGTATAAAGTTAACGCTATAAGTTAAAGA	9042
3S-5.4	TATTCTCTAAGAGAATCACTTAAATTTATAAGGTATAAAGTTAACGCTATAAGTTAAAGA	9073
4L-5.9	TATTCTCTAAGAGAATCACTTAAATTTATAAGATATAAAGTTAACGCTATAAGTTAAAGA	9241
5L-5.9	TATTCTCTAAGAGAATCACTTAAATTTATAAGGTATAAAGTTAACGCTATAAGTTAAAGA	9245

5S-5.9	GGTCATTTTTTAGATAAATAGGTCACCTTGTATGTAATAGGTCACCTTCTACTAAAATTTT	9102
3S-5.4	GGTCATTTTTTAGATAAATAGGTCACCTTGTATGTAATAGGTCACCTTCTACTAAAATTTT	9133
4L-5.9	GGTCATTTTTTAGATAAATAGGTCACCTTGTATGTAATAGGTCACCTTCTACTAAAATTTT	9301
5L-5.9	GGTCATTTTTTAGATAAATAGGTCACCTTGTATGTAATAGGTCACCTTCTACTAAAATTTT	9305
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5S-5.9	CCCGTATAGCAAGTTACAATTGTGTTAACCCAAATTATGGTAACATTTTGTACTTTTATC	9162
3S-5.4	CCCGTATAGCAAGTTACAATTGTGTTAACCCAAATTATGGTAACATTTTGTACTTTTATC	9193
4L-5.9	CCCGTATAGCAAGTTACAATTGTGTTAACCCAAATTATGGTAACATTTTGTACTTTTATC	9361
5L-5.9	CCCGTATAGCAAGTTACAATTGTGTTAACCCAAATTATGGTAACATTTTGTACTTTTATC	9365

5S-5.9	AACTCCGACTCATACTTGATATTCGAATAACCTCACTTATCAAGTCAATGCAAGCAAATC	9222
3S-5.4	AACTCCGACTCATACTTGATATTCGAATAACCTCACTTATCAAGTCAATGCAAGCAAATC	9253
4L-5.9	AACTCCGACTCATACTTGATATTCGAATAACCTCACTTATCAAGTCAATGCAAGCAAATC	9421
5L-5.9	AACTCCGACTCATACTTGATATTCGAATAACCTCACTTATCAAGTCAATGCAAGCAAATC	9425

5S-5.9	ATGTTAAACTTTGTTCGCCCTTAATGTCGAGACCAGTCTATCTAAAAGAA--TTTTTTTTT	9280
3S-5.4	ATGTTAAACTTTGTTCGCCCTTAATGTCGAGACCAGTCTATCTAAAAGAACTTTTTTTTTT	9313
4L-5.9	ATGTTAAACTTTGTTCGCCCTTAATGTCGAGACCAGTCTATCTAAAAGAACTTTTTTTTTT	9481
5L-5.9	ATGTTAAACTTTGTTCGCCCTTAATGTCGAGACCAGTCTATCTAAAAGAACTTTTTTTTTT	9485

5S-5.9	TTTTACAATTACCTAAAAGAACTTATTATTAGTTATTGGCTACAAAACCACACAAATATT	9340
3S-5.4	TTTTACAATTACCTAAAAGAACTTATTATTAGTTATTGGCTACAAAACCACACAAATATT	9373
4L-5.9	TTTTACAATTACCTAAAAGAACTTATTATTAGTTATTGGCTACAAAACCACACAAATATT	9541
5L-5.9	TTTTACAATTACCTAAAAGAACTTATTATTAGTTATTGGCTACAAAACCACACAAATATT	9545

5S-5.9	CAATACAATCTCAAGCTACAACCTCAAAGATTAAAGATTCCCTCACCCATCACATTCATA	9400
3S-5.4	CAATACAATCTCAAGCTACAACCTCAAAGATTAAAGATTCCCTCACCCATCACATTCATA	9433
4L-5.9	CAATACAATCTCAAGCTACAACCTCAAAGATTAAAGATTCCCTCACCCATCACATTCATA	9601
5L-5.9	CAATACAATCTCAAGCTACAACCTCAAAGATTAAAGATTCCCTCACCCATCACATTCATA	9605

5S-5.9	TACAATATATTGGTCTATCAGTGATATGATTGAATAAGTTGCACTCAATTGTATTGACCT	9460
3S-5.4	TACAATATATTGGTCTATCAGTGATATGATTGAATAAGTTGCACTCAATTGTATTGACCT	9493
4L-5.9	TACAATATATTGGTCTATCAGTGATATGATTGAATAAGTTGCACTCAATTGTATTGACCT	9661
5L-5.9	TACAATATATTGGTCTATCAGTGATATGATTGAATAAGTTGCACTCAATTGTATTGACCT	9665

5S-5.9	ACATAAGTATGGCCTTTATAATTACATAAAGGTGATC-GAAGTTCCAATAATATCAATGA	9519
3S-5.4	ACATAAGTATGGCCTTTATAATTACATAAAGGTGATCCAAAGTTCCAATAATATCAATGA	9553
4L-5.9	ACATAAGTATGGCCTTTATAATTACATAAAGGTGATCCAAAGTTCCAATAATATCAATGA	9721
5L-5.9	ACATAAGTATGGCCTTTATAATTACATAAAGGTGATCCAAAGTTCCAATAATATCAATGA	9725

5S-5.9	GATTTGAAGATTGTTTTCCAAATATTCACCTCAACCAAATATACCTTACGACAACCTTCATC	9579
3S-5.4	GATTTGAAGATTGTTTT-CCAGATATTCACCTCAACCAAATATACCTTACGACAACCTTCATC	9612
4L-5.9	GATTTGAAGATTGTTTT-CCAGATATTCACCTCAACCAAATATACCTTACGACAACCTTCATC	9780
5L-5.9	GATTTGAAGATTGTTTT-CCAGATATTCACCTCAACCAAATATACCTTACGACAACCTTCATC	9784

5S-5.9	CTGAAATCTTCGGTTTGTGACAGTACTCCACTTTTAATTCAATGGTCAAATATTTATACC	9639
3S-5.4	CTGAAATCTTCGGTTTGTGACAGTACTCCACTTTTAATTCAATGGTCAAATATTTATACC	9672
4L-5.9	CTGAAATCTTCGGTTTGTGACAGTACTCCACTTTTAATTCAATGGTCAAATATTTATACC	9840
5L-5.9	CTGAAATCTTCGGTTTGTGACAGTACTCCACTTTTAATTCAATGGTCAAATATTTATACC	9844

5S-5.9	TTACCCCTTAATTCAATGCCCATAAATGTTGATGATCATGTGAAGTAGTGCAATATATAGC	9699
3S-5.4	TTAACCCTTAATTCAATGCCCATAAATGTTGATGATCATGTGAAGTAGTGCAATATATAGC	9732
4L-5.9	TTAACCCTTAATTCAATGCCCATAAATGTTGATGATCATGTGAAGTAGTGCAATATATAGC	9900
5L-5.9	TTACCCCTTAATTCAATGCCCATAAATGTTGATGATCATGTGAAGTAGTGCAATATATAGC	9904
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5S-5.9	TTTACTTCATCTAAAAATGCATTAAAAAATTTAGTCAATTGATTGAATATAAACTAGCTA	9759
3S-5.4	TTTACTTCATCTAAAAATGCATTAAAAAATTTAGTCAATTGATTGAATATAAACTAGCTA	9792
4L-5.9	TTTACTTCATCTAAAAATGCATTAAAAAATTTAGTCAATTGATTGAATATAAACCAGCTA	9960
5L-5.9	TTTACTTCATCTAAAAATGCATTAAAAAATTTAGTCAATTGATTGAATATAAACCAGCTA	9964

5S-5.9	ACTCGTGTACTIONACTCAACCAAGATGGTTTCATGTCAATGATAAATAGCTCATTTGTTCTG	9819
3S-5.4	ACTCGTGTACTIONACTCAACCAAGATGGTTTCATGTCAATGATAAATAGCTCATTTGTTCTG	9852
4L-5.9	ACTCGTGTACTIONACTCAACCAAGATGGTTTTCATGTCAATGATAAATAGCTCATTTGTTCTG	10020
5L-5.9	ACTCGTGTACTIONACTCAACCAAGATGGTTTTCATGTCAATGATAAATAGCTCATTTGTTCTG	10024

5S-5.9	AACC-----ATATCATCTCCTTCATCACACCATGAAGGGAGCTTCTTTCAAG	9866
3S-5.4	AACCTCATAAATTTTCCATATCATCTCCTTCATCACACCATGAAGGGAGCTTCTTTCAAG	9912
4L-5.9	AACCTCATAAATTTTCCATATCATATCCTTCATTACACCATGAAGGGAGCTTCTTTCAAG	10080
5L-5.9	AACC-----ATATCATCTCCTTCATCACACCATGAAGGGAGCTTCTTTCAAG	10071

5S-5.9	CTGTCGATTCTGATTTTCGTCCTTGTGGCTTTCGCTTCGTGTAAGTGTCTTTTATCTCTT	9926
3S-5.4	CTGTCGATTCTGATTTTCGTCCTTGTGGCTTTCGCTTCATGTAAGTGTCTTTTATCTCTT	9972
4L-5.9	CTGTCGATTCTGATTTTCGTCCTTGTGGCTTTCGCTTCGTGTAAGTGTCTTTTATCTCTT	10140
5L-5.9	CTGTCGATTCTGATTTTCGTCCTTGTGGCTTTCGCTTCGTGTAAGTGTCTTTTATCTCTT	10131

5S-5.9	ATGATTCTTGCATGTAAATTAAGATGCATACATGGTTTGTCTTGATATAGTTTTCTTCAC	9986
3S-5.4	ATGATTCTTGCATGTGAATTAAGATGCATATATGGTT-GTCTTGATATAGTTTTCTTCAC	10031
4L-5.9	ATGATTCTTGCATGTAAATTAAGATGCATACATGGTT-GTCTTGATATAGTTTTCTTCAC	10199
5L-5.9	ATGATTCTTGCATGTAAATTAAGATGCATACATGGTTTGTCTTGATATAGTTTTCTTCAC	10191

5S-5.9	CTAAATAGCTCTTCTAGTATTATTATTGATTGGTTGGGGTCATACTATATTGCAGTTCTT	10046
3S-5.4	CTAAACAGCTCTTCTAGTACTATTATCGATTGATGGAGTTTATACTATATTGCAGTTCTT	10091
4L-5.9	CTAAACAGCTCTTCTAGTATTATTATTGATTGGGGAGGGTCATACTATATTGCAGTTCTT	10259
5L-5.9	CTAAATAGCTCTTCTAGTATTATTATTGATTGGTTGGGGTCATACTATATTGCAGTTCTT	10251

5S-5.9	TGTCCATTTACAGCAGAAGCAAGACACAAGCACGTGCATCATAGTAATTGCCACCATCGT	10106
3S-5.4	TGTCCATTTACAGCAGAAGCAAGACACAAGCACGTGCATCATAGTAATTGCCACCATCGT	10151
4L-5.9	TGTCCATTTACAGCAGAAGCAAGACACAAGCATGTACATCATAGTAATTGCCACCATCGT	10319
5L-5.9	TGTCCATTTACAGCAGAAGCAAGACACAAGCACGTGCATCATAGTAATTGCCACCATCGT	10311

5S-5.9	CGTGGACGTCCTGATCCAGCACCAACACCGGCGCCTGTGCCAGCATCTAATGAAGGCATA	10166
3S-5.4	CGTGGACGTCCTGATCCAGCACCAACACCGGCGCCTGTGCCAGCATCTAATGAAGGCATA	10211
4L-5.9	CGTGGACGTCCTGATCCAGCACCAACACCGGCGCCTGTGCCAGCATCTAATGAAGGCATA	10379
5L-5.9	CGTGGACGTCCTGATCCAGCACCAACACCGGCGCCTGTGCCAGCATCTAATGAAGGCATA	10371

5S-5.9	CCACCATATCAAATCCATGGTTGTGGTTACCCATGTAGTGACTCCAACGACTGTGATTGG	10226
3S-5.4	CCACCATATCAAATCCATGGTTGTGGTTACCCATGTAGTGACTCCAACGACTGTGATTGG	10271
4L-5.9	CCACCATATCAAATCCATGGTTGTGGTTACCCATGTAGTGACTCCAACGACTGTGATTGG	10439
5L-5.9	CCACCATATCAAATCCATGGTTGTGGTTACCCATGTAGTGACTCCAACGACTGTGATTGG	10431

5S-5.9	CCTTGACAGAATGCGGTGTCAACAGAACTTGTGCTTATGAAGAGCCCTTCTTTCCATCA	10286
3S-5.4	CCTTGACAGAATGCGGTGTCAACAGAACTTGTGCTTATGAAGAGCCCTTCTTTCCATCA	10331
4L-5.9	CCTTGACAGAATGCGGTGTCAACAGAACTTGTGCTTATGAAGAGCCCTTCTTTCCATCA	10499
5L-5.9	CCTTGACAGAATGCGGTGTCAACAGAACTTGTGCTTATGAAGAGCCCTTCTTTCCATCA	10491

5S-5.9	CCATCACCTGTTCCATCACCAAGTATGGAACCCCAACACAAGAACCACCACGTGCACCA	10346
3S-5.4	CCA-----AGTATGGAACCCCAACACAAGAATCACCACATACCA	10373
4L-5.9	CCATCACCTGTTCCATCACCAAGTATGGAACCCCAACACAAGAACCACCACGTGTACCA	10559
5L-5.9	CCATCACCTGTTCCATCACCAAGTATGGAACCCCAACACAAGAACCACCACGTGCACCA	10551

5S-5.9	GCACCGGCACCTGATAATGGCATTGGCGTAGGTGTGCCACCATATCAAATCCACGGTTGT	10406
3S-5.4	GCACCGGCACCTGATAATGGCATTGGCGTAGGTGTGCCACCATATCAAATCCACGGTTGT	10433
4L-5.9	GCACCGGCACCTGATAATGGCATTGGCGTAGGTGTGCCACCATATCAAATCCACGGTTGT	10619
5L-5.9	GCACCGGCACCTGATAATGGCATTGGCGTAGGTGTGCCACCATATCAAATCCACGGTTGT	10611

5S-5.9	GGCTACCCATGTAGTGACTCCAATGATTGTGATTGGCCTTGTACAGTATGTGGTGTCAAC	10466
3S-5.4	GGCTACCCATGTAGTGACTCCAATGATTGTGATTGGCCTTGTACAGTATGTGGTGTCAAC	10493
4L-5.9	GGCTACCCATGTAGTGACTCCAATGATTGTGATTGGCCTTGTACAGTATGTGGTGTCAAC	10679
5L-5.9	GGCTACCCATGTAGTGACTCCAATGATTGTGATTGGCCTTGTACAGTATGTGGTGTCAAC	10671

5S-5.9	GGAACCTTGTGCTTTTGAAGAGCCATTCTTTCCATCAT--CACCTGTTCCATCACCAAGT	10523
3S-5.4	GGAACCTTGTGCTTTTGAAGAGCCCTTCTTTCCATCATCATCACCTGTTCCATCACCAAGT	10553
4L-5.9	GGAACCTTGTGCTTTTGAAGAGCCATTCTTTCCATCAT--CACCTGTTCCATCACCAAGT	10736
5L-5.9	GGAACCTTGTGCTTTTGAAGAGCCATTCTTTCCATCAT--CACCTGTTCCATCACCAAGT	10728

5S-5.9	ATAGAAACTCCAACACAAGAACCACCACCTATCACCAGCACC	GGCACCTGATAATGGCATT	10583
3S-5.4	ATGAAAACCCCAACACAAGAACCACCACCTATCACCAGCACC	GGCACCTGATAATGGCATT	10613
4L-5.9	ATAGAAACTCCAACACAAGAACCACCACCTATCACCAGCACC	GGCACCTGATAATGGCATT	10796
5L-5.9	ATAGAAACTCCAACACAAGAACCACCACCTATCACCAGCACC	GGCACCTGATAATGGCATT	10788
	** **** *		
5S-5.9	GGCGTAGGTGTGCCACCATATCAAATCCACGGTTGTGGCTACCCATGTAGTGACTCTAAT		10643
3S-5.4	GGCGTAGGTGTGCCACCATATCAAATCCACGGTTGTGGCTACCCATGTAGTGACTCTAAT		10673
4L-5.9	GGCGTAGGTGTGCCACCATATCAAATCCACGGTTGTGGCTACCCATGTAGTGACTCTAAT		10856
5L-5.9	GGCGTAGGTGTGCCACCATATCAAATCCACGGTTGTGGCTACCCATGTAGTGACTCTAAT		10848
	***** *		
5S-5.9	GATTGTGATTGGCCTTGTACAATCTGTGGTGCTGACCAAACCTGTACTTTTGATGAACCC		10703
3S-5.4	GATTGTGATTGGCCTTGTACAATCTGTGGTGCTGACCAAACCTGTACTTTTGATGAGCCC		10733
4L-5.9	GATTGTGATTGGCCTTGTACAATCTGTGGTGCTGACCAAACCTGTACTTTTGATGAACCC		10916
5L-5.9	GATTGTGATTGGCCTTGTACAATCTGTGGTGCTGACCAAACCTGTACTTTTGATGAACCC		10908
	***** *		
5S-5.9	TTCTTTACATCACCTCGCTTGCTCCATTACCTCTCACAGAAGCACCCATTCCACAATGG		10763
3S-5.4	TTCTTTACATCACCTCGCTTGCTCCATTACCTCTCACAGAAGCACCCATTCCACAATGG		10793
4L-5.9	TTCTTTACATCACCTCGCTTGCTCCATTACCTCTCACAGAAGCACCCATTCCACAATGG		10976
5L-5.9	TTCTTTACATCACCTCGCTTGCTCCATTACCTCTCACAGAAGCACCCATTCCACAATGG		10968
	***** *		
5S-5.9	GTACCTGGTAATGGTATCGCGGCACCACCATATCAGATTTCATGGTTGTGGTTACCCATGT		10823
3S-5.4	GTACCTGGTAATGGCATCGCGGCACCACCATATCAGATTTCATGGTTGTGGTTACCCATGT		10853
4L-5.9	GTACCTGGTAATGGCATCGCGGCACCACCATATCAGATTTCATGGTTGTGGTTACCCATGT		11036
5L-5.9	GTACCTGGTAATGGTATCGCGGCACCACCATATCAGATTTCATGGTTGTGGTTACCCATGT		11028
	***** *		
5S-5.9	AACGACTCCAATGACTGTGATGCACCCTGTACAGTCTGTTGTGCAAACTATACCTGCTGT		10883
3S-5.4	AACGACTCCAATGACTGTGATGCACCCTGTACAGTCTGTTGTGCAAACTATACCTGCTGT		10913
4L-5.9	AGTGACTCCAATGACTGTGATGCACCCTGTACAGTCTGTTGTGCAAACTATACCTGCTGT		11096
5L-5.9	AACGACTCCAATGACTGTGATGCACCCTGTACAGTCTGTTGTGCAAACTATACCTGCTGT		11088
	* *****		
5S-5.9	TATGATGTGGCTGATCCTGAGTACATGCTACCACCTATGTACCCCTCTGAGCCACCGAAA		10943
3S-5.4	TATGATGTGGCTGATCCTGAGTACATGCTACCACCTATGTACCCCTCTGAGCCACCGAAA		10973
4L-5.9	TATGATGTGGCTGATCCCGAGTACATGCTACCACCTATGCCACCCTCTGAGCCACCGAAA		11156
5L-5.9	TATGATGTGGCTGATCCTGAGTACATGCTACCACCTATGTACCCCTCTGAGCCACCGAAA		11148
	***** *		
5S-5.9	TTATTACCTCTTCCACCATCTCCACCTCCATCTACAGAGGATGTAGAAAATGATGATATG		11003
3S-5.4	TTATTACCTCTTCCACCATCTCCACCTCCATCTACAGAGGATGTAGAAATATGATGATATG		11033
4L-5.9	TTATTACCTCTTCCACCATCTCCACCTCCATCTACAGAGGATGTAGAAAATGATGATATG		11216
5L-5.9	TTATTACCTCTTCCACCATCTCCACCTCCATCTACAGAGGATGTAGAAAATGATGATATG		11208
	***** *		
5S-5.9	TTTGCACCACAACCTGCTTATGATATAGGAACGCCTGCGGAACTTCCACCACCAGGATAC		11063
3S-5.4	TTTGCACCACAACCTGCTTATGATATAGGAACGCCTGCGGAACTTCCACCACCAGGATAC		11093
4L-5.9	TTTACACCACAACCTGCTTATGATATAGGAACGCCTGCAGAACTTCCACCACCAGGATAC		11276
5L-5.9	TTTGCACCACAACCTGCTTATGATATAGGAACGCCTGCGGAACTTCCACCACCAGGATAC		11268
	*** *****		
5S-5.9	GAATTCCCGCCGTATCAAATCCATGGTTGTGGCTATGGCCCCCTGCATGGACTCCAACGAC		11123
3S-5.4	GAATTCCCGCCGTATCAAATCCATGGTTGTGGCTATGGCCCCCTGCATGGACTCCAACGAC		11153
4L-5.9	GAATTCCCGCCATATCAAATCCATGGTTGTGGCTATGGCCCCCTGCATGGACTCCAACGAC		11336
5L-5.9	GAATTCCCGCCATATCAAATCCATGGTTGTGGCTATGGCCCCCTGCATGGACTCCAACGAC		11328
	***** *		
5S-5.9	TGCGATTGGCCCTGCACATCCTGCTGCTCTAATCATAACATGTTGCTATGAGGAGCCTATG		11183
3S-5.4	TGCGATTGGCCCTGCACATCCTGCTGCTCTAATCATAACATGTTGCTATGAGGAGCCTATG		11213
4L-5.9	TGTGATTGGCCCTGCACATCCTGCTGCTCTAATCATAACATGTTGCTATGAGGAGCCTATG		11396
5L-5.9	TGCGATTGGCCCTGCACATCCTGCTGCTCTAATCATAACATGTTGCTATGAGGAGCCTATG		11388
	** *****		
5S-5.9	TTTCGATGAAAAATCCTCAAACACACAAATTCCAAAGAAAAAGTATAGTAACACAATGTAA		11243
3S-5.4	TTTCGATGAAAAATCCTCAAACACACAAATTCCAAAGAAAAAGTATAGTAACACAATGTAA		11273
4L-5.9	TTTCGATGAAAAATCCTCAAACACACAAATGCCAAAGAAAAAGTATAGTAACACAATGTAA		11456
5L-5.9	TTTCGATGAAAAATCCTCAAACACACAAATTCCAAAGAAAAAGTATAGTAACACAATGTAA		11448
	***** *		

5S-5.9	TAAAACTTA-GTGTTCTGTATTACTTTAAATCACATTTGACCTATATTCTTCAATTGCT	11302
3S-5.4	TAAAACTTA-GTGTTCTGTATTACTTTAAATCACATTTGACCTATATTCTTCAATTGCT	11332
4L-5.9	TAAAACTAAAGTGTTCTT-TATTACTTAAATCACATTTGACCTATATTCTTCAATTGCT	11515
5L-5.9	TAAAACTTA-GTGTTCTGTATTACTTTAAATCACATTTGACCTATATTCTTCAATTGCT	11507
	***** * ***** ***** *****	
5S-5.9	ATGTCATTGTCTAATGATTGAAAGCAAGTACTTTTATTTCTGTGTCATACAAATGTAAGC	11362
3S-5.4	ATGTCATTGTCTAATGATTGAAAGCAAGTACTTTTATTTCTGTGTCATACAAATGTAAGC	11392
4L-5.9	ATGTCATTGTCTGGTAATTGCAAGCAAGTACTTCTATTTCTGTGTCATACAAATGTAAGC	11575
5L-5.9	ATGTCATTGTCTAATGATTGAAAGCAAGTACTTTTATTTCTGTGTCATACAAATGTAAGC	11567
	***** * **** ***** *****	
5S-5.9	AAGATCAATAAAGAATATATACAACCTACGTTAATCAATTGCTACTATTAACGCATTTT	11422
3S-5.4	AAGATCAATAAAGAATATATACAACCTACGTTAATCAATTGCTACTATCAAACGCATTTT	11452
4L-5.9	AAAATTAATAAAGAATATATACAACCTACGTTAATCAATTGCTACTATCAAATGCATTTT	11635
5L-5.9	AAGATCAATAAAGAATATATACAACCTACGTTAATCAATTGCTACTATCAAACGCATTTT	11627
	** ** ***** ** *****	
5S-5.9	CTATCAAACAACAGTATAATTATTCTGA-----CGTACTCTAATAATTAAAGTGGGT	11474
3S-5.4	CTGTCAAACAACAGTATAATTATTGTGAATTTGTGACGCACCTAGTAAATAAAGTGGGT	11512
4L-5.9	CTATCAAACAACAGTATAATTATTGTGA-----CGTACTCTAATAAATAAAGTGGGT	11687
5L-5.9	CTATCAAACAACAGTATAATTATTCTGA-----CGTGTCTAATAATTAAAGTGGGT	11679
	** ***** ** ** *****	
5S-5.9	TGAACTAAGCCTTTAATGACTGATTCATCTGCTCTACGCCTATATCACAATTTTCAGAGTA	11534
3S-5.4	TGAAGTAAGCATTAATGACTGATTCATCAGCTCTACGCCTATATCACAATTTTCAGAGTA	11572
4L-5.9	TGAACTAAGCATTAATGACTGATTCATCAGCTCTACGCCTATATCACAATTTTCAGAGTA	11747
5L-5.9	TGAACATAAGCCTTTAATGACTGATTCATCTGCTCTACGCCTATATCACAATTTTCAGAGTA	11739
	**** ***** ** *****	
5S-5.9	GATACATTGCGAGATTTCTGTTGTAAGAACCATTTTGATCATGTTGCTGTTACAGACAAC	11594
3S-5.4	GATACATTGCGAGATTTCTGTTGTAAGAACCATTTTGATCATGTTTCTGTAACAG-CAAC	11631
4L-5.9	GATACATTGCGAGATTTCTGTTGTAAGAACCATTTTGATCATGTTGCTGTTACAGACAAC	11807
5L-5.9	GATACATTGCGAGATTTCTGCTGTAAGAACCATTTTGATCATGTTGCTGTTACAGACAAC	11799
	***** ***** *****	
5S-5.9	GTGATTTTTCAGTATATTTTGTGTTACAACTTCCTTCGTCGAGGAAATTCTGGCATGTATT	11654
3S-5.4	ATGATTTTCCAGTATATTTTGTGTTACAAATTTCCCTTCGTCGAGGAAATTGTGACAT---T	11687
4L-5.9	ATGATTTTTCAGTATATTTTGTGTTGCAAATTTCCCTTCGTCGAGGAAATTTTGACATGTATT	11867
5L-5.9	ATGATTTTTCAGTATATTTTGTGTTACAAATTTCCCTTCGTCGAGGAAATTCTGGCATGTATT	11859
	***** ***** ***** ** ** *	
5S-5.9	ATTAAGATACCAACTTAAATTCTGGTATAGGTTCCATTCTAATTAATATCATCGGCATAC	11714
3S-5.4	ATTAAGATACCAACT-----CTA-----	11705
4L-5.9	ATTATGATACCAACTTAAATTCTGGTAGATGTTCCATTCTAATTAATATAACCGGCATAC	11927
5L-5.9	ATTAAGATACCAACTTAAATTCTGGTATAGGTTCCATTCTAATTAATATCATCGGCATAC	11919
	**** ***** ***	
5S-5.9	TCCTCAACTTAGATTCAATTCCTTAGTTGATTTACATCTTAATTCGTCAACTTTCATAGAG	11774
3S-5.4	-----	
4L-5.9	TCCTCAACTTAGATTCAATTCCTTAGTTGATTTACATCTTAATTCGTCAACTTTCATAGAG	11987
5L-5.9	TCCTCAACTTAGATTCAATTCCTTAGTTGATTTACATCTTAATTCGTCAACTTTCATAGAG	11979
5S-5.9	AACTCATCACAGGATAAGCCAGTTTAGTTCAACAATAGTATATTCCTCCGCCAAAATCCA	11834
3S-5.4	-----	
4L-5.9	AACTTATCACCGGATAAGCCAGTTTAGTTCAACAATAGTATATTC-CCACCAAAATCCA	12046
5L-5.9	AACTCATCACAGGATAAGCCAGTTTAGTTCAACAATAGTATATTCCTCCGCCAAAATCCA	12039
5S-5.9	CATAATGTTTTGAGAGTTTTAATTGCAAGTGGTATACCATCATGCTTTTTTCAGTTTTTCAC	11894
3S-5.4	-----	
4L-5.9	CATAATGTTTTGAGAGTTTTAATTGCAAGTG-TATACCATCATGCTTTTTTCAGTTTTGAC	12105
5L-5.9	CATAATGTTTTGAGAGTTTTAATTGCAAGTGGTATACCATCATGCTTTTTTCAGTTTTTCAC	12099
5S-5.9	TTTCGATAAAT-----CAAAAT-----CAATATAAATCCTT----	11925
3S-5.4	-----	
4L-5.9	TT--GATAAATTCCTCCATTTTCATATTATTCGCTATACTTTTCAATTCAGACTCCTAGGC	12163
5L-5.9	TTTCGATAAAT-----CAAAAT-----CAATATAAA-TCCT----	12129

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5S-5.9      ---TCCTCAAAAAGA-----AAAACGATATAAATCC----- 11954
3S-5.4      -----
4L-5.9      AATTTTGGAAAAGAGAGAGATAGAGAGTAAAAAGAAAGGGACCCATGTGAGAGGAAAG 12223
5L-5.9      --TTCCTCAAAAAGA-----AAAACGATATAAATCC----- 12159

5S-5.9      ---TAGCTCCAATTCGT-----AAAAGAATTTTACCAAAGTACTT--CCTCCGTTTC 12001
3S-5.4      -----
4L-5.9      AGATAGAGAGAGTTTGTGGCCCAAAAAGAAGTGTAGCAAATAATGTGAAACTTCCCATATA 12283
5L-5.9      ---TAGCTCCAATTCGT-----AAAAGAATTTTACCAAAGTACTT--CCTCCGTTTC 12206

5S-5.9      GTTTCAAATGCAACAAAAGGGTATTATTTGTGAGATATAAAATTTCCAATTGTTGCGTTT 12061
3S-5.4      -----
4L-5.9      ATGAAAAGTGTAGCGAA---TATTAT--GAAACGGATGAAGTA---AATCCTTGC-CTC 12333
5L-5.9      GTTTCAAATGCAACAAAAGGGTATTATTTGTGAGATATAAAATTTCCAATTGTTGCGTTT 12266

5S-5.9      AAAACGAGATGGAG-----GAAGCATTAAGTTGTAAGACAA 12099
3S-5.4      -----CGTTAAAAGTTGTAAGACAA 11725
4L-5.9      AAAAAGAAAAGCGTTATAAATCCTAGCTCCAATTCGAAGTATTAAGTTGTAAGACAG 12393
5L-5.9      AAAACGAGATGGAG-----GAAGCATTAAGTTGTAAGACAA 12304
                        *****

5S-5.9      CAAAATGAAAACAAATGGATAAATTTTATAATATATTCAACTCTACCTTCTTTTGCTCAA 12159
3S-5.4      CAAAATGAAAACAAATGGATAAATTTTATAATATATTCAACTCTACCTTCTTTTGCTCAA 11785
4L-5.9      CAAAATGAAAACAAATGGATAAATTTTATAATATATTCAACTCTACCTTCTTTTGCTCAA 12453
5L-5.9      CAAAATGAAAACAAATGGATAAATTTTATAATATATTCAACTCTACCTTCTTTTGCTCAA 12364
                        *****

5S-5.9      CATCACATACACACATCCGCACCTGACAATCATTATTCATTAAAAACACCCGATAAAATAA 12219
3S-5.4      CATCACATAAACACATCCGCACCTGACAATCATTATTCATTAAAAACACCCGATAAAATAA 11845
4L-5.9      CATCACATAAACACATCCGCACCTGACAATCATTATTCATTAAAAACACCCGATAAAATAA 12513
5L-5.9      CATCACATACACACATCCGCACCTGACAATCATTATTCATTAAAAACACCCGATAAAATAA 12424
                        *****

5S-5.9      ATACCAGTTCTGAAATCATGGATATGAAACTCACAGTAAAAAGA-GTAT-AAAAACACC 12277
3S-5.4      ATACCAGTTCTGAAATCATGGATATGAAATTCACAGTAAAAAGTATTAAAAACACC 11905
4L-5.9      ATACCAGTTCTGAAATCATGGATATGAAACTCACAGTAAAAAGA-GTATAGAAAAACACC 12572
5L-5.9      ATACCAGTTCTGAAATCATGGATATGAAACTCACAGTAAAAAGA-GTATA-AAAAACACC 12482
                        *****

5S-5.9      AGCTGAAGCAAACACAAGATCAACAAAGAGGTAAAAATCAAAAAATGGTCGTATCAAA-- 12335
3S-5.4      AGCTGAGGCAAACACAAGATCAACAAAGAGGTAAAAATCAAAAAATGGTCG----- 11956
4L-5.9      AGCTGAAGCAAACACAAGATCAACAAAGAGGTAAAAATCAAAAAATGGTCGTATCAAGAT 12632
5L-5.9      AGCTGAAGCAAACACAAGATCAACAAAGAGGTAAAAATCAAAAAATGGTCGTATCAAAAT 12542
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5S-5.9      ----- 12335
3S-5.4      ----- 11956
4L-5.9      ATTATTCT 12640
5L-5.9      ATTATTCT 12550

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Fig. S1 Alignment of the nucleotide sequences of the *rfl* regions from DNA-marker haplotypes 5S-5.9, 3S-5.4, 4L-5.9, and 5L-5.9. The source of the 4L-5.9 sequence was DDBJ/EMBL/GenBank accession number AB646136. Dashes are incorporated for maximum matching. Asterisks denote conserved residues in all four sequences. Boundaries of exons and introns are shown by vertical bars.

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219-2  GTATATAAACTATTCATGGGACTCCAATTATGTGCTTAAGCTGATGGTTAATA----- 54
219-3  GTATATAAACTATTCGTGGGACTCCAACCATCGGCTTAAGCTCATGGTTGATA----- 54
219-1  GTATATAAACTATTCCTGGGACTCCAACATCTGCTTAAGCTGATGGTTAATACTTAAT 60

219-2  -GAA----- 57
219-3  -GAATATAAAATTATTTCTGGGACTCCAACCAAAGCT--CAGGAATAGCTTTATATTCT 111
219-1  AGAATATAAACTATTCCTGGGACTCCAACCAAAGCTTCCTGAAATAGCTTTATATTCT 120

219-2  -----
219-3  ATCAGTAGCTTGTAGTAGTTCTTTACTAGACTGCAGGAATAGATAATATTTGGTTATCAA 171
219-1  ATCAGTATCTTGTAGTAGTTCTTTACTAGACTGCAGCAATAGATAATATTTGGTTATTAA 180

219-2  -----
219-3  TATACATGGGTGATTCCGGTTCATATTTAGGCGTATCAAATGATTTAAGATATTGTATGA 231
219-1  TATTCATGGGTGATTCCGGTTCATATTTAGGCGTATCAAATGATTCAGATATTGTATGA 240

219-2  -----CTATACAAAAACATGAAAGGAATTATATGAAAAAAAAA-CTGATGAATTT 107
219-3  AGTTATGAACATATACAAAAACATGAAAGAAATTATATGAAAAAAAAAACTGATGAATTT 291
219-1  AGTTATGAACATATACAAAAACATGAAAGGAATTATATGAAATTTTTT-TTGATGAATTT 299

219-2  TAGGTTATCAGATTACATTATGAATGTCATATGTCAATGTGGTGGTATGTATTTGTTAG 166
219-3  TAGGTTATTATATTGCATTATGAATGTCATATGTCAATGTGGTGGTATATATTTGTTAG 350
219-1  TAGGTTATCAGGTTACATTATGAATGTCATACGTCAATTTGGTGGTATGTATTTGTTAG 358

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Fig. S3 Alignment of nucleotide sequences of the first introns of *bvORF20L₂₁₉₋₁* (219-1), *bvORF20L₂₁₉₋₂* (219-2) and *bvORF20L₂₁₉₋₃* (219-3). The recognition site for HindIII is identified by a rectangular box. Dashes are incorporated for maximum matching.

Table S1 Mitotypes and DNA-marker types of US maintainer lines

Accession	Plant ID	Mitotype	DNA-marker type			
			s17/20L-int	Size of signal bands on DNA gel blot		
PI372277	12-139	Normal-2	44L		5.9	
PI372277	12-140	Normal-2	44L		5.9	
PI411128	12-187	Owen	55LS	7.2	5.9	1.9
PI411128	12-171	min06/-orf129	45LS	7.2	5.9	1.9
PI411128	12-170	min06/-orf129	45L		5.9	
PI411128	12-172	min06/-orf129	45L		5.9	
PI411128	12-178	min06/-orf129	44LS		5.9	
PI411128	12-179	min06/-orf129	44L		5.9	
PI486358	12-550	Normal-1	45LS	7.2	5.9	
PI486358	12-543	Normal-1	55S	7.2	5.9	
PI486358	12-552	Normal-1	55S	7.2	5.9	
PI486358	12-553	Normal-1	44L		5.9	
PI512298	12-475	Normal-1	55S		5.9	
PI518644	12-77	Normal-1	55L		5.9	
PI518644	12-79	Normal-1	55LS	7.9	5.9	2.1
PI558514	12-162	Normal-1	45LS		5.9	
PI558514	12-166	Normal-1	45L		5.9	
PI558515	12-64	Normal-2	55LS	7.9	5.9	2.1
PI564757	12-152	Normal-2	44L		5.9	
PI564758	12-96	Normal-2	45LS	7.9	5.9	2.1
PI564758	12-94	Normal-2	44L		5.9	
PI590689	12-348	Normal-1	55S		5.9	
PI590694	12-15	Normal-1	44L		5.9	
PI590697	12-224	Normal-1	44L		5.9	
PI590720	12-464	Normal-2	55LS	7.9	5.9	2.1
PI590720	12-465	Normal-2	55LS	7.9	5.9	2.1
PI590771	12-404	Normal-1	45LS	7.9	5.9	2.1
PI590772	12-422	Normal-1	45L		5.9	
PI590772	12-423	Normal-1	45L		5.9	
PI590772	12-424	Normal-1	55L		5.9	
PI590773	12-436	Normal-1	55LS	7.9	5.9	2.1
PI590774	12-5	Normal-1	55LS	7.9	5.9	2.1
PI590774	12-2	Normal-1	55L		5.9	
PI590775	12-307	Normal-1	45LS	7.9	5.9	2.1
PI590821	12-25	Normal-2	44L		5.9	
PI590823	12-117	Normal-1	44L		5.9	
PI590839	12-319	Normal-2	55S		5.9	
PI590841	12-332	Normal-2	44L		5.9	

PI590841	12-333	Normal-2	44L			5.9		
PI590847	12-293	Normal-2	55LS	7.9		5.9		2.1
PI590867	12-484	Normal-1	35LS	7.9		5.9	5.4	2.1
PI590871	12-46	Normal-1	45L			5.9		
PI594910	12-498	Normal-1	55S			5.9		
PI607897	12-72	Normal-1	45LS	7.2		5.9		
PI607897	12-72	Normal-1	45LS	7.2		5.9		
PI607897	12-70	Normal-1	44L			5.9		
PI610319	12-527	Normal-2	55S			5.9		
PI610319	12-528	Normal-2	35S	7.2		5.9	5.4	
PI615522	12-281	Normal-1	33S				5.4	
PI615522	12-282	Normal-1	33S				5.4	
PI615522	12-279	Normal-1	34LS			5.9	5.4	
PI615522	12-284	Normal-1	34LS			5.9	5.4	
PI632251	12-365	Normal-1	55S			5.9		
PI633934	12-55	Normal-2	35LS	7.9		5.9	5.4	2.1
PI634210	12-470	Normal-2	45LS			5.9		
PI634217	12-260	Normal-1	55LS	7.9		5.9		2.1
PI634217	12-264	Normal-1	45LS	7.9		5.9		2.1
W617112	12-383	Normal-2	44L			5.9		
W617122	12-391	Normal-1	55L			5.9		
TK-81mm-O	-	-	44L			5.9		
NK-198	-	-	11S	7.9	7.0	5.9		1.9

Table S2 Male fertility of F1 plants derived from test crosses

Pollen parent			F1			
Accession	Plant ID	Possible genotype	s17/20L-int marker type	Transmitted allele from the pollen parent	No. of plants	
					Fertile + partial fertile	Sterile
PI411128	12-171	4L-5.9/5LS-7.2+5.9+1.9	44L	4L-5.9	0	6
			45LS	5LS-7.2+5.9+1.9	4	1
PI486358	12-178	4L-5.9/4S-5.9	44L	4L-5.9	0	14
	12-550	4L-5.9/5S-7.2+5.9	44L	4L-5.9	0	5
			45LS	5S-7.2+5.9	4	0
	12-543	5S-7.2+5.9/5S-7.2+5.9	45LS	5S-7.2+5.9	8	0
	12-552	5S-7.2+5.9/5S-7.2+5.9	45LS	5S-7.2+5.9	20	0
PI518644	12-77	5L-5.9/5L-5.9	45L	5L-5.9	0	8
	12-79	5LS-7.9+5.9+2.1/5LS-7.9+5.9+2.1	45LS	5LS-7.9+5.9+2.1	0	15
PI558514	12-162	4L-5.9/5S-5.9	44L	4L-5.9	0	2
			45LS	5S-5.9	0	3
	12-166	4L-5.9/5L-5.9	44L	4L-5.9	0	2
PI590689	12-348	5S-5.9/5S-5.9	45LS	5S-5.9	0	5
PI590867	12-484	3S-5.4/5LS -7.9+5.9+2.1	34LS	3S-5.4	0	4
			45LS	5LS -7.9+5.9+2.1	0	5
PI590871	12-46	4L-5.9/5L-5.9	45L	5L-5.9	0	1
PI607897	12-72	4L-5.9/5S-7.2+5.9	44L	4L-5.9	0	12
			45LS	5S-7.2+5.9	10	0
PI610319	12-528	3S-5.4/5S-7.2+5.9	34LS	3S-5.4	0	3
PI615522	12-279	3S-5.4/4L-5.9	34LS	3S-5.4	0	5
	12-282	3S-5.4/3S-5.4	34LS	3S-5.4	0	1
PI633934	12-55	3S-5.4/5LS -7.9+5.9+2.1	34LS	3S-5.4	0	7
			45LS	5LS -7.9+5.9+2.1	0	3
PI634217	12-264	4L-5.9/5LS-7.9+5.9+2.1	44L	4L-5.9	0	11
			45LS	5LS -7.9+5.9+2.1	0	4
W617122	12-391	5L-5.9/5L-5.9	45L	5L-5.9	0	3