

Molecular characterization of foreign and domestic isolates of Rhizoctonia solani for the biological control of leafy spurge Euphorbia esula
by Deanna Lynne Nash

A thesis submitted in partial fulfillment of the requirements for the degree of Master of Science in Microbiology
Montana State University
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Abstract:
Fungal isolates belonging to the genus Rhizoctonia are often very diverse and difficult to characterize. The most recognized method for identification and characterization is anastomosis testing, and more recently molecular characterization using regions of ribosomal RNA genes. The present study sought to determine the phylogenetic relationship among foreign and domestic Rhizoctonia isolates being screened as possible biocontrol agents of Euphorbia esula. Restriction enzyme analysis (REA) of a 28s rDNA region, and sequence data of internal transcribed spacer (ITS) regions were used to infer phylogeny. The results obtained from REA and from the sequence data of ITS regions are similar, and the results of both methods indicate that several foreign isolates are very similar to domestic isolates.

MOLECULAR CHARACTERIZATION OF FOREIGN AND DOMESTIC ISOLATES OF *RHIZOCTONIA SOLANI* FOR THE BIOLOGICAL CONTROL OF LEAFY SPURGE *EUPHORBIA ESULA*

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APPROVAL

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Deanna Lynne Nash

This thesis has been read by each member of the thesis committee and has been found to be satisfactory regarding content, English usage, format, citations, bibliographic style, and consistency, and is ready for submission to the college of graduate studies.

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Signature Deanna Lynn Cash

Date Jan 12, 1998

I dedicate this work to my family,
for their patience, because some things...
arrive in their own mysterious hour,
on their own mysterious terms.

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ABSTRACT

Fungal isolates belonging to the genus *Rhizoctonia* are often very diverse and difficult to characterize. The most recognized method for identification and characterization is anastomosis testing, and more recently molecular characterization using regions of ribosomal RNA genes. The present study sought to determine the phylogenetic relationship among foreign and domestic *Rhizoctonia* isolates being screened as possible biocontrol agents of *Euphorbia esula*. Restriction enzyme analysis (REA) of a 28s rDNA region, and sequence data of internal transcribed spacer (ITS) regions were used to infer phylogeny. The results obtained from REA and from the sequence data of ITS regions are similar, and the results of both methods indicate that several foreign isolates are very similar to domestic isolates.

CHAPTER 1

MOLECULAR CHARACTERIZATION OF *RHIZOCTONIA SOLANI* FOR THE BIOLOGICAL CONTROL OF LEAFY SPURGE *EUPHORBIA ESULA*: INTRODUCTION

Economic losses based on the infestation of the common weed *Euphorbia esula (E. esula)* alone are estimated at more than $100 million in the United States (5). Due to the fact that conventional methods for controlling *E. esula* (leafy spurge) are extremely costly and that it is difficult to achieve long term control, we are looking at alternative solutions such as biological control. The biological control agent that we are particularly interested in is the soil-borne fungus *Rhizoctonia solani (R. solani)* due to its ability to decrease stands of *E. esula* (8). In order to consider the release of this agent as a biological control agent, it must be better characterized using molecular tools.

The Plant *Euphorbia esula*

The perennial plant leafy spurge, *E. esula*, belonging to the family *Euphorbiacea*, is a plant species native to Eurasia. The introduction of *E. esula* to the United States from Eurasia, occurred in approximately 1827 through the importation of impure seed (37). Leafy spurge is present on all continents with the exception of Australia (23), but only in North America, in a region encompassing southern Canada and the north central United States, is the presence of *E. esula* considered a serious problem. In these areas alone, nearly 2.5

million acres are infested by *E. esula* (23,37). The infestation chokes out native plant and grass species, thereby depleting valuable grazing areas that wildlife and livestock depend on for survival. *E. esula* is considered to be an irritant foodstuff for animals due to a white milky latex that is present in all parts of the plant. The latex, which seals any wounds that the plant may endure, can cause blisters and dermatitis in both man and cattle, as well as serve as a mouth and digestive tract irritant leading to scours and death in cattle (23; 28). Economic losses due to the infestation of *E. esula* are estimated at more than $100 million in the affected states (5).

The flowers of this plant are small, yellowish-green and arranged in bountiful small clusters. The plant itself may reach three feet in height and reproduce by either root stalks or seed. The seeds of *E. esula* are oblong shaped, grayish to purple in color and are contained in a tri-compartmental capsule that explodes when dry, projecting seeds as far away as fifteen feet from the plant. Once established, *E. esula* is very difficult to control due to it's extensive root system, with root depths exceeding fourteen feet, and extremely hardy seeds, able to germinate after lying dormant in soils for up to eight years (23,28,37).

Conventional Control of *Euphorbia esula*

It is extremely difficult to achieve long-term control of *E. esula*. The most appropriate control of *E. esula* is assessed on a case by case basis. The options include chemicals, cultivation, sheep grazing, insects and pathogens, or a combination of these techniques used over a long period of time. The two most commonly used chemicals to control *E. esula* are the herbicides 2,4-D, dicamba (brand name Banvel®) and picloram (brand name Tordon™) (23). Both broadleaf herbicides work well, but application is prohibited if *E.*

esula occurs around water. Cultivation practices, such as cropping, can also diminish *E. esula* populations, but may not be a practical choice for pasture and rangeland situations. The use of sheep grazing does not eradicate *E. esula,* but provides a reduction in stands in addition to being a well suited control measure along waterways. The use of insects and pathogens for the biological control of *E. esula* is another measure that is effective, but generally takes longer to obtain visible results (5,16,23,28). The term biological control agent encompasses any native biotic factors that may suppress the population of another organism, in this case, *E. esula*. Currently the trend is to implement ecologically sound biological control measures to achieve long-term control of *E. esula.*

Rhizoctonia solani as a Biological Control Agent

In the search for biological control agents, an increasing number of fungi are being collected and screened for their potential use against plant pathogens and weeds. However, before the release of such agents can be considered, a responsible assessment of the risks involved must be made. For imported pathogens, quarantine guidelines, such as extensive host range, pathogenicity testing and the development of genetic markers, which allow characterization and monitoring of the released biological control agent, must be met (32).

Strains of *Rhizoctonia solani (R. solani)* are among the few pathogens in the U.S. that are capable of reducing *E. esula* populations naturally and through field applications, as a biological control agent. Field observations, where *R. solani* is involved in abating populations of *E. esula*, confirm that surrounding grasses are largely unaffected by strains of *R. solani* that are pathogenic to leafy spurge (8). Observations by Caesar et al. (10) are that diseased plants of *Euphorbia* in Eurasia are pervasive and may provide a larger pool of highly virulent, well adapted, and narrow host range strains for the control of *E. esula*. Greenhouse tests

conducted by Caesar et al. (11) using *Fusarium* species show that the onset of symptoms was in general more rapid using foreign strains than domestic strains. As found earlier, the most virulent domestic strains pathogenic to *E. esula* were in association with root damage caused by insect biological control agents. Because *Fusarium* spp and *Rhizoctonia* spp both reduce stands of *E. esula*, and insect associated *Fusarium* spp collected in Eurasia are more effective at causing disease due to a more rapid onset of symptoms, insect associated foreign strains of *R. solani* may also be excellent candidates as biological control agents of this noxious weed (10,11). The ideal *R. solani* candidate selected for biological control is one that exhibits aggressiveness towards *E. esula* while maintaining a narrow host range.

Classification of the *Rhizoctonia solani* Complex

Fungi named *R. solani* occur world-wide, are economically important plant pathogens, and may actually include several different species (21). These plant pathogens have an extended host range that infect over 150 plant species, including agriculturally important crops as well as weed species. *R. solani* causes a variety of diseases including root rot, cankers, damping-off, fruit decay and foliage disease. These fungi do not produce spores, and therefore must be identified on the basis of their mycelial characteristics (2,26).

Historically, fungi classified as *Rhizoctonia* species have been lumped together and classified as such due to their lack of distinctive taxonomic features (24,34). With this classification scheme, it is not surprising that *Rhizoctonia* species are extremely diverse and may belong to several different orders of basidiomycetes as well as ascomycetes. Because of the importance of numerous *Rhizoctonia* species as plant pathogens, an assortment of practical approaches have been developed for identifying these species. These approaches are needed because conventional taxonomic measures are difficult to apply to *Rhizoctonia*, due to its

high levels of phenotypic variation and the inability of most strains to fruit in culture (34). Isolates of *R. solani* vary greatly in their cultural appearance, growth characteristics and pathogenicity towards plants as well as virulence (20). To date, the most unambiguous method for the characterization of *Rhizoctonia* is based on the occurrence of hyphal cell wall fusion between related isolates, and is called anastomosis grouping.

Hyphal Anastomosis Grouping

In a typical anastomosis reaction test, two different fungal isolates are placed on agar near each other but not touching. Isolates belonging to the same anastomosis group (AG) are generally attracted to each other, evident by hyphal growth toward each other, that leads to hyphal fusion and the killing reaction (35). Isolates belonging to different AGs typically do not undergo hyphal fusion with each other, and isolates belonging to the same AG do not always anastomose with each other at equal frequencies. Some isolates cannot be assigned to an AG because they have not been observed to anastomose with any representatives of known AGs (24). At least 12 AGs have been delineated within the *Rhizoctonia solani* complex, and in practice, when an isolate is unable to anastomose with existing representatives, it is assigned to a new AG. Table 1 lists the classification criteria of hyphal anastomosis reactions of MacNish et al. Even with such straightforward criteria to follow, determining the anastomosis group of an *R. solani* isolate can be very difficult. Environmental conditions such as humidity, temperature, light, and nutritional requirements need to be perfect for hyphal fusion to occur (13).

An intraspecific group is a further subdivision of isolates within an AG that anastomose with each other more frequently, or else possess other unique, distinguishing characters. Such distinguishing characteristics may include host-range specificity, nutrient utilization

or genetic differences based on molecular markers (20,34).

Though the AG classification scheme described allows a method for dividing *R. solani* isolates into more distinct groups, it does not offer other significant pieces of information such as distinguishing pathogenic isolates from nonpathogenic isolates. AG grouping as an indicator of genetic relatedness has been substantiated by DNA/DNA hybridization (34), though the mechanisms of anastomosis are not fully understood (24), which perpetuates an ill-defined *Rhizoctonia solani* complex.

Table 1. Classification of hyphal anastomosis reactions using the criteria of MacNish et al. to delimit anastamosis groups (AG) in *Rhizoctonia solani* (13).

Reaction	Phenotype	Nature of genetic relationship between isolates
C0: No interaction	Hyphae grow past each other, no recognition	Isolates have no genetic relationship and belong to different AG
C1: Hyphal contact only	No evidence of wall or membrane contact, reaction may or may not be accompanied by cell death	Isolates have a distant genetic relationship and belong to either the same or different AG
C2: Killing reaction	Wall fusion (anastomosis) evident, with cell death of anastomosing and adjacent cells, somatic incompatibility response often macroscopically visible	Isolates represent genetically distinct individuals that belong to the same AG
C3: Perfect fusion	Wall and membrane fusion evident, point of anastomosis not clearly visible, cell death absent	Isolates are genetically identical or closely related, individuals belong to the same AG and may represent clones

Systematics of *Rhizoctonia*

The term *systematics* is the comparative study of biotic diversity at any level (18). Systematics of *Rhizoctonia* is hindered by the ambiguity and shortage of credible, morphological characteristics to soundly characterize this genus. Therefore molecular approaches offer a new avenue for the characterization of *Rhizoctonia*. Looking at molecular data can yield much information for establishing classification systems and phylogenetic relationships at the species level (34). In particular, conserved evolutionary markers, such as the genes coding for ribosomal RNA, appear to be appropriate for comparisons of evolution at the species level because the rRNA genes evolve at a slower rate than other parts of the genome (1,6,35).

Several other properties of the rRNA gene make this gene a useful launching point for comparative analysis. Ribosomal DNA genes in basidiomycetes are tandemly repeated multigene families containing both genic and nongenic, or spacer regions. Each repeat contains a copy of the 18s, 5.8s, and 28s ribosomal subunit RNAs in addition to two spacer regions (internal transcribed spacer or ITS). As shown in Figure 1, the 5.8s rDNA gene is typically flanked by ITS1 and ITS2, which separates the 5.8s rDNA from the 18s and 28s genes (31). This gene in particular possesses highly conserved gene regions that are valuable in identifying organisms, as well as exhibiting regions such as the ITS regions that are considerably variable. Foremost, there is a homolog of this gene in every living cell, making it a well suited gene region as a basis for molecular comparison. In addition, genetic exchange between organisms has not been shown to occur in the rRNA operon, strengthening the rationale for using this region (38). Examinations of the variable ITS regions can often reveal differences present among separate isolates of the same species that may not present themselves when only examining the ribosomal subunit regions (15,20,29).

Having chosen the ribosomal subunit genes and the ITS regions to base our molecular comparisons, we elected to amplify them using the polymerase chain reaction (PCR). The PCR allowed us to exponentially amplify the rDNA region of interest. The specific portion to be amplified was governed by the choice of the oligonucleotide primers. One advantage that exists by using PCR is that it enabled us to amplify homologous gene segments in each of the isolates for comparison. A second advantage of using the PCR is the relatively short length of time needed to complete the reaction. Typically, each PCR run using the thermal cycler was under four hours and we were able to use crude DNA samples. Theoretically, the PCR is sensitive enough to detect a single target molecule for amplification without having to use other potentially harmful methods that, for example, may involve radioactivity (17).

The PCR was the initial step for each of the two methods we chose to analyze our isolates. The first method was the creation of a restriction fragment length polymorphism (RFLP) library using restriction enzyme analysis (REA), and the second method was sequence analysis. Both PCRs were identical except for the oligonucleotide primers chosen to amplify different portions of the rRNA gene (see Table 2).

Table 2. Oligonucleotides primer sequences used to amplify rRNA gene of *Rhizoctonia solani* isolates.

Primer	Nucleotide sequence 5'--3'
LR7	TACTACCACCAAGATCT
LROR	ACCCGCTGAACTTAAGC
ITS4	TCCTCCGCTTATTGATATGC
ITS5	GGAAGTAAAAGTCGTAACAAGG

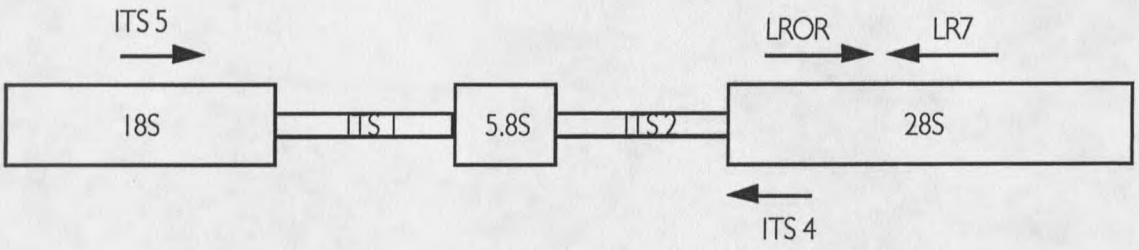


Figure 1. Schematic representation of the internal transcribed spacer regions. The boxes represent the ribosomal subunits. The arrows indicate the direction of the oligonucleotide primers (4).

CHAPTER 2

COLLECTION OF FOREIGN AND DOMESTIC *RHIZOCTONIA* ISOLATES FOR MOLECULAR CHARACTERIZATION

Introduction

Our objective in collecting both foreign and domestic isolates for molecular characterization stems from the fact that *E. esula* originated from Eurasia. There, *E. esula* populations are kept in check by a natural complex of insect and plant pathogens, including *R. solani* (8). We were looking for foreign and domestic isolates that appeared to be closely related. Ideally, we wanted to find foreign isolates that are related to isolates that already exist in the U.S., that show aggressiveness towards *E. esula,* and exhibit a narrow host range. Release of such isolates as biocontrol agents, in essence, would not be as risky as releasing an isolate or a new pathogen that does not already exist in the U.S. Equally as interesting is the basic information gained and possible future correlations that can be made by not only comparing the isolates to each other, but by using all the information we can gather to better characterize *R. solani*.

Field Materials and Methods

Surveys for disease within stands of *Euphorbia* spp. were undertaken in Eurasia 1993, 1994, 1995 and 1996. Entire plants were uprooted, placed in plastic bags and stored in an insulated container, then were cultured as soon as possible. Samples of *Euphorbia* which

exhibited wilting or stem necrosis were examined for decay in crown tissue or dead root buds, then washed thoroughly. The sample was then vigorously wiped with sterile cotton saturated with 0.5% NaOCl. Tissue from the sample was excised with a sterile scalpel and placed on acidified potato dextrose agar (PDA) for isolation. The cultures obtained were initially determined to be *Rhizoctonia* spp. based on microscopic characteristics, such as hyphal branching at 90° angles, and constriction at the septa, as well as cultural characteristics, including rapid growth, colony morphology, and sclerotia formation. Apparent *Rhizoctonia* spp. were hyphal-tipped and transferred to agar again (8).

The *Rhizoctonia* isolates from the diseased plants were evaluated for their ability to anastomose with thirteen isolates representing *R. solani*. Field isolates and tester strains were coupled on 2% water agar plates at a distance of 2.5 centimeters apart and assessed for anastomosis. To better visualize anastomosis reactions, hyphae were stained with a Methyl blue/lactophenol solution. The nuclear condition of the isolates was determined by vegetative cell staining with a solution of 4, 6-diamidino-2-phenyl indole (DAPI) (8).

Results

Tables 3 and 4 summarize information obtained for the 41 isolates collected. The tables list the *R. solani* sample, the original host of isolation, the geographic location, the identity determined by anastomosis testing and staining, and whether or not insects were present. Pathogenicity and virulence testing on all the isolates is incomplete (data not shown). Preliminary results indicate that isolates 01 and 06 may be good biological control candidates because they exhibited high aggressiveness to roots of *E. esula* (7).

Table 3. Identification and Features of Domestic Isolates of *Rhizoctonia solani*

Sample #	Designation	Identity of *Rhizoctonia* spp	Host	Insect Presence	Location
01	94-Lyman	AG-4	*Euphorbia esula*	Yes	Lyman Creek Bozeman, MT
02	94-WSS-M	AG-4	*Euphorbia esula*	No	White Sulfur Springs, MT
03	94-Miss-M	AG-4	*Euphorbia esula*	No	Missoula, MT
04	94-CC#2JL	AG-4	*Euphorbia esula*	No	Cabin Creek, MT
05	94-6J Rhiz.	AG-4	*Euphorbia esula*	No	Fort Benton, MT
06	93-2	AG-4	*Euphorbia esula*	No	Sidney, MT
07	93-1	AG-4	*Euphorbia esula*	No	Sidney, MT
08	94-20	binucleate	*Euphorbia esula*	No	Two Dot, MT
09	94-11	multinucleate	*Euphorbia esula*	No	Devil's Tower, WY
10	95-3	binucleate	*Euphorbia esula*	Yes	Stillwater, MT
11	95-6	multinucleate	*Euphorbia esula*	No	Knutson Creek, Theodore Roosevelt National Park (TRNP), ND
12	tester isolate	AG-4-HGI	n/a	No	n/a
13	95-5	binucleate	*Euphorbia esula*	No	TRNP, ND
14	95-10	binucleate	*Euphorbia esula*	No	Two Dot, MT
15	95-9	binucleate	*Centaurea maculosa*	No	Hill Co, MT
16	tester isolate	AG-4	n/a	No	n/a
17	KVAM 4	multinucleate	*Euphorbia esula*	Yes	Lambert, MT
18	KVAM 2	multinucleate	*Euphorbia esula*	Yes	Lambert, MT
19	KVAM 5X01	binucleate	*Euphorbia esula*	Yes	Lambert, MT
20	96-2	binucleate	*Euphorbia esula*	Yes	Fremont Co, WY
21	96 Johno 3	multinucleate	*Euphorbia esula*	Yes	Savage, MT

Table 4. Identification and Features of Foreign Isolates of *Rhizoctonia solani*

Sample #	Designation	Identity of *Rhizoctonia* spp	Host	Insect Presence	Location
22	93f-23C	multinucleate/ AG-4	*E. esula/virgata*	No	Volgograd, Russia
23	93f-16c	binucleate	*E. stepposa*	No	Novomarieskaya, Russia
24	93f-23A	multinucleate	*E. esula/virgata*	No	Volgograd, Russia
25	94f-15	binucleate	*E. esula/virgata*	No	Spakovskoe, Russia
26	94f-38	binucleate	*E. esula/virgata*	Yes	Cavaillon, France
27	95f-14	binucleate	*E. esula/virgata*	Yes	Fuzesabony, Hungary
28	95f-13	multinucleate	*E. esula/virgata*	Yes	Puspokladany, Hungary
29	95f-20	multinucleate	*E. esula/virgata*	Yes	Izsa, Slovak Republic
30	94f-18	multinucleate	*C. diffusa*	Yes	Novomarieskaya, Russia
31	94f-38a	binucleate	*E. esula/virgata*	No	Cavaillon, France
32	94f-38b	binucleate	*E. esula/virgata*	No	Cavaillon, France
33	94f-3N	binucleate	*Centaurea maculosa*	Yes	Spakovskoe Sniish, Russia
34	95f-18	binucleate	*E. stepposa*	No	Vesprem, Hungary
35	95f-16	binucleate	*Centaurea maculosa*	Yes	Vesprem, Hungary
36	95f-19	binucleate	*Centaurea maculosa*	Yes	Izsa, Slovak Republic
37	95f-10	multinucleate	*E. esula/virgata*	Yes	Balmasurvos, Hungary
38	96f-10	binucleate	*E. esula/virgata*	No	Xilinhot, China
39	96f-14	binucleate	*E. esula/virgata*	Yes	Inner Mongolia, China
40	96f-17	multinucleate	*E. esula/virgata*	Yes	Bautou, China
41	96f-12	binucleate	*E. esula/virgata*	No	Inner Mongolia, China

CHAPTER 3

RESTRICTION ENZYME ANALYSIS TO CREATE A RESTRICTION FRAGMENT LENGTH POLYMORPHISM LIBRARY

Introduction

The first approach we employed to characterize *R. solani* involved the PCR to amplify regions of rDNA to create our restriction fragment length polymorphism (RFLP) fingerprint library using restriction enzyme analysis (REA). REA is based on the capability of restriction enzymes to identify DNA sequences that are 4 to 8 bases in length and cleave the double helix at these sites. The number of restriction sites that exist for each isolate determines the number of fragments generated for each isolate and the distance between each restriction site governs the size of the fragments produced by these cuts. The products of these restriction digests are separated by standard agarose gel electrophoresis. The banding patterns produced by these restriction enzyme cuts are reproducible but usually vary somewhat between gels. Banding patterns produced by this method are known as the RFLP fingerprints. The banding pattern or RFLP fingerprint will change if changes in the DNA occur such as a point mutation, that would result in the loss or gain of a restriction site, or chromosomal rearrangement (38). By comparing the RFLP fingerprints, we can estimate the genetic similarity of the isolates (30,36).

Materials and Methods

Fungal cultures

A total of 41 foreign and domestic *Rhizoctonia solani* isolates, representing anastomosis group 4, intraspecific groups 1 and 2, were analyzed. All isolates were maintained on potato dextrose agar at 4°C. Each isolate was grown in 250 ml potato dextrose broth at room temperature with shaking for seven days.

DNA preparation

Mycelia from each isolate was sterile filtered and dehydrated on a lyopholizer for 24 hours. The dehydrated isolates were then ground with 12.5 grams of non-sterile sand to a fine powder in a sterilized mortar with a pestle. The DNA was prepared using the "Sand Prep " method (14). The powder-sand mixtures were transferred to polypropylene centrifugation tubes containing nine ml of extraction buffer and gently mixed by rolling the tubes back and forth on the bench top. The tubes were placed on their sides and gently rocked on an electric rocker for at least one hour at 60° C. After a one hour incubation, 6 ml of chloroform-octanol (24:1) were added to each tube. Each tube was then gently rolled on its side for 5 minutes and centrifuged for ten minutes at 4000 rpm. The aqueous layer of each tube was poured into new tubes each containing 1 ml 10% CTAB (56 ml H_2O, 10 g CTAB, 33ml 2.5M NaCl), then balanced with the addition of at least 4 ml of chloroform-octanol and centrifuged for ten minutes at 4000 rpm. Following centrifugation, the aqueous layer of each sample was pipetted into centrifugation tubes containing 6 ml isopropanol. The DNA in these tubes were allowed to precipitate for 30 minutes and then centrifuged for 20 minutes at 7000 rpm. The aqueous layer of each sample was discarded and the pellets that

remained were left to dry on the bench top overnight. The dried DNA pellets were then suspended in 1 ml TE buffer and stored at -20°C until later use.

Polymerase Chain Reaction

PCR reactions were performed using the oligonucleotide primers LROR and LR7 (see Figure 1 and Table 2) with template DNA obtained from the Sand Prep DNA extraction method. The DNA samples were diluted 1:100 before performing PCR in order to obtain the greatest yield of PCR products. Thirty PCR cycles were performed on an automated thermal cycler, using the following parameters: 1 minute denaturation step at 94°C, 1 minute annealing step at 50°C, and 1 minute primer extension step at 72°C followed by a final 7 minute incubation step at 72°C to ensure complete polymerization of any remaining PCR products (36). PCR products were examined on a 2% ethidium bromide-stained agarose gel over an ultraviolet light transilluminator, and photographed.

Restriction Enzyme Analysis of PCR Products

Restriction enzyme analysis was performed directly on the PCR products according to the manufacturer's directions (New England Biolabs). The restriction enzymes used to digest the PCR products are as follows: *Ava*II, *Hha*1, *Hpa*II, *Msp*1 and *Taq*1. The RFLPs were analyzed by separation of the fragments using electrophoresis on a 4% agarose gel. Figure 2 shows an example of RFLP banding patterns obtained from restriction enzyme *Hha*1. Four gels per restriction enzyme were run to accommodate all 41 isolates, and photos of these gels are found in Appendix A. The 1kb DNA ladder standard was run with each group of isolates for each restriction enzyme. The fragments of the standard are of known size, so the fragment size was plotted against the distance travelled from the origin. An

example of a calibration curve of the 1kb DNA ladder is shown in Figure 3 for the *Hha*1 gel shown in Figure 2. A calibration curve for each gel and for each restriction enzyme was plotted. This allowed us to determine the size of the fragments produced for each isolate by each restriction enzyme.

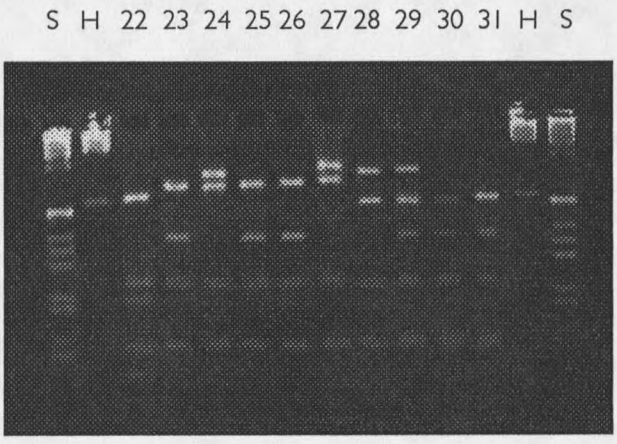


Figure 2. RFLP fingerprints produced by the digestion of LROR, LR7 amplified rDNA with restriction enzyme *Hha*1 analyzed on a 4% agarose gel. Isolate numbers and ladder identification are shown. The 1kb DNA ladder is labeled "S" and the *Hin*dIII lambda ladder is labeled "H".

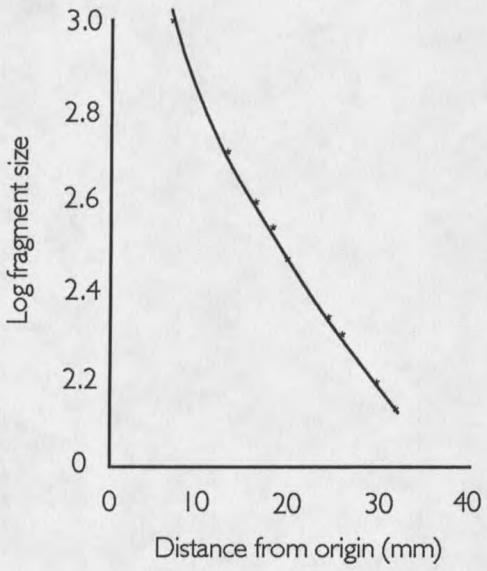


Figure 3. Calibration curve based on the 1kb DNA ladder for the RFLP fingerprint shown in Figure 2 (18).

Letter designations for RFLP banding patterns were assigned to all isolates for each restriction enzyme used. Isolates with identical RFLP banding patterns were placed in the same letter group. If the patterns of the lettered groups were the same for all six restriction enzymes, the isolates were placed in the same class. This is summarized in Tables 5 & 6.

Table 5. Genotype classes and restriction phenotypes of the domestic isolates.

Sample #	Class	Restriction phenotype of fragment digested with:					
		AvaII	*HhaI*	*HpaII*	*MspI*	*Sau3AI*	*TaqI*
01	I	A	A	A	A	A	A
02	I	A	A	A	A	A	A
03	I	A	A	A	A	A	A
04	I	A	A	A	A	A	A
05	I	A	A	A	A	A	A
06	I	A	A	A	A	A	A
07	II	B	B	B	B	B	A
08	III	A	A	C	C	C	A
09	IV	A	A	A	A	C	A
10	III	A	A	C	C	C	A
11	I	A	A	A	A	A	A
12	V	A	C	D	D	C	B
13	VI	C	C	E	E	D	C
14	VII	A	D	F	F	E	A
15	VIII	D	E	G	G	B	D
16	IX	A	F	H	H	F	D
17	I	A	A	A	A	A	A
18	X	A	A	A	A	A	E
19	XI	D	F	I	I	K	D
20	XII	A	A	C	C	G	A
21	XIII	E	G	J	J	H	F

Table 6. Genotype classes and restriction phenotypes of the foreign isolates.

Sample #	Class	Restriction phenotype of fragment digested with:					
		AvaII	*HhaI*	*HpaII*	*MspI*	*Sau3AI*	*TaqI*
22	XIV	A	C	A	A	A	A
23	XV	A	C	N	N	C	A
24	XVI	A	D	A	A	A	A
25	XVII	A	E	C	C	C	A
26	XVIII	G	F	O	O	L	J
27	III	A	A	C	C	C	A
28	I	A	A	A	A	A	A
29	XIX	A	F	N	N	C	A
30	XX	A	A	P	P	K	D
31	XXI	D	G	G	G	I	K
32	XXII	D	F	G	G	I	G
33	VIII	D	E	G	G	B	D
34	XXIII	C	H	K	K	J	H
35	XXIV	D	F	G	G	K	D
36	VIII	D	E	G	G	B	D
37	X	A	A	A	A	A	E
38	XXV	A	A	C	C	C	E
39	XXV	A	A	C	C	C	E
40	XXVI	F	I	L	L	C	I
41	XXVII	A	J	M	M	C	A

A distance matrix was calculated by using the equation

$$D = 1 - 2(\sum n_{xy})/(\sum n_x + \sum n_y),$$

where D represents the distance to be entered into the matrix; n_x represents the number of fragments found in the first of the two isolates being compared; n_y represents the number of fragments found in the second of the two isolates being compared; and n_{xy} represents the number of restriction fragments the two isolates have in common. The $\sum$ sign indicates the summation of the values for each restriction digest (19,36). The RFLP banding patterns and classes aided in the construction of a distance matrix. Figure 4 is an example of one "cell" used in calculating the matrix. Appendix B contains the entire collection of cell calculations in

matrix form, and Appendix C contains the distance, or *D*, values only. This matrix is the distance matrix manipulated by the phylogenetic software to infer phylogeny.

Neighbor, from Felsenstein's *Phylip* version 3.572 software package, was the first step towards inferring phylogeny. This used the Neighbor Joining method to create a phylogenetic tree from the distance matrix data. The Neighbor Joining method is an estimation procedure to make the best estimate of evolutionary history based on the data set. It uses an algorithm, or specific sequence of steps, that leads to a phylogenetic tree. This program took the raw data provided by the distance matrix and drew an initial tree. It then adjusted the nodes on the tree based on the average divergence from all the other nodes by constructing a modified distance matrix. From here, a phenogram using Felsenstein's *Drawgram* was produced to give us a visual representation of the data set.

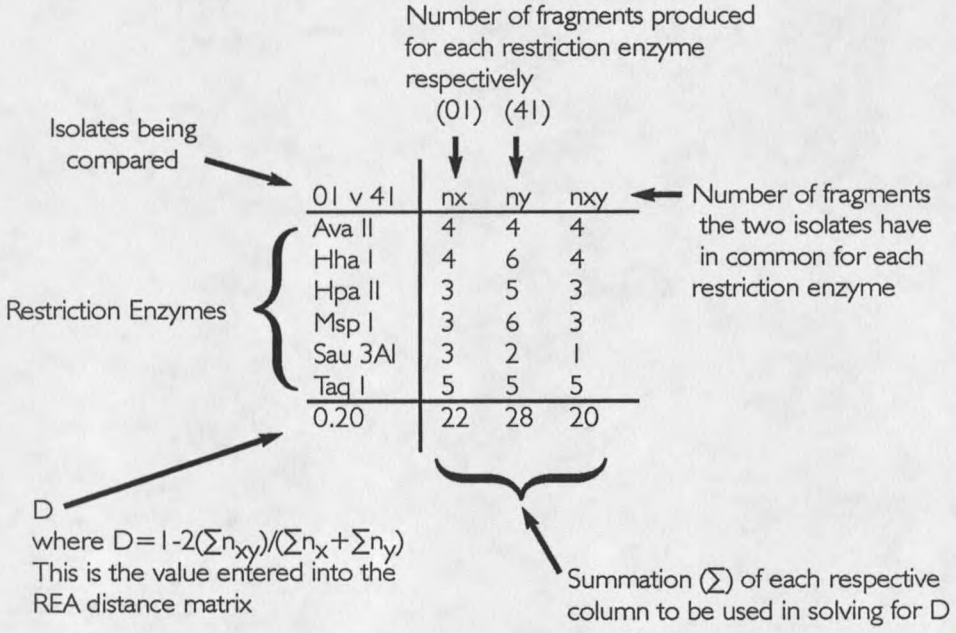


Figure 4. Diagram of the calculation cell used to evaluate the Distance Matrix. The number of fragments produced for each restriction enzyme was visually determined from RFLP fingerprints.

Results

Two different bands were produced during the PCR reaction using the primers LROR and LR7 (Figure 5). Out of 41 isolates, 27 isolates produced a 1.4 kilobase (kb) band, 11 isolates produced a 1.8 kb band, and 3 isolates presented both the 1.4 and 1.8 kb bands. These findings are in agreement with results obtained by Cubeta et al, 1991 (12). They reported that when using the primers LROR and LR7, they also observed a 1.4 kb band, a 1.8 kb band, or both. Occasionally, their isolates containing both the 1.4 and 1.8 kb fragments produced an additional 1.6 kb band, we did not observe the production of this additional 1.6 kb band. They theorized that "The intermediate 1.6 kb band may be the result of heteroduplex formation between DNA strands of different lengths, and that these bands may represent different length variants of the rRNA gene that individual isolates can possess (34)." They could not explain the similarity of restriction patterns from isolates that produced different length variants of rDNA, which is consistent with our results and RFLP banding patterns. These length variants did not appear to be artifacts of PCR due to the fact that they are consistent and repeatable, and they did not cluster together on the REA phenogram (Figure 6).

Discussion

Five groups of isolates presented identical RFLP fingerprints and were placed in RFLP classes I, III, VIII, X, and XXV (see Tables 5 & 6). It is interesting to note that each of four of the classes (I, III, VIII, and X) include at least one foreign isolate. RFLP classes I, III, and X included domestic isolates from Montana and foreign isolates from Hungary. Isolates from Montana, Russia, and Slovak Republic (samples 15, 33, and 36 respectively) all possessed identical banding patterns and were placed in class VIII. Class XXV includes isolates 38 and

39, both isolated in China, but from two very different geographic areas, located hundreds of miles apart. These class assignments suggest relatedness of the isolates but it is important to keep in mind that the assignment is based solely on banding patterns from the RFLP analysis. This assessment method does not supply information on a mutational basis and could yield erroneous estimates of genetic similarity (35). If, for example, a new restriction site evolves due to mutation between two pre-existing restriction sites, one large fragment may disappear resulting in the creation of two new, shorter fragments. This may be a serious problem because even though two isolates may share two out of three restriction sites, they no longer have fragments in common (18). It is also noted that insertions, possibly of transposable elements, and deletions are difficult to handle when using REA and that gaining a restriction site is less likely than losing one. RFLP interpretation is also complicated by isolates that may contain more than one rDNA length variant (12). Nevertheless, some argue that if you have a substantially large data set such as this, RFLP data can still be useful in determining relatedness (18).

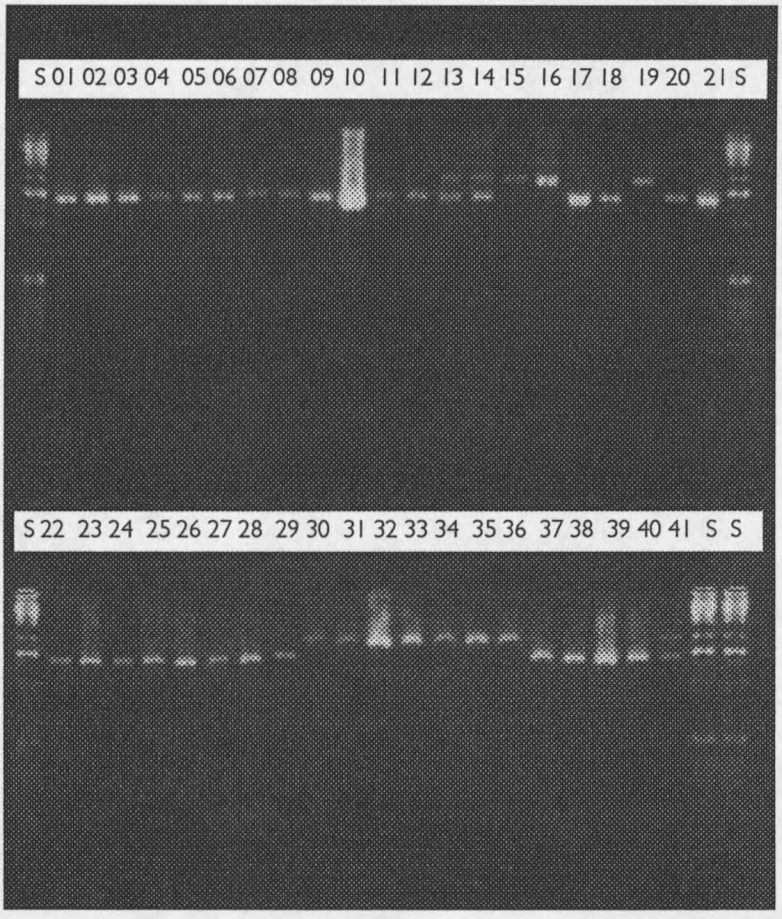


Figure 5. PCR products of rDNA amplified by restriction enzymes LROR and LR7. This depicts different length variants of 1.4 kb or 1.8 kb bands. Three of the isolates produced both 1.4 kb and 1.8 kb bands. Isolate numbers and ladder identification are shown. The 1kb DNA ladder is labeled "S".

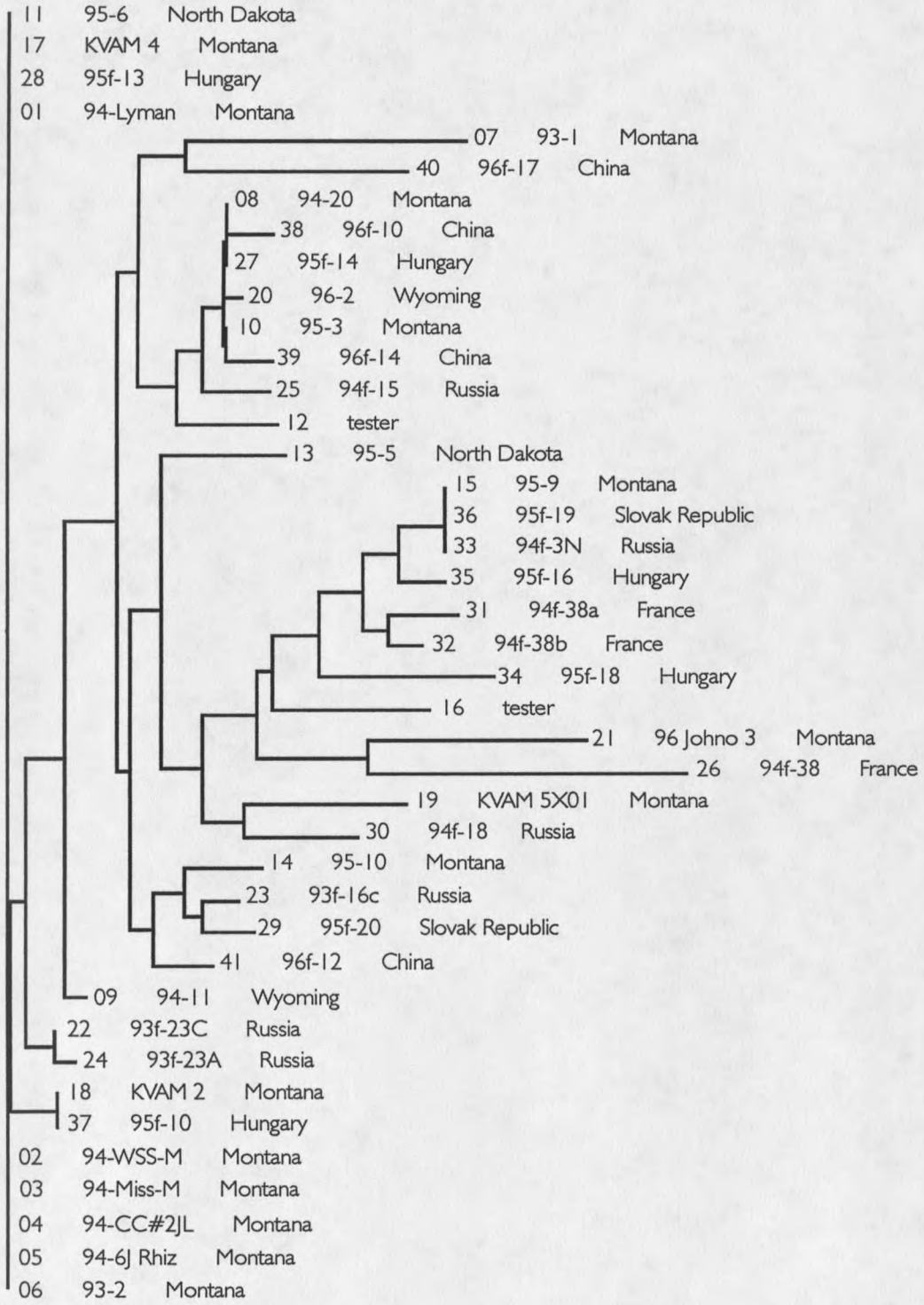


Figure 6. Neighbor joining phenogram of *R. solani* based on restriction enzyme analysis.

CHAPTER 4

PHYLOGENETIC RELATIONSHIPS INFERRED FROM SEQUENCES OF INTERNAL TRANSCRIBED SPACER REGIONS AND RIBOSOMAL DNA

Introduction

For further characterization we elected to sequence rDNA and ITS regions of *R. solani*. While RFLPs can often differentiate strains, data on sequences of DNA can also be used to infer phylogeny (38). The most practical approach is to analyze sequences of homologous segments. The rRNA gene is the best studied sequence used in phylogenetic comparisons evident by resources such as GenBank and the Ribosomal RNA Database Project that offer free alignment services by e-mail. Sequence data may confirm previous findings, contradict previous findings, or provide new insight. Sequencing ultimately provides us with a wealth of information and will undoubtedly play an increasing role in taxonomy. Obtaining sequence data for our isolates allowed us to infer phylogeny using Felsenstein's *Phylip* software package.

Materials and Methods

Fungal cultures

See Chapter 3 Materials and Methods.

DNA preparation

See Chapter 3 Materials and Methods.

Polymerase Chain Reaction

The polymerase chain reaction (PCR) was performed using the same thermal cycler parameters as described in Chapter 2 (p. 15). The reaction differed only by the region of the ribosomal RNA gene amplified using the primers ITS4 and ITS5 (Figure 1). The primers from this reaction were removed from the PCR products prior to sequencing by using a Qiagen QIAquick PCR purification kit according to manufacturers' instructions. Concentrations of the samples were determined by reading A_{260} with a spectrophotometer.

Automated Sequencing

DNA sequencing was conducted by Joan Strange at the University of Montana, Missoula, with an automated sequencer. This method is termed "automatic" in that one does not have to manually record the results. Rather than radioactively labeled DNA fragments, the DNA fragments are fluorescently labeled and detected by a laser during electrophoresis. The sequence is directed to a computer and recorded in chromatograph form. From this point, the chromatograph can be translated into a DNA sequence either visually or by computer software. Sequence data from these reactions were aligned "on-line" using the BLASTN database, producing 100% homology with several *Rhizoctonia solani* in the sequence database. This confirmed that we in fact had amplified and sequenced the 5.8s rDNA, ITS region that we had targeted.

Alignment of Sequences

The sequences obtained did not allow for complete alignment of all 700 nucleotides. Therefore, a combined sequence data set of 400 nucleotides was used for the alignment. Alignment of the isolates' sequences was accomplished using the *Align Plus*, version 2 software package with isolate "01" serving as the reference molecule. The aligned sequences are found in Appendix D.

To compare the isolates, I chose the Distance Method, which creates a distance matrix from the aligned sequence data. Distance comparison methods calculate the percent changes for the data set, taking each nucleotide position and determining simply whether it is the same or different for all the isolates in the data set. This is unlike Maximum Likelihood Methods that weight transversion and transition nucleotide changes differently. *Neighbor*, utilizing the Neighbor Joining method was used to create a phylogenetic tree, which was then used by *Drawgram* to produce a visual representation of the data set (Figure 7) (18).

Bootstrapping

The application of bootstrap methods is used to create a reliable phylogenetic tree by decreasing stochastic effects that may influence the branching of the tree. In situations where resampling is impractical or impossible, bootstrapping creates pseudoreplicate data sets by randomly sampling the original matrix to create new matrices. We used 100 bootstrap replications with bootstrap proportions listed to the left of the branches (Figure 8). The bootstrap proportion represents the frequency with which a given branch is found by analysis of the pseudoreplicate data sets (18). Again, Felsenstein's *Phylip* software was used. First *Seqboot* created 100 randomized sequence alignments, and then *DNADist* created distance matrices for each bootstrap replication. The Neighbor Joining method followed using

Neighbor and the phenogram was constructed using *Drawgram*.

Results

PCR products obtained using ITS 4 and ITS 5 oligonucleotide primers were approximately 700 base pairs in length (data not shown). Researchers claimed that they were able to distinguish their *R, solani* isolates according to virulence, based on differences in the size of the PCR product using the same primers (4). Due to the fact that our virulence testing has not been completed, we are unable to make such claims at this point in time. However, if in the future we are able to make the same claim of distinguishing virulence based on the size of the PCR product, it would definitely hasten the screening process of choosing appropriate isolates for biocontrol. Figure 7 shows the phenogram constructed from the sequence data. Figure 8 shows the phenogram constructed from the bootstrap data. Branches on the tree that have bootstrap proportions greater than 50 have been bolded.

No correlations for insect damaged isolates were detected by obvious clustering on the Neighbor-Joining or bootstrap consensus tree. On the bootstrap consensus tree, isolates 23 and 34 did not cluster together, and were the only two isolates to have *E. stepposa* as a host. However, all four isolates, including one domestic and three foreign isolates, originating from the host plant *Centaurea maculosa,* cluster at the top of the bootstrapping phenogram to the right of a bootstrap proportion of 63. Sixteen out of nineteen of the domestic isolates collected originated in Montana and are distributed evenly over the tree. Isolates from Hungary did not cluster together, nor did isolates from China. Hungarian isolate 28 and isolate 11 from North Dakota branch together with a bootstrap proportion of 65 and differ by only one nucleotide. Though isolates 27 and 36 were isolated from different countries (Hungary and Slovak Republic) and from different hosts, they group together on

the tree with a bootstrap proportion of 100, and differ by only nine nucleotides. Two out of three isolates collected from a small field in France clustered together while the third isolate branches by itself. This helps depict the diversity of *R. solani* isolates in a small geographical area. Russian isolates 22 and 24 are identical to each other as are China isolates 38 and 39 which were isolated in separate regions of Inner Mongolia.

The nucleotide differences referenced above were obtained by using the *Align Plus* software package to help interpret the trees. The matrix depicting the number of nucleotide matches between each isolate is listed in Appendix E. Keep in mind that the phylogenetic tree is just a visual representation of the sequence data and that the interpretation of the tree is subjective. Paired isolates 38 and 39 have identical sequences matching 400 out of 400 nucleotides. Given that, one might interpret isolates 23 and 34 to be identical or isolates 21 and 26 to be identical but they differ by 138 and 133 nucleotides respectively. This is not to say that the inferred trees are not informative, just that caution should be taken in the interpretation. Slight differences in the number of nucleotide matches arise each time a different reference molecule is selected. Regardless of which molecule is chosen as the reference molecule, the obvious clustering of isolates shown in Figure 8 remain fairly constant. One mistake to avoid in interpreting the bootstrap consensus tree, given by Hillis et al, is not to focus on individual branches, but to look at the tree as a whole.

Discussion

Our study revealed that although *R. solani* isolates display a high level of sequence variation in the rDNA ITS regions, some foreign and domestic strains are identical. This is not surprising considering that most of the isolates were collected from the same host species *E. esula*. Recently, Boysen et al. (1996) reported that phylogenetic analysis showed

that the AG-4 isolates they examined could be divided into three subgroups that correlate with habitat and virulence. Following that study, Kuninaga et al. (1997) evaluated the genetic diversity within and between anastomosis groups in *R. solani*. They were able to distinguish hybridization groups AG4-HG-I and AG4-HG-II as well as correlate the information to two of the three subgroups of Boysen et al. (1996). The hypovirulent subgroups of Boysen et al. evaluated by Kuninaga et al. showed low homology to subgroups HG-I and HG-II but did show high relatedness to a binucleate *Rhizoctonia* isolate belonging to the group with a *Ceratobasidium* sexual state. This is intriguing due to the fact that our sample collection consists of both multinucleate and binucleate isolates. Perhaps our virulence tests will yield similar results and we may find that our multinucleate and binucleate strains merit separate species. One of the advantages of having used sequence analysis here is that when our virulence tests are complete, we can compare the results of different studies to our own without performing the experiments.

The findings in this study show that several of the foreign isolates are identical to the domestic isolates, suggesting that a larger survey is needed. A consistent relationship of soilborne pathogens with insect root damage has been observed (9), and we need to apply virulence and insect data to the rDNA, ITS sequence data. To do this, a critical mass of foreign isolates is needed to assess AG and insect association. The determination, by sequence analysis, that some foreign and domestic isolates are identical should qualify these foreign isolates as possible release agents. This information proves that these fungi already exist in U.S. soil and, in essence, a foreign isolate may simply be a more effective pathogen and a better adapted biocontrol agent.

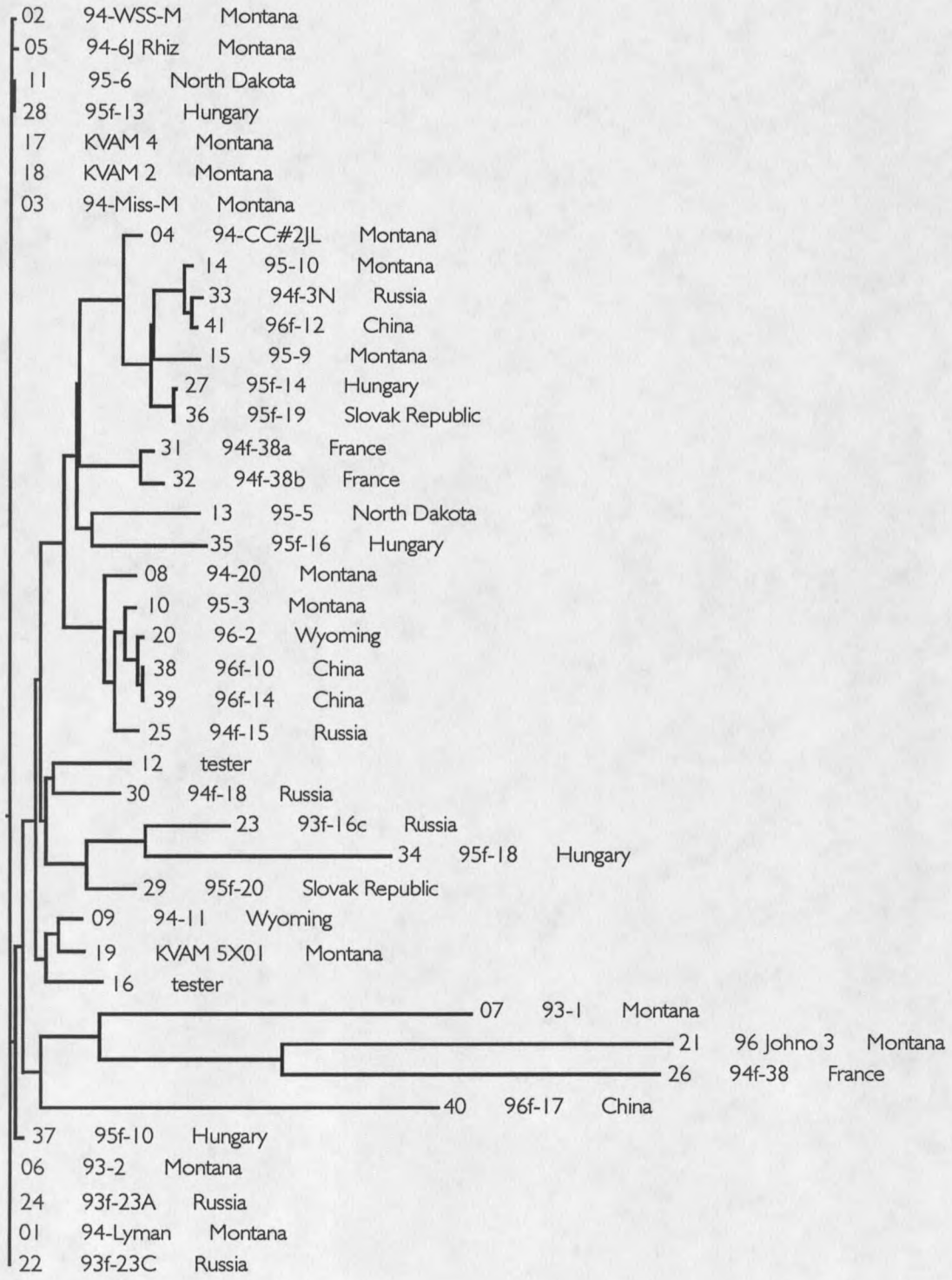


Figure 7. Neighbor joining tree for *Rhizoctonia solani* inferred from 400 alignable sites of rDNA sequence data.

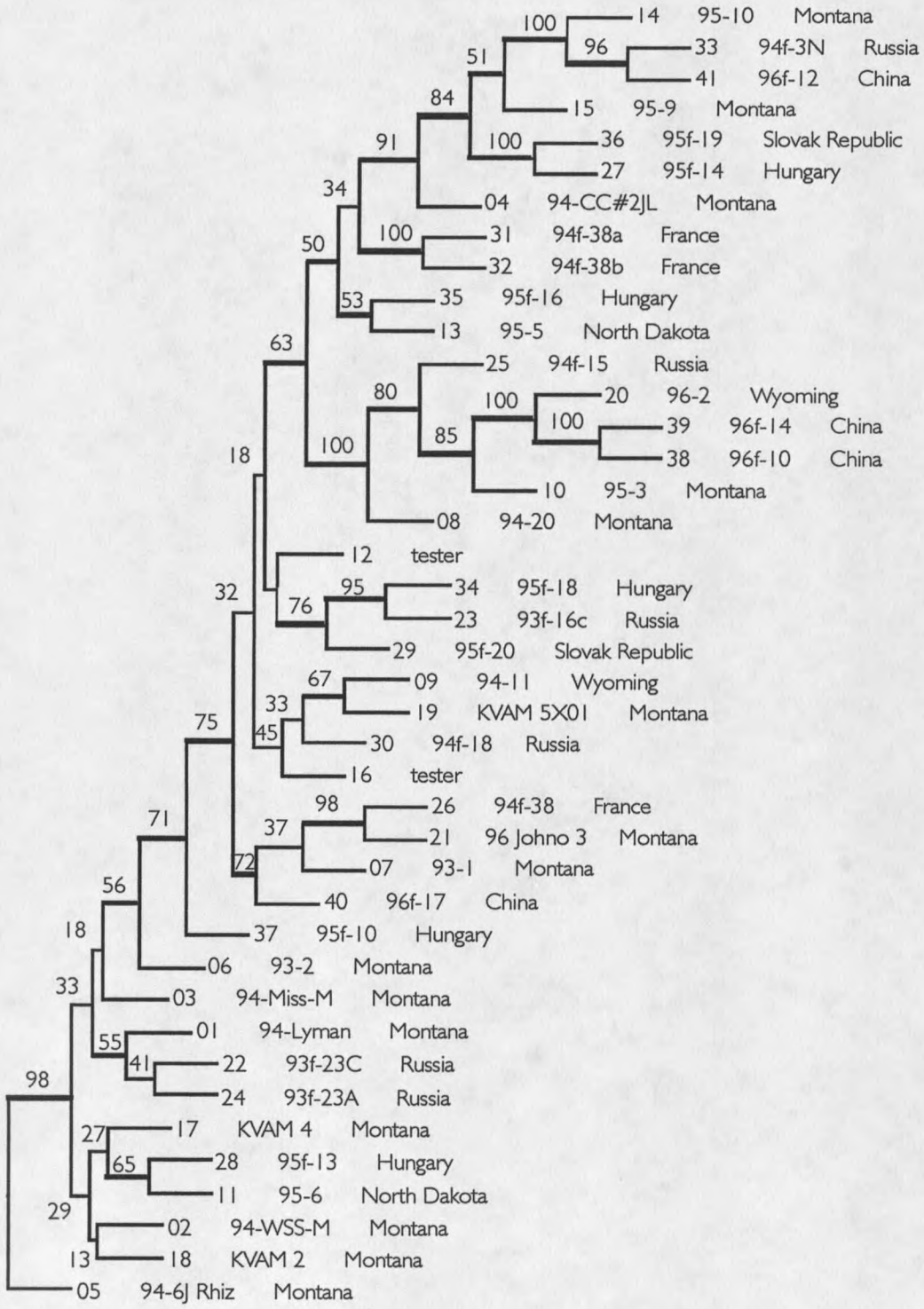


Figure 8. Bootstrap consensus tree generated from 100 bootstrap replications of 400 alignable sites of rDNA sequence data.

EPILOGUE

Results of the sequence data reinforce some of the results obtained by REA data. The results are not identical, and this may be due to some of the problems associated with REA, such as not being able to detect mutational changes as the result of a loss or gain of a restriction site due to insertions or deletions. In addition, the regions of the rDNA that we used for REA and for sequence analysis differ, which may also explain some slight variance in the results. This same variance, however strengthens the evidence for similarity of isolates that appear to be the same using both methods. Small errors, such as the incorporation of the wrong nucleotide, is also to be expected when using the PCR. Given these possible avenues for error, it is still obvious that several foreign and domestic isolates appear to be very similar using both methods. These comparative results, along with the pathogenicity and virulence testing, will aid in the selection of the appropriate isolates for biocontrol of *E. esula*.

In comparing both of the methods used, I would choose sequencing over REA for most applications. In the past few years, sequencing has become relatively cheap and easy to obtain. The time required for sequencing is shorter than that for REA and it ultimately gives more information. Given the sequence data, restriction sites can be found visually or by using computer software packages. These software packages are capable of searching for restriction sites, displaying the position of the sites, and determining the exact size of the bands that are produced given a particular restriction enzyme. This capability aids in the selection of restriction enzymes that are informative which saves time and money.

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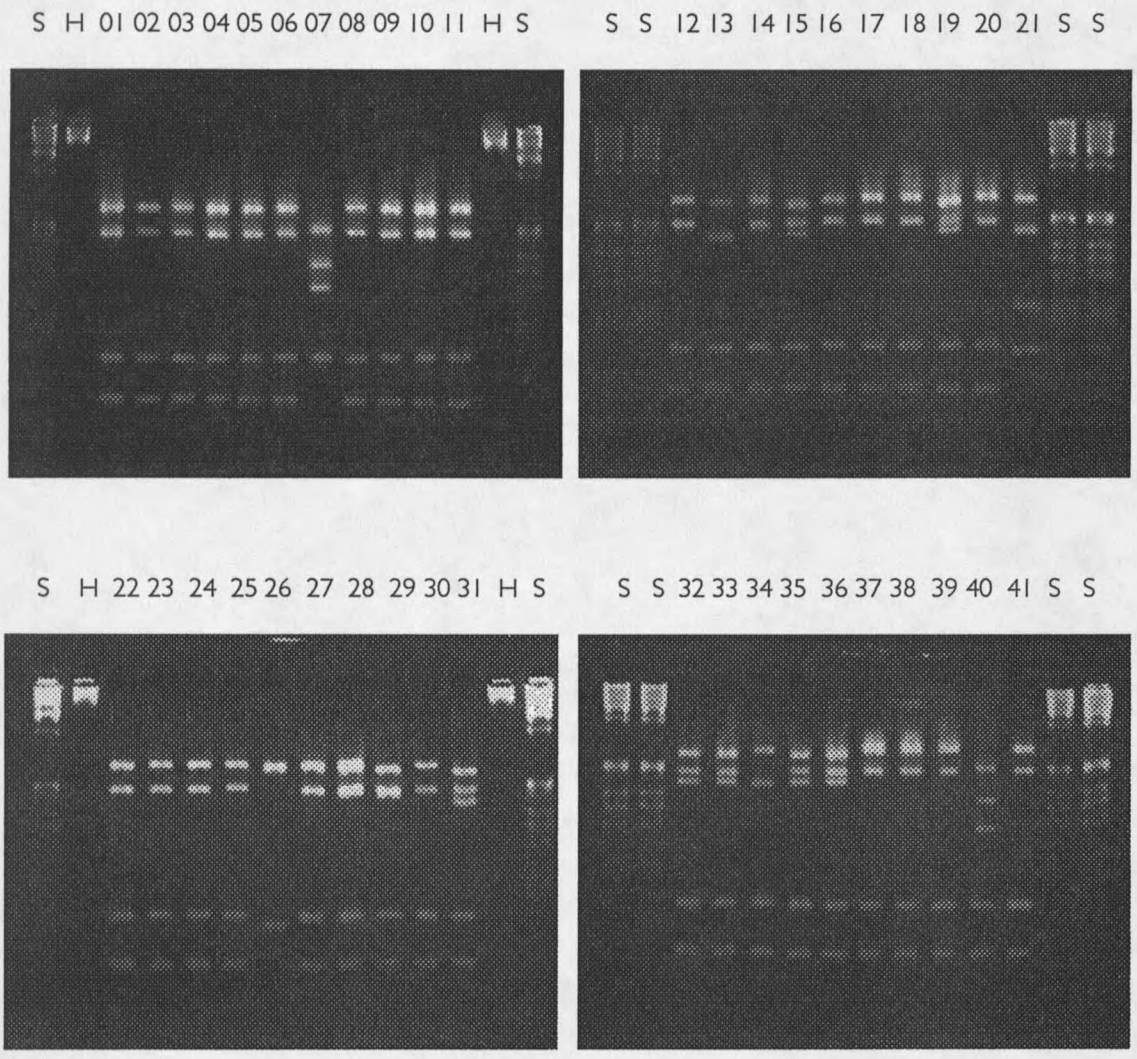
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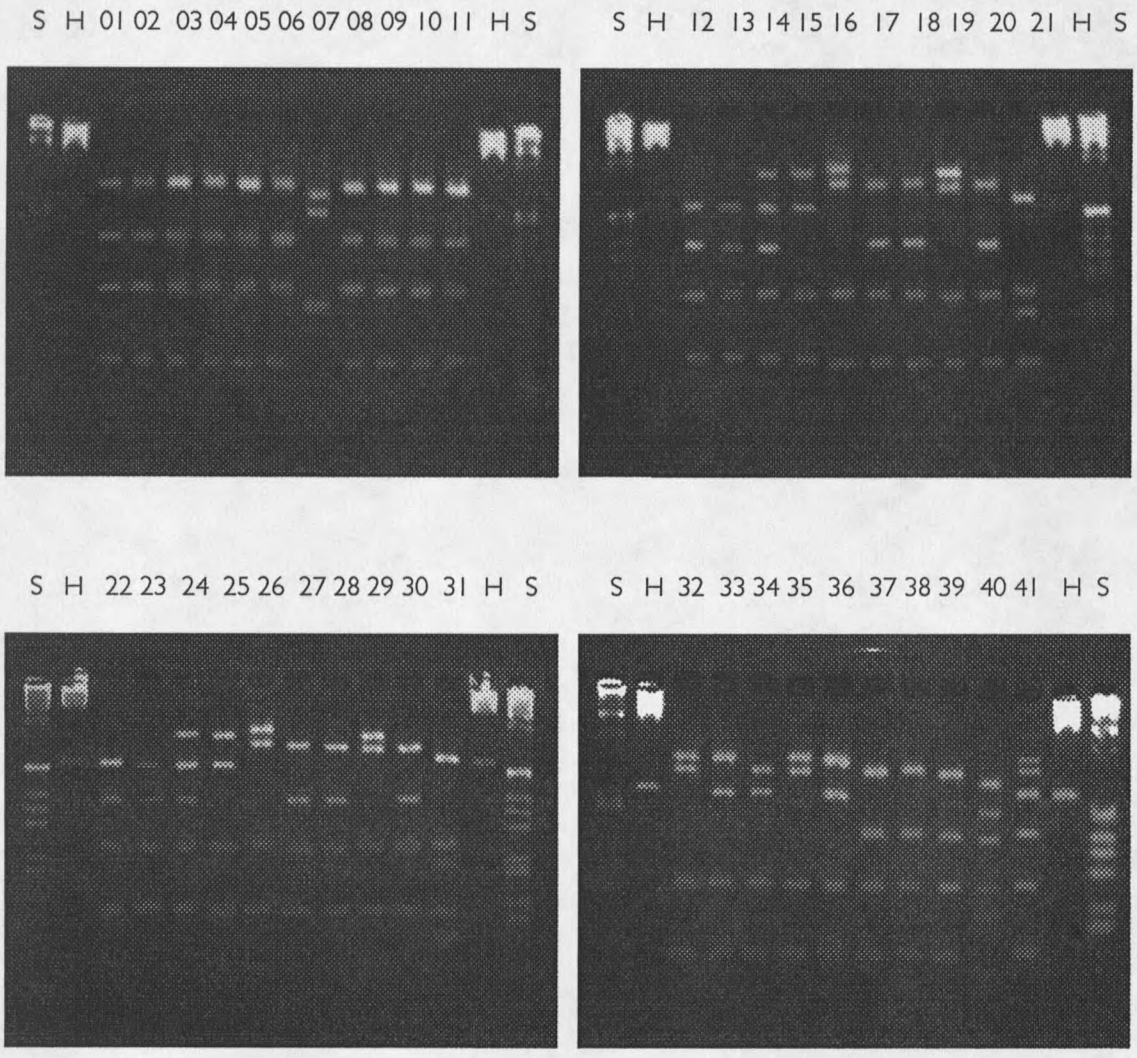
APPENDICES

APPENDIX A

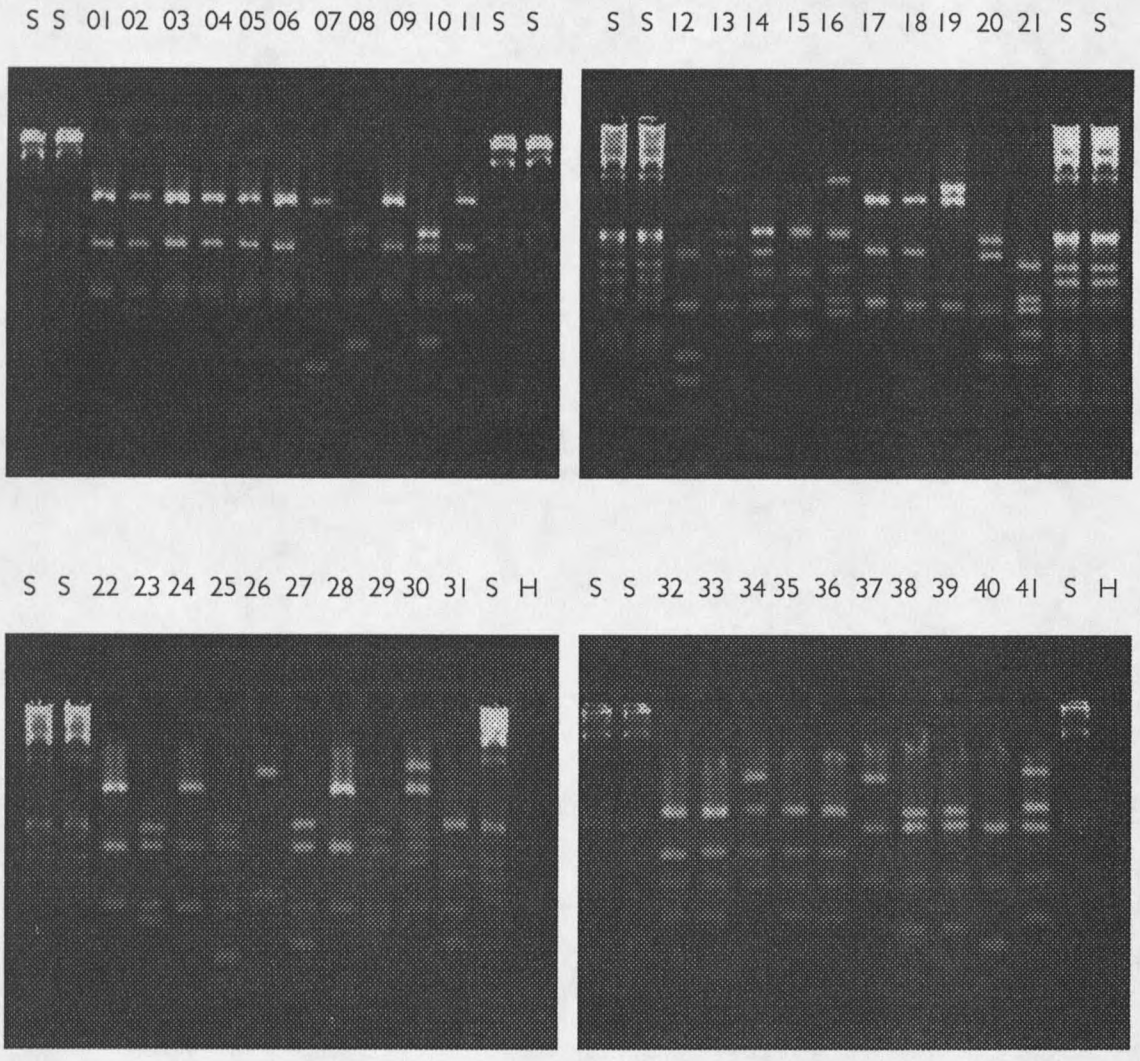
RFLP FINGERPRINTS



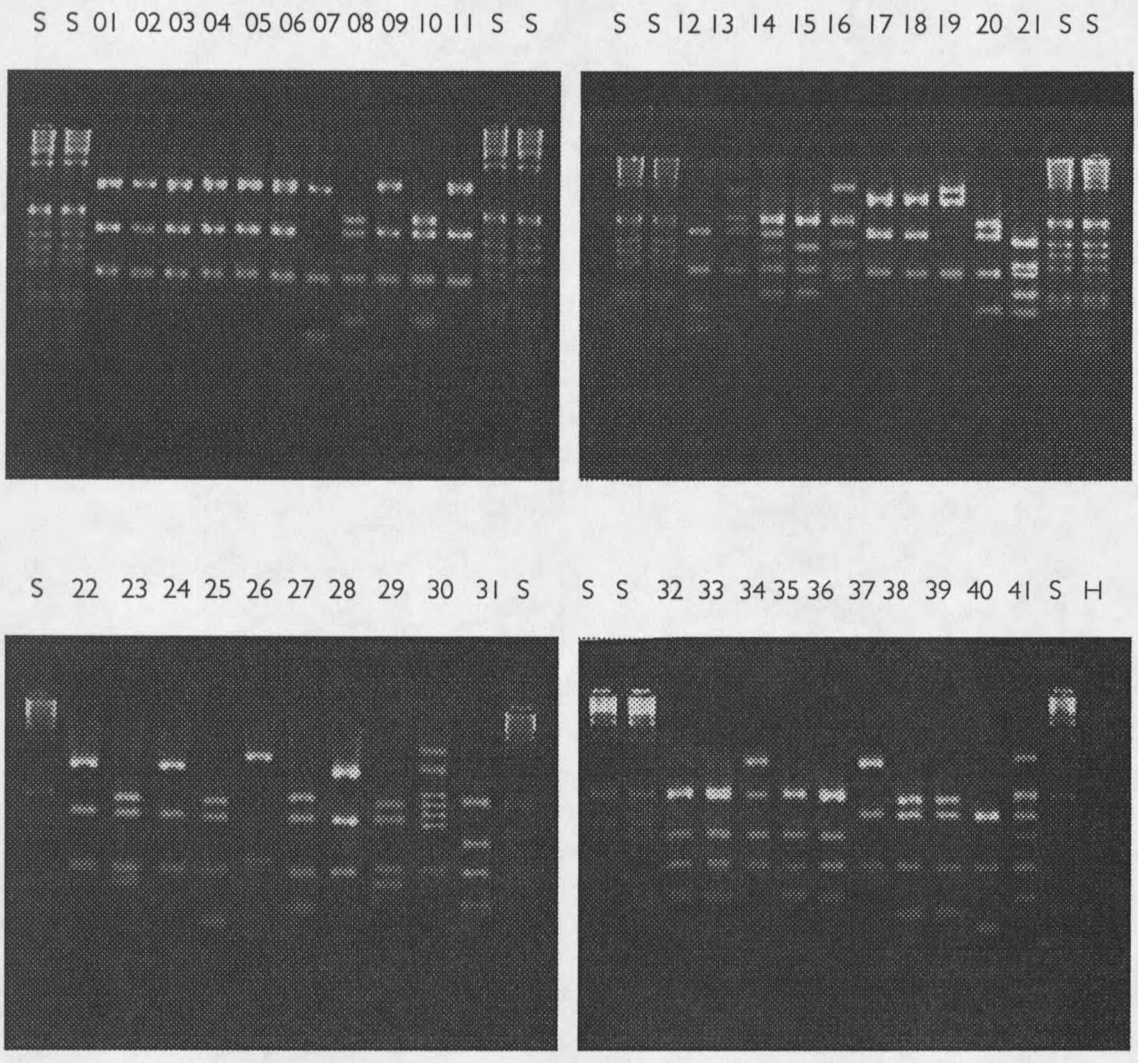
RFLP fingerprints produced by the digestion of LROR, LR7 amplified rDNA with restriction enzyme *Ava*II analyzed on a 4% agarose gel. Isolate numbers and ladder identification are shown. The 1kb DNA ladder is labeled "S" and the *Hin*dIII lambda ladder is labeled "H".



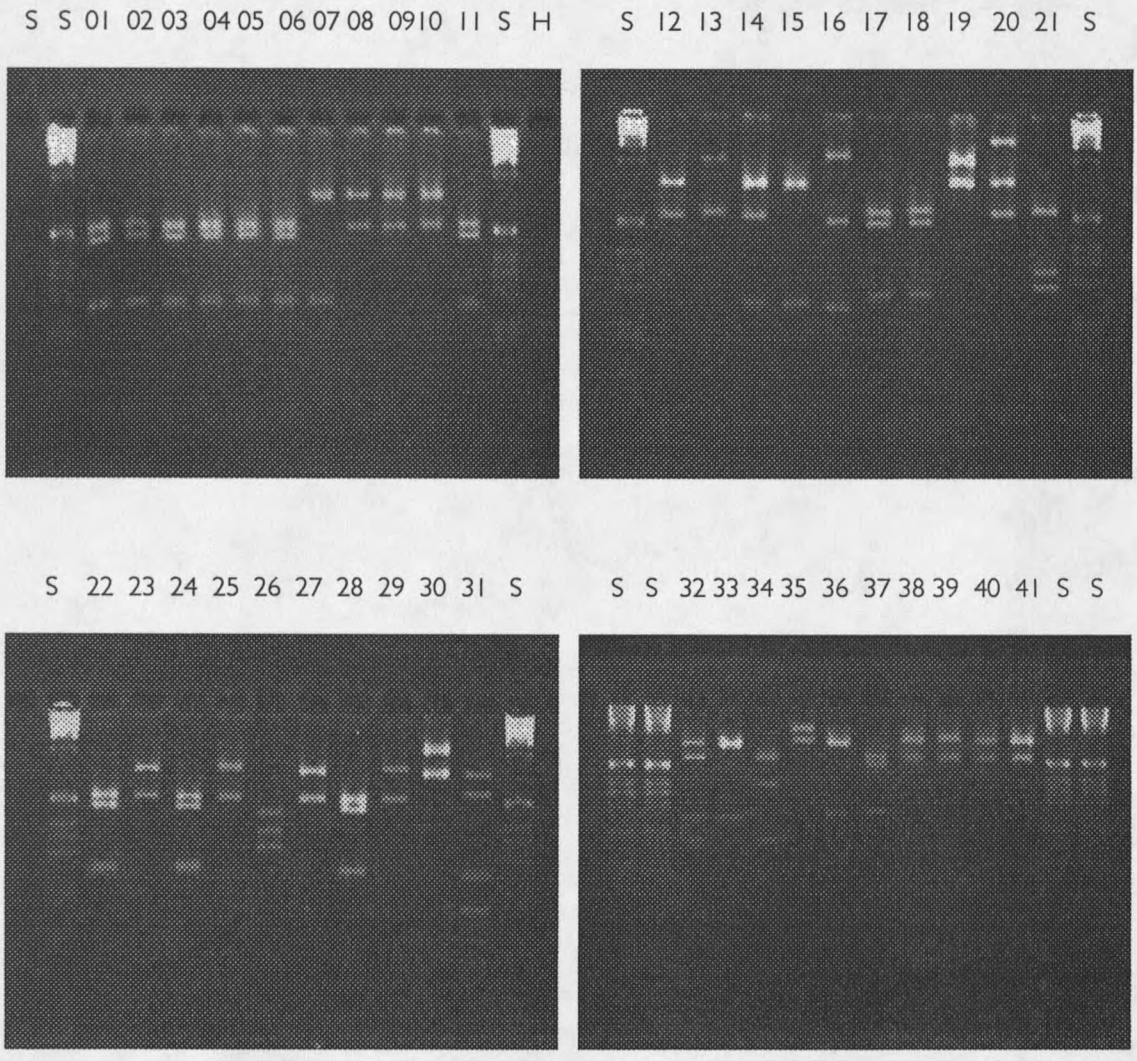
RFLP fingerprints produced by the digestion of LROR, LR7 amplified rDNA with restriction enzyme *Hha*I analyzed on a 4% agarose gel. Isolate numbers and ladder identification are shown. The 1kb DNA ladder is labeled "S" and the *Hin*dIII lambda ladder is labeled "H".



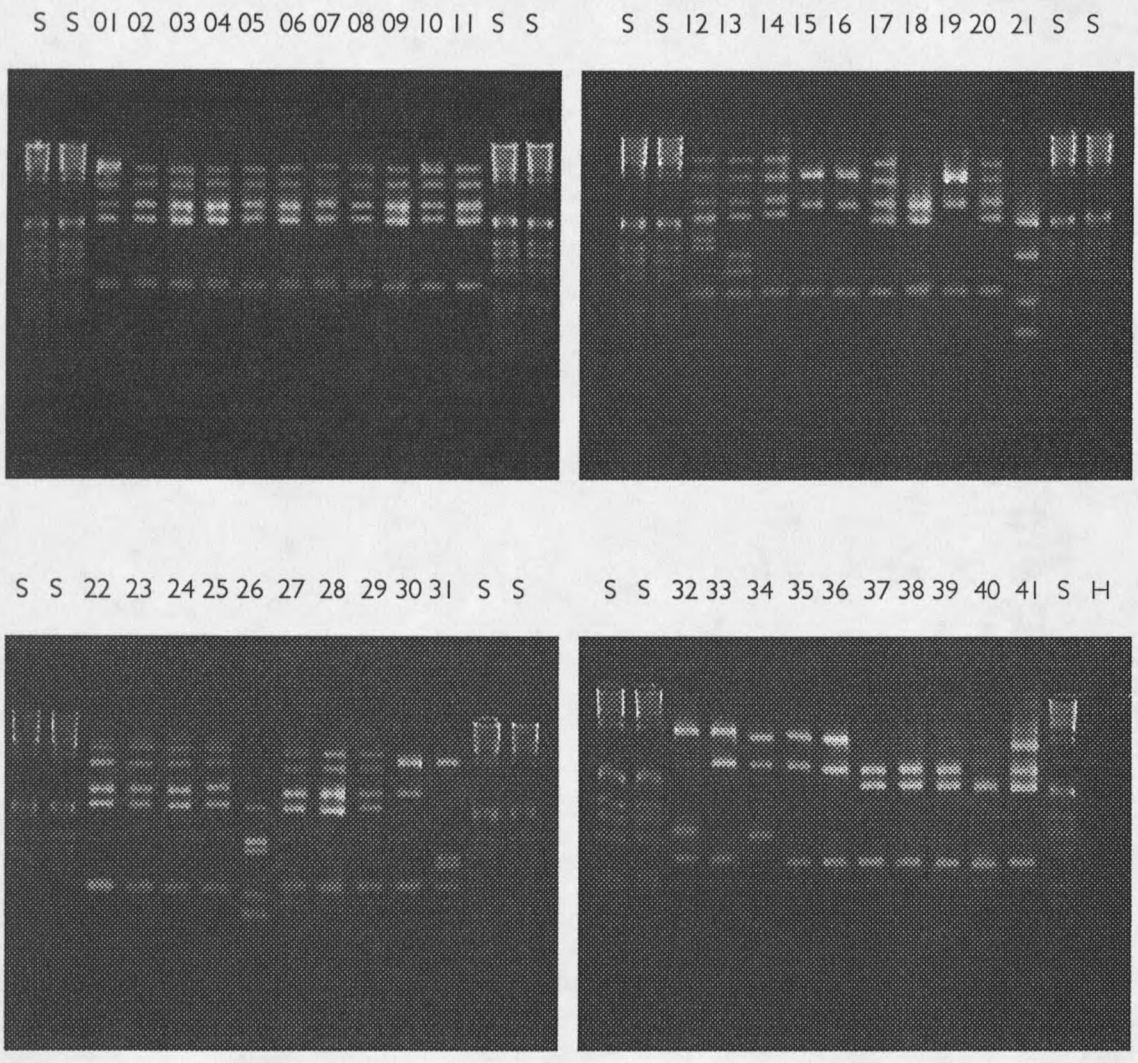
RFLP fingerprints produced by the digestion of LROR, LR7 amplified rDNA with restriction enzyme *Hpa*II analyzed on a 4% agarose gel. Isolate numbers and ladder identification are shown. The 1kb DNA ladder is labeled "S" and the *Hin*dIII lambda ladder is labeled "H".



RFLP fingerprints produced by the digestion of LROR, LR7 amplified rDNA with restriction enzyme *Msp*I analyzed on a 4% agarose gel. Isolate numbers and ladder identification are shown. The 1kb DNA ladder is labeled "S" and the *Hin*dIII lambda ladder is labeled "H".



RFLP fingerprints produced by the digestion of LROR, LR7 amplified rDNA with restriction enzyme *Sau*3AI analyzed on a 4% agarose gel. Isolate numbers and ladder identification are shown. The 1kb DNA ladder is labeled "S" and the *Hin*dIII lambda ladder is labeled "H".



RFLP fingerprints produced by the digestion of LROR, LR7 amplified rDNA with restriction enzyme *Taq*I analyzed on a 4% agarose gel. Isolate numbers and ladder identification are shown. The 1kb DNA ladder is labeled "S" and the *Hin*dIII lambda ladder is labeled "H".

APPENDIX B

COLLECTION OF DISTANCE MATRIX CALCULATIONS

01 v 41	nx	ny	nxy
Ava II	4	4	4
*Hha*I	4	6	4
*Hpa*II	3	5	3
*Msp*I	3	6	3
Sau 3AI	3	2	1
*Taq*I	5	5	5
0.20	22	28	20

01 v 40	nx	ny	nxy
*Ava*II	4	5	3
*Hha*I	4	5	2
*Hpa*II	3	3	2
*Msp*I	3	3	2
Sau 3AI	3	2	1
*Taq*I	5	2	2
0.43	22	20	12

01 v 39	nx	ny	nxy
*Ava*II	4	4	4
*Hha*I	4	4	4
*Hpa*II	3	4	2
*Msp*I	3	4	2
Sau 3AI	3	2	1
*Taq*I	5	3	3
0.26	22	21	16

02 v 41	nx	ny	nxy
*Ava*II	4	4	4
*Hha*I	4	6	4
*Hpa*II	3	5	3
*Msp*I	3	6	3
*Sau*3AI	3	2	1
*Taq*I	5	5	5
0.20	22	28	20

02 v 40	nx	ny	nxy
*Ava*II	4	5	3
*Hha*I	4	5	2
*Hpa*II	3	3	2
*Msp*I	3	3	2
*Sau*3AI	3	2	1
*Taq*I	5	2	2
0.43	22	20	12

02 v 39	nx	ny	nxy
*Ava*II	4	4	4
*Hha*I	4	4	4
*Hpa*II	3	4	2
*Msp*I	3	4	2
*Sau*3AI	3	2	1
*Taq*I	5	3	3
0.26	22	21	16

03 v 41	nx	ny	nxy
*Ava*II	4	4	4
*Hha*I	4	6	4
*Hpa*II	3	5	3
*Msp*I	3	6	3
*Sau*3AI	3	2	1
*Taq*I	5	5	5
0.20	22	28	20

03 v 40	nx	ny	nxy
*Ava*II	4	5	3
*Hha*I	4	5	2
*Hpa*II	3	3	2
*Msp*I	3	3	2
*Sau*3AI	3	2	1
*Taq*I	5	2	2
0.43	22	20	12

03 v 39	nx	ny	nxy
*Ava*II	4	4	4
*Hha*I	4	4	4
*Hpa*II	3	4	2
*Msp*I	3	4	2
*Sau*3AI	3	2	1
*Taq*I	5	3	3
0.26	22	21	16

04 v 41	nx	ny	nxy
*Ava*II	4	4	4
*Hha*I	4	6	4
*Hpa*II	3	5	3
*Msp*I	3	6	3
*Sau*3AI	3	2	1
*Taq*I	5	5	5
0.20	22	28	20

04 v 40	nx	ny	nxy
*Ava*II	4	5	3
*Hha*I	4	5	2
*Hpa*II	3	3	2
*Msp*I	3	3	2
*Sau*3AI	3	2	1
*Taq*I	5	2	2
0.43	22	20	12

04 v 39	nx	ny	nxy
*Ava*II	4	4	4
*Hha*I	4	4	4
*Hpa*II	3	4	2
*Msp*I	3	4	2
*Sau*3AI	3	2	1
*Taq*I	5	3	3
0.26	22	21	16

05 v 41	nx	ny	nxy
*Ava*II	4	4	4
*Hha*I	4	6	4
*Hpa*II	3	5	3
*Msp*I	3	6	3
*Sau*3AI	3	2	1
*Taq*I	5	5	5
0.20	22	28	20

05 v 40	nx	ny	nxy
*Ava*II	4	5	3
*Hha*I	4	5	2
*Hpa*II	3	3	2
*Msp*I	3	3	2
*Sau*3AI	3	2	1
*Taq*I	5	2	2
0.43	22	20	12

05 v 39	nx	ny	nxy
*Ava*II	4	4	4
*Hha*I	4	4	4
*Hpa*II	3	4	2
*Msp*I	3	4	2
*Sau*3AI	3	2	1
*Taq*I	5	3	3
0.26	22	21	16

01 v 38	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	3	3
0.26	22	21	16

01 v 37	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	3	3
0.05	22	20	20

01 v 36	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	1
TaqI	5	3	2
0.50	22	22	11

02 v38	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	3	3
0.26	22	21	16

02 v 37	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	3	3
0.05	22	20	20

02 v 36	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	1
TaqI	5	3	2
0.50	22	22	11

03 v 38	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	3	3
0.26	22	21	16

03 v 37	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	3	3
0.05	22	20	20

03 v 36	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	1
TaqI	5	3	2
0.50	22	22	11

04 v 38	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	3	3
0.26	22	21	16

04 v 37	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	3	3
0.05	22	20	20

04 v 36	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	1
TaqI	5	3	2
0.50	22	22	11

05 v 38	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	3	3
0.26	22	21	16

05 v 37	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	3	3
0.05	22	20	20

05 v 36	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	1
TaqI	5	3	2
0.50	22	22	11

01 v 35	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	0
TaqI	5	3	2
0.50	22	22	11

01 v 34	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	3	1
TaqI	5	3	1
0.50	22	22	11

01 v 33	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	1
TaqI	5	3	2
0.50	22	22	11

02 v 35	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	0
TaqI	5	3	2
0.50	22	22	11

02 v 34	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	3	1
TaqI	5	3	1
0.50	22	22	11

02 v 33	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	1
TaqI	5	3	2
0.50	22	22	11

03 v 35	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	0
TaqI	5	3	2
0.50	22	22	11

03 v 34	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	3	1
TaqI	5	3	1
0.50	22	22	11

03 v 33	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	1
TaqI	5	3	2
0.50	22	22	11

04 v 35	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	0
TaqI	5	3	2
0.50	22	22	11

04 v 34	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	3	1
TaqI	5	3	1
0.50	22	22	11

04 v 33	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	1
TaqI	5	3	2
0.50	22	22	11

05 v 35	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	0
TaqI	5	3	2
0.50	22	22	11

05 v 34	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	3	1
TaqI	5	3	1
0.50	22	22	11

05 v 33	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	1
TaqI	5	3	2
0.50	22	22	11

01 v 32	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	4	2
TaqI	5	3	2
0.43	22	24	13

01 v 31	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	4	2
TaqI	5	4	2
0.49	22	25	12

01 v 30	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	7	3
MspI	3	7	3
Sau3AI	3	2	0
TaqI	5	3	2
0.35	22	27	16

02 v 32	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	4	2
TaqI	5	3	2
0.43	22	24	13

02 v 31	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	4	2
TaqI	5	4	2
0.49	22	25	12

02 v 30	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	7	3
MspI	3	7	3
Sau3AI	3	2	0
TaqI	5	3	2
0.35	22	27	16

03 v 32	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	4	2
TaqI	5	3	2
0.43	22	24	13

03 v 31	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	4	2
TaqI	5	4	2
0.49	22	25	12

03 v 30	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	7	3
MspI	3	7	3
Sau3AI	3	2	0
TaqI	5	3	2
0.35	22	27	16

04 v 32	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	4	2
TaqI	5	3	2
0.43	22	24	13

04 v 31	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	4	2
TaqI	5	4	2
0.49	22	25	12

04 v 30	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	7	3
MspI	3	7	3
Sau3AI	3	2	0
TaqI	5	3	2
0.35	22	27	16

05 v 32	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	4	2
TaqI	5	3	2
0.43	22	24	13

05 v 31	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	4	2
TaqI	5	4	2
0.49	22	25	12

05 v 30	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	7	3
MspI	3	7	3
Sau3AI	3	2	0
TaqI	5	3	2
0.35	22	27	16

01 v 29	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.24	22	23	17

01 v 28	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

01 v 27	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.20	22	23	18

02 v 29	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.24	22	23	17

02 v 28	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

02 v 27	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.20	22	23	18

03 v 29	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.24	22	23	17

03 v 28	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

03 v 27	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.20	22	23	18

04 v 29	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.24	22	23	17

04 v 28	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

04 v 27	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.20	22	23	18

05 v 29	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.24	22	23	17

05 v 28	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

05 v 27	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.20	22	23	18

01 v 26	nx	ny	nxy
AvaII	4	2	2
HhaI	4	4	3
HpaII	3	2	0
MspI	3	2	0
Sau3AI	3	3	1
TaqI	5	5	1
0.65	22	18	7

01 v 25	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	2
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.29	22	23	16

01 v 24	nx	ny	nxy
AvaII	4	4	4
HhaI	4	5	3
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.07	22	23	21

02 v 26	nx	ny	nxy
AvaII	4	2	2
HhaI	4	4	3
HpaII	3	2	0
MspI	3	2	0
Sau3AI	3	3	1
TaqI	5	5	1
0.65	22	18	7

02 v 25	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	2
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.29	22	23	16

02 v 24	nx	ny	nxy
AvaII	4	4	4
HhaI	4	5	3
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.07	22	23	21

03 v 26	nx	ny	nxy
AvaII	4	2	2
HhaI	4	4	3
HpaII	3	2	0
MspI	3	2	0
Sau3AI	3	3	1
TaqI	5	5	1
0.65	22	18	7

03 v 25	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	2
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.29	22	23	16

03 v 24	nx	ny	nxy
AvaII	4	4	4
HhaI	4	5	3
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.07	22	23	21

04 v 26	nx	ny	nxy
AvaII	4	2	2
HhaI	4	4	3
HpaII	3	2	0
MspI	3	2	0
Sau3AI	3	3	1
TaqI	5	5	1
0.65	22	18	7

04 v 25	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	2
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.29	22	23	16

04 v 24	nx	ny	nxy
AvaII	4	4	4
HhaI	4	5	3
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.07	22	23	21

05 v 26	nx	ny	nxy
AvaII	4	2	2
HhaI	4	4	3
HpaII	3	2	0
MspI	3	2	0
Sau3AI	3	3	1
TaqI	5	5	1
0.65	22	18	7

05 v 25	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	2
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.29	22	23	16

05 v 24	nx	ny	nxy
AvaII	4	4	4
HhaI	4	5	3
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.07	22	23	21

01 v 23	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.24	22	23	17

01 v 22	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.05	22	22	21

01 v 21	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	2
HpaII	3	5	1
MspI	3	5	2
Sau3AI	3	3	1
TaqI	5	4	1
0.62	22	25	9

02 v 23	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.24	22	23	17

02 v 22	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.05	22	22	21

02 v 21	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	2
HpaII	3	5	1
MspI	3	5	2
Sau3AI	3	3	1
TaqI	5	4	1
0.62	22	25	9

03 v 23	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.24	22	23	17

03 v 22	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.05	22	22	21

03 v 21	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	2
HpaII	3	5	1
MspI	3	5	2
Sau3AI	3	3	1
TaqI	5	4	1
0.62	22	25	9

04 v 23	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.24	22	23	17

04 v 22	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.05	22	22	21

04 v 21	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	2
HpaII	3	5	1
MspI	3	5	2
Sau3AI	3	3	1
TaqI	5	4	1
0.62	22	25	9

05 v 23	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.24	22	23	17

05 v 22	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.05	22	22	21

05 v 21	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	2
HpaII	3	5	1
MspI	3	5	2
Sau3AI	3	3	1
TaqI	5	4	1
0.62	22	25	9

01 v 20	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	3	1
TaqI	5	5	5
0.22	22	24	18

01 v 19	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	3	2
MspI	3	3	2
Sau3AI	3	2	0
TaqI	5	3	2
0.38	22	20	13

01 v 18	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	3	3
0.05	22	20	20

02 v 20	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	3	1
TaqI	5	5	5
0.22	22	24	18

02 v 19	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	3	2
MspI	3	3	2
Sau3AI	3	2	0
TaqI	5	3	2
0.38	22	20	13

02 v 18	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	3	3
0.05	22	20	20

03 v 20	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	3	1
TaqI	5	5	5
0.22	22	24	18

03 v 19	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	3	2
MspI	3	3	2
Sau3AI	3	2	0
TaqI	5	3	2
0.38	22	20	13

03 v 18	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	3	3
0.05	22	20	20

04 v 20	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	3	1
TaqI	5	5	5
0.22	22	24	18

04 v 19	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	3	2
MspI	3	3	2
Sau3AI	3	2	0
TaqI	5	3	2
0.38	22	20	13

04 v 18	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	3	3
0.05	22	20	20

05 v 20	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	3	1
TaqI	5	5	5
0.22	22	24	18

05 v 19	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	3	2
MspI	3	3	2
Sau3AI	3	2	0
TaqI	5	3	2
0.38	22	20	13

05 v 18	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	3	3
0.05	22	20	20

01 v 17	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

01 v 16	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	5	1
MspI	3	5	1
Sau3AI	3	3	2
TaqI	5	3	2
0.43	22	24	13

01 v 15	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	1
TaqI	5	3	2
0.50	22	22	11

02 v 17	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

02 v 16	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	5	1
MspI	3	5	1
Sau3AI	3	3	2
TaqI	5	3	2
0.43	22	24	13

02 v 15	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	1
TaqI	5	3	2
0.50	22	22	11

03 v 17	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

03 v 16	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	5	1
MspI	3	5	1
Sau3AI	3	3	2
TaqI	5	3	2
0.43	22	24	13

03 v 15	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	1
TaqI	5	3	2
0.50	22	22	11

04 v 17	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

04 v 16	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	5	1
MspI	3	5	1
Sau3AI	3	3	2
TaqI	5	3	2
0.43	22	24	13

04 v 15	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	1
TaqI	5	3	2
0.50	22	22	11

05 v 17	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

05 v 16	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	5	1
MspI	3	5	1
Sau3AI	3	3	2
TaqI	5	3	2
0.43	22	24	13

05 v 15	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	1
TaqI	5	3	2
0.50	22	22	11

01 v 14	nx	ny	nxy
AvaII	4	4	4
HhaI	4	5	3
HpaII	3	5	2
MspI	3	5	2
Sau3AI	3	3	2
TaqI	5	5	5
0.27	22	27	18

01 v 13	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	3
Sau3AI	3	2	1
TaqI	5	7	5
0.28	22	25	17

01 v 12	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	7	5
0.28	22	25	17

02 v 14	nx	ny	nxy
AvaII	4	4	4
HhaI	4	5	3
HpaII	3	5	2
MspI	3	5	2
Sau3AI	3	3	2
TaqI	5	5	5
0.27	22	27	18

02 v 13	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	3
Sau3AI	3	2	1
TaqI	5	7	5
0.28	22	25	17

02 v 12	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	7	5
0.28	22	25	17

03 v 14	nx	ny	nxy
AvaII	4	4	4
HhaI	4	5	3
HpaII	3	5	2
MspI	3	5	2
Sau3AI	3	3	2
TaqI	5	5	5
0.27	22	27	18

03 v 13	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	3
Sau3AI	3	2	1
TaqI	5	7	5
0.28	22	25	17

03 v 12	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	7	5
0.28	22	25	17

04 v 14	nx	ny	nxy
AvaII	4	4	4
HhaI	4	5	3
HpaII	3	5	2
MspI	3	5	2
Sau3AI	3	3	2
TaqI	5	5	5
0.27	22	27	18

04 v 13	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	3
Sau3AI	3	2	1
TaqI	5	7	5
0.28	22	25	17

04 v 12	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	7	5
0.28	22	25	17

05 v 14	nx	ny	nxy
AvaII	4	4	4
HhaI	4	5	3
HpaII	3	5	2
MspI	3	5	2
Sau3AI	3	3	2
TaqI	5	5	5
0.27	22	27	18

05 v 13	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	3
Sau3AI	3	2	1
TaqI	5	7	5
0.28	22	25	17

05 v 12	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	7	5
0.28	22	25	17

01 v 11	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

01 v 10	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.20	22	23	18

01 v 09	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	2	1
TaqI	5	5	5
0.07	22	21	20

02 v 11	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

02 v 10	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.20	22	23	18

02 v 09	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	2	1
TaqI	5	5	5
0.07	22	21	20

03 v 11	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

03 v 10	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.20	22	23	18

03 v 09	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	2	1
TaqI	5	5	5
0.07	22	21	20

04 v 11	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

04 v 10	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.20	22	23	18

04 v 09	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	2	1
TaqI	5	5	5
0.07	22	21	20

05 v 11	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

05 v 10	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.20	22	23	18

05 v 09	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	2	1
TaqI	5	5	5
0.07	22	21	20

01 v 08	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.20	22	23	18

01 v 07	nx	ny	nxy
AvaII	4	4	2
HhaI	4	3	0
HpaII	3	3	2
MspI	3	3	2
Sau3AI	3	2	1
TaqI	5	5	5
0.43	22	20	12

01 v 06	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

02 v 08	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.20	22	23	18

02 v 07	nx	ny	nxy
AvaII	4	4	2
HhaI	4	3	0
HpaII	3	3	2
MspI	3	3	2
Sau3AI	3	2	1
TaqI	5	5	5
0.43	22	20	12

02 v 06	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

03 v 08	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.20	22	23	18

03 v 07	nx	ny	nxy
AvaII	4	4	2
HhaI	4	3	0
HpaII	3	3	2
MspI	3	3	2
Sau3AI	3	2	1
TaqI	5	5	5
0.43	22	20	12

03 v 06	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

04 v 08	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.20	22	23	18

04 v 07	nx	ny	nxy
AvaII	4	4	2
HhaI	4	3	0
HpaII	3	3	2
MspI	3	3	2
Sau3AI	3	2	1
TaqI	5	5	5
0.43	22	20	12

04 v 06	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

05 v 08	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.20	22	23	18

05 v 07	nx	ny	nxy
AvaII	4	4	2
HhaI	4	3	0
HpaII	3	3	2
MspI	3	3	2
Sau3AI	3	2	1
TaqI	5	5	5
0.43	22	20	12

05 v 06	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

01 v 05	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

01 v 04	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

01 v 03	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

02 v 05	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

02 v 04	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

02 v 03	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

03 v 05	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

03 v 04	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

03 v 03	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

04 v 05	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

04 v 04	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

05 v 05	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

01 v 02	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

01 v 01	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

02 v 02	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

06 v 41	nx	ny	nxy
AvaII	4	4	4
HhaI	4	6	4
HpaII	3	5	3
MspI	3	6	3
Sau3AI	3	2	1
TaqI	5	5	5
0.20	22	28	20

06 v 40	nx	ny	nxy
AvaII	4	5	3
HhaI	4	5	2
HpaII	3	3	2
MspI	3	3	2
Sau3AI	3	2	1
TaqI	5	2	2
0.43	22	20	12

06 v 39	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	3	3
0.26	22	21	16

07 v 41	nx	ny	nxy
AvaII	4	4	2
HhaI	3	6	0
HpaII	3	5	2
MspI	3	6	2
Sau3AI	2	2	1
TaqI	5	5	5
0.50	20	28	12

07 v 40	nx	ny	nxy
AvaII	4	5	2
HhaI	3	5	1
HpaII	3	3	2
MspI	3	3	2
Sau3AI	2	2	1
TaqI	5	2	2
0.50	20	20	10

07 v 39	nx	ny	nxy
AvaII	4	4	2
HhaI	3	4	0
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	2	1
TaqI	5	3	3
0.61	20	21	8

08 v 41	nx	ny	nxy
AvaII	4	4	4
HhaI	4	6	4
HpaII	4	5	3
MspI	4	6	3
Sau3AI	2	2	2
TaqI	5	5	5
0.18	23	28	21

08 v 40	nx	ny	nxy
AvaII	4	5	3
HhaI	4	5	2
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	2	2
TaqI	5	2	2
0.40	23	20	13

08 v 39	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	2
TaqI	5	3	3
0.05	23	21	21

09 v 41	nx	ny	nxy
AvaII	4	4	4
HhaI	4	6	4
HpaII	3	5	3
MspI	3	6	3
Sau3AI	2	2	2
TaqI	5	5	5
0.14	21	28	21

09 v 40	nx	ny	nxy
AvaII	4	5	3
HhaI	4	5	2
HpaII	3	3	2
MspI	3	3	2
Sau3AI	2	2	2
TaqI	5	2	2
0.37	21	20	13

09 v 39	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	2	2	2
TaqI	5	3	3
0.19	21	21	17

10 v 41	nx	ny	nxy
AvaII	4	4	4
HhaI	4	6	4
HpaII	4	5	3
MspI	4	6	3
Sau3AI	2	2	2
TaqI	5	5	5
0.18	23	28	21

10 v 40	nx	ny	nxy
AvaII	4	5	3
HhaI	4	5	2
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	2	2
TaqI	5	2	2
0.40	23	20	13

10 v 39	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	2
TaqI	5	3	3
0.05	23	21	21

06 v 38	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	3	3
0.26	22	21	16

06 v 37	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	3	3
0.05	22	20	20

06 v 36	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	1
TaqI	5	3	2
0.50	22	22	11

07 v 38	nx	ny	nxy
AvaII	4	4	2
HhaI	3	4	0
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	2	1
TaqI	5	3	3
0.61	20	21	8

07 v 37	nx	ny	nxy
AvaII	4	4	2
HhaI	3	4	0
HpaII	3	3	2
MspI	3	3	2
Sau3AI	2	3	1
TaqI	5	3	3
0.50	20	20	10

07 v 36	nx	ny	nxy
AvaII	4	5	2
HhaI	3	4	1
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	2	2
TaqI	5	3	2
0.57	20	22	9

08 v 38	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	2
TaqI	5	3	3
0.05	23	21	21

08 v 37	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	3	1
TaqI	5	3	3
0.26	23	20	16

08 v 36	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	2	1
TaqI	5	3	2
0.42	23	22	13

09 v 38	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	2	2	2
TaqI	5	3	3
0.19	21	21	17

09 v 37	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	2	3	1
TaqI	5	3	3
0.12	21	20	18

09 v 36	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	2	1
TaqI	5	3	2
0.49	21	22	11

10 v 38	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	2
TaqI	5	3	3
0.05	23	21	21

10 v 37	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	3	1
TaqI	5	3	3
0.26	23	20	16

10 v 36	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	2	1
TaqI	5	3	2
0.42	23	22	13

06 v 35	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	0
TaqI	5	3	2
0.50	22	22	11

06 v 34	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	3	1
TaqI	5	3	1
0.50	22	22	11

06 v 33	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	1
TaqI	5	3	2
0.50	22	22	11

07 v 35	nx	ny	nxy
AvaII	4	5	2
HhaI	3	4	0
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	2	1
TaqI	5	3	2
0.67	20	22	7

07 v 34	nx	ny	nxy
AvaII	4	4	1
HhaI	3	4	1
HpaII	3	4	2
MspI	3	4	2
Sau3AI	2	3	0
TaqI	5	3	1
0.67	20	22	7

07 v 33	nx	ny	nxy
AvaII	4	5	2
HhaI	3	4	1
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	2	2
TaqI	5	3	2
0.57	20	22	9

08 v 35	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	2	1
TaqI	5	3	2
0.38	23	22	14

08 v 34	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	3	1
TaqI	5	3	1
0.47	23	22	12

08 v 33	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	2	1
TaqI	5	3	2
0.42	23	22	13

09 v 35	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	2	1
TaqI	5	3	2
0.44	21	22	12

09 v 34	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	2	3	1
TaqI	5	3	1
0.49	21	22	11

09 v 33	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	2	1
TaqI	5	3	2
0.49	21	22	11

10 v 35	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	2	1
TaqI	5	3	2
0.38	23	22	14

10 v 34	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	3	1
TaqI	5	3	1
0.47	23	22	12

10 v 33	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	2	1
TaqI	5	3	2
0.42	23	22	13

06 v 32	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	4	2
TaqI	5	3	2
0.43	22	24	13

06 v 31	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	4	2
TaqI	5	4	2
0.49	22	25	12

06 v 30	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	7	3
MspI	3	7	3
Sau3AI	3	2	0
TaqI	5	3	2
0.35	22	27	16

07 v 32	nx	ny	nxy
AvaII	4	5	2
HhaI	3	4	0
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	4	2
TaqI	5	3	2
0.64	20	24	8

07 v 31	nx	ny	nxy
AvaII	4	5	2
HhaI	3	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	4	2
TaqI	5	4	2
0.56	20	25	10

07 v 30	nx	ny	nxy
AvaII	4	4	2
HhaI	3	4	0
HpaII	3	7	2
MspI	3	7	2
Sau3AI	2	2	1
TaqI	5	3	2
0.62	20	27	9

08 v 32	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	4	2
TaqI	5	3	2
0.36	23	24	15

08 v 31	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	4	2
TaqI	5	4	2
0.42	23	25	14

08 v 30	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	7	3
MspI	4	7	3
Sau3AI	2	2	1
TaqI	5	3	2
0.32	23	27	17

09 v 32	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	4	2
TaqI	5	3	2
0.42	21	24	13

09 v 31	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	4	2
TaqI	5	4	2
0.48	21	25	12

09 v 30	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	7	3
MspI	3	7	3
Sau3AI	2	2	1
TaqI	5	3	2
0.29	21	27	17

10 v 32	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	4	2
TaqI	5	3	2
0.36	23	24	15

10 v 31	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	4	2
TaqI	5	4	2
0.42	23	25	14

10 v 30	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	7	3
MspI	4	7	3
Sau3AI	2	2	1
TaqI	5	3	2
0.32	23	27	17

06 v 29	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.24	22	23	17

06 v 28	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

06 v 27	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.20	22	23	18

07 v 29	nx	ny	nxy
AvaII	4	4	2
HhaI	3	4	0
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	2	1
TaqI	5	5	5
0.53	20	23	10

07 v 28	nx	ny	nxy
AvaII	4	4	2
HhaI	3	4	0
HpaII	3	3	2
MspI	3	3	2
Sau3AI	2	3	1
TaqI	5	5	5
0.43	20	22	12

07 v 27	nx	ny	nxy
AvaII	4	4	2
HhaI	3	4	0
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	2	1
TaqI	5	5	5
0.53	20	23	10

08 v 29	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	4	3
MspI	4	4	3
Sau3AI	2	2	2
TaqI	5	5	5
0.13	23	23	20

08 v 28	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	3	1
TaqI	5	5	5
0.20	23	22	18

08 v 27	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	2
TaqI	5	5	5
0.00	23	23	23

09 v 29	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	2	2	2
TaqI	5	5	5
0.18	21	23	18

09 v 28	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	2	3	1
TaqI	5	5	5
0.07	21	22	20

09 v 27	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	2	2	2
TaqI	5	5	5
0.14	21	23	19

10 v 29	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	4	3
MspI	4	4	3
Sau3AI	2	2	2
TaqI	5	5	5
0.13	23	23	20

10 v 28	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	3	1
TaqI	5	5	5
0.20	23	22	18

10 v 27	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	2
TaqI	5	5	5
0.00	23	23	23

06 v 26	nx	ny	nxy
AvaII	4	2	2
HhaI	4	4	3
HpaII	3	2	0
MspI	3	2	0
Sau3AI	3	3	1
TaqI	5	5	1
0.65	22	18	7

06 v 25	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	2
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.29	22	23	16

06 v 24	nx	ny	nxy
AvaII	4	4	4
HhaI	4	5	3
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.07	22	23	21

07 v 26	nx	ny	nxy
AvaII	4	2	1
HhaI	3	4	0
HpaII	3	2	0
MspI	3	2	2
Sau3AI	2	3	0
TaqI	5	5	1
0.79	20	18	4

07 v 25	nx	ny	nxy
AvaII	4	4	2
HhaI	3	4	1
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	2	1
TaqI	5	5	5
0.49	20	23	11

07 v 24	nx	ny	nxy
AvaII	4	4	2
HhaI	3	5	1
HpaII	3	3	2
MspI	3	3	2
Sau3AI	2	3	1
TaqI	5	5	5
0.40	20	23	13

08 v 26	nx	ny	nxy
AvaII	4	2	2
HhaI	4	4	3
HpaII	4	2	0
MspI	4	2	0
Sau3AI	2	3	0
TaqI	5	5	1
0.71	23	18	6

08 v 25	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	2
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	2
TaqI	5	5	5
0.09	23	23	21

08 v 24	nx	ny	nxy
AvaII	4	4	4
HhaI	4	5	3
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	3	1
TaqI	5	5	5
0.26	23	23	17

09 v 26	nx	ny	nxy
AvaII	4	2	2
HhaI	4	4	3
HpaII	3	2	0
MspI	3	2	0
Sau3AI	2	3	0
TaqI	5	5	1
0.69	21	18	6

09 v 25	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	2
HpaII	3	4	2
MspI	3	4	2
Sau3AI	2	2	2
TaqI	5	5	5
0.23	21	23	17

09 v 24	nx	ny	nxy
AvaII	4	4	4
HhaI	4	5	3
HpaII	3	3	3
MspI	3	3	3
Sau3AI	2	3	1
TaqI	5	5	5
0.14	21	23	19

10 v 26	nx	ny	nxy
AvaII	4	2	2
HhaI	4	4	3
HpaII	4	2	0
MspI	4	2	0
Sau3AI	2	3	0
TaqI	5	5	1
0.71	23	18	6

10 v 25	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	2
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	2
TaqI	5	5	5
0.09	23	23	21

10 v 24	nx	ny	nxy
AvaII	4	4	4
HhaI	4	5	3
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	3	1
TaqI	5	5	5
0.26	23	23	17

06 v 23	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.24	22	23	17

06 v 22	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.05	22	22	21

06 v 21	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	2
HpaII	3	5	1
MspI	3	5	2
Sau3AI	3	3	1
TaqI	5	4	1
0.62	22	25	9

07 v 23	nx	ny	nxy
AvaII	4	4	2
HhaI	3	4	1
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	2	1
TaqI	5	5	5
0.49	20	23	11

07 v 22	nx	ny	nxy
AvaII	4	4	2
HhaI	3	4	1
HpaII	3	3	2
MspI	3	3	2
Sau3AI	2	3	1
TaqI	5	5	5
0.38	20	22	13

07 v 21	nx	ny	nxy
AvaII	4	4	1
HhaI	3	4	2
HpaII	3	5	1
MspI	3	5	2
Sau3AI	2	3	1
TaqI	5	4	1
0.64	20	25	8

08 v 23	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	4	3
MspI	4	4	3
Sau3AI	2	2	2
TaqI	5	5	5
0.13	23	23	20

08 v 22	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	3	1
TaqI	5	5	5
0.24	23	22	17

08 v 21	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	2
HpaII	4	5	2
MspI	4	5	2
Sau3AI	2	3	1
TaqI	5	4	1
0.58	23	25	10

09 v 23	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	2	2	2
TaqI	5	5	5
0.18	21	23	18

09 v 22	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	3	3
MspI	3	3	3
Sau3AI	2	3	1
TaqI	5	5	5
0.12	21	22	19

09 v 21	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	2
HpaII	3	5	1
MspI	3	5	2
Sau3AI	2	3	1
TaqI	5	4	1
0.61	21	25	9

10 v 23	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	4	3
MspI	4	4	3
Sau3AI	2	2	2
TaqI	5	5	5
0.13	23	23	20

10 v 22	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	3	1
TaqI	5	5	5
0.24	23	22	17

10 v 21	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	2
HpaII	4	5	2
MspI	4	5	2
Sau3AI	2	3	1
TaqI	5	4	1
0.58	23	25	10

06 v 20	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	3	1
TaqI	5	5	5
0.22	22	24	18

06 v 19	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	3	2
MspI	3	3	2
Sau3AI	3	2	0
TaqI	5	3	2
0.38	22	20	13

06 v 18	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	3	3
0.05	22	20	20

07 v 20	nx	ny	nxy
AvaII	4	4	2
HhaI	3	4	0
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	3	1
TaqI	5	5	5
0.55	20	24	10

07 v 19	nx	ny	nxy
AvaII	4	5	2
HhaI	3	4	0
HpaII	3	3	2
MspI	3	3	2
Sau3AI	2	2	1
TaqI	5	3	2
0.55	20	20	9

07 v 18	nx	ny	nxy
AvaII	4	4	2
HhaI	3	4	0
HpaII	3	3	2
MspI	3	3	2
Sau3AI	2	3	1
TaqI	5	3	3
0.50	20	20	10

08 v 20	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	3	2
TaqI	5	5	5
0.02	23	24	23

08 v 19	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	4	3	1
MspI	4	3	1
Sau3AI	2	2	1
TaqI	5	3	2
0.44	23	20	12

08 v 18	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	3	1
TaqI	5	3	3
0.26	23	20	16

09 v 20	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	2	3	2
TaqI	5	5	5
0.16	21	24	19

09 v 19	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	3	2
MspI	3	3	2
Sau3AI	2	2	1
TaqI	5	3	2
0.32	21	20	14

09 v 18	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	2	3	1
TaqI	5	3	3
0.12	21	20	18

10 v 20	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	3	2
TaqI	5	5	5
0.02	23	24	23

10 v 19	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	4	3	1
MspI	4	3	1
Sau3AI	2	2	1
TaqI	5	3	2
0.44	23	20	12

10 v 18	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	3	1
TaqI	5	3	3
0.26	23	20	16

06 v 17	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

06 v 16	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	5	1
MspI	3	5	1
Sau3AI	3	3	2
TaqI	5	3	2
0.43	22	24	13

06 v 15	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	1
TaqI	5	3	2
0.50	22	22	11

07 v 17	nx	ny	nxy
AvaII	4	4	2
HhaI	3	4	0
HpaII	3	3	2
MspI	3	3	2
Sau3AI	2	3	1
TaqI	5	5	5
0.43	20	22	12

07 v 16	nx	ny	nxy
AvaII	4	4	2
HhaI	3	4	0
HpaII	3	5	1
MspI	3	5	1
Sau3AI	2	3	1
TaqI	5	3	2
0.68	20	24	7

07 v 15	nx	ny	nxy
AvaII	4	5	2
HhaI	3	4	1
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	2	2
TaqI	5	3	2
0.57	20	22	9

08 v 17	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	3	1
TaqI	5	5	5
0.20	23	22	18

08 v 16	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	5	1
MspI	4	5	2
Sau3AI	2	3	1
TaqI	5	3	2
0.45	23	24	13

08 v 15	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	2	1
TaqI	5	3	2
0.42	23	22	13

09 v 17	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	2	3	1
TaqI	5	5	5
0.07	21	22	20

09 v 16	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	5	1
MspI	3	5	1
Sau3AI	2	3	1
TaqI	5	3	2
0.47	21	24	12

09 v 15	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	2	1
TaqI	5	3	2
0.49	21	22	11

10 v 17	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	3	1
TaqI	5	5	5
0.20	23	22	18

10 v 16	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	5	1
MspI	4	5	2
Sau3AI	2	3	1
TaqI	5	3	2
0.45	23	24	13

10 v 15	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	2	1
TaqI	5	3	2
0.42	23	22	13

06 v 14	nx	ny	nxy
AvaII	4	4	4
HhaI	4	5	3
HpaII	3	5	2
MspI	3	5	2
Sau3AI	3	3	2
TaqI	5	5	5
0.27	22	27	18

06 v 13	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	3
Sau3AI	3	2	1
TaqI	5	7	5
0.28	22	25	17

06 v 12	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	7	5
0.28	22	25	17

07 v 14	nx	ny	nxy
AvaII	4	4	2
HhaI	3	5	1
HpaII	3	5	1
MspI	3	5	1
Sau3AI	2	3	2
TaqI	5	5	5
0.49	20	27	12

07 v 13	nx	ny	nxy
AvaII	4	4	1
HhaI	3	4	1
HpaII	3	4	2
MspI	3	4	2
Sau3AI	2	2	0
TaqI	5	7	5
0.51	20	25	11

07 v 12	nx	ny	nxy
AvaII	4	4	2
HhaI	3	4	1
HpaII	3	4	2
MspI	3	4	2
Sau3AI	2	2	1
TaqI	5	7	5
0.42	20	25	13

08 v 14	nx	ny	nxy
AvaII	4	4	4
HhaI	4	5	3
HpaII	4	5	2
MspI	4	5	3
Sau3AI	2	3	2
TaqI	5	5	5
0.24	23	27	19

08 v 13	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	3
Sau3AI	2	2	1
TaqI	5	7	5
0.29	23	25	17

08 v 12	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	4	3
MspI	4	4	3
Sau3AI	2	2	2
TaqI	5	7	5
0.17	23	25	20

09 v 14	nx	ny	nxy
AvaII	4	4	4
HhaI	4	5	3
HpaII	3	5	2
MspI	3	5	2
Sau3AI	2	3	2
TaqI	5	5	5
0.25	21	27	18

09 v 13	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	3
Sau3AI	2	2	1
TaqI	5	7	5
0.26	21	25	17

09 v 12	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	2	2	2
TaqI	5	7	5
0.22	21	25	18

10 v 14	nx	ny	nxy
AvaII	4	4	4
HhaI	4	5	3
HpaII	4	5	2
MspI	4	5	3
Sau3AI	2	3	2
TaqI	5	5	5
0.24	23	27	19

10 v 13	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	3
Sau3AI	2	2	1
TaqI	5	7	5
0.29	23	25	17

10 v 12	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	4	3
MspI	4	4	3
Sau3AI	2	2	2
TaqI	5	7	5
0.17	23	25	20

06 v 14	nx	ny	nxy
AvaII	4	4	4
HhaI	4	5	3
HpaII	3	5	2
MspI	3	5	2
Sau3AI	3	3	2
TaqI	5	5	5
0.27	22	27	18

06 v 13	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	3
Sau3AI	3	2	1
TaqI	5	7	5
0.28	22	25	17

06 v 12	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	7	5
0.28	22	25	17

07 v 14	nx	ny	nxy
AvaII	4	4	2
HhaI	3	5	1
HpaII	3	5	1
MspI	3	5	1
Sau3AI	2	3	2
TaqI	5	5	5
0.49	20	27	12

07 v 13	nx	ny	nxy
AvaII	4	4	1
HhaI	3	4	1
HpaII	3	4	2
MspI	3	4	2
Sau3AI	2	2	0
TaqI	5	7	5
0.51	20	25	11

07 v 12	nx	ny	nxy
AvaII	4	4	2
HhaI	3	4	1
HpaII	3	4	2
MspI	3	4	2
Sau3AI	2	2	1
TaqI	5	7	5
0.42	20	25	13

08 v 14	nx	ny	nxy
AvaII	4	4	4
HhaI	4	5	3
HpaII	4	5	2
MspI	4	5	3
Sau3AI	2	3	2
TaqI	5	5	5
0.24	23	27	19

08 v 13	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	3
Sau3AI	2	2	1
TaqI	5	7	5
0.29	23	25	17

08 v 12	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	4	3
MspI	4	4	3
Sau3AI	2	2	2
TaqI	5	7	5
0.17	23	25	20

09 v 14	nx	ny	nxy
AvaII	4	4	4
HhaI	4	5	3
HpaII	3	5	2
MspI	3	5	2
Sau3AI	2	3	2
TaqI	5	5	5
0.25	21	27	18

09 v 13	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	3
Sau3AI	2	2	1
TaqI	5	7	5
0.26	21	25	17

09 v 12	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	2	2	2
TaqI	5	7	5
0.22	21	25	18

10 v 14	nx	ny	nxy
AvaII	4	4	4
HhaI	4	5	3
HpaII	4	5	2
MspI	4	5	3
Sau3AI	2	3	2
TaqI	5	5	5
0.24	23	27	19

10 v 13	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	3
Sau3AI	2	2	1
TaqI	5	7	5
0.29	23	25	17

10 v 12	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	4	3
MspI	4	4	3
Sau3AI	2	2	2
TaqI	5	7	5
0.17	23	25	20

06 v 11	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

06 v 10	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.20	22	23	18

06 v 09	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	2	1
TaqI	5	5	5
0.07	22	21	20

07 v 11	nx	ny	nxy
AvaII	4	4	2
HhaI	3	4	0
HpaII	3	3	2
MspI	3	3	2
Sau3AI	2	3	1
TaqI	5	5	5
0.43	20	22	12

07 v 10	nx	ny	nxy
AvaII	4	4	2
HhaI	3	4	0
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	2	1
TaqI	5	5	5
0.53	20	23	10

07 v 09	nx	ny	nxy
AvaII	4	4	2
HhaI	3	4	0
HpaII	3	3	2
MspI	3	3	2
Sau3AI	2	2	1
TaqI	5	5	5
0.41	20	21	12

08 v 11	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	3	1
TaqI	5	5	5
0.20	23	22	18

08 v 10	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	2
TaqI	5	5	5
0.00	23	23	23

08 v 09	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	2	2
TaqI	5	5	5
0.14	23	21	19

09 v 11	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	2	3	1
TaqI	5	5	5
0.07	21	22	20

09 v 10	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	2	2	2
TaqI	5	5	5
0.14	21	23	19

09 v 09	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	2	2	2
TaqI	5	5	5
0	21	21	21

10 v 11	nx	ny	nxy
AvaII	4	4	4
Hind fl	0	0	0
HhaI	4	4	4
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	3	1
TaqI	5	5	5
0.20	23	22	18

10 v 10	nx	ny	nxy
AvaII	4	4	4
Hind fl	0	0	0
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	2
TaqI	5	5	5
0.00	23	23	23

06 v 08	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.20	22	23	18

06 v 07	nx	ny	nxy
AvaII	4	4	2
HhaI	4	3	0
HpaII	3	3	2
MspI	3	3	2
Sau3AI	3	2	1
TaqI	5	5	5
0.43	22	20	12

06 v 06	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

07 v 08	nx	ny	nxy
AvaII	4	4	2
HhaI	3	4	0
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	2	1
TaqI	5	5	5
0.53	20	23	10

07 v 07	nx	ny	nxy
AvaII	4	4	4
HhaI	3	3	3
HpaII	3	3	3
MspI	3	3	3
Sau3AI	2	2	2
TaqI	5	5	5
0.00	20	20	20

08 v 08	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	2
TaqI	5	5	5
0.00	23	23	23

11 v 41	nx	ny	nxy
AvaII	4	4	4
HhaI	4	6	4
HpaII	3	5	3
MspI	3	6	3
Sau3AI	3	2	1
TaqI	5	5	5
0.20	22	28	20

11 v 40	nx	ny	nxy
AvaII	4	5	3
HhaI	4	5	2
HpaII	3	3	2
MspI	3	3	2
Sau3AI	3	2	1
TaqI	5	2	2
0.43	22	20	12

11 v 39	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	3	3
0.26	22	21	16

12 v 41	nx	ny	nxy
AvaII	4	4	4
HhaI	4	6	3
HpaII	4	5	3
MspI	4	6	2
Sau3AI	2	2	2
TaqI	7	5	5
0.28	25	28	19

12 v 40	nx	ny	nxy
AvaII	4	5	3
HhaI	4	5	2
HpaII	4	3	3
MspI	4	3	3
Sau3AI	2	2	2
TaqI	7	2	2
0.33	25	20	15

12 v 39	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	4	3
MspI	4	4	3
Sau3AI	2	2	2
TaqI	7	3	3
0.22	25	21	18

13 v 41	nx	ny	nxy
AvaII	4	4	3
HhaI	4	6	3
HpaII	4	5	4
MspI	4	6	4
Sau3AI	2	2	1
TaqI	7	5	5
0.25	25	28	20

13 v 40	nx	ny	nxy
AvaII	4	5	2
HhaI	4	5	2
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	2	1
TaqI	7	2	2
0.51	25	20	11

13 v 39	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	3
Sau3AI	2	2	1
TaqI	7	3	3
0.35	25	21	15

14 v 41	nx	ny	nxy
AvaII	4	4	4
HhaI	5	6	5
HpaII	5	5	4
MspI	5	6	4
Sau3AI	3	2	2
TaqI	5	5	5
0.13	27	28	24

14 v 40	nx	ny	nxy
AvaII	4	5	3
HhaI	5	5	3
HpaII	5	3	2
MspI	5	3	2
Sau3AI	3	2	2
TaqI	5	2	2
0.40	27	20	14

14 v 39	nx	ny	nxy
AvaII	4	4	4
HhaI	5	4	3
HpaII	5	4	2
MspI	5	4	3
Sau3AI	3	2	2
TaqI	5	3	3
0.29	27	21	17

15 v 41	nx	ny	nxy
AvaII	5	4	4
HhaI	4	6	4
HpaII	4	5	3
MspI	4	6	3
Sau3AI	2	2	1
TaqI	3	5	2
0.32	22	28	17

15 v 40	nx	ny	nxy
AvaII	5	5	3
HhaI	4	5	1
HpaII	4	3	1
MspI	4	3	1
Sau3AI	2	2	1
TaqI	3	2	1
0.62	22	20	8

15 v 39	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	2
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	2	1
TaqI	3	3	2
0.40	22	21	13

11 v 38	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	3	3
0.26	22	21	16

11 v 37	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	3	3
0.05	22	20	20

11 v 36	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	1
TaqI	5	3	2
0.50	22	22	11

12 v 38	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	4	3
MspI	4	4	3
Sau3AI	2	2	2
TaqI	7	3	3
0.22	25	21	18

12 v 37	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	3	1
TaqI	7	3	3
0.33	25	20	15

12 v 36	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	4	4	1
MspI	4	4	1
Sau3AI	2	2	1
TaqI	7	3	3
0.45	25	22	13

13 v 38	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	3
Sau3AI	2	2	1
TaqI	7	3	3
0.35	25	21	15

13 v 37	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	4	3	2
MspI	4	3	3
Sau3AI	2	3	1
TaqI	7	3	3
0.33	25	20	15

13 v 36	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	2	0
TaqI	7	3	3
0.40	25	22	14

14 v 38	nx	ny	nxy
AvaII	4	4	4
HhaI	5	4	3
HpaII	5	4	2
MspI	5	4	3
Sau3AI	3	2	2
TaqI	5	3	3
0.29	27	21	17

14 v 37	nx	ny	nxy
AvaII	4	4	4
HhaI	5	4	3
HpaII	5	3	2
MspI	5	3	2
Sau3AI	3	3	2
TaqI	5	3	3
0.32	27	20	16

14 v 36	nx	ny	nxy
AvaII	4	5	4
HhaI	5	4	4
HpaII	5	4	4
MspI	5	4	4
Sau3AI	3	2	2
TaqI	5	3	2
0.18	27	22	20

15 v 38	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	2
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	2	1
TaqI	3	3	2
0.40	22	21	13

15 v 37	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	2
HpaII	4	3	1
MspI	4	3	1
Sau3AI	2	3	1
TaqI	3	3	2
0.48	22	20	11

15 v 36	nx	ny	nxy
AvaII	5	5	5
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	2
TaqI	3	3	3
0.00	22	22	22

11 v 35	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	0
TaqI	5	3	2
0.50	22	22	11

11 v 34	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	3	1
TaqI	5	3	1
0.50	22	22	11

11 v 33	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	1
TaqI	5	3	2
0.50	22	22	11

12 v 35	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	4	4	1
MspI	4	4	1
Sau3AI	2	2	1
TaqI	7	3	3
0.49	25	22	12

12 v 34	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	2
HpaII	4	4	1
MspI	4	4	1
Sau3AI	2	3	1
TaqI	7	3	1
0.66	25	22	8

12 v 33	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	4	4	1
MspI	4	4	1
Sau3AI	2	2	1
TaqI	7	3	3
0.45	25	22	13

13 v 35	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	2	1
TaqI	7	3	3
0.40	25	22	14

13 v 34	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	2
HpaII	4	4	2
MspI	4	4	3
Sau3AI	2	3	1
TaqI	7	3	2
0.40	25	22	14

13 v 33	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	2	0
TaqI	7	3	3
0.40	25	22	14

14 v 35	nx	ny	nxy
AvaII	4	5	4
HhaI	5	4	3
HpaII	5	4	4
MspI	5	4	4
Sau3AI	3	2	1
TaqI	5	3	2
0.27	27	22	18

14 v 34	nx	ny	nxy
AvaII	4	4	2
HhaI	5	4	4
HpaII	5	4	3
MspI	5	4	2
Sau3AI	3	3	1
TaqI	5	3	1
0.47	27	22	13

14 v 33	nx	ny	nxy
AvaII	4	5	4
HhaI	5	4	4
HpaII	5	4	4
MspI	5	4	4
Sau3AI	3	2	2
TaqI	5	3	2
0.18	27	22	20

15 v 35	nx	ny	nxy
AvaII	5	5	5
HhaI	4	4	3
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	1
TaqI	3	3	3
0.09	22	22	20

15 v 34	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	3
HpaII	4	4	3
MspI	4	4	3
Sau3AI	2	3	0
TaqI	3	3	2
0.32	22	22	15

15 v 33	nx	ny	nxy
AvaII	5	5	5
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	2
TaqI	3	3	3
0.00	22	22	22

11 v 32	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	4	2
TaqI	5	3	2
0.43	22	24	13

11 v 31	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	4	2
TaqI	5	4	2
0.49	22	25	12

11 v 30	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	7	3
MspI	3	7	3
Sau3AI	3	2	0
TaqI	5	3	2
0.35	22	27	16

12 v 32	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	4	4	1
MspI	4	4	1
Sau3AI	2	4	2
TaqI	7	3	2
0.51	25	24	12

12 v 31	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	4	4	1
MspI	4	4	1
Sau3AI	2	4	2
TaqI	7	4	2
0.48	25	25	13

12 v 30	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	7	2
MspI	4	7	2
Sau3AI	2	2	1
TaqI	7	3	3
0.42	25	27	15

13 v 32	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	4	1
TaqI	7	3	3
0.43	25	24	14

13 v 31	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	4	1
TaqI	7	4	4
0.36	25	25	16

13 v 30	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	4	7	4
MspI	4	7	4
Sau3AI	2	2	1
TaqI	7	3	3
0.31	25	27	18

14 v 32	nx	ny	nxy
AvaII	4	5	4
HhaI	5	4	3
HpaII	5	4	4
MspI	5	4	4
Sau3AI	3	4	3
TaqI	5	3	2
0.22	27	24	20

14 v 31	nx	ny	nxy
AvaII	4	5	4
HhaI	5	4	3
HpaII	5	4	4
MspI	5	4	4
Sau3AI	3	4	3
TaqI	5	4	2
0.23	27	25	20

14 v 30	nx	ny	nxy
AvaII	4	4	4
HhaI	5	4	3
HpaII	5	7	3
MspI	5	7	2
Sau3AI	3	2	1
TaqI	5	3	2
0.44	27	27	15

15 v 32	nx	ny	nxy
AvaII	5	5	5
HhaI	4	4	3
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	4	2
TaqI	3	3	2
0.13	22	24	20

15 v 31	nx	ny	nxy
AvaII	5	5	5
HhaI	4	4	3
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	4	2
TaqI	3	4	2
0.15	22	25	20

15 v 30	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	2
HpaII	4	7	2
MspI	4	7	2
Sau3AI	2	2	1
TaqI	3	3	3
0.43	22	27	14

11 v 29	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.24	22	23	17

11 v 28	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

11 v 27	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.20	22	23	18

12 v 29	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	2
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	2	2
TaqI	7	5	5
0.29	25	23	17

12 v 28	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	3	1
TaqI	7	5	5
0.28	25	22	17

12 v 27	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	4	3
MspI	4	4	3
Sau3AI	2	2	2
TaqI	7	5	5
0.17	25	23	20

13 v 29	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	2
HpaII	4	4	3
MspI	4	4	3
Sau3AI	2	2	1
TaqI	7	5	5
0.29	25	23	17

13 v 28	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	4	3	2
MspI	4	3	3
Sau3AI	2	3	1
TaqI	7	5	5
0.28	25	22	17

13 v 27	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	3
Sau3AI	2	2	1
TaqI	7	5	5
0.29	25	23	17

14 v 29	nx	ny	nxy
AvaII	4	4	4
HhaI	5	4	3
HpaII	5	4	3
MspI	5	4	4
Sau3AI	3	2	2
TaqI	5	5	5
0.16	27	23	21

14 v 28	nx	ny	nxy
AvaII	4	4	4
HhaI	5	4	3
HpaII	5	3	2
MspI	5	3	2
Sau3AI	3	3	2
TaqI	5	5	5
0.27	27	22	18

14 v 27	nx	ny	nxy
AvaII	4	4	4
HhaI	5	4	3
HpaII	5	4	2
MspI	5	4	3
Sau3AI	3	2	2
TaqI	5	5	5
0.24	27	23	19

15 v 29	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	3
HpaII	4	4	1
MspI	4	4	1
Sau3AI	2	2	1
TaqI	3	5	2
0.47	22	23	12

15 v 28	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	2
HpaII	4	3	1
MspI	4	3	1
Sau3AI	2	3	1
TaqI	3	5	2
0.50	22	22	11

15 v 27	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	2
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	2	1
TaqI	3	5	2
0.42	22	23	13

11 v 26	nx	ny	nxy
AvaII	4	2	2
HhaI	4	4	3
HpaII	3	2	0
MspI	3	2	0
Sau3AI	3	3	1
TaqI	5	5	1
0.65	22	18	7

11 v 25	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	2
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.29	22	23	16

11 v 24	nx	ny	nxy
AvaII	4	4	4
HhaI	4	5	3
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.07	22	23	21

12 v 26	nx	ny	nxy
AvaII	4	2	2
HhaI	4	4	2
HpaII	4	2	0
MspI	4	2	0
Sau3AI	2	3	0
TaqI	7	5	3
0.67	25	18	7

12 v 25	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	4	3
MspI	4	4	3
Sau3AI	2	2	2
TaqI	7	5	5
0.17	25	23	20

12 v 24	nx	ny	nxy
AvaII	4	4	4
HhaI	4	5	4
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	3	1
TaqI	7	5	5
0.25	25	23	18

13 v 26	nx	ny	nxy
AvaII	4	2	2
HhaI	4	4	2
HpaII	4	2	0
MspI	4	2	2
Sau3AI	2	3	0
TaqI	7	5	2
0.63	25	18	8

13 v 25	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	3
Sau3AI	2	2	1
TaqI	7	5	5
0.29	25	23	17

13 v 24	nx	ny	nxy
AvaII	4	4	3
HhaI	4	5	4
HpaII	4	3	2
MspI	4	3	3
Sau3AI	2	3	1
TaqI	7	5	5
0.25	25	23	18

14 v 26	nx	ny	nxy
AvaII	4	2	2
HhaI	5	4	3
HpaII	5	2	0
MspI	5	2	0
Sau3AI	3	3	0
TaqI	5	5	1
0.73	27	18	6

14 v 25	nx	ny	nxy
AvaII	4	4	4
HhaI	5	4	4
HpaII	5	4	2
MspI	5	4	3
Sau3AI	3	2	2
TaqI	5	5	5
0.20	27	23	20

14 v 24	nx	ny	nxy
AvaII	4	4	4
HhaI	5	5	5
HpaII	5	3	2
MspI	5	3	2
Sau3AI	3	3	2
TaqI	5	5	5
0.20	27	23	20

15 v 26	nx	ny	nxy
AvaII	5	2	1
HhaI	4	4	3
HpaII	4	2	0
MspI	4	2	0
Sau3AI	2	3	0
TaqI	3	5	0
0.80	22	18	4

15 v 25	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	4
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	2	1
TaqI	3	5	2
0.33	22	23	15

15 v 24	nx	ny	nxy
AvaII	5	4	4
HhaI	4	5	4
HpaII	4	3	1
MspI	4	3	1
Sau3AI	2	3	1
TaqI	3	5	2
0.42	22	23	13

11 v 23	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.24	22	23	17

11 v 22	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.05	22	22	21

11 v 21	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	2
HpaII	3	5	1
MspI	3	5	2
Sau3AI	3	3	1
TaqI	5	4	1
0.62	22	25	9

12 v 23	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	2	2
TaqI	7	5	5
0.21	25	23	19

12 v 22	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	3	1
TaqI	7	5	5
0.23	25	22	18

12 v 21	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	3
HpaII	4	5	2
MspI	4	5	2
Sau3AI	2	3	1
TaqI	7	4	1
0.56	25	25	11

13 v 23	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	4
HpaII	4	4	3
MspI	4	4	3
Sau3AI	2	2	1
TaqI	7	5	5
0.21	25	23	19

13 v 22	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	4
HpaII	4	3	2
MspI	4	3	3
Sau3AI	2	3	1
TaqI	7	5	5
0.23	25	22	18

13 v 21	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	4	5	1
MspI	4	5	1
Sau3AI	2	3	1
TaqI	7	4	2
0.56	25	25	11

14 v 23	nx	ny	nxy
AvaII	4	4	4
HhaI	5	4	4
HpaII	5	4	3
MspI	5	4	4
Sau3AI	3	2	2
TaqI	5	5	5
0.12	27	23	22

14 v 22	nx	ny	nxy
AvaII	4	4	4
HhaI	5	4	4
HpaII	5	3	2
MspI	5	3	2
Sau3AI	3	3	2
TaqI	5	5	5
0.22	27	22	19

14 v 21	nx	ny	nxy
AvaII	4	4	2
HhaI	5	4	3
HpaII	5	5	3
MspI	5	5	3
Sau3AI	3	3	2
TaqI	5	4	1
0.46	27	25	14

15 v 23	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	3
HpaII	4	4	1
MspI	4	4	1
Sau3AI	2	2	1
TaqI	3	5	2
0.47	22	23	12

15 v 22	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	3
HpaII	4	3	1
MspI	4	3	1
Sau3AI	2	3	1
TaqI	3	5	2
0.45	22	22	12

15 v 21	nx	ny	nxy
AvaII	5	4	3
HhaI	4	4	3
HpaII	4	5	3
MspI	4	5	3
Sau3AI	2	3	1
TaqI	3	4	0
0.45	22	25	13

11 v 20	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	3	1
TaqI	5	5	5
0.22	22	24	18

11 v 19	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	3	2
MspI	3	3	2
Sau3AI	3	2	0
TaqI	5	3	2
0.38	22	20	13

11 v 18	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	3	3
0.05	22	20	20

12 v 20	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	4	3
MspI	4	4	3
Sau3AI	2	3	2
TaqI	7	5	5
0.18	25	24	20

12 v 19	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	4	3	1
MspI	4	3	1
Sau3AI	2	2	1
TaqI	7	3	3
0.47	25	20	12

12 v 18	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	3	1
TaqI	7	3	3
0.33	25	20	15

13 v 20	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	3
Sau3AI	2	3	1
TaqI	7	5	5
0.31	25	24	17

13 v 19	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	2	1
TaqI	7	3	3
0.38	25	20	14

13 v 18	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	4	3	2
MspI	4	3	3
Sau3AI	2	3	1
TaqI	7	3	3
0.33	25	20	15

14 v 20	nx	ny	nxy
AvaII	4	4	4
HhaI	5	4	3
HpaII	5	4	2
MspI	5	4	3
Sau3AI	3	3	2
TaqI	5	5	5
0.25	27	24	19

14 v 19	nx	ny	nxy
AvaII	4	5	4
HhaI	5	4	3
HpaII	5	3	1
MspI	5	3	1
Sau3AI	3	2	1
TaqI	5	3	2
0.49	27	20	12

14 v 18	nx	ny	nxy
AvaII	4	4	4
HhaI	5	4	3
HpaII	5	3	2
MspI	5	3	2
Sau3AI	3	3	2
TaqI	5	3	3
0.32	27	20	16

15 v 20	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	2
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	3	1
TaqI	3	5	2
0.43	22	24	13

15 v 19	nx	ny	nxy
AvaII	5	5	5
HhaI	4	4	3
HpaII	4	3	1
MspI	4	3	1
Sau3AI	2	2	1
TaqI	3	3	3
0.33	22	20	14

15 v 18	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	2
HpaII	4	3	1
MspI	4	3	1
Sau3AI	2	3	1
TaqI	3	3	2
0.48	22	20	11

11 v 17	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

11 v 16	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	5	1
MspI	3	5	1
Sau3AI	3	3	2
TaqI	5	3	2
0.43	22	24	13

11 v 15	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	1
TaqI	5	3	2
0.50	22	22	11

12 v 17	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	3	1
TaqI	7	5	5
0.28	25	22	17

12 v 16	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	2
HpaII	4	5	1
MspI	4	5	1
Sau3AI	2	3	1
TaqI	7	3	3
0.51	25	24	12

12 v 15	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	4	4	1
MspI	4	4	1
Sau3AI	2	2	1
TaqI	7	3	3
0.45	25	22	13

13 v 17	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	4	3	2
MspI	4	3	3
Sau3AI	2	3	1
TaqI	7	5	5
0.28	25	22	17

13 v 16	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	2
HpaII	4	5	2
MspI	4	5	3
Sau3AI	2	3	1
TaqI	7	3	3
0.43	25	24	14

13 v 15	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	2	0
TaqI	7	3	3
0.40	25	22	14

14 v 17	nx	ny	nxy
AvaII	4	4	4
HhaI	5	4	3
HpaII	5	3	2
MspI	5	3	2
Sau3AI	3	3	2
TaqI	5	5	5
0.27	27	22	18

14 v 16	nx	ny	nxy
AvaII	4	4	4
HhaI	5	4	3
HpaII	5	5	3
MspI	5	5	3
Sau3AI	3	3	2
TaqI	5	3	2
0.33	27	24	17

14 v 15	nx	ny	nxy
AvaII	4	5	4
HhaI	5	4	4
HpaII	5	4	4
MspI	5	4	4
Sau3AI	3	2	2
TaqI	5	3	2
0.18	27	22	20

15 v 17	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	2
HpaII	4	3	1
MspI	4	3	1
Sau3AI	2	3	1
TaqI	3	5	2
0.50	22	22	11

15 v 16	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	3
HpaII	4	5	3
MspI	4	5	3
Sau3AI	2	3	1
TaqI	3	3	3
0.26	22	24	17

15 v 15	nx	ny	nxy
AvaII	5	5	5
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	2
TaqI	3	3	3
0.00	22	22	22

11 v 14	nx	ny	nxy
AvaII	4	4	4
HhaI	4	5	3
HpaII	3	5	2
MspI	3	5	2
Sau3AI	3	3	2
TaqI	5	5	5
0.27	22	27	18

11 v 13	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	3
Sau3AI	3	2	1
TaqI	5	7	5
0.28	22	25	17

11 v 12	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	7	5
0.28	22	25	17

12 v 14	nx	ny	nxy
AvaII	4	4	4
HhaI	4	5	4
HpaII	4	5	2
MspI	4	5	2
Sau3AI	2	3	2
TaqI	7	5	5
0.27	25	27	19

12 v 13	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	4
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	2	1
TaqI	7	7	5
0.32	25	25	17

12 v 12	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	2
TaqI	7	7	7
0.00	25	25	25

13 v 14	nx	ny	nxy
AvaII	4	4	3
HhaI	4	5	4
HpaII	4	5	3
MspI	4	5	3
Sau3AI	2	3	1
TaqI	7	5	5
0.27	25	27	19

13 v 13	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	2
TaqI	7	7	7
0.00	25	25	25

14 v 14	nx	ny	nxy
AvaII	4	4	4
HhaI	5	5	5
HpaII	5	5	5
MspI	5	5	5
Sau3AI	3	3	3
TaqI	5	5	5
0.00	27	27	27

I I v I I	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
*Sau*3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

16 v 41	nx	ny	nxy
AvaII	4	4	4
HhaI	4	6	4
HpaII	5	5	2
MspI	5	6	4
Sau3AI	3	2	1
TaqI	3	5	2
0.35	24	28	17

16 v 40	nx	ny	nxy
AvaII	4	5	3
HhaI	4	5	1
HpaII	5	3	1
MspI	5	3	1
Sau3AI	3	2	1
TaqI	3	2	1
0.64	24	20	8

16 v 39	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	5	4	1
MspI	5	4	2
Sau3AI	3	2	1
TaqI	3	3	2
0.42	24	21	13

17 v 41	nx	ny	nxy
AvaII	4	4	4
HhaI	4	6	4
HpaII	3	5	3
MspI	3	6	3
Sau3AI	3	2	1
TaqI	5	5	5
0.20	22	28	20

17 v 40	nx	ny	nxy
AvaII	4	5	3
HhaI	4	5	2
HpaII	3	3	2
MspI	3	3	2
Sau3AI	3	2	1
TaqI	5	2	2
0.43	22	20	12

17 v 39	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	3	3
0.26	22	21	16

18 v 41	nx	ny	nxy
AvaII	4	4	4
HhaI	4	6	4
HpaII	3	5	3
MspI	3	6	3
Sau3AI	3	2	1
TaqI	3	5	3
0.25	20	28	18

18 v 40	nx	ny	nxy
AvaII	4	5	3
HhaI	4	5	2
HpaII	3	3	2
MspI	3	3	2
Sau3AI	3	2	1
TaqI	3	2	2
0.40	20	20	12

18 v 39	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	3	3	3
0.22	20	21	16

19 v 41	nx	ny	nxy
AvaII	5	4	4
HhaI	4	6	4
HpaII	3	5	2
MspI	3	6	2
Sau3AI	2	2	1
TaqI	3	5	2
0.38	20	28	15

19 v 40	nx	ny	nxy
AvaII	5	5	3
HhaI	4	5	1
HpaII	3	3	1
MspI	3	3	1
Sau3AI	2	2	1
TaqI	3	2	1
0.60	20	20	8

19 v 39	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	2	1
TaqI	3	3	2
0.41	20	21	12

20 v 41	nx	ny	nxy
AvaII	4	4	4
HhaI	4	6	4
HpaII	4	5	3
MspI	4	6	3
Sau3AI	3	2	2
TaqI	5	5	5
0.19	24	28	21

20 v 40	nx	ny	nxy
AvaII	4	5	3
HhaI	4	5	2
HpaII	4	3	2
MspI	4	3	2
Sau3AI	3	2	2
TaqI	5	2	2
0.41	24	20	13

20 v 39	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	3	2	2
TaqI	5	3	3
0.07	24	21	21

16 v 38	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	5	4	1
MspI	5	4	2
Sau3AI	3	2	1
TaqI	3	3	2
0.42	24	21	13

16 v 37	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	5	3	1
MspI	5	3	1
Sau3AI	3	3	2
TaqI	3	3	2
0.41	24	20	13

16 v 36	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	5	4	3
MspI	5	4	3
Sau3AI	3	2	1
TaqI	3	3	3
0.26	24	22	17

17 v 38	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	3	3
0.26	22	21	16

17 v 37	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	3	3
0.05	22	20	20

17 v 36	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	1
TaqI	5	3	2
0.50	22	22	11

18 v 38	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	3	3	3
0.22	20	21	16

18 v 37	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	3	3	3
0.00	20	20	20

18 v 36	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	1
TaqI	3	3	2
0.48	20	22	11

19 v 38	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	2	1
TaqI	3	3	2
0.41	20	21	12

19 v 37	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	3
HpaII	3	3	2
MspI	3	3	2
Sau3AI	2	3	0
TaqI	3	3	2
0.35	20	20	13

19 v 36	nx	ny	nxy
AvaII	5	5	5
HhaI	4	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	2	1
TaqI	3	3	3
0.33	20	22	14

20 v 38	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	3	2	2
TaqI	5	3	3
0.07	24	21	21

20 v 37	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	3	2
MspI	4	3	2
Sau3AI	3	3	1
TaqI	5	3	3
0.27	24	20	16

20 v 36	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	4	4	2
MspI	4	4	2
Sau3AI	3	2	1
TaqI	5	3	2
0.43	24	22	13

16 v 35	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	4
HpaII	5	4	3
MspI	5	4	3
Sau3AI	3	2	1
TaqI	3	3	3
0.22	24	22	18

16 v 34	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	3
HpaII	5	4	3
MspI	5	4	2
Sau3AI	3	3	1
TaqI	3	3	2
0.43	24	22	13

16 v 33	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	5	4	3
MspI	5	4	3
Sau3AI	3	2	1
TaqI	3	3	3
0.26	24	22	17

17 v 35	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	0
TaqI	5	3	2
0.50	22	22	11

17 v 34	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	3	1
TaqI	5	3	1
0.50	22	22	11

17 v 33	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	1
TaqI	5	3	2
0.50	22	22	11

18 v 35	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	0
TaqI	3	3	2
0.48	20	22	11

18 v 34	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	3	1
TaqI	3	3	1
0.48	20	22	11

18 v 33	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	1
TaqI	3	3	2
0.48	20	22	11

19 v 35	nx	ny	nxy
AvaII	5	5	5
HhaI	4	4	4
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	2	2
TaqI	3	3	3
0.24	20	22	16

19 v 34	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	2	3	0
TaqI	3	3	2
0.38	20	22	13

19 v 33	nx	ny	nxy
AvaII	5	5	5
HhaI	4	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	2	1
TaqI	3	3	3
0.33	20	22	14

20 v 35	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	2
Sau3AI	3	2	1
TaqI	5	3	2
0.39	24	22	14

20 v 34	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	2
Sau3AI	3	3	1
TaqI	5	3	1
0.48	24	22	12

20 v 33	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	4	4	2
MspI	4	4	2
Sau3AI	3	2	1
TaqI	5	3	2
0.43	24	22	13

16 v 32	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	4
HpaII	5	4	3
MspI	5	4	3
Sau3AI	3	4	2
TaqI	3	3	2
0.25	24	24	18

16 v 31	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	5	4	3
MspI	5	4	3
Sau3AI	3	4	2
TaqI	3	4	2
0.35	24	25	16

16 v 30	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	5	7	3
MspI	5	7	4
Sau3AI	3	2	1
TaqI	3	3	3
0.29	24	27	18

17 v 32	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	4	2
TaqI	5	3	2
0.43	22	24	13

17 v 31	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	4	2
TaqI	5	4	2
0.49	22	25	12

17 v 30	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	7	3
MspI	3	7	3
Sau3AI	3	2	0
TaqI	5	3	2
0.35	22	27	16

18 v 32	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	4	2
TaqI	3	3	1
0.45	20	24	12

18 v 31	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	4	2
TaqI	3	4	1
0.51	20	25	11

18 v 30	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	7	3
MspI	3	7	3
Sau3AI	3	2	0
TaqI	3	3	2
0.32	20	27	16

19 v 32	nx	ny	nxy
AvaII	5	5	5
HhaI	4	4	4
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	4	1
TaqI	3	3	2
0.36	20	24	14

19 v 31	nx	ny	nxy
AvaII	5	5	5
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	4	1
TaqI	3	4	2
0.47	20	25	12

19 v 30	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	3
HpaII	3	7	2
MspI	3	7	3
Sau3AI	2	2	2
TaqI	3	3	3
0.28	20	27	17

20 v 32	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	2
Sau3AI	3	4	1
TaqI	5	3	2
0.42	24	24	14

20 v 31	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	4	4	2
MspI	4	4	2
Sau3AI	3	4	1
TaqI	5	4	2
0.47	24	25	13

20 v 30	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	7	3
MspI	4	7	3
Sau3AI	3	2	1
TaqI	5	3	2
0.33	24	27	17

16 v 29	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	5	4	3
MspI	5	4	3
Sau3AI	3	2	1
TaqI	3	5	2
0.28	24	23	17

16 v 28	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	5	3	1
MspI	5	3	1
Sau3AI	3	3	2
TaqI	3	5	2
0.43	24	22	13

16 v 27	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	5	4	1
MspI	5	4	2
Sau3AI	3	2	1
TaqI	3	5	2
0.45	24	23	13

17 v 29	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.24	22	23	17

17 v 28	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

17 v 27	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.20	22	23	18

18 v 29	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	3	5	3
0.30	20	23	15

18 v 28	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	3	5	3
0.05	20	22	20

18 v 27	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	3	5	3
0.26	20	23	16

19 v 29	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	4
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	2	1
TaqI	3	5	2
0.40	20	23	13

19 v 28	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	3
HpaII	3	3	2
MspI	3	3	2
Sau3AI	2	3	0
TaqI	3	5	2
0.38	20	22	13

19 v 27	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	2	1
TaqI	3	5	2
0.44	20	23	12

20 v 29	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	4	3
MspI	4	4	3
Sau3AI	3	2	2
TaqI	5	5	5
0.15	24	23	20

20 v 28	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	3	2
MspI	4	3	2
Sau3AI	3	3	1
TaqI	5	5	5
0.22	24	22	18

20 v 27	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	3	2	2
TaqI	5	5	5
0.02	24	23	23

16 v 26	nx	ny	nxy
AvaII	4	2	2
HhaI	4	4	4
HpaII	5	2	1
MspI	5	2	1
Sau3AI	3	3	1
TaqI	3	5	0
0.57	24	18	9

16 v 25	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	5	4	1
MspI	5	4	2
Sau3AI	3	2	1
TaqI	3	5	2
0.45	24	23	13

16 v 24	nx	ny	nxy
AvaII	4	4	4
HhaI	4	5	3
HpaII	5	3	1
MspI	5	3	1
Sau3AI	3	3	2
TaqI	3	5	2
0.45	24	23	13

17 v 26	nx	ny	nxy
AvaII	4	2	2
HhaI	4	4	3
HpaII	3	2	0
MspI	3	2	0
Sau3AI	3	3	1
TaqI	5	5	1
0.65	22	18	7

17 v 25	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	2
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.29	22	23	16

17 v 24	nx	ny	nxy
AvaII	4	4	4
HhaI	4	5	3
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.07	22	23	21

18 v 26	nx	ny	nxy
AvaII	4	2	2
HhaI	4	4	3
HpaII	3	2	0
MspI	3	2	0
Sau3AI	3	3	1
TaqI	3	5	1
0.63	20	18	7

18 v 25	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	2
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	3	5	3
0.35	20	23	14

18 v 24	nx	ny	nxy
AvaII	4	4	4
HhaI	4	5	3
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	3	5	3
0.12	20	23	19

19 v 26	nx	ny	nxy
AvaII	5	2	1
HhaI	4	4	4
HpaII	3	2	1
MspI	3	2	1
Sau3AI	2	3	0
TaqI	3	5	0
0.63	20	18	7

19 v 25	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	2	1
TaqI	3	5	2
0.44	20	23	12

19 v 24	nx	ny	nxy
AvaII	5	4	4
HhaI	4	5	3
HpaII	3	3	2
MspI	3	3	2
Sau3AI	2	3	0
TaqI	3	5	2
0.40	20	23	13

20 v 26	nx	ny	nxy
AvaII	4	2	2
HhaI	4	4	3
HpaII	4	2	0
MspI	4	2	0
Sau3AI	3	3	0
TaqI	5	5	1
0.71	24	18	6

20 v 25	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	2
HpaII	4	4	4
MspI	4	4	4
Sau3AI	3	2	2
TaqI	5	5	5
0.11	24	23	21

20 v 24	nx	ny	nxy
AvaII	4	4	4
HhaI	4	5	3
HpaII	4	3	2
MspI	4	3	2
Sau3AI	3	3	1
TaqI	5	5	5
0.28	24	23	17

16 v 23	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	2
HpaII	5	4	3
MspI	5	4	3
Sau3AI	3	2	1
TaqI	3	5	2
0.36	24	23	15

16 v 22	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	2
HpaII	5	3	1
MspI	5	3	1
Sau3AI	3	3	2
TaqI	3	5	2
0.48	24	22	12

16 v 21	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	2
HpaII	5	5	3
MspI	5	5	3
Sau3AI	3	3	2
TaqI	3	4	0
0.51	24	25	12

17 v 23	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.24	22	23	17

17 v 22	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.05	22	22	21

17 v 21	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	2
HpaII	3	5	1
MspI	3	5	2
Sau3AI	3	3	1
TaqI	5	4	1
0.62	22	25	9

18 v 23	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	3	5	3
0.30	20	23	15

18 v 22	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	3	5	3
0.10	20	22	19

18 v 21	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	2
HpaII	3	5	1
MspI	3	5	2
Sau3AI	3	3	1
TaqI	3	4	1
0.60	20	25	9

19 v 23	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	4
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	2	1
TaqI	3	5	2
0.40	20	23	13

19 v 22	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	2
HpaII	3	3	2
MspI	3	3	2
Sau3AI	2	3	0
TaqI	3	5	2
0.43	20	22	12

19 v 21	nx	ny	nxy
AvaII	5	4	3
HhaI	4	4	2
HpaII	3	5	1
MspI	3	5	1
Sau3AI	2	3	0
TaqI	3	4	0
0.69	20	25	7

20 v 23	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	4	3
MspI	4	4	3
Sau3AI	3	2	2
TaqI	5	5	5
0.15	24	23	20

20 v 22	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	3	2
MspI	4	3	2
Sau3AI	3	3	1
TaqI	5	5	5
0.26	24	22	17

20 v 21	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	2
HpaII	4	5	2
MspI	4	5	2
Sau3AI	3	3	1
TaqI	5	4	1
0.59	24	25	10

16 v 20	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	5	4	1
MspI	5	4	2
Sau3AI	3	3	1
TaqI	3	5	2
0.46	24	24	13

16 v 19	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	4
HpaII	5	3	1
MspI	5	3	2
Sau3AI	3	2	1
TaqI	3	3	3
0.32	24	20	15

16 v 18	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	5	3	1
MspI	5	3	1
Sau3AI	3	3	2
TaqI	3	3	2
0.41	24	20	13

17 v 20	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	3	1
TaqI	5	5	5
0.22	22	24	18

17 v 19	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	3	2
MspI	3	3	2
Sau3AI	3	2	0
TaqI	5	3	2
0.38	22	20	13

17 v 18	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	3	3
0.05	22	20	20

18 v 20	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	3	1
TaqI	3	5	3
0.27	20	24	16

18 v 19	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	3	2
MspI	3	3	2
Sau3AI	3	2	0
TaqI	3	3	2
0.35	20	20	13

18 v 18	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	3	3	3
0.00	20	20	20

19 v 20	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	2	3	1
TaqI	3	5	2
0.45	20	24	12

19 v 19	nx	ny	nxy
AvaII	5	5	5
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	2	2	2
TaqI	3	3	3
0.00	20	20	20

20 v 20	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	3	3	3
TaqI	5	5	5
0.00	24	24	24

16 v 17	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	5	3	1
MspI	5	3	1
Sau3AI	3	3	2
TaqI	3	5	2
0.43	24	22	13

16 v 16	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	5	5	5
MspI	5	5	5
Sau3AI	3	3	3
TaqI	3	3	3
0.00	24	24	24

17 v 17	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

21 v 41	nx	ny	nxy
AvaII	4	4	2
HhaI	4	6	3
HpaII	5	5	2
MspI	5	6	2
Sau3AI	3	2	1
TaqI	4	5	1
0.58	25	28	11

21 v 40	nx	ny	nxy
AvaII	4	5	1
HhaI	4	5	2
HpaII	5	3	1
MspI	5	3	2
Sau3AI	3	2	1
TaqI	4	2	1
0.64	25	20	8

21 v 39	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	2
HpaII	5	4	2
MspI	5	4	2
Sau3AI	3	2	1
TaqI	4	3	1
0.57	25	21	10

22 v 41	nx	ny	nxy
AvaII	4	4	4
HhaI	4	6	3
HpaII	3	5	3
MspI	3	6	3
Sau3AI	3	2	1
TaqI	5	5	5
0.24	22	28	19

22 v 40	nx	ny	nxy
AvaII	4	5	3
HhaI	4	5	2
HpaII	3	3	2
MspI	3	3	2
Sau3AI	3	2	1
TaqI	5	2	2
0.43	22	20	12

22 v 39	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	3	3
0.30	22	21	15

23 v 41	nx	ny	nxy
AvaII	4	4	4
HhaI	4	6	3
HpaII	4	5	3
MspI	4	6	3
Sau3AI	2	2	2
TaqI	5	5	5
0.22	23	28	20

23 v 40	nx	ny	nxy
AvaII	4	5	3
HhaI	4	5	2
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	2	2
TaqI	5	2	2
0.40	23	20	13

23 v 39	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	4	3
MspI	4	4	3
Sau3AI	2	2	2
TaqI	5	3	3
0.18	23	21	18

24 v 41	nx	ny	nxy
AvaII	4	4	4
HhaI	5	6	5
HpaII	3	5	3
MspI	3	6	3
Sau3AI	3	2	1
TaqI	5	5	5
0.18	23	28	21

24 v 40	nx	ny	nxy
AvaII	4	5	3
HhaI	5	5	3
HpaII	3	3	2
MspI	3	3	2
Sau3AI	3	2	1
TaqI	5	2	2
0.40	23	20	13

24 v 39	nx	ny	nxy
AvaII	4	4	4
HhaI	5	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	3	3
0.32	23	21	15

25 v 41	nx	ny	nxy
AvaII	4	4	4
HhaI	4	6	4
HpaII	4	5	3
MspI	4	6	3
Sau3AI	2	2	2
TaqI	5	5	5
0.18	23	28	21

25 v 40	nx	ny	nxy
AvaII	4	5	3
HhaI	4	5	1
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	2	2
TaqI	5	2	2
0.44	23	20	12

25 v 39	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	2
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	2
TaqI	5	3	3
0.14	23	21	19

21 v 38	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	2
HpaII	5	4	2
MspI	5	4	2
Sau3AI	3	2	1
TaqI	4	3	1
0.57	25	21	10

21 v 37	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	2
HpaII	5	3	1
MspI	5	3	2
Sau3AI	3	3	1
TaqI	4	3	1
0.60	25	20	9

21 v 36	nx	ny	nxy
AvaII	4	5	3
HhaI	4	4	3
HpaII	5	4	3
MspI	5	4	3
Sau3AI	3	2	1
TaqI	4	3	0
0.45	25	22	13

22 v 38	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	3	3
0.30	22	21	15

22 v 37	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	3	3
0.10	22	20	19

22 v 36	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	1
TaqI	5	3	2
0.45	22	22	12

23 v 38	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	4	3
MspI	4	4	3
Sau3AI	2	2	2
TaqI	5	3	3
0.18	23	21	18

23 v 37	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	3	1
TaqI	5	3	3
0.30	23	20	15

23 v 36	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	4	4	1
MspI	4	4	1
Sau3AI	2	2	1
TaqI	5	3	2
0.47	23	22	12

24 v 38	nx	ny	nxy
AvaII	4	4	4
HhaI	5	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	3	3
0.32	23	21	15

24 v 37	nx	ny	nxy
AvaII	4	4	4
HhaI	5	4	3
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	3	3
0.12	23	20	19

24 v 36	nx	ny	nxy
AvaII	4	5	4
HhaI	5	4	4
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	1
TaqI	5	3	2
0.42	23	22	13

25 v 38	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	2
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	2
TaqI	5	3	3
0.14	23	21	19

25 v 37	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	2
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	3	1
TaqI	5	3	3
0.35	23	20	14

25 v 36	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	4
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	2	1
TaqI	5	3	2
0.33	23	22	15

21 v 35	nx	ny	nxy
AvaII	4	5	3
HhaI	4	4	2
HpaII	5	4	3
MspI	5	4	3
Sau3AI	3	2	0
TaqI	4	3	0
0.53	25	22	11

21 v 34	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	5	4	2
MspI	5	4	2
Sau3AI	3	3	1
TaqI	4	3	1
0.49	25	22	12

21 v 33	nx	ny	nxy
AvaII	4	5	3
HhaI	4	4	3
HpaII	5	4	3
MspI	5	4	3
Sau3AI	3	2	1
TaqI	4	3	0
0.45	25	22	13

22 v 35	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	0
TaqI	5	3	2
0.55	22	22	10

22 v 34	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	2
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	3	1
TaqI	5	3	1
0.55	22	22	10

22 v 33	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	1
TaqI	5	3	2
0.45	22	22	12

23 v 35	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	4	4	1
MspI	4	4	1
Sau3AI	2	2	1
TaqI	5	3	2
0.51	23	22	11

23 v 34	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	2
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	3	1
TaqI	5	3	1
0.56	23	22	10

23 v 33	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	4	4	1
MspI	4	4	1
Sau3AI	2	2	1
TaqI	5	3	2
0.47	23	22	12

24 v 35	nx	ny	nxy
AvaII	4	5	4
HhaI	5	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	0
TaqI	5	3	2
0.51	23	22	11

24 v 34	nx	ny	nxy
AvaII	4	4	2
HhaI	5	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	3	1
TaqI	5	3	1
0.47	23	22	12

24 v 33	nx	ny	nxy
AvaII	4	5	4
HhaI	5	4	4
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	1
TaqI	5	3	2
0.42	23	22	13

25 v 35	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	2	1
TaqI	5	3	2
0.38	23	22	14

25 v 34	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	3	1
TaqI	5	3	1
0.47	23	22	12

25 v 33	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	4
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	2	1
TaqI	5	3	2
0.33	23	22	15

21 v 32	nx	ny	nxy
AvaII	4	5	3
HhaI	4	4	2
HpaII	5	4	3
MspI	5	4	3
Sau3AI	3	4	2
TaqI	4	3	1
0.43	25	24	14

21 v 31	nx	ny	nxy
AvaII	4	5	3
HhaI	4	4	4
HpaII	5	4	3
MspI	5	4	3
Sau3AI	3	4	2
TaqI	4	4	1
0.36	25	25	16

21 v 30	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	2
HpaII	5	7	2
MspI	5	7	2
Sau3AI	3	2	0
TaqI	4	3	0
0.69	25	27	8

22 v 32	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	4	2
TaqI	5	3	2
0.48	22	24	12

22 v 31	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	4	2
TaqI	5	4	2
0.45	22	25	13

22 v 30	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	7	3
MspI	3	7	3
Sau3AI	3	2	0
TaqI	5	3	2
0.39	22	27	15

23 v 32	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	4	4	1
MspI	4	4	1
Sau3AI	2	4	2
TaqI	5	3	2
0.49	23	24	12

23 v 31	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	4	4	1
MspI	4	4	1
Sau3AI	2	4	2
TaqI	5	4	2
0.46	23	25	13

23 v 30	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	7	3
MspI	4	7	3
Sau3AI	2	2	1
TaqI	5	3	2
0.36	23	27	16

24 v 32	nx	ny	nxy
AvaII	4	5	4
HhaI	5	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	4	2
TaqI	5	3	2
0.45	23	24	13

24 v 31	nx	ny	nxy
AvaII	4	5	4
HhaI	5	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	4	2
TaqI	5	4	2
0.46	23	25	13

24 v 30	nx	ny	nxy
AvaII	4	4	4
HhaI	5	4	3
HpaII	3	7	3
MspI	3	7	3
Sau3AI	3	2	0
TaqI	5	3	2
0.40	23	27	15

25 v 32	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	4	2
TaqI	5	3	2
0.36	23	24	15

25 v 31	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	4	2
TaqI	5	4	2
0.38	23	25	15

25 v 30	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	2
HpaII	4	7	3
MspI	4	7	3
Sau3AI	2	2	1
TaqI	5	3	2
0.40	23	27	15

21 v 29	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	2
HpaII	5	4	1
MspI	5	4	3
Sau3AI	3	2	1
TaqI	4	5	1
0.58	25	23	10

21 v 28	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	2
HpaII	5	3	1
MspI	5	3	2
Sau3AI	3	3	1
TaqI	4	5	1
0.62	25	22	9

21 v 27	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	2
HpaII	5	4	2
MspI	5	4	2
Sau3AI	3	2	1
TaqI	4	5	1
0.58	25	23	10

22 v 29	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	2
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.29	22	23	16

22 v 28	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.05	22	22	21

22 v 27	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.24	22	23	17

23 v 29	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	2
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	2
TaqI	5	5	5
0.09	23	23	21

23 v 28	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	3	1
TaqI	5	5	5
0.24	23	22	17

23 v 27	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	4	3
MspI	4	4	3
Sau3AI	2	2	2
TaqI	5	5	5
0.13	23	23	20

24 v 29	nx	ny	nxy
AvaII	4	4	4
HhaI	5	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.26	23	23	17

24 v 28	nx	ny	nxy
AvaII	4	4	4
HhaI	5	4	3
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.07	23	22	21

24 v 27	nx	ny	nxy
AvaII	4	4	4
HhaI	5	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.26	23	23	17

25 v 29	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	4	3
MspI	4	4	3
Sau3AI	2	2	2
TaqI	5	5	5
0.13	23	23	20

25 v 28	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	2
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	3	1
TaqI	5	5	5
0.29	23	22	16

25 v 27	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	2
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	2
TaqI	5	5	5
0.09	23	23	21

21 v 26	nx	ny	nxy
AvaII	4	2	2
HhaI	4	4	2
HpaII	5	2	1
MspI	5	2	1
Sau3AI	3	3	1
TaqI	4	5	3
0.53	25	18	10

21 v 25	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	3
HpaII	5	4	2
MspI	5	4	2
Sau3AI	3	2	1
TaqI	4	5	1
0.54	25	23	11

21 v 24	nx	ny	nxy
AvaII	4	4	2
HhaI	4	5	3
HpaII	5	3	1
MspI	5	3	2
Sau3AI	3	3	1
TaqI	4	5	1
0.58	25	23	10

22 v 26	nx	ny	nxy
AvaII	4	2	2
HhaI	4	4	2
HpaII	3	2	0
MspI	3	2	0
Sau3AI	3	3	1
TaqI	5	5	1
0.70	22	18	6

22 v 25	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.24	22	23	17

22 v 24	nx	ny	nxy
AvaII	4	4	4
HhaI	4	5	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.02	22	23	22

23 v 26	nx	ny	nxy
AvaII	4	2	2
HhaI	4	4	2
HpaII	4	2	1
MspI	4	2	0
Sau3AI	2	3	0
TaqI	5	5	1
0.71	23	18	6

23 v 25	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	4	3
MspI	4	4	3
Sau3AI	2	2	2
TaqI	5	5	5
0.13	23	23	20

23 v 24	nx	ny	nxy
AvaII	4	4	4
HhaI	4	5	4
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	3	1
TaqI	5	5	5
0.22	23	23	18

24 v 26	nx	ny	nxy
AvaII	4	2	2
HhaI	5	4	3
HpaII	3	2	0
MspI	3	2	0
Sau3AI	3	3	1
TaqI	5	5	1
0.66	23	18	7

24 v 25	nx	ny	nxy
AvaII	4	4	4
HhaI	5	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.22	23	23	18

24 v 24	nx	ny	nxy
AvaII	4	4	4
HhaI	5	5	5
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	23	23	23

25 v 26	nx	ny	nxy
AvaII	4	2	2
Hind fl	0	0	0
HhaI	4	4	3
HpaII	4	2	0
MspI	4	2	0
Sau3AI	2	3	0
TaqI	5	5	1
0.71	23	18	6

25 v 25	nx	ny	nxy
AvaII	4	4	4
Hind fl	0	0	0
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	2
TaqI	5	5	5
0.00	23	23	23

21 v 23	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	3
HpaII	5	4	1
MspI	5	4	3
Sau3AI	3	2	1
TaqI	4	5	1
0.54	25	23	11

21 v 22	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	3
HpaII	5	3	1
MspI	5	3	2
Sau3AI	3	3	1
TaqI	4	5	1
0.57	25	22	10

21 v 21	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	5	5	5
MspI	5	5	5
Sau3AI	3	3	3
TaqI	4	4	4
0.00	25	25	25

22 v 23	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.20	22	23	18

22 v 22	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

23 v 23	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	2
TaqI	5	5	5
0.00	23	23	23

26 v 41	nx	ny	nxy
AvaII	2	4	2
HhaI	4	6	4
HpaII	2	5	0
MspI	2	6	1
Sau3AI	3	2	0
TaqI	5	5	1
0.65	18	28	8

26 v 40	nx	ny	nxy
AvaII	2	5	1
HhaI	4	5	1
HpaII	2	3	0
MspI	2	3	0
Sau3AI	3	2	0
TaqI	5	2	1
0.84	18	20	3

26 v 39	nx	ny	nxy
AvaII	2	4	2
HhaI	4	4	3
HpaII	2	4	0
MspI	2	4	0
Sau3AI	3	2	0
TaqI	5	3	1
0.69	18	21	6

27 v 41	nx	ny	nxy
AvaII	4	4	4
HhaI	4	6	4
HpaII	4	5	3
MspI	4	6	3
Sau3AI	2	2	2
TaqI	5	5	5
0.18	23	28	21

27 v 40	nx	ny	nxy
AvaII	4	5	3
HhaI	4	5	2
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	2	2
TaqI	5	2	2
0.40	23	20	13

27 v 39	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	2
TaqI	5	3	3
0.05	23	21	21

28 v 41	nx	ny	nxy
AvaII	4	4	4
HhaI	4	6	4
HpaII	3	5	3
MspI	3	6	3
Sau3AI	3	2	1
TaqI	5	5	5
0.20	22	28	20

28 v 40	nx	ny	nxy
AvaII	4	5	3
HhaI	4	5	2
HpaII	3	3	2
MspI	3	3	2
Sau3AI	3	2	1
TaqI	5	2	2
0.43	22	20	12

28 v 39	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	3	3
0.26	22	21	16

29 v 41	nx	ny	nxy
AvaII	4	4	4
HhaI	4	6	4
HpaII	4	5	3
MspI	4	6	3
Sau3AI	2	2	2
TaqI	5	5	5
0.18	23	28	21

29 v 40	nx	ny	nxy
AvaII	4	5	3
HhaI	4	5	1
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	2	2
TaqI	5	2	2
0.44	23	20	12

29 v 39	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	4	3
MspI	4	4	3
Sau3AI	2	2	2
TaqI	5	3	3
0.18	23	21	18

30 v 41	nx	ny	nxy
AvaII	4	4	4
HhaI	4	6	4
HpaII	7	5	4
MspI	7	6	4
Sau3AI	2	2	1
TaqI	3	5	2
0.31	27	28	19

30 v 40	nx	ny	nxy
AvaII	4	5	3
HhaI	4	5	2
HpaII	7	3	2
MspI	7	3	2
Sau3AI	2	2	1
TaqI	3	2	1
0.53	27	20	11

30 v 39	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	7	4	3
MspI	7	4	3
Sau3AI	2	2	1
TaqI	3	3	2
0.29	27	21	17

26 v 38	nx	ny	nxy
AvaII	2	4	2
HhaI	4	4	3
HpaII	2	4	0
MspI	2	4	0
Sau3AI	3	2	0
TaqI	5	3	1
0.69	18	21	6

26 v 37	nx	ny	nxy
AvaII	2	4	2
HhaI	4	4	3
HpaII	2	3	0
MspI	2	3	0
Sau3AI	3	3	1
TaqI	5	3	1
0.63	18	20	7

26 v 36	nx	ny	nxy
AvaII	2	5	1
HhaI	4	4	3
HpaII	2	4	0
MspI	2	4	0
Sau3AI	3	2	0
TaqI	5	3	0
0.80	18	22	4

27 v 38	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	2
TaqI	5	3	3
0.05	23	21	21

27 v 37	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	3	1
TaqI	5	3	3
0.26	23	20	16

27 v 36	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	2	1
TaqI	5	3	2
0.42	23	22	13

28 v 38	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	3	3
0.26	22	21	16

28 v 37	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	3	3
0.05	22	20	20

28 v 36	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	1
TaqI	5	3	2
0.50	22	22	11

29 v 38	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	4	3
MspI	4	4	3
Sau3AI	2	2	2
TaqI	5	3	3
0.18	23	21	18

29 v 37	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	3	1
TaqI	5	3	3
0.30	23	20	15

29 v 36	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	4	4	1
MspI	4	4	1
Sau3AI	2	2	1
TaqI	5	3	2
0.47	23	22	12

30 v 38	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	7	4	3
MspI	7	4	3
Sau3AI	2	2	1
TaqI	3	3	2
0.29	27	21	17

30 v 37	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	7	3	3
MspI	7	3	3
Sau3AI	2	3	0
TaqI	3	3	2
0.32	27	20	16

30 v 36	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	7	4	2
MspI	7	4	2
Sau3AI	2	2	1
TaqI	3	3	3
0.43	27	22	14

26 v 35	nx	ny	nxy
AvaII	2	5	1
HhaI	4	4	4
HpaII	2	4	0
MspI	2	4	0
Sau3AI	3	2	0
TaqI	5	3	0
0.75	18	22	5

26 v 34	nx	ny	nxy
AvaII	2	4	2
HhaI	4	4	3
HpaII	2	4	0
MspI	2	4	1
Sau3AI	3	3	1
TaqI	5	3	0
0.65	18	22	7

26 v 33	nx	ny	nxy
AvaII	2	5	1
HhaI	4	4	3
HpaII	2	4	0
MspI	2	4	0
Sau3AI	3	2	0
TaqI	5	3	0
0.80	18	22	4

27 v 35	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	2	1
TaqI	5	3	2
0.38	23	22	14

27 v 34	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	3	1
TaqI	5	3	1
0.47	23	22	12

27 v 33	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	2	1
TaqI	5	3	2
0.42	23	22	13

28 v 35	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	0
TaqI	5	3	2
0.50	22	22	11

28 v 34	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	3	1
TaqI	5	3	1
0.50	22	22	11

28 v 33	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	2	1
TaqI	5	3	2
0.50	22	22	11

29 v 35	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	4
HpaII	4	4	1
MspI	4	4	1
Sau3AI	2	2	1
TaqI	5	3	2
0.42	23	22	13

29 v 34	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	3	1
TaqI	5	3	1
0.51	23	22	11

29 v 33	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	4	4	1
MspI	4	4	1
Sau3AI	2	2	1
TaqI	5	3	2
0.47	23	22	12

30 v 35	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	7	4	2
MspI	7	4	2
Sau3AI	2	2	2
TaqI	3	3	3
0.35	27	22	16

30 v 34	nx	ny	nxy
AvaII	4	4	2
HhaI	4	4	3
HpaII	7	4	3
MspI	7	4	3
Sau3AI	2	3	0
TaqI	3	3	2
0.47	27	22	13

30 v 33	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	7	4	2
MspI	7	4	2
Sau3AI	2	2	1
TaqI	3	3	3
0.43	27	22	14

26 v 32	nx	ny	nxy
AvaII	2	5	1
HhaI	4	4	4
HpaII	2	4	0
MspI	2	4	0
Sau3AI	3	4	0
TaqI	5	3	0
0.76	18	24	5

26 v 31	nx	ny	nxy
AvaII	2	5	1
HhaI	4	4	2
HpaII	2	4	0
MspI	2	4	0
Sau3AI	3	4	0
TaqI	5	4	0
0.86	18	25	3

26 v 30	nx	ny	nxy
AvaII	2	4	2
HhaI	4	4	3
HpaII	2	7	1
MspI	2	7	1
Sau3AI	3	2	0
TaqI	5	3	0
0.69	18	27	7

27 v 32	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	4	2
TaqI	5	3	2
0.36	23	24	15

27 v 31	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	4	2
TaqI	5	4	2
0.42	23	25	14

27 v 30	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	7	3
MspI	4	7	3
Sau3AI	2	2	1
TaqI	5	3	2
0.32	23	27	17

28 v 32	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	4	2
TaqI	5	3	2
0.43	22	24	13

28 v 31	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	3	4	1
MspI	3	4	1
Sau3AI	3	4	2
TaqI	5	4	2
0.49	22	25	12

28 v 30	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	7	3
MspI	3	7	3
Sau3AI	3	2	0
TaqI	5	3	2
0.35	22	27	16

29 v 32	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	4
HpaII	4	4	1
MspI	4	4	1
Sau3AI	2	4	2
TaqI	5	3	2
0.40	23	24	14

29 v 31	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	4	4	1
MspI	4	4	1
Sau3AI	2	4	2
TaqI	5	4	2
0.50	23	25	12

29 v 30	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	7	3
MspI	4	7	3
Sau3AI	2	2	1
TaqI	5	3	2
0.36	23	27	16

30 v 32	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	7	4	2
MspI	7	4	2
Sau3AI	2	4	1
TaqI	3	3	2
0.45	27	24	14

30 v 31	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	7	4	2
MspI	7	4	2
Sau3AI	2	4	1
TaqI	3	4	2
0.50	27	25	13

30 v 30	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	7	7	7
MspI	7	7	7
Sau3AI	2	2	2
TaqI	3	3	3
0.00	27	27	27

26 v 29	nx	ny	nxy
AvaII	2	4	2
HhaI	4	4	4
HpaII	2	4	1
MspI	2	4	0
Sau3AI	3	2	0
TaqI	5	5	1
0.61	18	23	8

26 v 28	nx	ny	nxy
AvaII	2	4	2
HhaI	4	4	3
HpaII	2	3	0
MspI	2	3	0
Sau3AI	3	3	1
TaqI	5	5	1
0.65	18	22	7

26 v 27	nx	ny	nxy
AvaII	2	4	2
HhaI	4	4	3
HpaII	2	4	0
MspI	2	4	0
Sau3AI	3	2	0
TaqI	5	5	1
0.71	18	23	6

27 v 29	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	4	4	3
MspI	4	4	3
Sau3AI	2	2	2
TaqI	5	5	5
0.13	23	23	20

27 v 28	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	3	1
TaqI	5	5	5
0.20	23	22	18

27 v 27	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	2
TaqI	5	5	5
0.00	23	23	23

28 v 29	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	3
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	5	5	5
0.24	22	23	17

28 v 28	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	5	5	5
0.00	22	22	22

29 v 29	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	2
TaqI	5	5	5
0.00	23	23	23

26 v 26	nx	ny	nxy
AvaII	2	2	2
HhaI	4	4	4
HpaII	2	2	2
MspI	2	2	2
Sau3AI	3	3	3
TaqI	5	5	5
0.00	18	18	18

31 v 41	nx	ny	nxy
AvaII	5	4	4
HhaI	4	6	3
HpaII	4	5	3
MspI	4	6	3
Sau3AI	4	2	2
TaqI	4	5	2
0.36	25	28	17

31 v 40	nx	ny	nxy
AvaII	5	5	3
HhaI	4	5	2
HpaII	4	3	1
MspI	4	3	1
Sau3AI	4	2	2
TaqI	4	2	1
0.56	25	20	10

31 v 39	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	2
HpaII	4	4	2
MspI	4	4	2
Sau3AI	4	2	2
TaqI	4	3	1
0.43	25	21	13

32 v 41	nx	ny	nxy
AvaII	5	4	4
HhaI	4	6	4
HpaII	4	5	3
MspI	4	6	3
Sau3AI	4	2	2
TaqI	3	5	2
0.31	24	28	18

32 v 40	nx	ny	nxy
AvaII	5	5	3
HhaI	4	5	1
HpaII	4	3	1
MspI	4	3	1
Sau3AI	4	2	2
TaqI	3	2	1
0.59	24	20	9

32 v 39	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	2
Sau3AI	4	2	2
TaqI	3	3	1
0.38	24	21	14

33 v 41	nx	ny	nxy
AvaII	5	4	4
HhaI	4	6	4
HpaII	4	5	3
MspI	4	6	3
Sau3AI	2	2	1
TaqI	3	5	2
0.32	22	28	17

33 v 40	nx	ny	nxy
AvaII	5	5	3
HhaI	4	5	1
HpaII	4	3	1
MspI	4	3	1
Sau3AI	2	2	1
TaqI	3	2	1
0.62	22	20	8

33 v 39	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	2
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	2	1
TaqI	3	3	2
0.40	22	21	13

34 v 41	nx	ny	nxy
AvaII	4	4	3
HhaI	4	6	4
HpaII	4	5	3
MspI	4	6	3
Sau3AI	3	2	1
TaqI	3	5	1
0.40	22	28	15

34 v 40	nx	ny	nxy
AvaII	4	5	2
HhaI	4	5	1
HpaII	4	3	1
MspI	4	3	1
Sau3AI	3	2	1
TaqI	3	2	0
0.71	22	20	6

34 v 39	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	2
Sau3AI	3	2	1
TaqI	3	3	1
0.44	22	21	12

35 v 41	nx	ny	nxy
AvaII	5	4	4
HhaI	4	6	4
HpaII	4	5	3
MspI	4	6	3
Sau3AI	2	2	1
TaqI	3	5	2
0.32	22	28	17

35 v 40	nx	ny	nxy
AvaII	5	5	3
HhaI	4	5	1
HpaII	4	3	1
MspI	4	3	1
Sau3AI	2	2	1
TaqI	3	2	1
0.62	22	20	8

35 v 39	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	2	1
TaqI	3	3	2
0.35	22	21	14

31 v 38	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	2
HpaII	4	4	2
MspI	4	4	2
Sau3AI	4	2	2
TaqI	4	3	1
0.43	25	21	13

31 v 37	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	2
HpaII	4	3	1
MspI	4	3	1
Sau3AI	4	3	2
TaqI	4	3	1
0.51	25	20	11

31 v 36	nx	ny	nxy
AvaII	5	5	5
HhaI	4	4	3
HpaII	4	4	4
MspI	4	4	4
Sau3AI	4	2	2
TaqI	4	3	2
0.15	25	22	20

32 v 38	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	2
Sau3AI	4	2	2
TaqI	3	3	1
0.38	24	21	14

32 v 37	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	3
HpaII	4	3	1
MspI	4	3	1
Sau3AI	4	3	2
TaqI	3	3	1
0.45	24	20	12

32 v 36	nx	ny	nxy
AvaII	5	5	5
HhaI	4	4	3
HpaII	4	4	4
MspI	4	4	4
Sau3AI	4	2	2
TaqI	3	3	2
0.13	24	22	20

33 v 38	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	2
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	2	1
TaqI	3	3	2
0.40	22	21	13

33 v 37	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	2
HpaII	4	3	1
MspI	4	3	1
Sau3AI	2	3	1
TaqI	3	3	2
0.48	22	20	11

33 v 36	nx	ny	nxy
AvaII	5	5	5
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	2
TaqI	3	3	3
0.00	22	22	22

34 v 38	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	2
Sau3AI	3	2	1
TaqI	3	3	1
0.44	22	21	12

34 v 37	nx	ny	nxy
AvaII	4	4	3
HhaI	4	4	3
HpaII	4	3	2
MspI	4	3	2
Sau3AI	3	3	1
TaqI	3	3	1
0.43	22	20	12

34 v 36	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	2
HpaII	4	4	3
MspI	4	4	3
Sau3AI	3	2	0
TaqI	3	3	2
0.36	22	22	14

35 v 38	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	3
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	2	1
TaqI	3	3	2
0.35	22	21	14

35 v 37	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	3
HpaII	4	3	1
MspI	4	3	1
Sau3AI	2	3	0
TaqI	3	3	2
0.48	22	20	11

35 v 36	nx	ny	nxy
AvaII	5	5	5
HhaI	4	4	3
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	1
TaqI	3	3	3
0.09	22	22	20

31 v 35	nx	ny	nxy
AvaII	5	5	5
HhaI	4	4	2
HpaII	4	4	4
MspI	4	4	4
Sau3AI	4	2	1
TaqI	4	3	2
0.23	25	22	18

31 v 34	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	3
HpaII	4	4	3
MspI	4	4	3
Sau3AI	4	3	2
TaqI	4	3	2
0.28	25	22	17

31 v 33	nx	ny	nxy
AvaII	5	5	5
HhaI	4	4	3
HpaII	4	4	4
MspI	4	4	4
Sau3AI	4	2	2
TaqI	4	3	2
0.15	25	22	20

32 v 35	nx	ny	nxy
AvaII	5	5	5
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	4	2	1
TaqI	3	3	2
0.13	24	22	20

32 v 34	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	3
HpaII	4	4	3
MspI	4	4	3
Sau3AI	4	3	2
TaqI	3	3	2
0.26	24	22	17

32 v 33	nx	ny	nxy
AvaII	5	5	5
HhaI	4	4	3
HpaII	4	4	4
MspI	4	4	4
Sau3AI	4	2	2
TaqI	3	3	2
0.13	24	22	20

33 v 35	nx	ny	nxy
AvaII	5	5	5
HhaI	4	4	3
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	1
TaqI	3	3	3
0.09	22	22	20

33 v 34	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	3
HpaII	4	4	3
MspI	4	4	3
Sau3AI	2	3	0
TaqI	3	3	2
0.32	22	22	15

33 v 33	nx	ny	nxy
AvaII	5	5	5
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	2
TaqI	3	3	3
0.00	22	22	22

34 v 35	nx	ny	nxy
AvaII	4	5	4
HhaI	4	4	3
HpaII	4	4	3
MspI	4	4	3
Sau3AI	3	2	0
TaqI	3	3	2
0.32	22	22	15

34 v 34	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	3	3	3
TaqI	3	3	3
0.00	22	22	22

35 v 35	nx	ny	nxy
AvaII	5	5	5
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	2
TaqI	3	3	3
0.00	22	22	22

31 v 32	nx	ny	nxy
*Aval*I	5	5	5
*Hha*I	4	4	2
*Hpa*II	4	4	4
*Msp*I	4	4	4
*Sau*3AI	4	4	4
*Taq*I	4	3	3
0.10	25	24	22

31 v 31	nx	ny	nxy
*Aval*I	5	5	5
*Hha*I	4	4	4
*Hpa*II	4	4	4
*Msp*I	4	4	4
*Sau*3AI	4	4	4
*Taq*I	4	4	4
0.00	25	25	25

32 v 32	nx	ny	nxy
*Aval*I	5	5	5
*Hha*I	4	4	4
*Hpa*II	4	4	4
*Msp*I	4	4	4
*Sau*3AI	4	4	4
*Taq*I	3	3	3
0.00	24	24	24

36 v 41	nx	ny	nxy
AvaII	5	4	4
HhaI	4	6	4
HpaII	4	5	3
MspI	4	6	3
Sau3AI	2	2	1
TaqI	3	5	2
0.32	22	28	17

36 v 40	nx	ny	nxy
AvaII	5	5	3
HhaI	4	5	1
HpaII	4	3	1
MspI	4	3	1
Sau3AI	2	2	1
TaqI	3	2	1
0.62	22	20	8

36 v 39	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	2
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	2	1
TaqI	3	3	2
0.40	22	21	13

37 v 41	nx	ny	nxy
AvaII	4	4	4
HhaI	4	6	4
HpaII	3	5	3
MspI	3	6	3
Sau3AI	3	2	1
TaqI	3	5	3
0.25	20	28	18

37 v 40	nx	ny	nxy
AvaII	4	5	3
HhaI	4	5	2
HpaII	3	3	2
MspI	3	3	2
Sau3AI	3	2	1
TaqI	3	2	2
0.40	20	20	12

37 v 39	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	3	3	3
0.22	20	21	16

38v 41	nx	ny	nxy
AvaII	4	4	4
HhaI	4	6	4
HpaII	4	5	3
MspI	4	6	3
Sau3AI	2	2	2
TaqI	3	5	3
0.22	21	28	19

38v 40	nx	ny	nxy
AvaII	4	5	3
HhaI	4	5	2
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	2	2
TaqI	3	2	2
0.37	21	20	13

38v 39	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	1
Sau3AI	2	2	2
TaqI	3	3	3
0.14	21	21	18

39 v 41	nx	ny	nxy
AvaII	4	4	4
HhaI	4	6	4
HpaII	4	5	3
MspI	4	6	3
Sau3AI	2	2	2
TaqI	3	5	3
0.22	21	28	19

39 v 40	nx	ny	nxy
AvaII	4	5	3
HhaI	4	5	2
HpaII	4	3	2
MspI	4	3	2
Sau3AI	2	2	2
TaqI	3	2	2
0.37	21	20	13

39 v 39	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	2
TaqI	3	3	3
0.00	21	21	21

40 v 41	nx	ny	nxy
AvaII	5	4	3
Hind fl	0	0	0
HhaI	5	6	2
HpaII	3	5	2
MspI	3	6	2
Sau3AI	2	2	2
TaqI	2	5	1
0.50	20	28	12

40 v 40	nx	ny	nxy
AvaII	5	5	5
Hind fl	0	0	0
HhaI	5	5	5
HpaII	3	3	3
MspI	3	3	3
Sau3AI	2	2	2
TaqI	2	2	2
0.00	20	20	20

36 v 38	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	2
HpaII	4	4	2
MspI	4	4	2
Sau3AI	2	2	1
TaqI	3	3	2
0.40	22	21	13

36 v 37	nx	ny	nxy
AvaII	5	4	4
HhaI	4	4	2
HpaII	4	3	1
MspI	4	3	1
Sau3AI	2	3	1
TaqI	3	3	2
0.48	22	20	11

36 v 36	nx	ny	nxy
AvaII	5	5	5
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	2
TaqI	3	3	3
0.00	22	22	22

37 v 38	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	4	2
MspI	3	4	2
Sau3AI	3	2	1
TaqI	3	3	3
0.22	20	21	16

37 v 37	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	3	3	3
MspI	3	3	3
Sau3AI	3	3	3
TaqI	3	3	3
0.00	20	20	20

38v 38	nx	ny	nxy
AvaII	4	4	4
HhaI	4	4	4
HpaII	4	4	4
MspI	4	4	4
Sau3AI	2	2	2
TaqI	3	3	3
0.00	21	21	21

41 v 41	nx	ny	nxy
AvaII	4	4	4
HhaI	6	6	6
HpaII	5	5	5
MspI	6	6	6
Sau3AI	2	2	2
TaqI	5	5	5
0.00	28	28	28

APPENDIX C

REA DISTANCE MATRIX VALUES

isolate # → / ↓	01	02	03	04	05	06	07	08	09	10	11
01	0.00	0.00	0.00	0.00	0.00	0.00	0.43	0.20	0.07	0.20	0.00
02	0.00	0.00	0.00	0.00	0.00	0.00	0.43	0.20	0.07	0.20	0.00
03	0.00	0.00	0.00	0.00	0.00	0.00	0.43	0.20	0.07	0.20	0.00
04	0.00	0.00	0.00	0.00	0.00	0.00	0.43	0.20	0.07	0.20	0.00
05	0.00	0.00	0.00	0.00	0.00	0.00	0.43	0.20	0.07	0.20	0.00
06	0.00	0.00	0.00	0.00	0.00	0.00	0.43	0.20	0.07	0.20	0.00
07	0.43	0.43	0.43	0.43	0.43	0.43	0.00	0.53	0.41	0.53	0.43
08	0.20	0.20	0.20	0.20	0.20	0.20	0.53	0.00	0.14	0.00	0.20
09	0.07	0.07	0.07	0.07	0.07	0.07	0.41	0.14	0.00	0.14	0.07
10	0.20	0.20	0.20	0.20	0.20	0.20	0.53	0.00	0.14	0.00	0.20
11	0.00	0.00	0.00	0.00	0.00	0.00	0.43	0.20	0.07	0.20	0.00
12	0.28	0.28	0.28	0.28	0.28	0.28	0.42	0.17	0.22	0.17	0.28
13	0.28	0.28	0.28	0.28	0.28	0.28	0.51	0.29	0.26	0.29	0.28
14	0.27	0.27	0.27	0.27	0.27	0.27	0.49	0.24	0.25	0.24	0.27
15	0.50	0.50	0.50	0.50	0.50	0.50	0.57	0.42	0.49	0.42	0.50
16	0.43	0.43	0.43	0.43	0.43	0.43	0.68	0.45	0.47	0.45	0.43
17	0.00	0.00	0.00	0.00	0.00	0.00	0.43	0.20	0.07	0.20	0.00
18	0.05	0.05	0.05	0.05	0.05	0.05	0.50	0.26	0.12	0.26	0.05
19	0.38	0.38	0.38	0.38	0.38	0.38	0.55	0.44	0.32	0.44	0.38
20	0.22	0.22	0.22	0.22	0.22	0.22	0.55	0.02	0.16	0.02	0.22
21	0.62	0.62	0.62	0.62	0.62	0.62	0.64	0.58	0.61	0.58	0.62
22	0.05	0.05	0.05	0.05	0.05	0.05	0.38	0.24	0.12	0.24	0.05
23	0.24	0.24	0.24	0.24	0.24	0.24	0.49	0.13	0.18	0.13	0.24
24	0.07	0.07	0.07	0.07	0.07	0.07	0.40	0.26	0.14	0.26	0.07
25	0.29	0.29	0.29	0.29	0.29	0.29	0.49	0.09	0.23	0.09	0.29
26	0.65	0.65	0.65	0.65	0.65	0.65	0.79	0.71	0.69	0.71	0.65
27	0.20	0.20	0.20	0.20	0.20	0.20	0.53	0.00	0.14	0.00	0.20
28	0.00	0.00	0.00	0.00	0.00	0.00	0.43	0.20	0.07	0.20	0.00
29	0.24	0.24	0.24	0.24	0.24	0.24	0.53	0.13	0.18	0.13	0.24
30	0.35	0.35	0.35	0.35	0.35	0.35	0.62	0.32	0.29	0.32	0.35
31	0.49	0.49	0.49	0.49	0.49	0.49	0.56	0.42	0.48	0.42	0.49
32	0.43	0.43	0.43	0.43	0.43	0.43	0.64	0.36	0.42	0.36	0.43
33	0.50	0.50	0.50	0.50	0.50	0.50	0.57	0.42	0.49	0.42	0.50
34	0.50	0.50	0.50	0.50	0.50	0.50	0.67	0.47	0.49	0.47	0.50
35	0.50	0.50	0.50	0.50	0.50	0.50	0.67	0.38	0.44	0.38	0.50
36	0.50	0.50	0.50	0.50	0.50	0.50	0.57	0.42	0.49	0.42	0.50
37	0.05	0.05	0.05	0.05	0.05	0.05	0.50	0.26	0.12	0.26	0.05
38	0.26	0.26	0.26	0.26	0.26	0.26	0.61	0.05	0.19	0.05	0.26
39	0.26	0.26	0.26	0.26	0.26	0.26	0.61	0.05	0.19	0.05	0.26
40	0.43	0.43	0.43	0.43	0.43	0.43	0.50	0.40	0.37	0.40	0.43
41	0.20	0.20	0.20	0.20	0.20	0.20	0.50	0.18	0.14	0.18	0.20

sample # → / ↓	12	13	14	15	16	17	18	19	20	21	22
01	0.28	0.28	0.27	0.50	0.43	0.00	0.05	0.38	0.22	0.62	0.05
02	0.28	0.28	0.27	0.50	0.43	0.00	0.05	0.38	0.22	0.62	0.05
03	0.28	0.28	0.27	0.50	0.43	0.00	0.05	0.38	0.22	0.62	0.05
04	0.28	0.28	0.27	0.50	0.43	0.00	0.05	0.38	0.22	0.62	0.05
05	0.28	0.28	0.27	0.50	0.43	0.00	0.05	0.38	0.22	0.62	0.05
06	0.28	0.28	0.27	0.50	0.43	0.00	0.05	0.38	0.22	0.62	0.05
07	0.42	0.51	0.49	0.57	0.68	0.43	0.50	0.55	0.55	0.64	0.38
08	0.17	0.29	0.24	0.42	0.45	0.20	0.26	0.44	0.02	0.58	0.24
09	0.22	0.26	0.25	0.49	0.47	0.07	0.12	0.32	0.16	0.61	0.12
10	0.17	0.29	0.24	0.42	0.45	0.20	0.26	0.44	0.02	0.58	0.24
11	0.28	0.28	0.27	0.50	0.43	0.00	0.05	0.38	0.22	0.62	0.05
12	0.00	0.32	0.27	0.45	0.51	0.28	0.33	0.47	0.18	0.56	0.23
13	0.32	0.00	0.27	0.40	0.43	0.28	0.33	0.38	0.31	0.56	0.23
14	0.27	0.27	0.00	0.18	0.33	0.27	0.32	0.49	0.25	0.46	0.22
15	0.45	0.40	0.18	0.00	0.26	0.50	0.48	0.33	0.43	0.45	0.45
16	0.51	0.43	0.33	0.26	0.00	0.43	0.41	0.32	0.46	0.51	0.48
17	0.28	0.28	0.27	0.50	0.43	0.00	0.05	0.38	0.22	0.62	0.05
18	0.33	0.33	0.32	0.48	0.41	0.05	0.00	0.35	0.27	0.60	0.10
19	0.47	0.38	0.49	0.33	0.32	0.38	0.35	0.00	0.45	0.69	0.43
20	0.18	0.31	0.25	0.43	0.46	0.22	0.27	0.45	0.00	0.59	0.26
21	0.56	0.56	0.46	0.45	0.51	0.62	0.60	0.69	0.59	0.00	0.57
22	0.23	0.23	0.22	0.45	0.48	0.05	0.10	0.43	0.26	0.57	0.00
23	0.21	0.21	0.12	0.47	0.36	0.24	0.30	0.40	0.15	0.54	0.20
24	0.25	0.25	0.20	0.42	0.45	0.07	0.12	0.40	0.28	0.58	0.02
25	0.17	0.29	0.20	0.33	0.45	0.29	0.35	0.44	0.11	0.54	0.24
26	0.67	0.63	0.73	0.80	0.57	0.65	0.63	0.63	0.71	0.53	0.70
27	0.17	0.29	0.24	0.42	0.45	0.20	0.26	0.44	0.02	0.58	0.24
28	0.28	0.28	0.27	0.50	0.43	0.00	0.05	0.38	0.22	0.62	0.05
29	0.29	0.29	0.16	0.47	0.28	0.24	0.30	0.40	0.15	0.58	0.29
30	0.42	0.31	0.44	0.43	0.29	0.35	0.32	0.28	0.33	0.69	0.39
31	0.48	0.36	0.23	0.15	0.35	0.49	0.51	0.47	0.47	0.36	0.45
32	0.51	0.43	0.22	0.13	0.25	0.43	0.45	0.36	0.42	0.43	0.48
33	0.45	0.40	0.18	0.00	0.26	0.50	0.48	0.33	0.43	0.45	0.45
34	0.66	0.40	0.47	0.32	0.43	0.50	0.48	0.38	0.48	0.49	0.55
35	0.49	0.40	0.27	0.09	0.22	0.50	0.48	0.24	0.39	0.53	0.55
36	0.45	0.40	0.18	0.00	0.26	0.50	0.48	0.33	0.43	0.45	0.45
37	0.33	0.33	0.32	0.48	0.41	0.05	0.00	0.35	0.27	0.60	0.10
38	0.22	0.35	0.29	0.40	0.42	0.26	0.22	0.41	0.07	0.57	0.30
39	0.22	0.35	0.29	0.40	0.42	0.26	0.22	0.41	0.07	0.57	0.30
40	0.33	0.51	0.40	0.62	0.64	0.43	0.40	0.60	0.41	0.64	0.43
41	0.28	0.25	0.13	0.32	0.35	0.20	0.25	0.38	0.19	0.58	0.24

sample # → / ↓	23	24	25	26	27	28	29	30	31	32	33
01	0.24	0.07	0.29	0.65	0.20	0.00	0.24	0.35	0.49	0.43	0.50
02	0.24	0.07	0.29	0.65	0.20	0.00	0.24	0.35	0.49	0.43	0.50
03	0.24	0.07	0.29	0.65	0.20	0.00	0.24	0.35	0.49	0.43	0.50
04	0.24	0.07	0.29	0.65	0.20	0.00	0.24	0.35	0.49	0.43	0.50
05	0.24	0.07	0.29	0.65	0.20	0.00	0.24	0.35	0.49	0.43	0.50
06	0.24	0.07	0.29	0.65	0.20	0.00	0.24	0.35	0.49	0.43	0.50
07	0.49	0.40	0.49	0.79	0.53	0.43	0.53	0.62	0.56	0.64	0.57
08	0.13	0.26	0.09	0.71	0.00	0.20	0.13	0.32	0.42	0.36	0.42
09	0.18	0.14	0.23	0.69	0.14	0.07	0.18	0.29	0.48	0.42	0.49
10	0.13	0.26	0.09	0.71	0.00	0.20	0.13	0.32	0.42	0.36	0.42
11	0.24	0.07	0.29	0.65	0.20	0.00	0.24	0.35	0.49	0.43	0.50
12	0.21	0.25	0.17	0.67	0.17	0.28	0.29	0.42	0.48	0.51	0.45
13	0.21	0.25	0.29	0.63	0.29	0.28	0.29	0.31	0.36	0.43	0.40
14	0.12	0.20	0.20	0.73	0.24	0.27	0.16	0.44	0.23	0.22	0.18
15	0.47	0.42	0.33	0.80	0.42	0.50	0.47	0.43	0.15	0.13	0.00
16	0.36	0.45	0.45	0.57	0.45	0.43	0.28	0.29	0.35	0.25	0.26
17	0.24	0.07	0.29	0.65	0.20	0.00	0.24	0.35	0.49	0.43	0.50
18	0.30	0.12	0.35	0.63	0.26	0.05	0.30	0.32	0.51	0.45	0.48
19	0.40	0.40	0.44	0.63	0.44	0.38	0.40	0.28	0.47	0.36	0.33
20	0.15	0.28	0.11	0.71	0.02	0.22	0.15	0.33	0.47	0.42	0.43
21	0.54	0.58	0.54	0.53	0.58	0.62	0.58	0.69	0.36	0.43	0.45
22	0.20	0.02	0.24	0.70	0.24	0.05	0.29	0.39	0.45	0.48	0.45
23	0.00	0.22	0.13	0.71	0.13	0.24	0.09	0.36	0.46	0.49	0.47
24	0.22	0.00	0.22	0.66	0.26	0.07	0.26	0.40	0.46	0.45	0.42
25	0.13	0.22	0.00	0.71	0.09	0.29	0.13	0.40	0.38	0.36	0.33
26	0.71	0.66	0.71	0.00	0.71	0.65	0.61	0.69	0.86	0.76	0.80
27	0.13	0.26	0.09	0.71	0.00	0.20	0.13	0.32	0.42	0.36	0.42
28	0.24	0.07	0.29	0.65	0.20	0.00	0.24	0.35	0.49	0.43	0.50
29	0.09	0.26	0.13	0.61	0.13	0.24	0.00	0.36	0.50	0.40	0.47
30	0.36	0.40	0.40	0.69	0.32	0.35	0.36	0.00	0.50	0.45	0.43
31	0.46	0.46	0.38	0.86	0.42	0.49	0.50	0.50	0.00	0.10	0.15
32	0.49	0.45	0.36	0.76	0.36	0.43	0.40	0.45	0.10	0.00	0.13
33	0.47	0.42	0.33	0.80	0.42	0.50	0.47	0.43	0.15	0.13	0.00
34	0.56	0.47	0.47	0.65	0.47	0.50	0.51	0.47	0.28	0.26	0.32
35	0.51	0.51	0.38	0.75	0.38	0.50	0.42	0.35	0.23	0.13	0.09
36	0.47	0.42	0.33	0.80	0.42	0.50	0.47	0.43	0.15	0.13	0.00
37	0.30	0.12	0.35	0.63	0.26	0.05	0.30	0.32	0.51	0.45	0.48
38	0.18	0.32	0.14	0.69	0.05	0.26	0.18	0.29	0.43	0.38	0.40
39	0.18	0.32	0.14	0.69	0.05	0.26	0.18	0.29	0.43	0.38	0.40
40	0.40	0.40	0.44	0.84	0.40	0.43	0.44	0.53	0.56	0.59	0.62
41	0.22	0.18	0.18	0.65	0.18	0.20	0.18	0.31	0.36	0.31	0.32

sample # → / ↓	34	35	36	37	38	39	40	41
01	0.50	0.50	0.50	0.05	0.26	0.26	0.43	0.20
02	0.50	0.50	0.50	0.05	0.26	0.26	0.43	0.20
03	0.50	0.50	0.50	0.05	0.26	0.26	0.43	0.20
04	0.50	0.50	0.50	0.05	0.26	0.26	0.43	0.20
05	0.50	0.50	0.50	0.05	0.26	0.26	0.43	0.20
06	0.50	0.50	0.50	0.05	0.26	0.26	0.43	0.20
07	0.67	0.67	0.57	0.50	0.61	0.61	0.50	0.50
08	0.47	0.38	0.42	0.26	0.05	0.05	0.40	0.18
09	0.49	0.44	0.49	0.12	0.19	0.19	0.37	0.14
10	0.47	0.38	0.42	0.26	0.05	0.05	0.40	0.18
11	0.50	0.50	0.50	0.05	0.26	0.26	0.43	0.20
12	0.66	0.49	0.45	0.33	0.22	0.22	0.33	0.28
13	0.40	0.40	0.40	0.33	0.35	0.35	0.51	0.25
14	0.47	0.27	0.18	0.32	0.29	0.29	0.40	0.13
15	0.32	0.09	0.00	0.48	0.40	0.40	0.62	0.32
16	0.43	0.22	0.26	0.41	0.42	0.42	0.64	0.35
17	0.50	0.50	0.50	0.05	0.26	0.26	0.43	0.20
18	0.48	0.48	0.48	0.00	0.22	0.22	0.40	0.25
19	0.38	0.24	0.33	0.35	0.41	0.41	0.60	0.38
20	0.48	0.39	0.43	0.27	0.07	0.07	0.41	0.19
21	0.49	0.53	0.45	0.60	0.57	0.57	0.64	0.58
22	0.55	0.55	0.45	0.10	0.30	0.30	0.43	0.24
23	0.56	0.51	0.47	0.30	0.18	0.18	0.40	0.22
24	0.47	0.51	0.42	0.12	0.32	0.32	0.40	0.18
25	0.47	0.38	0.33	0.35	0.14	0.14	0.44	0.18
26	0.65	0.75	0.80	0.63	0.69	0.69	0.84	0.65
27	0.47	0.38	0.42	0.26	0.05	0.05	0.40	0.18
28	0.50	0.50	0.50	0.05	0.26	0.26	0.43	0.20
29	0.51	0.42	0.47	0.30	0.18	0.18	0.44	0.18
30	0.47	0.35	0.43	0.32	0.29	0.29	0.53	0.31
31	0.28	0.23	0.15	0.51	0.43	0.43	0.56	0.36
32	0.26	0.13	0.13	0.45	0.38	0.38	0.59	0.31
33	0.32	0.09	0.00	0.48	0.40	0.40	0.62	0.32
34	0.00	0.32	0.36	0.43	0.44	0.44	0.71	0.40
35	0.32	0.00	0.09	0.48	0.35	0.35	0.62	0.32
36	0.36	0.09	0.00	0.48	0.40	0.40	0.62	0.32
37	0.43	0.48	0.48	0.00	0.22	0.22	0.40	0.25
38	0.44	0.35	0.40	0.22	0.00	0.14	0.37	0.22
39	0.44	0.35	0.40	0.22	0.14	0.00	0.37	0.22
40	0.71	0.62	0.62	0.40	0.37	0.37	0.00	0.50
41	0.40	0.32	0.32	0.25	0.22	0.22	0.50	0.00

APPENDIX D
ALIGNED SEQUENCES

GUIDE TO ALIGNED SEQUENCES

"A" Adenine
"C" Cytosine
"G" Guanine
"T" Thymine
"N" A,C,G, or T
"-" Deletion
"." Match to Reference Molecule

Isolate 01 is the reference molecule

Isolate	Sequence
01	t--c--c-gtaggtgaa-c-t-gcggaaggatcattattgaa--tt----
02	.t-.--.-.....-.c.-.....--..----
03	.t-.--.-.....-.c.-.....--..----
04	.t-.--.-.....-.-.-.....--.g----
05	.t-.--.-.....-.-.-.....--..----
06	.tt.--.-.....-.c.-.....--..----
07	.--.--.-.....-.-.-.....aa..t--.c----
08	.t-.--.-...t.....-.-.-.....--.g----
09	.t-.--.-.....-.c.-.....--..ttt-
10	.t-.--.-.....-.-.-.....--.g----
11	.t-.--.-.....-.c.-.....--..----
12	.t-.--.-.....-.c.-.....t--..ttct
13	.t-.--.-.....-.-.-.....--.g----
14	.t-.--.-.....-.-.-.....--.g----
15	.t-.--.-.....-.-.-.....--.g----
16	.t-.--.-.....-.-.-.....--..t---
17	.t-.--.-.....-.-.-.....--..----
18	.t-.--.-.....-.-.-.....--..----
19	.t-.--.-.....-.-.-.....at..----
20	.g-.--.-.....-.c.-.....--.g----
21	.--.tc.-..t.....-.-ca....g.....cc..---------
22	.--.--.-.....-.-.-.....--..----
23	.t-.--.-.....-.-.-.....--..t---
24	.--.--.-.....-.-.-.....--..----
25	.t-.--.-.....-.-.-.....--.g----
26	.--.tc.-..t.....-.-ca....g.....----------
27	.t-.--.-.....-.-.-.....--.g----
28	.t-.--.-.....-.-.-.....--..----
29	.t-.--.-.....-.c.-.....--..t---
30	.--.--.-.....-.-.-.....--..tt--
31	.--t--.n.....-.-.-.....--.g----
32	.t-.--.-.....-.c.-.....--.g----
33	.--.--.-.....-.-.-.....--.g----
34	.--g--.t...t..t..n.-.-nt...cn..nn.....n--.n----
35	.t-.--.-.....-.c.-.....--.g----
36	.t-.--.-.....-.-.-.....--.g----
37	.t-.--.-.....-.c.-.....--..----
38	.t-.--.-.....-.c.-.....--.g----
39	.t-.--.-.....-.c.-.....--.g----
40	.t-.--.-.....-.c.-.....ac...--.a----
41	.t-.--.-.....-.-.-.....--.g----

Isolate	Sequence
01	aatgtagagt---ttggt--tgtagctggctccta----attaaa--ctt
02	.....---.....--.....----.....--...
03	.....---.....--.....----.....--...
04	..ct.g...----.c...--...c.....--------g.ctt.--t..
05	.....---.....--.....----.....--...
06	.....---.....--.....----.....--...
07	g.cc.----------.--c.ggt..at..t..c----t.c.gc--tg.
08	...ta....----.....--...t.....----------...
09	....a.....---.....--.....c.-------.....g--t.-
10	...ta....----.....--...t.....----------...
11	.....---.....--.....----.....--...
12	....ag....---.ga..--...t.....ct..gggg-....nttt..c
13	.....----.....--...c.....ct..----------t--ngc
14	..ct.g...----.c...--...c.....--------g.ctt.--t..
15	..ct.g...----.c...--...c.....--------g.ctt.--t..
16	.....----.....--.....--..cg----...t..--ta.
17	.....---.....--.....----.....--...
18	.....---.....--.....----.....--...
19	....a.....---.....--.....c.a..----t.c.t.--t..
20	...ta....----.....--...t.....----------...
21	----------.t.--.ac.a..cc.----------...--.--
22	.....---.....--.....----.....--...
23	.....----.....--.....c.ncg----gan.n.--t..
24	.....---.....--.....----.....--...
25	...ta....----.....--...t.....----------...
26	----------.c--..g.a.gc..c..ag---gcnc.c--.cg
27	..ct.g...----.c...--...c.....--------g.ctt.--t..
28	.....---.....--.....----.....--...
29	.....----.....--.....n..cngag-..nn.t--..c
30	....a.....att.....--.....c.----------.tt--.a.
31	...a.....----.....--...c.....----------cc
32	...a.....----.....--...c.....----------cc
33	..ct.g...----.c...--...c.....--------g.ctt.--t..
34	.nca.g.n..---ng..n--gt.gn.n...c..----------.n--.an
35	.....a---g.t..gc...c.....ggg.tggg.....t--t.c
36	..ct.g...----.c...--...c.....--------g.ctt.--t..
37	.....---.....--.....----.....--...
38	...ta....----.....--...t.....----------...
39	...ta....----.....--...t.....----------...
40	.c.a.g.t..c--....c--.....----------...
41	..ct.g...----.c...--...c.....--------g.ctt.--tg.

Isolate	Sequence
01	---g-gg--ggca-tg-tgc------acac-ctttc--tctttcatc--c
02	---.-..--....-..-...------....-....--.....--.
03	---.-..--....-..-...------....-....--.....--.
04	---.-.c--a...-..-...------..g.-...ct--ct.....--.
05	---.-..--....-..-...------....-....--.....--.
06	---.-..--....-..-...------....-....--.....--.
07	---.-c.--cttt-..c...------..g.-tg..g--aa....------
08	---cc..--....-..-...------....-.-...--.....---.
09	------.--....-..-...------....-...a.--.....--.
10	---cc..--....-..-..n------....-.-...--...n....---.
11	---.-..--....-..-...------....-....--.....--.
12	---c-aa--....-..-...------....-.-...--.....---.
13	---.-.a--....-..-...------..g.-.-...--.....---.
14	---.-.c--a...-..-...------..g.-...ct--ct.....--.
15	---.-.c--a...-..-...------..g.-...ct--ct.....--.
16	---t-t.--....-..-...------....-.-..--.....---.
17	---.-..--....-..-...------....-....--.....--.
18	---.-..--....-..-...------....-....--.....--.
19	------.--....-..-...------....-...c.--.....--.
20	---cc..--....-..-...------....-.-...--.....---.
21	----------c,.-..-..a------...ta.c.a.--.g..g.t..gg.
22	---.-..--....-..-...------....-....--.....--.
23	ctc.-..--..gg-g.-..n------tn..-.-nc.--..c.c...---.
24	---.-..--....-..-...------....-....--.....--.
25	---cc..--....-..-...------....-.-...--.....---.
26	---.-aa--an.c-.t-..tgaactt.t..-..ga.--.g.ng.c..--g
27	---.-.c--a...-..-...------..g.-...ct--ct.....--.
28	---.-..--....-..-...------....-....--.....--.
29	ngg.-..--..nt-n.-...------n.n.-.-.c.--..nn..-nn--.
30	---t-t.--....-..-...------....-....gnt.t.....--.
31	---.-..--a...-..-...------..-g-.....--.....---.
32	---.-..--a...-..-...------..-g-.....--.....---.
33	---.-.c--a...-..-...------..g.-...ct--ct.....--.
34	---.-..--..an-at-..n------.ng.-t.c..--...ccacct--.
35	---t-.ttc....-..-...------..g.-.-.g.--.....tcat--.
36	---.-.c--a...-..-...------..g.-...ct--ct.....--.
37	---.-..--....-..-...------....-....--.....--.
38	---cc..--....-..-...------....-.-...--.....---.
39	---cc..--....-..-...------....-.-...--.....---.
40	---c-..--a...a..-...------..g.-.cgc.--at...t...---
41	---.-.c--a...-..-...------..g.-...ct--ct.....--.

Isolate	Sequence
01	-------catacacacctgtgcacc---t-gtgagacag----------
02	-------.....---.-.....----------
03	-------.....---.-.....----------
04	a------..c....c.....t---.-.....----------
05	-------.....---.-.....----------
06	-------.....---.-.....----------
07	----------.....----------
08	-------..c.....t---.-.....----------
09	-------..c.....a...---.-.....----------
10	-------..c.....t---.-.....----------
11	-------.....---.-.....----------
12	-------..c....c.....t---.-.....----------
13	-------..c.....t---.-.....g.----------
14	a------..c....c.....t---.-.....----------
15	a------..c....c.....t---.-.....t.gagaccggtaa
16	-------..c.....---.-.....g...----------
17	-------.....---.-.....----------
18	-------.....---.-.....----------
19	-------..c.....a...---.-.....----------
20	-------..c.....t---.-.....----------
21	-------ggg.ttgc..c.g..g..---.c...t.c.cc----------
22	-------.....---.-.....----------
23	-------..cn.n.n..nc.nat.n---n-c.n.t.nna----------
24	-------.....---.-.....----------
25	-------..c.....t---.-.....----------
26	gcgcacg.cgg.c.c.ag.g..c..---.-cg..a...a----------
27	a------..c....c.....t---.-.....----------
28	-------.....---.-.....----------
29	-------..c....n....nan..---.-....n.----------
30	a------..c....nn....aann.---.-...gng..----------
31	-------..c.....t---.-.....g.----------
32	-------..c.....t---.-.....g.----------
33	a------..c....c.....t---.-.....----------
34	-------..c....nn....aan.t---.-....cng..----------
35	-------..c.....t---.-.....----------
36	a------..c....c.....t---.-.....----------
37	-------.....---.-.....----------
38	-------..c.....t---.-.....----------
39	-------..c.....t---.-.....----------
40	---------.ttc.....gac.-..ag.t.t.----------
41	a------..cn...c.....t---.-.....----------

Isolate	Sequence
01	---a----------tg----------ttttgt----ggggg
02	---.----------..----------.....----.....
03	---.----------..----------.....----.....
04	----------.g.a----.acc.
05	---.----------.t----------a.....----.....
06	---.----------..----------.....----.....
07	----------ac----------..cg..----t.ta.
08	----------.
09	---.----------..gggaatttacttgttgc...tg----.aata
10	----------
11	---.----------..----------...:...----.....
12	---taaggtt------.c----------....t.----t....
13	---.----------g.cctt----------...ct.----tcac.
14	----------.g.a----.acc.
15	aaa.----------a.----------.c..ca----.tct.
16	---.----------a.----------.----------.
17	---.----------..----------.....----.....
18	---.----------..----------.....----.....
19	---.----------..gggaa----------...ac.----t.ct.
20	----------
21	---g----------ga----------.cag.c----.ccc.
22	---.----------..----------.....----.....
23	---t----------a.----------.----------n..
24	---.----------..----------.....----.....
25	----------
26	---g----------na----------gcag.c----ac.cc
27	----------.g.a----.acc.
28	---.----------..----------.....----.....
29	----------t----------.g..n.----.....
30	----------.----a....
31	---.----------..acc
32	---.----------..acc
33	----------..g----a.acc
34	---.----------.n----------c..nnccccc.....
35	----------..g----..acc
36	----------.g.a----.acc.
37	---.----------..----------.....----.....
38	----------
39	----------
40	---gatacctctcgtc.c----------.c...a----.a..c
41	----------..g----a.acc

Isolate	Sequence
01	gg----------aag--g-------aa--ct---tt-------a----
02	..----------...--.-------..--..---..-------.----
03	..----------...--.-------..--..---..-------.----
04	.t----------..a--a-------..--ag---.n-------c----
05	..----------...--.-------..--..---..-------.----
06	..----------...--.-------..--..---..-------.----
07	ct----------.gt--t-------..--..---c.-------.gctg
08	..----------n..--.-------gc--..---cc-------n----
09	ca----------...--.-------c.--a.agg..-------.----
10	..----------g..--.-------gn--n.---n.-------.----
11	..----------...--.-------..--..---..-------.----
12	..----------.c---..-------g----
13	a.----------.g.--.-------gg--gc---..-------c----
14	.t----------..a--a-------..--aa---g.-------c----
15	ct----------..a--t-------cc--a.---a.-------.----
16	..----------.ct--tttaattc..--t.---.a-------.----
17	..----------...--.-------..--..---..-------.----
18	..----------...--.-------..--..---..-------.----
19	ctttttgaaataca...--.-------t.--a.agg..-------.----
20	..----------g..--.-------gc--..---.c-------.----
21	cc----------t..--.-------..--ac---..-------.----
22	..----------...--.-------..--..---..-------.----
23	..----------.g.--.-------.----------n----
24	..----------...--.-------..--..---..-------.----
25	..----------g..--.-------gc--..---.c-------.----
26	..----------c..--cc------..--g.---.n-------.----
27	.t----------..a--a-------..--ag---.n-------c----
28	..----------...--.-------..--..---..-------.----
29	.----------.--.n---n.-------g----
30	..----------..ttt.-------tg--.g---n.-------.----
31	.t----------..a--a-------..--g.---c.tccgtct.----
32	.t----------..a--a-------..--g.---c.tccgtct.----
33	..----------t.a--a-------..--aa---g.-------c----
34	..----------g.t--c-------.g--.c---cn-------g----
35	.t----------..a--a-------..gt..---.c-------.----
36	.t----------..a--a-------..--ag---.n-------c----
37	..----------..a--.-------n.--n.---..-------.----
38	..----------g..--.-------gc--..---.c-------.----
39	..----------g..--.-------gc--..---.c-------.----
40	..----------.t.----------
41	..----------t.a--a-------..--aa---g.-------c----

Isolate	Sequence
01	-------ttggacctt------ct----actc----------ccccct
02	-------.........------..----....----------.....
03	-------.........------..----....----------.....
04	-------.ccatn.gg------..----.a.n----------..nnn
05	-------.........------..----....----------.....
06	-------.........------..----....----------.....
07	cttccgc..tt..a..------ta----..aa----------..aag
08	-------.g..ntt..------.c----ngnn----------.nnn.
09	-------.....----------
10	-------...ntt..tccngt..----.t.t----------ta.ac
11	-------.........------..----....----------.....
12	-------c..-----.------..----...t----------aat..
13	-------cgtctg.ca------a.----..at----------ata..
14	-------..cagt..g------..----.aat----------..ata
15	-------caaac..a.------t.----.a.t----------gaa..
16	-------...t...c.------..gtct....aatccacacaaac..aa.
17	-------.........------..----....----------.....
18	-------.........------..----....----------.....
19	-------.....----------
20	-------....ctt..tcctgt..----...t----------ta.ac
21	-------a.tcttg..------t.----.t.----------
22	-------.........------..----....----------.....
23	-------a.....nna------.n----c.nn----------t.tnn
24	-------.........------..----....----------.....
25	-------....-.t..------t.----c..g----------t.ta.
26	-------c.----...------g.----tt.n----------a.a..
27	-------.ccatn.gg------..----.a.n----------..nnn
28	-------.........------..----....----------....
29	-------na.....---------.----------a.tnn
30	-------..tct.ta.------ta----ta..----------n.agg
31	-------..aa...ac------ac----.aa.----------...a.
32	-------..aa...ac------ac----.aa.----------...a.
33	-------..cagt..g------..----.aat----------..ata
34	-------.nt.--.n.------nn----nn.----------..a..
35	-------g.ct..t.a------a.----.ta.----------aaa..
36	-------.ccntnngg------n.----.a..----------.nnnn
37	-------.....a.n.------.c----..n.----------....c
38	-------....ctt..tcctgt..----...t----------ta.ac
39	-------....ctt..tcctgt..----...t----------ta.ac
40	--------...gga..----------g.t.g
41	-------..cagt..g------..----.aat----------..ata

Isolate	Sequence
01	tg-------a-------cttctg----------tct-----ac-------
02	..-------.-------.....----------...-----..-------
03	..-------.-------.....----------...-----..-------
04	.cc------.-------acc.cn----------.t.-----.n-------
05	..-------.-------.....----------...-----..-------
06	..-------.-------.....----------...-----..-------
07	.c-------t-------agaa..----------..a-----.a-------
08	.a-------nnncaann.cnt.t----------.t.-----.aaannnan
09	----------------.c....----------...-----..-------
10	aa-------.-------..ca.t----------.a.tttaa..-------
11	..-------.-------.....----------...-----..-------
12	ac-------.-------.-a.ac----------...-----.t-------
13	ca-------t-------a.a..t----------.aa-----..-------
14	.acaaaccc.-------t..aat----------.ga-----..-------
15	ga-------.-------tg.aa.----------...-----g.-------
16	.t-------.-------t..t.c----------a.a-----c.-------
17	..-------.-------.....----------...-----..-------
18	..-------.-------.....----------...-----..-------
19	----------------.c....----------...-----..-------
20	aa-------.-------..ca.t----------.t.-----.a-------
21	..-------gaat----.....----------ag.-----.g-------
22	..-------.-------.....----------...-----..-------
23	nt-------.-------n...atacanaatcaa...-----.n-------
24	..-------.-------.....----------...-----..-------
25	.ttacacaa.-------..ca.t----------.a.ttaaa..-------
26	aa-------.-------ac..n----------aga-----.naanacnn
27	.cc------.-------acc.cn----------.t.-----.n-------
28	..-------.-------.....----------...-----..-------
29	n.-------t-------..a..t----------..n-----t.-------
30	a.-------.-------.cc..c----------...nn---..-------
31	..tattta-.-------a..gaa----------.g.-----.a-------
32	..tattta-.-------a..gaa----------.g.-----.a-------
33	.acaaaccc.-------t..aat----------.ga-----..-------
34	cc-------.-------n.ngan----------a.a-----nt-------
35	cc-------.-------t..aat----------.aa-----..-------
36	.cc------.-------acc.nn----------.t.-----.n-------
37	..-------.-------a...n.----------.nn-----..-------
38	aa-------.-------..ca.t----------.t.ttaaa..-------
39	aa-------.-------..ca.t----------.t.ttaaa..-------
40	.a-------.-------ggg..c----------..c-----t.-------
41	.anaaaccc.-------t..aat----------.ga-----..-------

Isolate	Sequence
01	-----t---------taa----t-------------------------t
02	-----.---------.------g-------------------------.
03	-----.---------..-------------------------------.
04	-----.---------...----nngnangnta----------------.
05	-----.---------.n.------------------------------.
06	-----.----------------.------------------------.
07	-----.acaataaaa...----c-------------------------a
08	gnttg.---------...----.gntgtactaacatctgc---------.
09	-----.---------c.c----acacctgc------------------.
10	-----.---------g..----.gtnnttnatgtancactaacatctgc.
11	-----.---------.-n----c-------------------------.
12	-----.---------.c.cacg.-------------------------.
13	-----.---------g..----.gtaaagatccacgtctgc--------.
14	-----.---------g..----.gtaagtctgc----------------.
15	--.
16	-----.----------g----c-------------------------.
17	-----.---------...-----------------------------.
18	-----.---------...-----------------------------.
19	-----.---------c.c----acctgc--------------------.
20	-----a---------a..----n-------------------------.
21	-----.---------.tt----.-------------------------a
22	-----.---------...----.-------------------------.
23	-----.---------.t.----.-------------------------.
24	-----.---------...----.-------------------------.
25	-----.---------g..----.gtaattgatgtaacgcatacatctgc.
26	aa---.---------g..----.-------------------------a
27	-----.---------...----nngnangntagtctgc----------.
28	-----.---------.n.----c-------------------------.
29	-----a---------..t----a-------------------------.
30	-----.---------ctn----.ntacacctgc---------------.
31	-----.---------.g.----.gtaaccacagtctgc----------.
32	-----.---------.g.----.gtaacacagtctgc-----------.
33	-----.---------g..----.gtaaaacagtctgc-----------.
34	-----.---------.n.----.ntnngna------------------.
35	-----.---------g.c----agtctgc-------------------.
36	-----.---------n..----nngaangttagtctgc----------.
37	-----n---------.------.-------------------------.
38	-----.---------g..----.gtaattgatgtaacgtaacatctgc-.
39	-----.---------g..----.gtaattgatgtaacgtaacatctgc-.
40	-----a---------a.t----.-------------------------.
41	-----.---------g..----.gtaagtntgc---------------.

Isolate	Sequence
01	----------cct----------c-----
02	----------...----------.-----
03	----------...----------.-----
04	----------...----------.-----
05	----------...----------.-----
06	----------...----------.-----
07	----------a..----------t-----
08	----------...----------.-----
09	----------...----------.-----
10	----------...----------.-----
11	----------...----------.-----
12	----------.tn----------.-----
13	----------...----------.-----
14	----------...----------.-----
15	----------...----------.-----
16	----------...----------.-----
17	----------...----------.-----
18	----------...----------.-----
19	----------...----------.-----
20	gaatgtaattgatgtaacataacatctgct...----------.-----
21	----------.aaataaataaaaa.-----
22	----------...----------.-----
23	----------gg.----------.-----
24	----------...----------.-----
25	----------...----------.-----
26	----------aac----------.-----
27	----------...----------.-----
28	----------...----------.-----
29	----------.a.----------.nntnt
30	----------...----------.-----
31	----------...----------.-----
32	----------...----------.-----
33	----------...----------.-----
34	----------naa----------g-----
35	----------...----------.-----
36	----------...----------.-----
37	----------...----------.-----
38	----------...----------.-----
39	----------...----------.-----
40	----------..a----------g-----
41	----------...----------.-----

Isolate	Sequence
01	----------t----------ttg-tgcat---t---ag--
02	----------.----------...-.....---.---..--
03	----------.----------...-.....---.---..--
04	----------.----------...-.....---.---..--
05	----------.----------...-.....---.---..--
06	----------.----------...-.....---.---..--
07	----------.cattgtggtggatttgga...-...cg---.---.a--
08	----------.----------.aaa.tt..---.---..--
09	----------.----------...-.....---.---..--
10	----------.----------.aaa.tt..---.---..--
11	----------.----------...-.....---.---..--
12	----------.----------n..-...nc---a---..--
13	----------.----------caaa.....---.---..--
14	----------.----------.aaa.aa..---.---..--
15	----------.----------.aaa.aa..---.---..--
16	----------.----------...-.....---.---..--
17	----------.----------...-.....---.---..--
18	----------.----------...-.....---.---..--
19	----------.----------...-.....---.---..--
20	----------.----------.aaa.tt..---.---..--
21	----------.----------..c-aa..c---.---catg
22	----------.----------...-.....---.---..--
23	----------c----------..n-.tgg.nna.---..--
24	----------.----------...-.....---.---..--
25	----------.----------.aaa.t...---.---..--
26	----------c----------.ca-....c---.----.--
27	----------.----------.aaa.aa..---.---..--
28	----------.----------...-.....---.---..--
29	tacggtncttn.----------.n.-.....---n---n.--
30	----------.----------...-.....---.---..--
31	----------.----------.aaa.aa..---.---..--
32	----------.----------.aaa.aa..---.---..--
33	----------.----------.aaa.aa..---.---..--
34	----------.----------...-gt.c.---.nta.a--
35	----------.----------.aaa.tt..---.---..--
36	----------.----------.aaa.aa..---.---..--
37	----------.----------...-.....---.---..--
38	----------.----------.aaa.tt..---.---..--
39	----------.----------.aaa.tt..---.---..--
40	----------g----------c.c-..g..---g---t.gg
41	----------n----------.aaa.aa..---.---..--

Isolate	Sequence
01	--------ctgg--atctcagtgttatgct-----tgg----------t
02	--------....--.............-----...----------.
03	--------....--.............-----...----------.
04	--------....--.............-----...----------.
05	--------....--.............-----...----------.
06	--------....--.............-----...----------.
07	--------.....--c..atcc..aa....a-----.tagcttgtgcttt.
08	--------....--........-a.....-----...----------.
09	--------....--.............-----...----------.
10	--------....--........-a.....-----...----------.
11	--------....--.............-----...----------.
12	--------ag..nt....nn.........-----...----------.
13	--------....--.........---a...-----c..----------.
14	--------....--........-a..ca..-----...----------.
15	--------....--........-a..ca..-----...----------.
16	--------....--.............-----...----------.
17	--------....--.............-----...----------.
18	--------....--.............-----...----------.
19	--------....--.............-----...----------.
20	--------....--........-a.....-----...----------.
21	ccc-----..a.--gg.gtg.....gg.ga-----.c.----------g
22	--------....--.............-----...----------.
23	--------gn..--n.t..n.g.g..n.gn-----...----------g
24	--------....--.............-----...----------.
25	--------....--........-a.....-----...----------.
26	--------..t.--g.g.tg.gncac...c-----.tt----------.
27	--------....--........-a..ca..-----...----------.
28	--------....--.............-----...----------.
29	--------nn..--n.nn.n.n..n.g...-----g..----------.
30	--------....--.............-----...----------.
31	--------....--........-a.....-----...----------.
32	--------....--........-a....g-----gtt----------.
33	--------....--........-a..ca..-----...----------.
34	--------a.nn--n.aggn.gn..t.tanngaan...----------g
35	--------.....--.....g..a.a.ca..-----...----------.
36	--------....--........-a..ca..-----...----------.
37	--------....--.............-----...----------.
38	--------....--........-a.....-----...----------.
39	--------....--........-a.....-----...----------.
40	ggtttgtg.a..--c.gc.tt.c.ggc.g.-----ct.----------c
41	--------....--........-a..ca..-----...----------.

Isolate	Sequence
01	tcca---ctca-gcgtgataagt--------tatctatcgctgaggacac
02	....---....-..........--------..................
03	....---....-..........--------..................
04	....---....-..........--------..................
05	....---....-..........--------..................
06	....---....-..........--------..................
07	.a..gtg...g-..a..g.gt.a--------..at....tgc.cc.t.g.
08	....---...g-..........--------....ac............-
09	....---...g-.........a.--------.................-
10	....---...g-..........--------....ac............-
11	....---....-..........--------..................
12	....---....-..........--------.................-
13	....---...g-..........---------....ac...........
14	....---...g-..........---------....ac............-
15	....---...g-..........---------....ac............-
16	....---....-..........---------.................-
17	....---....-..........--------..................
18	....---....-..........--------..................
19	....---...g-.........a.--------.................-
20	....---...g-..........--------....ac............-
21	c.a.---ag.cc...a.gg.c.gccggcccc..aa.c.a.tg.c....c.
22	....---....-..........--------..................
23	.n..---a.nn-.gnn.gn..nn--------...tn..t.--.n..gg.n
24	....---....-..........--------..................
25	....---...g-..........--------....ac............-
26	...g---gaag-..ag.ccnt.a--------a..tc.gt.gc...ct.g.
27	....---...g-..........---------....ac............-
28	....---....-..........--------..................
29	..n.---n..g-...g..n....--------nt..nt.n..g.n.n....
30	....---...g-..........--------.................-
31	....---...g-..........---------....ac............-
32	....---...g-..........---------....ac............-
33	....---...g-..........---------....ac............-
34	...n---a.ng-.g.n.gn.n.---------g...a..t.--.n..gg.n
35	....---...g-..........---------....at............-
36	....---...g-..........---------....ac............-
37	....---....-..........--------..................
38	....---...g-..........--------....ac............-
39	....---...g-..........--------....ac............-
40	...c---..g.-aatgc..t..c--------g.gt.cata.....ct.cg
41	....---...g-..........---------....ac............-

Isolate	Sequence
01	cctgttaaa----------aaggggtggccaa----ggtaaatgcag
02	.....----------.....----.....
03	.....----------.....----.....
04	.....----------.....----.....
05	.....----------.....----.....
06	.....----------.....----.....
07	.t.----------...cc..----------t.ct.t
08	-....a...----------.....------.g....a...
09	-....a...----------.....----.....
10	-....a...----------.....------.g....a...
11	.....----------.....----.....
12	-...g....----------..--.....----.....c....
13	..--g....----------..--.....-------.gg.t.....
14	-.....----------..--.....------.gc.....
15	-.....----------..--.....------.gc.....
16	-....----------..ca.....----.....
17	.....----------.....----.....
18	.....----------.....----.....
19	-....a...----------.....----.....
20	-....a...----------.....------.g....a...
21	----------.tc.....tcctct.cg..g.agt.
22	.....----------.....----.....
23	nnn.nn...----------..n....c.----..nn..a.nn.
24	.....----------.....----.....
25	-....a...----------.....------.g....a...
26	.----------a..acc..g.----.cgc.--.t..
27	-.....----------..--.....------.gc.....
28	.....----------.....----.....
29	ng.----------..an..n.n.n.n----..n...g..n.
30	-....a...----------.---.....----.....
31	-....a...----------.....------.g.....
32	-....a...----------.....------.g.....
33	-.....----------..--.....------.gc.....
34	nnn.nn...----------..n....cg----..---n..gg.
35	-....----------..ca.....g----.aa.tt.a...
36	-.....----------..--.....------.gc.....
37	.....----------.....----.....
38	-....a...----------.....------.g....a...
39	-....a...----------.....------.g....a...
40	t..a..ggtgtgataattatct.c.cc....a.g.----...tc.-----
41	-.....----------..--.....------.gc.....

Isolate	Sequence
01	atgaacc---gcttctaatagtccattgacttggacaatat----ctaa-
02	.....---.....----....
03	.....---.....----....
04	.....---.....----....
05	.....---.....----....
06	.....---.....----....
07	...tg.a---.....c....c...---.....-------..t.-
08	.....---.....t...a.a..a....--..----ta.t-
09	.....---.....c.....c.c----.----
10	.....---.....t...a.a..a....--..----ta.t-
11	.....---.....----....
12	.....---.....c.....--------.t.-
13	.....---.....c.....t.....a..a.....--------gt.-
14	.....---.....at.----aa..a
15	.....---.....at.----aa..a
16	.....---.....c.....-------.act-
17	.....---.....----....
18	.....---.....----....
19	.....---.....c.....c----.----
20	.....---.....t...a.a..a....--..----ta.t-
21	..att..---..a..gg.g..cgacga.c.cct.c.gt..aaccc.c..-
22	.....---.....----....
23	gn.g...---.g..t.n.....nn...an...nnn.nga----a.n.a
24	.....---.....----....
25	.....---.....t...a.a..a....--..----ta.t-
26	t.a....ctc....-.gga..g..c.g.cgg..cc.tgccg----n...a
27	.....---.....at.----aa..a
28	.....---.....----....
29	.g..c..---....t...n.n.....gn.n.n.n....a.a----ta..-
30	.....---.....c.....----t.---
31	.....---.....a.a.....-..----ta..-
32	.....---.....a.a.....-..----ta..-
33	....g..---.....at.----aa..a
34	ga.g.nn---.g..t...ac....nn.t.gn...nnc.a.------n..-
35	.....---.....-------...-
36	.....---.....at.----aa..a
37	.....---.....----....
38	.....---.....t...a.a..a....--..----ta.t-
39	.....---.....t...a.a..a....--..----ta.t-
40	--..ctt---.....cc....----g.aa.....c----.----
41	.....---.....at.----aa..a

Isolate	Sequence
01	----------ttt--atga-tc--tgatctcaaatcaggtaggactaccc
02	----------..--....-..--..........................
03	----------..--....-..--..........................
04	----------..--....-..--..........................
05	----------..--....-..--..........................
06	----------..--....-..--..........................
07	----------c..--.ac.c.t--..gc.....................
08	----------..--.a..-..--..........................
09	----------..--....-..--..........................
10	----------..--.a..-..--..........................
11	----------..--....-..--..........................
12	----------..--....-..--..........................
13	----------..--....-..--..........................
14	----------..--....-..--..........................
15	----------..--....-..--..........................
16	----------c..--....-..--..........................
17	----------..--....-..--..........................
18	----------..--....-..--..........................
19	----------..--....-..--..........................
20	----------..--.a..-..--..........................
21	----------c..--tcc.-aggt...c....g..........a.....
22	----------..--....-..--..........................
23	tt--------..--....-..--..........................
24	----------..--....-..--..........................
25	----------..--.a..-.g--..........................
26	cccccaactc..g--.aa.-.t--...c...gg..........a.....
27	----------..--....-..--..........................
28	----------..--....-..--..........................
29	----------...tt....-..--..........................
30	----------..--....-..--..........................
31	----------..--....-..--..........................
32	----------..--....-..--..........................
33	----------..--....-..--..........................
34	----------n..--....-..--..........................
35	----------..--....-..--..........................
36	----------..--....-..--..........................
37	----------..--....-..--..........................
38	----------..--.a..-..--..........................
39	----------..--.a..-..--..........................
40	----------..g--.ca.-.t--...c.....................
41	----------..--....-..--..........................

Isolate	Sequence
01	gctgaacttaa
02	.....
03	.....
04	.....
05	.....
06	.....
07	.....---
08	.....
09	.....
10	.....
11	.....-.
12	.....-.
13	.....
14	.....
15	.....
16	.....
17	.....
18	.....
19	.....
20	.....
21	.....
22	.....
23	.....
24	.....
25	.....
26	.....
27	.....
28	.....-.
29	.....
30	.....
31	.....
32	.....
33	.....---
34	.....
35	.....
36	.....
37	.....
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40	.....
41	.....

APPENDIX E

MATRIX DEPICTING THE NUMBER OF NUCLEOTIDE MATCHES BETWEEN EACH ISOLATE OUT OF 400 ALIGNABLE SITES

This Appendix is in the form of a matrix, where each isolate's sequence is compared to every other isolate's sequence over 400 alignable sites. The isolate #s across the top are the reference molecules used to obain the number of nucleotide matches with every other isolate listed below the isolate #. For example, the first column used isolate 01 as a reference molecule in the Align Plus program. The numbers below it indicate how many nucleotide matches each isolate # (to the left) had to the reference molecule out of 400 alignable sites.

isolate #

	01	02	03	04	05	06	07	08	09	10	11
01	400	397	398	336	396	397	233	308	343	309	396
02	397	400	399	336	396	399	233	307	345	311	398
03	398	399	400	337	397	399	232	307	345	311	398
04	334	334	335	400	334	334	237	314	314	308	332
05	396	396	397	336	400	396	233	308	344	315	396
06	397	399	399	336	396	400	236	308	345	311	398
07	231	231	230	237	227	232	400	225	238	237	228
08	308	305	305	314	306	306	237	400	321	357	308
09	341	345	343	316	344	343	238	321	400	322	344
10	311	311	311	310	315	307	241	361	324	400	314
11	396	396	398	334	396	398	234	308	344	312	400
12	327	328	323	311	324	328	237	299	324	310	324
13	308	313	313	315	312	314	244	316	313	329	314
14	311	310	310	351	311	310	256	318	316	327	311
15	310	311	311	354	311	311	257	313	315	328	310
16	339	340	340	326	339	340	242	308	353	319	339
17	399	398	399	336	397	398	235	308	343	309	397
18	399	398	399	336	397	398	235	308	343	309	397
19	344	345	345	321	345	345	243	323	387	323	346
20	312	313	313	308	311	311	253	366	324	380	312
21	213	214	203	207	216	214	216	211	222	216	214
22	400	397	398	336	396	397	233	308	343	309	396
23	253	252	251	242	253	252	195	245	255	249	248
24	400	397	398	336	396	397	233	308	343	309	396
25	316	318	315	314	318	317	254	361	327	382	317
26	202	201	204	204	201	201	215	211	206	217	207
27	310	311	311	376	313	313	244	326	306	319	310
28	397	397	397	335	397	397	233	310	344	307	399
29	277	280	278	260	277	278	187	254	273	260	277
30	329	331	329	315	328	328	224	308	343	314	330
31	321	321	320	327	321	320	249	336	318	350	320
32	318	319	318	324	318	318	248	331	317	347	318
33	307	309	309	349	306	307	257	308	313	326	304
34	223	224	222	226	222	225	189	225	217	226	221
35	310	311	312	323	311	311	247	321	316	331	312
36	307	312	312	367	312	312	242	328	306	320	307
37	385	386	386	336	383	387	224	308	341	311	385
38	315	315	315	309	314	314	256	365	325	383	315
39	315	315	315	309	314	314	256	365	325	383	315
40	243	245	242	238	242	246	258	243	256	246	247
41	308	307	307	350	308	307	258	313	310	326	312

isolate # → / ↓	12	13	14	15	16	17	18	19	20	21
01	323	312	311	312	341	399	399	342	314	207
02	323	313	312	313	342	398	398	343	313	202
03	323	313	312	313	342	399	399	343	313	203
04	308	313	353	356	330	334	334	323	306	209
05	322	312	313	311	341	397	397	345	311	202
06	326	314	312	313	342	398	398	343	313	202
07	241	240	256	259	244	231	231	231	247	216
08	299	316	312	321	310	306	306	321	366	207
09	324	315	316	317	353	343	343	387	324	214
10	308	331	329	328	323	309	309	319	380	214
11	324	314	311	312	343	397	397	344	312	208
12	400	311	304	304	330	324	324	323	313	222
13	311	400	335	336	323	308	308	319	331	211
14	298	335	400	399	326	310	310	318	329	209
15	298	336	399	400	327	311	311	321	331	208
16	330	319	326	327	400	339	339	352	320	226
17	322	314	312	313	343	400	400	344	314	202
18	322	314	312	313	343	400	400	344	314	202
19	323	319	318	319	352	346	346	400	323	206
20	311	331	329	331	324	312	312	321	400	222
21	208	215	213	212	230	214	214	212	222	400
22	323	312	311	312	341	399	399	342	314	207
23	255	237	243	244	257	253	253	257	247	189
24	323	312	311	312	341	399	399	342	314	207
25	312	336	331	333	324	316	316	322	389	222
26	206	216	212	214	210	204	204	209	215	267
27	289	321	377	380	317	311	311	312	319	207
28	328	314	311	312	342	398	398	343	311	199
29	271	261	257	258	277	279	279	272	259	199
30	317	307	305	306	340	328	328	346	313	203
31	301	339	353	354	326	321	321	323	354	207
32	300	335	350	351	324	318	318	318	353	217
33	296	334	394	395	325	303	303	319	331	215
34	222	231	230	230	221	222	222	215	225	179
35	309	322	354	355	329	311	311	317	335	216
36	294	321	375	376	317	308	308	311	321	202
37	322	312	316	317	340	385	385	341	309	202
38	312	335	332	334	326	315	315	322	395	221
39	312	335	332	334	326	315	315	322	395	221
40	233	261	250	251	247	242	242	255	250	221
41	298	336	394	395	322	307	307	316	327	209

isolate # → / ↓	22	23	24	25	26	27	28	29	30	31
01	400	251	400	318	204	314	397	277	331	321
02	397	252	397	318	205	315	397	280	329	321
03	398	251	398	313	206	315	397	280	329	320
04	334	244	334	312	206	376	333	260	315	325
05	396	249	396	318	205	315	397	277	330	321
06	397	250	397	317	203	315	397	278	330	320
07	231	193	231	250	219	246	229	195	224	247
08	308	243	308	357	209	326	306	254	308	336
09	341	255	341	327	208	306	340	267	343	320
10	311	247	311	382	215	321	315	262	314	350
11	396	248	396	315	207	314	399	279	330	320
12	327	253	327	314	210	291	328	271	315	297
13	308	235	308	334	216	323	314	261	307	335
14	311	235	311	331	208	377	311	257	309	351
15	310	236	310	333	208	380	310	258	310	352
16	339	255	339	322	210	317	340	277	338	326
17	399	249	399	318	206	315	398	277	330	321
18	399	249	399	318	206	315	398	277	330	321
19	344	255	344	324	207	308	345	270	344	321
20	312	245	312	389	217	319	311	259	315	350
21	213	183	213	220	271	211	199	199	211	211
22	400	251	400	318	204	314	397	277	331	321
23	253	400	253	247	197	238	252	279	255	248
24	400	251	400	318	204	314	397	277	331	321
25	316	245	316	400	220	324	318	260	315	356
26	202	199	202	220	400	207	201	184	201	214
27	310	234	310	322	207	400	311	258	304	339
28	397	250	397	318	205	313	400	278	330	321
29	277	275	277	258	182	256	276	400	273	265
30	329	249	329	317	201	304	328	271	400	311
31	321	244	321	358	214	343	321	263	315	400
32	318	242	318	354	218	340	318	263	312	394
33	307	231	307	329	210	373	307	254	307	350
34	223	262	223	223	184	238	222	226	218	235
35	310	244	310	332	212	341	310	268	302	347
36	307	235	307	320	208	391	305	257	303	338
37	385	249	385	310	202	314	384	277	331	318
38	315	246	315	394	218	320	314	260	311	353
39	315	246	315	394	218	320	314	260	311	353
40	243	199	243	248	226	246	242	210	249	259
41	308	238	308	331	210	375	308	261	306	349

isolate # →	32	33	34	35	36	37	38	39	40	41
01	318	309	223	310	311	385	315	315	247	308
02	319	309	224	315	312	386	313	313	247	307
03	318	309	224	312	312	386	313	313	250	307
04	322	351	230	321	367	334	309	309	236	352
05	318	314	222	313	312	383	312	312	244	310
06	318	309	225	317	312	387	314	314	246	309
07	246	259	197	245	242	226	250	250	264	258
08	331	314	227	319	326	308	365	365	249	321
09	317	315	217	312	306	341	323	323	246	312
10	347	324	232	327	318	311	383	383	244	326
11	318	306	221	314	311	385	313	313	251	308
12	296	300	226	311	290	324	312	312	233	300
13	331	332	237	322	321	308	333	333	267	334
14	348	394	238	352	375	310	332	332	248	394
15	349	395	234	353	376	311	334	334	249	395
16	322	325	221	327	317	336	326	326	239	322
17	318	309	222	313	312	385	315	315	250	309
18	318	309	222	313	312	385	315	315	250	309
19	316	317	217	311	309	339	324	324	249	314
20	349	331	227	333	321	309	395	395	252	329
21	213	217	169	216	210	204	217	217	225	213
22	318	309	223	310	311	385	315	315	247	308
23	244	239	258	246	241	253	248	248	203	246
24	318	309	223	310	311	385	315	315	247	308
25	352	329	227	334	320	310	394	394	250	331
26	214	214	190	210	210	202	216	216	224	212
27	338	373	240	337	391	312	320	320	242	375
28	318	309	222	314	311	384	314	314	248	308
29	265	254	228	268	257	277	260	260	216	261
30	308	303	216	302	301	333	315	315	245	302
31	394	352	233	345	342	318	357	357	259	353
32	400	349	231	343	339	316	357	357	256	350
33	349	400	231	349	371	306	333	333	244	390
34	233	227	400	228	238	224	224	224	209	237
35	347	351	226	400	338	310	337	337	256	351
36	337	371	240	336	400	311	321	321	243	371
37	316	312	224	310	313	400	305	305	249	311
38	351	333	228	335	321	311	400	400	253	332
39	351	333	228	335	321	311	400	400	253	332
40	258	248	203	252	247	251	251	251	400	248
41	346	390	235	351	371	309	330	330	248	400

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