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MOLECULAR COEVOLUTION OF PACIFIC NORTHWEST HANTAVIRUSES AND THEIR HOST, THE DEER MOUSE, *PEROMYSCUS MANICULATUS*

by

PHILIP DARREN JONES

A dissertation submitted in partial fulfillment of the
requirements for the degree of

DOCTOR OF PHILOSOPHY
in
BIOLOGY

Portland State University
2009

DISSERTATION APPROVAL

The abstract and dissertation of Philip Darren Jones for the Doctor of Philosophy in Biology were presented February 13, 2009, and accepted by the dissertation committee and the doctoral program.

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ABSTRACT

An abstract of the dissertation of Philip Darren Jones for the Doctor of Philosophy in Biology presented February 13, 2009.

Title: Molecular Coevolution of Pacific Northwest Hantaviruses and their host, the Deer Mouse, *Peromyscus maniculatus*

Sin Nombre virus (SNV, family *Bunyaviridae*, genus Hantavirus), hosted by the deer mouse, *Peromyscus maniculatus* (family Cricetidae, Subfamily Neotominae), is the primary etiological agent of *Hantavirus* pulmonary syndrome (HPS) in the western United States. HPS, with known pathogenicity only to humans and for which there is no cure or prophylaxis, affects the epithelium of the lungs by making the capillaries leaky, thereby resulting in bilateral infiltrates, and eventually leading to respiratory failure and death by drowning in approximately 38% of hospitalized patients.

In the Americas, *Peromyscus* has been co–evolving with hantaviruses for approximately 12–20 million years, since the first cricetids crossed Beringia, radiating and differentiating into the Neotominae and Sigmodontinae currently found in the New World. As it stands, the evolutionary relationships of deer mice remains unclear, consequently, so too is the associated viral phylogeny, with twelve named quasispecies in the genus *Hantavirus* presently characterized in North America, and twenty five quasispecies in the Western Hemisphere. Evidence of this opacity is seen in the new species that are regularly being discovered from among these host

conspecifics suggesting that many uncharacterized hantaviruses remain to be described.

To improve our understanding of these co–evolutionary relationships, as well as the epidemiology of HPS, specimens of both host and virus were collected from throughout the Portland, Oregon region, as well as other locations across North America. Analyses of the ND3, ND4, ND4L, and arginine tRNA host mitochondrial genes yielded average genetic divergence estimates of 0.0413 among local (Portland, OR) deer mice relative to specimens from the type locality of the species, in Newfoundland. Phylogenetic analysis also revealed a deep division in the phylogeny of deer mice discriminating the distribution into two distinct clades on either side of the Mississippi River, and suggesting that western deer mice in fact are constituted by a formerly cryptic species distinct from those in Newfoundland and eastern North America. Sequencing and phylogenetic comparison of the Pacific Northwest hantaviral G1/G2 glycoprotein precursor encoding gene showed a large genetic distance ($p=0.143$) from Sin Nombre type specimens from New Mexico, suggesting that the Portland area virus minimally constitutes a new strain.

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Chapter 1: Introduction

Epizootiology-

In the last few decades there has been what appears to be a significant increase in the emergence of pathogenic infectious diseases such as Sudden Acute Respiratory Syndrome (SARS; emerging in SE Asia in 2002), Ebola Virus (sub-Saharan Africa, 1976), Human Immunodeficiency Virus (HIV; sub-Saharan Africa, 1970's), Marburg Virus (Sub-Saharan Africa, 1970's), and tick-borne diseases such as Lyme disease (NE USA, 1990's)(Daszak *et al.*, 2000). Among these recent discoveries are the hantaviruses, the causative agents of *Hantavirus* Pulmonary Syndrome (HPS; Western Hemisphere, 1993) and Hemorrhagic Fever with Renal Syndrome (HFRS; Eastern Hemisphere, 1950's). The appearance of these diseases are believed to be associated with a range of underlying causal factors including interactions with zoonotic pathogens, that would otherwise normally be contained within a host–parasite relationship, between wildlife and humans (Daszak *et al.*, 2000). The term "emerging infectious disease" (EID) has been coined to describe the plethora of pathogens implicated in these recent discoveries, and is specifically used to define diseases that have recently increased in occurrence or geographic range, moved into new host populations, or only recently been discovered (Daszak *et al.*, 2000).

In 1993 in the southwestern United States, an outbreak occurred of a previously unknown disease, now identified as *Hantavirus* Pulmonary Syndrome (HPS). The subsequent investigation led to the identification of the etiological agent—a novel hantavirus— *Sin Nombre* virus (SNV; Childs *et al.*, 1994; Nichol *et al.*, 1993). In the

years since this discovery, the number of *Hantavirus* geno– and serotypes identified in the Americas has grown to at least 23 (Johnson *et al.*, 1997; Morzunov *et al.*, 1998; Pini *et al.*, 2003; Rhodes *et al.*, 2000; Sanchez *et al.*, 2001; Schmaljohn *et al.*, 1995; Yates *et al.*, 2002), with this number on the increase as previously unknown hantaviruses are identified. In addition to *Sin Nombre* Virus some of the other most common hantaviruses known to cause HPS include; *New York* virus (NY), *Bayou* virus (BAY), *Black Creek Canal* virus (BCC), and *Andes* virus, with *Sin Nombre* virus being responsible for most of the 465 (Centers for Disease Control [CDC], 2007) known cases in the United States (Monroe *et al.*, 1999; Peters *et al.*, 1998; Schmaljohn *et al.*, 1997). Recent surveys for *Hantavirus* antibodies have revealed *Hantavirus*–infected rodents throughout most of North America (Holmes *et al.*, 2004; Monroe *et al.*, 1999; Rhodes *et al.*, 2000; Sanchez *et al.*, 2001; Schmaljohn *et al.*, 1995; Yates *et al.*, 2002). Hantaviruses have been proposed to be transmitted through aggressive encounters—primarily between individuals of the same sex (usually males)—or by infectious aerosols generated from contaminated urine, feces, blood, or saliva (Schmaljohn *et al.*, 1997; Olsson *et al.*, 2002).

Evolution-

It has been hypothesized by many that for every type of *Hantavirus* there is a specific rodent host species whose members can potentially acquire a chronic, asymptomatic, lifelong infection from the virus (Kaufman *et al.*, 1994; Morzunov *et al.*, 1998; Netski *et al.*, 1999). It has been shown through phylogenetic analyses that the topologies of the evolutionary relationships among hantaviruses were closely

correlated with those of their known or suspected primary mammal reservoirs (Borucki *et al.*, 2000; Monroe *et al.*, 1999; Plyusnin and Morzunov 2000; Sironen *et al.*, 2001; Yates *et al.*, 2002).

In the Americas, the deer mouse has been co–evolving with hantaviruses for approximately 12–20 million years, since the first cricetids crossed the Bering Land Bridge, radiating and differentiating into the Rodent subfamilies Neotominae and Sigmodontinae found in the New World today (Yates *et al.*, 2002). While much is known about deer mouse phylogeny, it remains less than fully understood, and as a result of the documented host-parasite specificity among deer mice and their hantaviruses (Yates *et al.*, 2002), the associated viral phylogeny may be unresolved as well. New species of Peromyscus are increasingly being revealed from among these former host conspecifics (Chirhart *et al.*, 2001; Zheng *et al.*, 2003), revealing the potential likelihood of many uncharacterized hantaviruses waiting to be described as well.

For many years it was believed that hantaviruses were maintained exclusively within Order Rodentia. Only very recently has that perception been challenged as genetically distinct hantaviruses have increasingly come to be found residing among members of the Order Soricomorpha (shrews) - family Soricidae (Xiao *et al.*, 1994; Arai *et al.*, 2007, 2008). In the former Soviet Union in the 1980's, antibodies to *Hantavirus* were found in members of families *Soricidae* and *Talpidae* (Gavrilovskaya *et al.*, 1983; Tkachenko *et al.*, 1983; Gligic *et al.*, 1989). At that time molecular techniques were not yet available to delineate genetic identity of potentially hosted viruses to confirm whether these were truly distinct viral evolutionary lineages or

merely cases of ecological spillover from a sympatric rodent host. As of yet, no human disease has been associated with shrew–borne hantaviruses (Arai *et al.* 2007).

Worldwide, most hantaviruses have been found in members of the rodent families Cricetidae (Subfamilies Neotominae and Arvicolinae) and Muridae (Subfamily Murinae), with genetically distinct viral lineages found associated with specific members of these taxa (Fig. 1). Hantaviruses are believed to have arisen at least 136 million years ago before the split of the Mammalian Orders Soricomorpha and Rodentia, evidenced by the presence of distinct hantaviral lineages found in both Orders (Carey *et al.*, 1971; Plyusnin *et al.*, 1996; Hughes and Friedman, 2000). Among the earliest described are those found in East Asia, including Hantaan virus from the Hantaan River valley, recognized during the Korean War, as well as Seoul virus, also found in Korea (Lee *et al.*, 1978)(fig. 3). These East Asian viral species have been found to be reservoired within members of the family Muridae, Subfamily Murinae, as *Apodemus agrarius* (Hantaan), and *Rattus norvegicus* (Seoul; Lee *et al.*, 1982). Another murine *Hantavirus* is the recently described Sangassou virus, shown to reside within the African wood mouse *Hylomyscus simus*, found in Sangassou, Guinea (Klempa *et al.*, 2006). Reducing the clarity of this strict regional relationship, but upholding the host Subfamily paradigm, is the presence of Dobrava virus found in Northern Europe and hosted by the murine *Apodemus flavicollis*, a congener of the Hantaan virus host (Avsic-Zupanc *et al.*, 1992; 2000). Phylogenetic analyses have supported placement of Dobrava virus in the murine-hosted viral clade (Avsic-Zupanc *et al.*, 1992) (Fig. 1). European and North Asian serotypes such as Tula virus, Topografov virus, and Puumala virus, among others, have been found within

arvicoline hosts such as *Microtus* and *Clethrionomys* species (Plyusnin *et al.*, 1994; Vapalahti *et al.*, 1999).

The more recently described members in *Hantavirus* are those found in the new world. In North and South America most of these infections are in species of the Subfamily Neotominae. Only a few Murid-hosted hantaviruses, consisting of Seoul virus in *Rattus norvegicus,* Subfamily Murinae, have been seen in the western hemisphere, primarily in urban environs (Monroe *et al.*, 1999). Cricetid rodents found hosting hantaviruses are many (table 1). In North America most common among these are hosts in the genus *Peromyscus* (Monroe *et al.*, 1999). The deer mouse, *Peromyscus maniculatus,* Subfamily Neotominae, has been identified as the reservoir for Sin Nombre virus (Childs *et al.*, 1994). In-depth studies of Sin Nombre virus in North America have shown substantial genetic diversity and geographic structure of genetic variants within the viral quasispecies that may be the result of the genetic diversity in *P. maniculatus* (Monroe *et al.*, 1999; Morzunov *et al.*, 1996; Nichol *et al.*, 1999; Plyusnin *et al.*, 1996; Plyusnin *et al.*, 2000; Salazar-Bravo *et al.*, 2002). This rodent genetic diversity is paralleled by that of the virus (Dragoo *et al.*, 2006). *Peromyscus maniculatus* as currently recognized have a vast range across the entire North American continent, excluding the southeastern U.S. (fig. 4). In addition, at least as many as 70 morphological subspecies are described in *P. maniculatus* (including sympatric subspecies), underscoring the variability in the species (Hall, 1981; Michaux *et al.*, 2001).

As pointed out by Wilson and Ruff (1999), the basis of the *Peromyscus* taxonomic framework was built upon morphological analyses, long before the advent of

molecular techniques. Recently, several former conspecifics, such as *P. maniculatus keeni, P. maniculatus sitkensis*; and congeners including *P. oreas* and *P. sitkensis* (now combined as *P. keeni)* have been removed from *maniculatus* and formally recognized as distinct taxa using chromosomal and molecular techniques (fig. 4) (Allard and Greenbaum, 1988; Avise *et al.*, 1983; Calhoun and Greenbaum, 1991; Chirhart *et al.*, 2005; Chirhart *et al.*, 2001; Greenbaum and Baker, 1978; Gunn, 1988; Hogan *et al.*, 1997; Hogan *et al.*, 1993; Michaux *et al.*, 2001; Smith *et al.*, 2000; Zheng *et al.*, 2003). Current literature has shown a wide range (2.5 - 16%) of intrageneric genetic divergence, being the percent difference in pair-wise comparisons of sequences, within *Peromyscus* (Bradley and Baker, 2001). In point of fact, Bradley and Baker (2001) show *Peromyscus boylii* only 2.5% genetically divergent from *P. simulus* in a well accepted sister (non-conspecific) relationship. In addition, much of the current data in the literature strongly suggest that co–speciation between hantaviruses and their hosts characterize the long–term evolution of these genera (Morzunov *et al.*, 1998; Yates *et al.*, 2002; Dragoo *et al.*, 2006).

While, as stated above, much analyses of *P. maniculatus* subspecies distributions have been morphologically based, analyses of hantaviruses have in contrast been undertaken using molecular techniques (Hjelle *et al.*, 1995a; Hjelle *et al.*, 1995b; Hjelle *et al.*, 1994; Johnson *et al.*, 1997; Li *et al.*,1995; Nichol *et al.*, 1993; Nichol *et al.*, 1999; Plyusnin and Morzunov, 2000; Dragoo *et al.*, 2006).

Virology-

Members of the genus *Hantavirus* of the family *Bunyaviridae* (5 genera, 250 species), are spherical, 100 nanometer diameter particles enclosed within a phospholipid bilayer envelope (Elliot *et al.*, 1991; Nichol *et al.*, 2005). Expressed within and extending above this envelope are two glycoproteins (G1 and G2) that facilitate cell entry via a clathrin coated pit (Elliot *et al.*, 1991; Nichol *et al.*, 2005). Within the envelope is a protein nucleocapsid that houses a segmented single-stranded negative-sense RNA genome ~12,100 nucleotides (nt) in length. These segments are small (S), medium (M), and large (L) (Plyusnin *et al.*, 1996). The S segment, approximately 2,000nt in length, encodes the genes for the nucleocapsid proteins that encase the RNA genome in daughter viral particles. The medium, or M segment (3,700nt), encodes the envelope glycoprotein precursor that is then co-translationally cleaved to yield the G1 and G2 glycoproteins (Elliot, 1990; Vapalahti *et al.*, 1992; Bohlman *et al.*, 2002). The L segment (6,500nt) encodes the RNA-specific polymerase that is used to replicate viral progeny genomes (Elliott *et al.*, 1991; Chizhikov *et al.*, 1995).

Purview of this study-

The genomes, or subsets thereof, of many different hantaviruses have been sequenced to varying extents (Schmaljohn *et al.*, 1990; Elliot *et al.*, 1991; Monroe *et al.*, 1999; Morzunov *et al.*, 1996; Nichol *et al.*, 1999; Plyusnin *et al.*, 1996, 2000; Salazar-Bravo *et al.*, 2002; Yates *et al.*, 2002). The majority of studies have chosen to examine the M segment (at the very least) as it is responsible for the glycoproteins used for cell

recognition, and thereby potentially the most variable since it is likely under the greatest amount of evolutionary pressure from the corresponding host. The L segment, coding for the RNA polymerase, is believed to be the most conserved of the *Hantavirus* genes (Schmaljohn, 1990; Elliott *et al.*, 1991; Chizhikov *et al.*, 1995). Many studies, especially those of hantaviruses with the greatest geographical proximity (and therefore *a priori* hypothesized to be the most genetically similar) to those found in the Pacific Northwest have used a fragment of the G1 and G2 encoding region of viral M segments, amplified by reverse transcriptase polymerase chain reaction (RT-PCR) (Avsic-Zupanc *et al.*, 2000; Hjelle *et al.*, 1995a; Hjelle *et al.*, 1995b; Hjelle *et al.*, 1994; Johnson *et al.*, 1997; Li *et al.*, 1995; Nichol *et al.*, 1993; Nichol, 1999; Plyusnin and Morzunov, 2000). Accordingly, to ensure that the viral analyses contained herein might be comparable across even the most potentially closely related species, similar M segment amplicons were pursued in this research. The PCR products were then sequenced and compared for genetic divergence as a direct indicator of viral speciation and for phylogenetic comparisons.

Mitochondrial DNA (mtDNA) is often the genetic material of choice for small mammal phylogenetic analyses (Avise *et al.*, 1983; Bradley *et al.*, 2001). Again, in order to enable meaningful comparison of Pacific Northwest specimens of mice, genus *Peromyscus*, to the bulk of data previously published, mtDNA was chosen for the analyses presented herein (Avise *et al.*, 1983; Allard *et al.*, 1988; Hogan *et al.*, 1993, 1997; Bradley *et al.*, 2001; Chirhart *et al.*, 2001; Michaux *et al.*, 2001; Zheng *et al.*, 2003).

To date, characterized hantaviruses geographically most proximal to the Pacific Northwest have been found in *Peromyscus*; indeed, all viruses associated with rodents in the genus *Peromyscus* form a well–supported monophyletic clade (Botten *et al.*, 2000; Monroe *et al.*, 1999; Plyusnin and Morzunov, 2000; Weidmann *et al.*, 2005; Yates *et al.*, 2002). This viral monophyly likely reflects adaptation of the virus to the rodent host and not just speciation due to geographic isolation of the virus variants (Botten *et al.*, 2000; Monroe *et al.*, 1999; Plyusnin and Morzunov, 2000; Weidmann *et al.*, 2005; Yates *et al.*, 2002). For instance, *P. maniculatus* and *P. leucopus* are sympatric in many regions and share microhabitat, but virus mixing between species is not seen (Monroe *et al.*, 1999). While extremely rare, cases of host switching (to hosts with no current *hantavirus* population), as well as spillover into neighboring species, do occur (Klingstrom *et al.*, 2002; Nemirov *et al.*, 2002; Vapalahti *et al.*, 1999; Weidmann *et al.*, 2005). Host switching is defined the result of formerly host-specific viruses having experienced genetic changes that allow the virus to be subsequently maintained in a different species population (Klingstrom *et al.*, 2002; Weidmann *et al.*, 2005). Spillover is the result of high population densities of the host species as well as another sympatric species leading, through increased encounters, to only a temporary presence (un-maintained) of the virus within that sympatric population, without any genetic change being seen in the virus (Nemirov *et al.*, 2002; Vapalahti *et al.*, 1999). A unique rodent host species would therefore be likely to have a novel *Hantavirus* as well. North American hantaviruses discovered among different rodent reservoir species have been found to range from one another in genetic percent divergence from as little as 5% to as much as 30% (Vincent *et al.*, 2000).

With so little known about *Hantavirus* distributions, it is important to understand the health risks faced by humans due to that lack of knowledge. Human mortality rates for HPS range from approximately 40% to 60% depending upon the strain of the virus encountered and the health and age of the patient (Peters, 1998; Schmaljohn and Hjelle, 1997). The current mortality rate among patients hospitalized and diagnosed with HPS in the U.S. is 38% but increases to 50% in Oregon. Three new cases occurred in Oregon during the span of this study with one of these three resulting in a fatality, underscoring the need for a clearer understanding of hantaviral species distributions.

No systematic studies of evolutionary relationships of deer mice have been undertaken in the Portland area or even Oregon in its entirety. Distribution maps show the Cascade Mountains forming a boundary between two subspecies of deer mice (fig. 4), with *Peromyscus maniculatus rubidus* on the West side, and *Peromyscus maniculatus gambelii* on the East (Michaux *et al.*, 2001; Wilson and Ruff, 1999; Hall, 1981), but with the upper habitation zone limits of both subspecies surpassing the passes within the Cascade Mountains, it is therefore likely that they constitute an incomplete barrier to migration, and it is suspected that some overlapping of populations may have occurred (Hall, 1981; Verts and Carraway, 1998; Wilson and Ruff, 1999). No molecular phylogenetic studies of Portland, OR region *Peromyscus* have previously been undertaken although, as previously mentioned, current phylogenies are based solely upon morphology, leading to the specific and sub-specific definitions described.

The objective of this research was to elucidate, using molecular analyses, whether the *Peromyscus* species found in the Portland area had been misidentified as well as to provide an initial characterization of the evolutionary relationships of the as yet uncharacterized regional *Hantavirus*. Hypothesized as:

$H_{0\text{-}1}$: Deer mice in the Portland, Oregon region are correctly classified as *Peromyscus maniculatus rubidus*.

Or, stated as a working hypothesis…

H_1: Based on molecular evidence, previously characterized *Peromyscus maniculatus rubidus* in the Portland, Oregon region, while a congener of *P. maniculatus*, is not conspecific.

$H_{0\text{-}2}$: The *Hantavirus* reservoired by deer mice in the Portland, Oregon region are in fact Sin Nombre virus.

Again, in working format…

H_2: The *Hantavirus* carried by the taxon currently recognized as *Peromyscus maniculatus rubidus*, constitutes a previously unrecognized species or strain of *Hantavirus*.

Hall (1981) suggested that the partially sympatric subspecies *P. m. rubidus* and *P. m. gambelii* may in fact not be interbreeding, although there have been no studies to confirm or deny this hypothesis (Hall, 1981). If this truly is the case, then according to the biological species concept (Mayr, 1982) some of these populations may have differentiated into recognizable distinct species.

In light of the foregoing research described above showing the gaps in our understanding of the biogeography of *Peromyscus*, as well as their hantaviruses, and in conjunction with the additional resolution to be provided by molecular analyses over morphological analyses alone (Hoelzel and Green, 1992), the reasoning for this research is evident. This study has attempted to yield a sharper image of the speciation patterns in the *Peromyscus maniculatus* species group, as well as the hantaviruses putatively coevolving with them, with a focus on the region in and around Portland, Oregon, and the greater Pacific Northwest.

Chapter 2: *Peromyscus* in the Pacific Northwest

Abstract-

The neotomine rodent *Peromyscus maniculatus* (deer mouse) is distributed and found throughout most of North America (fig. 3). With more than 70 subspecies described on a morphological basis (Hall, 1981; Osgood, 1909), evolutionary relationships among *Peromyscus maniculatus* subspecies, as well as those among the entire genus *Peromyscus*, remain complex and unclear. The research contained herein attempted to clarify some of these relationships, specifically the association of deer mice from the Pacific Northwest with their closest relatives, as well as their status within the larger generic taxonomic framework. To this end, phylogenetic analyses were performed on the mitochondrial DNA sequences of the ND3, ND4, ND4L, and Arginine tRNA from 84 individuals of *Peromyscus* representing the three putatively distinct subspecies from the Pacific Northwest. Specimens from beyond the Pacific Northwest region included subspecies from throughout the entire distribution of deer mice, including topotypical *Peromyscus maniculatus maniculatus* from Newfoundland. These sequences were compared to other congeners, including: *Peromyscus keeni, P. sejugis,* and *P. leucopus*, using Maximum Likelihood analysis with bootstrap support, genetic distance, and Bayesian analyses.

These molecular approaches to the problematic phylogenetic relationships among deer mice subspecies agreed in finding a taxonomic division in the molecular phylogeny of deer mice, separating *P. maniculatus* into two distinct clades. This division is equal in percent divergence to the divergence of *P. maniculatus* from *P. keeni* and *P. sejugis*. The division in the distribution of *P. maniculatus* occurs along

the Mississippi River and continues from its source in central Minnesota (after a 97 km break in the barrier) north along the Red River to Lake Winnipeg, then along the Nelson River to Hudson Bay essentially dividing *P. maniculatus* into an eastern and western clade along this barrier. The western clade may represent a separate—formerly cryptic—species, and is proposed in this investigation to be recognized as *Peromyscus sonoriensis.*

Introduction-

Description-

Peromyscus maniculatus, Order Rodentia, Family Cricetidae, Subfamily Neotominae, commonly known as the deer mouse, is a small, ubiquitous rodent with a range extending from the northeastern coast of North America across the continent to the west coast, north through most of Canada, and south into northern Mexico, but excluding most of the southeastern U.S. (fig. 3).

Peromyscus maniculatus varies in color from grayish to reddish-brown to black dorsally with a white venter, legs, and feet. The variation primarily depends on the habitat in which the population is found: color will generally tend toward the predominant local substrate. The tail is distinctly bi-colored, with dark above and white below (Huestis, 1931). Ears are large and semi–erect, and eyes are black and beady.

Adult *Peromyscus maniculatus* range from 10-30 grams with newborns at roughly 1.5-2 grams, and juveniles in the intervening range. Typically, adult deer mice will measure 106-222 mm in total length with tails from 46 to 123 mm, hind feet 14-25

mm, and ears 12-21mm (Hall, 1981). These wide ranges are seen as a result of the vast geographic range of the species (Hall, 1981). Local subspecies and populations exist within much smaller size ranges (Hall, 1981). A great deal of the variation seen throughout the deer mouse's range may also be seen on a smaller geographic scale in Oregon as a result of the highly disparate climates and habitats found on opposing sides of the Cascade mountains (Verts and Carraway, 1998; Woodley, 2007).

Habitat and Distribution-

Due to the vast range described above, *P. maniculatus* may be found in habitats as varied as agricultural fields, grassland, brushland, sub-alpine zones, northern boreal forest, desert, southern montane woodland, and dry subtropical climes. The species is most commonly found in prairies, bushy areas, and woodlands (King, 1968). In addition to these natural habitats, *P. maniculatus* is often seen in and around domestic dwellings.

The species has been divided into two subgroups: the grassland or prairie form in the Midwest and west, and the woodland form in the east and northeast (LTER, 1998). The woodland form of the east has a longer tail, ears, and hind foot than the more western prairie form. These differences have spawned controversy over whether or not they constitute distinct species.

Within the species' range as many as 70 subspecies of deer mice have been described (Hall, 1981; Michaux *et al.*, 2001) with some of these being sympatric and not considered to be interbreeding (Hall, 1981). To be considered a single species, some level of gene flow must occur among individuals throughout the range (Mayr,

1982). However, being a small organism with some relatively locally concentrated populations, it is clear that an individual *P. maniculatus* is incapable of migrating across the whole range. There also exist physical barriers within the range, such as the Rocky Mountains, Cascade Range, and Mississippi River, all of which serve to impede gene flow, thus isolating subspecies into allopatric populations. If these subspecies have not already diverged into separate species, they are therefore likely on that path.

Scope-

In consideration of the incomplete clarity of the phylogenetic relationships among members of the genus *Peromyscus*, this work was intended to use molecular data to test the monophyly of *Peromyscus maniculatus*, in particular, the subspecies from the Pacific Northwest currently assigned to *P. maniculatus*. While natural selection works upon phenotypes and not genotypes, the contents of genomes dictate those phenotypes. It is likely that molecular data will provide a more representative picture of evolutionary history than morphology because a portion phenotypic variation seen in/between species is the result of differential gene expression, not divergent genetic content.

Research Design and Methods-

Field Protocols-

Deer mice, *Peromyscus*, were collected from five sites in and around the Portland, Oregon metropolitan area from October 2002 through September 2004. Collection

sites were chosen based on their relative size to contain the trapping web. To ensure that samples were taken from locations where humans would be most likely to encounter infected mice, public parks were selected for specimen collection (fig. 5) (Kuenzi *et al.*, 2001). Sites chosen were: Forest Park, Multnomah Co., Tryon Creek State Park, Multnomah Co., Powell Butte Nature Park, Multnomah Co., Oxbow Regional Park, Multnomah Co., and Tualatin River National Wildlife Refuge (TRNWR), Washington Co.

The Forest Park site (5046892.5 N, 484267.53 E, UTM Zone 10, WGS-84), at a relatively flat 184 meters elevation near the top of the West Hills, on the northwest side of downtown Portland, consisted of a fairly dense second-growth mix of Douglas-fir (*Pseudotsuga menziesii*), western hemlock (*Tsuga heterophylla*), western red cedar (*Thuja plicata*), Oregon big-leaf maple (*Acer macrophyllum*), and red alder (*Alnus rubra*). Sword fern (*Polystichum munitum*), vine maple (*Acer cirinatum*), Oregon grape (*Berberis aquifolium*), and English ivy (*Hedera* helix) dominated the understory. Several trails crossed the study site, and were used daily by hikers, bikers, and dogs. While currently in a relatively natural state, it is known that this site has been logged in the past and replanted, in an attempt to restore a natural habitat. Other than the few hiking trails running through the area, it appears to have been left to develop along a natural course for many decades. The Tryon Creek State Park site (5031184.0 N, 474109.6 E, UTM Zone 10, WGS-84), at 105 m, on the south side of Portland contained essentially the same species composition as Forest Park, but with much greater proportion of ivy, a very undulating terrain, and two small creeks. The Tryon Creek research site was in an area of the park that did not have established trails

to or within it. Powell Butte Nature Park, is an extinct volcanic cinder cone on the east side of Portland, and the most anthropogenically altered of the sites with a relatively open canopy made up of big leaf maples and alders, with stinging nettles (*Urtica dioica*) and Himalayan blackberry (*Rubus discolor*) in the understory. This site, on the south shoulder of the summit at 135 meters (5036804.5 N, 461386.22 E, UTM Zone 10, WGS-84), had been logged thoroughly in the past and was flanked on the north by a large, maintained grass clearing. The Tualatin River National Wildlife Refuge (TRNWR), on the banks of the Tualatin River, was dominated by English Hawthorn (*Crataegus laevigata*) and Himalayan blackberry; it was mostly level, with dense vegetation, and wetlands encroaching into the site (34 m) (5026923.0 N, 486732.9 E, UTM Zone 10, WGS-84) during the rainy winter months. A newly established National Wildlife Refuge, the TRNWR had not yet opened to the public and had been temporarily left undisturbed to allow some reestablishment of the natural wildlife and ecology. Oxbow Regional Park on the Sandy River (site at 37 meters) (5037392.5 N, 445064.88 E, UTM Zone 10, WGS-84) is the only one of our sites containing a remnant patch of old growth forest. Douglas fir, western hemlock, and western red cedar almost completely shade the area. The ground is completely covered by sword fern, mosses, and large amounts of woody debris.

In addition to these five regular local collection centers, specimens were obtained from elsewhere in the range of *Peromyscus maniculatus* in order to provide comparative data (fig. 5). *Peromyscus maniculatus* tissues collected from the species type locality in northwestern Newfoundland were kindly donated by A. Lackey, State University of New York at Oswego. These tissues were included in the study to allow

direct comparison of local *P. maniculatus* genotypes to those representative of the voucher *P. m. maniculatus*. *Peromyscus* specimens also were collected from habitats adjacent to both the east and west of the Mississippi River in northeastern Missouri (west site) and western Illinois (east site); these specimens were collected and tissues generously donated by S. Burt, Truman State University, Kirksville, Missouri. It was hypothesized that these allopatric Missouri and Illinois populations, kept separate by the barrier of the Mississippi River, would provide a distinct and visible break in the genetic continuum (gradient) believed to reflect the *Peromyscus maniculatus* subspecies distribution across the continent (LTER, 1998; Dragoo *et al.*, 2006). This genetic continuum or gradient across the full range of *P. maniculatus* is seen as relative genetic similarity among subspecific populations, with that similarity inversely proportional to the geographic distance between subspecies.

Three types of live–capture traps were used to capture specimens: Sherman traps (H. B. Sherman Traps, Tallahassee, Florida), pitfall, and custom built mesh traps (O'Farrell et al., 1994). The Sherman traps were treadle-type collapsible aluminum boxes, models LFA and LFATDG, 8 cm x 8 cm x 23 cm. The mesh live traps were designed to be approximately the same size as the Sherman live-traps with square wire cloth creating the box. The closure mechanism consisted of a treadle trigger, and gravity drop door, both of galvanized metal (O'Farrell *et al.*, 1994). Pitfall traps consisted of a five-gallon bucket buried to the rim with a lid for a rain cover suspended above, leaving a 7-8 cm gap for specimen access. A trapping web design was selected over the more traditional trapping grid because absolute densities could be estimated from the capture data and because the estimation procedures required few

assumptions about capture probabilities and animal movement patterns (Parmenter *et al.*, 1998; Parmenter *et al.*, 2003; Wilson and Anderson, 1985).

The trapping webs used for this study consisted of 12 spokes radiating at 30–degrees from one-another from a center point (fig. 6). Each spoke measures 100 meters from the center to end and contains 12 trapping locations along its length. The first four traps are at 5–meter intervals, while the subsequent traps are 10 meters apart. Each trap station had a mesh and Sherman live–trap; trap stations 7 and 12 on each line also had a medium (48cm x 15cm x 15cm) or large (81cm x 25cm x 30cm) Tomahawk live–trap. In addition, trap stations 4, 7, and 12, of each line also had a pit fall trap as previously described. Lastly, 4 Sherman traps were located at the center–point of the web. This design results in 145 trap stations consisting of 144 mesh live-traps, 148 Sherman live-traps, 24 Tomahawk live-traps, and 36 pit fall traps (Parmenter *et al.*, 1998; Parmenter *et al.*, 2003) for a total of 353 traps. Mesh and Sherman traps were baited with a mixture of oats and peanut butter, while Tomahawk traps were baited with canned cat food. Pit falls remained unbaited. Poly-fiber nesting material was added to Sherman and mesh traps when warranted by weather. Traps were set out for four consecutive nights at each site with collection occurring at dawn the following day (Ritchie and Sullivan, 1989). After collection on the last morning, all Sherman and mesh traps were removed. To avoid extraneous captures, pitfalls were closed with a lid while not in use. Each park was trapped ten times over the course of this study, approximately every eight weeks. Total trap-nights were 65,200.

Captured animals were transferred from traps into clear, sealable plastic bags, labeled with the trap number, and transported to the center of the web for processing.

Captures from Tomahawk traps were left in the trap and also transported to the center of the web center. Due to the possibility of contracting HPS, standard precautionary methods were implemented, including the use of full-face powered air purifying respirators (PAPR) with highly efficient particulate air (HEPA) filters, and latex gloves under leather gloves (Mills *et al.*, 1995).

Each animal was identified to species and evaluated for gender, reproductive status, mass, relative age, and any other notable characteristics such as ectoparasites, wounds, or defects such as atypical coloration (appx. C). Heparinized glass micro-capillary tubes were used to draw blood from the retroorbital sinus and stored in cryovials, which were then placed in liquid nitrogen until testing (Kaufman *et al.*, 1994). After blood samples were taken, deer mice were euthanized in a chloroform chamber (Mills *et al., 1995*).

This research was conducted under the auspices of federal and state permits, and complied with the American Society of Mammalogists Guidelines (Gannon *et al.*, 2007) for the care and use of animals. Specimens were identified using museum tags including all relevant data mentioned above, sealed in plastic, then returned to the laboratory. Once in the laboratory, specimens were placed in a locked -70°C ultracold freezer for storage and further analyses.

Molecular Protocols-

Field collected blood samples were tested for the presence of antibodies cross-reactive to Sin Nombre virus (SNV) using Enzyme Linked Immunosorbent Assay (ELISA), by L. J. Dizney, Ph.D., of the Oregon State Health Laboratory, or Strip

Immunoblot Assay, by B. Hjelle, Ph.D., of the University of New Mexico, (SIA; Kaufman *et al.*, 1994; Mills *et al.*, 1995; Morzunov *et al.*, 1995; Rowe *et al.*, 1995).

Kidney samples were extracted from all *Peromyscus* specimens that were sero-positive for SNV antibodies as well as a random sample of those found negative (tables 2, 3; appx. D). Ultimately, including donated tissues from allopatric conspecifics (n=9) and congeners (n=4), tissues were collected for examination from 86 *Peromyscus* specimens.

Approximately 30-50 mg of tissue from each individual were used in DNA extraction. Whole cellular DNA was extracted and isolated from these tissue samples using the Qiagen DNeasy Tissue Kit (Valencia, CA) and protocols contained therein. To ensure comparison with sequence analyses in the literature, mitochondrial genes of the nicotinimide adenine dinucleotide (NADH) dehydrogenase subunit group were chosen as the targets for analysis. Specifically these consist of the ND3, ND4, ND4L, subunit mitochondrial genes and the Arginine tRNA mitochondrial gene that is located between the ND4L and the ND3 genes in the circular mitochondrial genome (Fig. 7). Amplification of gene targets was performed in two parallel but separate reactions for each DNA sample to obtain this entire gene set. Polymerase Chain Reactions (PCR) were set up utilizing Amersham Biosciences (UK) "puReTaq ready-To-Go PCR Beads" (each bead contains ~200μM final concentration dATP, dCTP, dGTP, and dTTP, 10mM Tris-HCl, 50mM KCl, 1.5mM $MgCl_2$), 0.4 μl (each) of 10.0 μM primers, and 1.0 μl of template DNA in a 25.0 μl final reaction volume. The first of the two fragments was amplified using the specific primers

5' – CGAACTAGTACAGCTGACTTCC – 3' (PI') for the (+) strand and 5' – CCGTAGGAGTTTGATAGTTTTGCT – 3' (MANR) for the (-) strand (Arevalo *et al.*, 1994). This PCR produced a mitochondrial DNA fragment of 734 bp. The second PCR reaction was set up with primers 5' – AGCAAAACTATCAAACTCCTACGG – 3' (MANF) (+) and 5' – TGGAGCTTCTACGTGGGCTTT – 3' (NAP2) (-), generating a 729 bp mitochondrial DNA fragment (Arevalo *et al.*, 1994). Reaction mixtures were placed in an Eppendorf – Master Cycler 96 well Thermocycler for PCR amplification. Thermocycler protocol (STANDARD) was delineated as:

Denature:	95°C	5min
35 cycles:	95°C	45sec
	50°C	30sec
	72°C	90sec
Extension:	72°C	10min
Hold:	4°C	

To verify successful PCR, the products from the reactions were evaluated using electrophoresis. 5 µl of amplified DNA product were combined with 12 µl water and mixed. These 17 µl solutions were then placed in each of the wells of an "E-Gel" (Invitrogen) 2% agarose gel. Lane one of the 12-lane gel was left empty to receive 10 µl of 80bp-1Kbp DNA ladder (Fermentas (Glen Bernie, MD) MassRuler™ DNA Ladder, Low Range) as well as 7 µl water. The gel was run for 15 minutes. After the run was complete the E-Gel was removed and placed on an ultraviolet viewer to

observe the fluorescently tagged DNA bands. In the E-Gel, fluorescent DNA stain is enclosed in the cartridge with the gel, allowing its interaction and binding with the DNA. Bands were seen, as expected, at the range of approximately 700bp-750bp as compared to the ladder.

After confirmation of PCR products the remaining reaction solutions were then subjected to PCR cleanup to remove excess polymerases, primers, dNTP's, and buffers using the QIAGEN (Valencia, CA) PCR Cleanup Kit and protocols contained therein.

The amplified products from each of these reactions were then utilized as template for sequencing using the modified Sanger chain terminator method (Sanger *et al.*, 1975, 1977). The sequencing reactions were set up with the 0.6 ml tubes recessed in an ice-bath to limit reactivity of constituents until placed in the thermocycler. Each reaction vessel was prepared with 2.0 µl Big Dye Terminator solution (Applied Biosystems), 2.1 µl of 2.5 µM appropriate primer, 1.0 µl 5x reaction buffer, 4.8 µl water, and 2.1 µl purified PCR product for a final reaction volume of 12 µl. These sequencing reaction vessels were then placed in the Eppendorf thermocycler and exposed to the sequencing thermo protocol (SEQ) as:

	96°C	5min
25 Cycles	96°C	30sec
	50°C	15sec
	60°C	4sec
Hold	4°C	

Upon completion of sequencing cycles, reactant solutions were plated in a 96 well micro titer plate that was then sealed and frozen at -70°C. The derived sequences were then shipped over night on dry ice to the Center for Genome Research and Bioinformatics (CGRB) Core Laboratories at Oregon State University, Corvallis, OR. There, sequences were analyzed on an Applied Biosystems (ABI) 3730 Capillary Sequence Machine.

Sequence File Preparation-

After the ABI 3730 generated the representative chromatograms they were downloaded via the internet from the CGRB Core Laboratories web site. Next, the sequence file chromatograms were uploaded into the software program SeqEd (Applied Biosystems v. 1.0.3). Within this program, sequences from corresponding primer pairs are viewed and edited for quality. First, the negative strand sequence, amplified from the reverse (ManR and Nap2) primers, is "reverse complimented" where the entire sequence is turned around to orient the last nucleotide first and the first nucleotide last. Then the bases of this reversed sequence are converted to their complementary nucleotide. Next, unidentifiable bases, artifacts of the sequencing process that occur at both the beginning and the end of the sequence, were removed. Sequences were aligned with SeqEd. These labeled mismatched bases were then examined based upon their corresponding peak in the sequence chromatogram. In most cases, one of the two opposing sequence chromatogram peaks was considerably cleaner, or stronger allowing the base to be "called" as the one indicative of the higher quality peak. In this way sequences were edited and aligned to produce a consensus

sequence for the target gene group from each individual *Peromyscus* specimen. This task was undertaken twice for each *Peromyscus* specimen because the target sequence (mitochondrial NAD gene group) was originally amplified and sequenced in two separate fragment subsets.

The two consensus sequence fragments from each specimen were concatenated in Text-Edit (Apple-Inc.). The concatenated sequences were imported into MacClade (Maddison and Maddison, 2003) for multiple sequence alignment where sequences from all *Peromyscus* were aligned with one another as well as with other out-group species obtained from NCBI GenBank. The multiple sequence alignment was adjusted as to codon reading frame to minimize the occurrence of stop codons and thereby represent the natural reading frame. The NADH dehydrogenase genes coded within the sequence contained the Arginine transfer RNA gene (between ND3 and ND4L) as well which is not translated into protein. Therefore, to separate the non-coding tRNA from the rest of the sequence, that is read in a triplet codon-reading frame, single spaces were inserted flanking the tRNA gene. In doing so, the tRNA was considered separately during phylogenetic analysis.

Phylogenetic Analysis-

The multiple sequence alignment file was saved in MacClade in Nexus format to allow use in the software programs PAUP (Phylogenetic Analysis Using Parsimony v. 4.0b10) (Swofford, 2002), MrBayes (v3.1.2) (Huelsenbeck and Ronquist, 2001), and GARLI (Genetic Algorithm for Rapid Likelihood Inference v 0.951) (Zwickl, 2006). The first step of phylogenetic analysis entailed selection of an evolutionary model to

enforce parameters of nucleotide substitution. To this end, the program MODELTEST v. 3.7 (Posada and Crandall, 1998) was utilized. Contained within the MODELTEST software package was the file modelblockPAUPb10. This file was inserted into the nexus sequence file and executed within PAUP. The purpose of this was to guide PAUP in analyzing the sequence data to choose from among 56 evolutionary models by using three different model selection frameworks: hierarchical likelihood ratio tests (hLRTs), Akaike information criterion (AIC), and Bayesian information criterion (BIC) (Posada and Crandall, 1998). The program also implements the assessment of model uncertainty and tools for model averaging and calculation of parameter importance, using the AIC or the BIC. Upon completion PAUP created an output file named *model.scores* that contained the results of the 56 analyses. The *model.scores* file was then read by MODELTEST that selected the model of nucleotide substitution that was the best fit. These analyses chose GTR+I+Γ (General Time Reversible + proportion Invariant + Gamma, 10 parameter) as the best fitting model. The GTR+I+Γ model is the most complex of the 56 model choices contained within the MODELTEST program where a proportion of sites are invariant (I) and a gamma-distributed substitution rate variation is implemented across sites (Γ). This more complex model allows more free parameters for the analyses. A command block for the purpose of directing PAUP in application of the evolutionary model, known as a model block, was rendered by MODELTEST and contained within the output file. Other PAUP block commands were added to the Nexus file as well to command PAUP to conduct further analyses.

These other commands included instructions for the type of analysis to be executed, in this case, Maximum Likelihood, which is a method for the inference of phylogeny. It evaluates a given hypothesis about the evolutionary history of the organisms involved (*Peromyscus*) in terms of the probability that the proposed model (GTR+I+Γ) and the hypothesized history would give rise to the observed data set. The supposition is that a phylogenetic history with a higher probability of reaching the observed state (condition of genetic divergence represented by the nucleotide data) is preferred to a history with a lower probability, or simply put, the higher probability phylogenetic history is more *likely*. The Maximum Likelihood method searches for the tree with the highest probability of occurrence.

In addition to Maximum Likelihood, Distance analysis (in PAUP) was used to evaluate the relative amount of genetic divergence among the *Peromyscus* included in this study. Distance provides a simple comparative matrix of the nucleotide differences among organisms stated as percent divergence.

Bayesian analyses, by way of MrBayes Markov chain Monte Carlo (MCMC) (Hulsenbeck and Ronquist, 2001) were also performed. Bayesian analysis, as implemented by MrBayes, uses the likelihood function as well but instead of testing the probability of the data given the hypothesis, Bayesian evaluates the probability of the hypothesis given the data. In Maximum Likelihood, free parameters are optimized, maximizing the likelihood, but in a Bayesian MCMC approach, free parameters are probability distributions, which are then sampled (Hulsenbeck and Ronquist, 2001).

Bayesian analysis expresses its result as the *posterior probability* (PP) of the tree

topologies and model parameters. The posterior probability is proportional to the likelihood, and, also proportional to the *prior probability* (Hulsenbeck and Ronquist, 2001). The best estimate of the phylogeny can be selected as the tree with the highest posterior probability (i.e., the MAximum Posterior probability [MAP] tree) (Rannala and Yang, 1996).

In a similar method to Bayesian posterior probabilities, Maximum Likelihood uses Bootstrapping (BS) (Felsenstein, 1985) to evaluate the probability that tree nodes are correct. These bootstrap values are reported as a percentage, being the percent of replicates that generated the same node. In the analyses conducted and described herein1000 bootstrap replicates were generated using PAUP and 1000 BS replicates were performed using the program GARLI.

Studies have shown some incongruity between Bootstrap and Posterior Probability (Leache and Reeder, 2002; Whittingham *et al.*, 2002). Although, when BS is plotted as a function of PP several examinations have revealed a correlation between BS and PP (Douady *et al.*, 2003). Rannala and Yang (1996) found that within this correlation, posterior probabilities are consistently higher than corresponding bootstrap percentages. Wilcox *et al.* (2002) found that both PP and BS are overly conservative estimates. Therefore, considering the higher PP results of Rannala and Yang (1996) and the fact that both are overly conservative (Wilcox *et al.*, 2002), it stands to reason that the Bayesian Posterior Probabilities may be slightly more representative of the true condition than Likelihood Bootstrap. That not withstanding, in a few circumstances, PP was found to have overestimated the hypothesis probability, and as such, over-reliance of Bayesian PP alone may be misleading (Douady *et al.*, 2003).

As a result of these findings both Bayesian Posterior Probabilities and Maximum Likelihood Bootstrapping have been included in these analyses to ensure the greatest possible representation of the *Peromyscus* phylogeny.

Results-

For comparison to five Rodent out-groups, consisting of *Microtus pennsylvanicus*, *Oryzomys palustrus*, *Sigmodon hispidus*, *Rattus norvegicus*, and *Reithrodontomys megalotis*, *Peromyscus maniculatus* mitochondrial ND3, ND4, ND4L, and arginine tRNA genes were sequenced (fig. 8) (appxs. E, G). Specimens included in these analyses were from the Portland, OR region (n=46), the greater Pacific Northwest (n=18), East-central California (n=1, *Peromyscus maniculatus rufinus*), the Midwest (n=9, *Peromyscus maniculatus bairdii, and P. leucopus*), and Newfoundland (n=4, *Peromyscus maniculatus maniculatus*), for a total of 78 sequence specimens generated by this study. Sequences for *Peromyscus keeni*, *Peromyscus leucopus* (one of six), and *Peromyscus sejugis* (n=2) were obtained from GenBank as well as the out-group sequences (n=5), These specific out-group species were selected due to their condition as known reservoirs of *Hantavirus* species.

Distance Analysis-

Distance analyses (*p* distances) (figs. 8, 9; appx. A) for 1,450 nucleotides of the mitochondrial ND3, ND4, and ND4L genes, as well as the Arginine tRNA sequence, revealed an average pair-wise nucleotide genetic distance (defined as percent divergence) of $p = 0.0413$ (4.13%) between the Newfoundland voucher *Peromyscus*

maniculatus maniculatus and the local *Peromyscus maniculatus rubidus* found west of the Cascade Mountains in Oregon (figs. 3, and 4). A relative pair-wise genetic distance of 0.0416 (figs. 8, 9) was found between voucher *P. m. maniculatus* and the greater Pacific Northwest (PNW) *Peromyscus maniculatus* subspecies clade (figs. 10-13) on the whole. Intra-PNW clade average genetic distance was found to be 0.0063 revealing no discernable structure signal (appx. A). In these analyses the PNW clade includes *P. m. rubidus*; *P. m. austerus,* from Washington, north of the Columbia River and west of the Cascade Mountains; *P. m. gambeli,* found east of the Cascade Mountains in Oregon and Northern California; and *P. m. austerus,* located in the San Juan Islands (fig. 4). At the same time, topo-typical *P. m. maniculatus* was shown to possess a genetic divergence of 0.0600 from the Pacific northwestern *P. keeni* (at least partially sympatric with the PNW *P. m.* clade), 0.0542 from *P. maniculatus rufinus*, the reservoir species of Sin Nombre Virus from the four corners region of New Mexico, and 0.0468 pair-wise genetic distance from *P. m. bairdii* from west of the Mississippi River in northeastern Missouri (figs. 8 and 9). This *P. m. bairdii/ P. m. maniculatus* pair-wise genetic distance (0.0468), taken with consideration that the genetic distance between the Pacific Northwest Clade and *P. m. bairdii* from the west side of the Mississippi River is only 0.0171, raises the possibility that a genetic break exists at or near the Mississippi River, dividing the *P. maniculatus* species into a western clade and an eastern Clade. Further to this point, when the *P. maniculatus baridii* subspecies from west of the Mississippi River are included with the Pacific Northwest specimens and compared as a group to the Newfoundland voucher specimens a pair-wise genetic distance of 0.0457 is resolved, strengthening the

possibility of two separate major *Peromyscus* (*maniculatus*) clades (figs. 8 and 9). Interestingly, the calculated genetic distance between two widely accepted species, *P. keeni*, from Washington and British Columbia (Zheng *et al.*, 2003), and *Peromyscus sejugis*, from San Diego and Santa Cruz Islands in the Gulf of California (Burt, 1932), is 0.0429, less than the other *P. maniculatus* subspecies in the western clade from the supposed conspecific *P. m. maniculatus* (figs. 8 and 9). *P. sejugis* itself has a similar genetic distance (0.0511), and is also recognized as a separate congener of *P. maniculatus* (fig. 8). That a previously described isolated insular species is only marginally more divergent (0.0511/0.0457) from the topo-type than are those from the rest of the western half of the continent as a whole raises the potential that speciation may have indeed occurred between the Newfoundland *Peromyscus maniculatus maniculatus* and the western *P. maniculatus* subspecies.

The Mississippi River only divides the majority of the United States, and not Canada, as it flows from West of Lake Superior in Central Minnesota to the Gulf of Mexico, therefore, it is an incomplete barrier for division of the entire North American *Peromyscus maniculatus* species distribution. Canadian populations may be similarly separated by a water barrier extending from Hudson Bay in the north to Lake Winnipeg (Lake Agassiz) via the Nelson River, and from there to the Lake of the Woods at the Canadian-Minnesota border, through the Boundary waters to the Mississippi River. The only opening in this barrier exists between the Red River, arising in Northern Minnesota, flowing to the southern tip of Lake Winnipeg, and the headwaters of the Mississippi River, a not so inconsequential 97 kilometers (60 mi.). Much more extensive sampling is required from these regions to further elucidate the

possibility of the occurrence of a genetic break within the *Peromyscus maniculatus* species along this mostly complete barrier.

Maximum Likelihood Analysis-

Taxa including *Peromyscus* genus and related outgroups (n=88) from within the rodent families Cricetidae and Muridae were examined for their phylogenetic relationship using Maximum Likelihood in PAUP (Swofford, 2002). Likelihood analyses rendered a likelihood tree with a negative log-likelihood (–lnL) = 8702.95284 for the resolved tree topology. The likelihood tree was calculated using the tree bisection-reconnection (TBR) swapping algorithm. Nucleotide frequencies were A=0.35450, T=0.29800, C=0.27910, G=0.06840. Among-site rate variation includes an assumed proportion of invariable sites of 0.2851. A gamma distribution of rates across variable sites was implemented with a shape parameter of 0.7693 and four rate categories. These parameters are determined by the GTR+I+Γ model of evolution as chosen by Modeltest (Posada and Crandall, 1998).

Node support for the likelihood tree was generated using 1000 bootstrap replicates. The consensus bootstrap tree yielded strong support for resolved nodes (Fig. 11). Fig. 11 shows the Pacific Northwest *Peromyscus* Clade (PNW) nested within a greater clade containing all those representative *Peromyscus* taxa from west of the Mississippi River (western clade). The consensus tree demonstrates the western *Peromyscus* clustering in a very well supported, yet distinct, clade, sister to the Newfoundland topotype specimens. The western clade is also separate at the same level from the other nearest (geographically and genetically) related congeners including *P. sejugis*

from San Diego and Santa Cruz Islands (Gulf of California) as well as *P. keeni* from the Pacific Northwest north of the Columbia River.

Consistent with widely accepted positions (Greenbaum *et al.*, 1978; Avise *et al.*, 1983) is the location in these analyses of *Peromyscus leucopus*, as a more distantly related member of the *Peromyscus* genus. As expected, all *Peromyscus* members represented in these analyses are seen as a separate monophyletic clade from the nearest regarded member of the Neotominae Subfamily that is included in these data, *Reithrodontomys megalotis*.

The genetic distance tree (fig. 10) resolved using the Neighbor Joining (NJ) method produced a tree with the same topology as the Bootstrapped Maximum Likelihood consensus tree (fig. 11). Branch lengths are shown above each corresponding branch with the change scale, representing the number of nucleotide changes from the previous node to the subsequent, located at the bottom-left of the figure. The Neighbor Joining analysis calculated a minimum evolution score of 3.18101 (analogous to sum of branch lengths) for these data.

A manually combined tree (fig. 12) includes branch lengths, likelihood scores, and bootstrap support at nodes present in both representative trees to allow direct comparison of these data.

Bayesian Analysis-

Bayesian analyses of these data were performed for 500,000 generations using two runs of four separate Markov chain Monte Carlo Metropolis coupling computations. Samples were taken from the tree-scape every 100 generations yielding 5,001 sample

trees for each run, or 10,002 total sample trees. The final average standard deviation of split frequencies was 0.0077 after completion of the 500,000 generations. The Metropolis-coupled Markov Chain Monte Carlo (MCMCMC) analysis led to burn-in after 100,000 generations, therefore, the first 1,000 sample trees were excluded from the majority-rule consensus tree search, resulting in a consensus tree derived from a total of 8,002 sample trees or 800,000 generations.

The Bayesian majority-rule consensus tree (Fig. 13) resolved the exact same topology as all other phylogenetic analyses contained herein (Likelihood, and Neighbor-Joining Distance), showing all subspecies of *Peromyscus* from west of the Mississippi River (that were included in this study) as one whole clade – sister at the same level to the topo-type *P. m. maniculatus* from Newfoundland as well as *P. keeni* and *P. sejugis*.

Discussion-

Peromyscus maniculatus is a diverse species said to span most of the North American continent, excluding the southeastern United States and extreme northern Canada (Hall, 1981). Included within this distribution are as many as 70 morphological subspecies (Hall, 1981; Michaux *et al.*, 2001). The vast majority of these sub specific relationships have not yet been evaluated by molecular analyses.

Being terrestrial and diminutive in size, deer mice possess limited vicariant abilities. With a home range of only 200-400 m^2 and highly susceptible to ecological barriers, they would therefore have great difficulty maintaining gene flow over this entire distribution (Hall, 1981; Verts and Carraway, 1998; Wilson and Ruff, 1999;

Michaux *et al.*, 2001). Without this exchange of genetic material, it is inevitable that allopatric populations would begin to genetically drift apart, or diverge (Mayr, 1982; Kimura, 1983). Winding through the middle of the North American continent is the Mississippi River that, along with the Red River in north central Minnesota, that flows to Lake Winnipeg (Lake Agassiz) in Canada and is ultimately connected to Hudson Bay via the Nelson River, come within 97 kilometers (60 miles) of completely dividing the continent in two. This very nearly complete ecological barrier may provide the very blockade to genetic exchange of flanking allopatric sub specific populations that could drive such a genetic drift. The literature focusing on *Peromyscus maniculatus* phylogenetic relationships are found with references to two distinct morphotypes, each consisting of many subspecies from within the species as a whole, the putative forest-form, found east of the Mississippi River and these other bodies of water, and the grassland-form, seen from west of the Mississippi River to the Pacific Ocean (LTER, 1998, Dragoo *et al.*, 2006).

In support of these previous findings, this study has resolved a similar division in the deer mouse distribution, in the form of a genetic break occurring at the Mississippi River. It should be noted however, that the discussion of a genetic break at this very specific location is based upon only four sequences from one site. It is apparent that the genetic break exists, only the exact location of it is in question. Further investigation into the populations distributed along this barrier would be needed to strengthen or refute these arguments.

Genetic distance analyses of the mitochondrial coding genes ND3, ND4, ND4L and the non-coding arginine tRNA, show the deer mouse subspecies nearest the

western banks of the Mississippi River, *P. m. bairdii*, virtually as genetically divergent (p distance=0.0468, figs. 8, 9) from the topotype *P. m. maniculatus* as are the western most deer mouse subspecies included in these analyses ({*P. m. rubidus, P. m. gambelii, P. m. austerus, P. m. rufinus*} at p=0.0457, figs. 8, 9). Conversely, the genetic distance between *P. m. bairdii* and these western subspecies is at most 0.0171, confirming their closer alliance with those western subspecies (figs. 8, 9). Interestingly, the haplotype distributions of the congener *P. leucopus*, with populations found on both sides of the Mississippi River, does not show this same division at the river (Morzunov *et al.*, 1998). One possible explanation for this lack of genetic division could be the result of more recent range expansion by *P. leucopus* than the expansion that led to the division in *P. maniculatus*. Simply, not enough time has passed since that expansion to make the division significant enough to be detected. In fact, Morzunov *et al.* (1998) show haplotypes of *P. leucopus* with "hydrid" haplotypes in over lapping regions of haplotype distributions. To that point, Morzunov *et al.* (1998) show that hantaviruses found in *P. leucopus*, with their more rapid genetic divergence than their hosts, do in fact show this division, with separate viral lineages found on opposite sides of the Mississippi River, and do not overlap. The faster genetic divergence of the viruses carried by *P. leucopus* may be revealing, through their own lineal division, a forthcoming division in the distribution of *P. leucopus*.

Distance analysis, with its susceptibility to underestimation of evolution due to the possibility of multiple changes at a given single nucleotide locus, would alone not be enough to confirm a division in *P. maniculatus*, or more importantly, clarify that *P. m. bairdii* is indeed clustering with those subspecies further west and not with the

Newfoundland topotype. Although, if underestimation is occurring, then correcting for that underestimation would only increase the resolved divergence, strengthening the argument for two separate east and west clades. Further phylogenetic analyses contained herein using methods less susceptible to underestimation of divergence reveal additional confirmation of the relationship espoused in these genetic distance analyses.

While considered an inferior phylogenetic method to the others used in these analyses - due to the simplicity of using least total branch length - Mihaescu *et al.* (2007) have shown that Neighbor Joining trees based upon genetic distance have proven to be reliable, and therefore worth inclusion in analyses. Genetic distance analysis may also suffer from one of the criticisms of Parsimony in that it may not be reflective of multiple changes within one nucleotide locus. This may result in an underestimate of the amount of change that may have historically occurred (Swofford, 1998). Conversely, with implementation of a more complex model (than used in Parsimony) such as GTR+I+Γ (used in these analyses), which allows a proportion of sites to be invariable (I), applies gamma-distributed variable rates (Γ), and among-site rate variation is taken into account, thereby alleviating at least most, if not all of the underestimation (Foster, 2003).

As expected, the distance Neighbor-Joining tree (Fig. 10), derived from the genetic distance matrix, separates the western subspecies of *P. maniculatus*, including *P. m. bairdii*, from the topotypical *P. maniculatus* at the species level, the same as the division between these and other previously accepted western congeners including *P.*

keeni, and *P. sejugis*. This association is repeated in other analyses as well. Fig. 11 shows the Bootstrapped Maximum Likelihood tree with the exact same topology as the NJ distance tree, showing all the subspecies from west of the Mississippi River contained within a single clade separate from, and at the same level as, the topotypical deer mouse. In point of fact, the node separating the western clade, the topotype, and *P. keeni* and *P. sejugis* in Fig. 11 was elucidated in 91% of 1000 bootstrap replicates.

There have been some purported advantages and disadvantages (Felsenstein, 1981; Cunningham *et al.*, 1998; Lewis, (CH 5 Soltis book 1998); Leache and Reeder, 2002) of Maximum Likelihood methods. Specifically, Maximum Likelihood methods have recently been preferred over other common methods such as Maximum Parsimony. Likelihood analyses often have lower variance than Parsimony, meaning, it is frequently the estimation method least affected by sampling error (Felsenstein, 1981). Analyses using Likelihood tend to be robust to many violations of the assumptions in the evolutionary model, and even with very short sequences they tend to outperform alternative methods such as Parsimony (Foster, 2003). Also, Likelihood considers branch length. Conversely, Parsimony assumes that you would have the same expectation that a character would change along both long and short branches of the phylogenetic tree. Likelihood and distance methods, using models, instead consider that change is more probable along long branches than along short branches and provide accurate branch lengths even when a particular site has undergone more than one mutation (Foster, 2003).

There have also been a few disadvantages proposed for Maximum Likelihood as well. While not detrimental to the quality of results, but possibly restrictive on the

number, depth, or types of analyses performed is the problem that Maximum Likelihood is very computationally intensive and thus extremely slow. Compared to Bayesian analysis, Maximum Likelihood has been shown to use 80% more computing time (Leache and Reeder, 2002). In these analyses, this has been alleviated to some extent by use of the research computer cluster at Portland State University. Another critique of Maximum Likelihood is that the result is dependent on the model of evolution used and therefore very susceptible to incorrect evolutionary model selection and application (Merl *et al.*, 2005).

One million generations of Bayesian analysis also resolved a phylogenetic tree (Fig. 13) that possessed the same topology as the Likelihood and Distance trees. The Majority-Rule consensus tree derived from the 800,000 sample trees, once again, partitions all western subspecies within a single clade, separate from Newfoundland deer mice at the same (species) level as they are split from *P. keeni* and *P. sejugis*. The Majority-Rule consensus tree contained a Bayesian posterior probability for this bipartition of 100, indicating the strongest possible probability of this node being representative of the natural state.

The results seen here displaying a clear division between the eastern and western clades are congruent with the conclusions reached by a concurrent study (Dragoo *et al.*, 2006). Dragoo *et al.* (2006) suggest in their analyses that further data were needed from Oregon to further the understanding of these relationships. These analyses have provided those data. Like Dragoo *et al.* (2006), the data contained herein have shown that *P. keeni* of the Pacific Northwest allies very closely with the insular *P. sejugis* of San Diego and Santa Cruz Islands in the Gulf of California. Conversely, while

Dragoo *et al.* (2006) suggest that coastal Pacific Northwest forms would ally more closely with *P. sejugis* and *P. keeni* than with *P. maniculatus*, these analyses, containing specimens from the coastal, insular, and non-coastal Pacific Northwest have resolved them as essentially equally distinct from *P. maniculatus* and the *P. keeni/sejugis* clade.

Therefore, it is concluded that deer mice in the western half of North America, possibly bound on the east by the Mississippi River and the northern bodies of water, and seen as the separate western clade resolved in Figs. 10-13, represent a formerly cryptic but distinct species from *Peromyscus maniculatus* in the east within the *Peromyscus* genus. As suggested elsewhere (Dragoo *et al.*, 2006), this western clade may be representative of the previously morphologically described taxon *Peromyscus sonoriensis* (Le Conte, 1853).

Chapter 3: *Hantavirus* in the Pacific Northwest

Abstract-

An outbreak of an illness in 1993 that came to be known as *Hantavirus* Pulmonary Syndrome (HPS) was later found to be caused by a novel *Hantavirus*, since named Sin Nombre virus. In the years since, as many as 34 previously unidentified hantaviruses have been discovered and characterized, with the vast majority of these occurring in the Western hemisphere. Until this study, no hantaviruses had been identified in Oregon in spite of the occurrence of five recognized cases of HPS in the state. To fill this gap, *Peromyscus maniculatus* (deer mice) were collected at 5 sites in parks and green-spaces in and around the Portland, OR region. Ultimately, 86 of 2084 (4.1%) deer mice sampled were found to be sero-positive for antibodies to *Hantavirus* (tables 1, 2; appx. D).

Phylogenetic analyses were performed on 23 *Hantavirus* sequences obtained from sero-positive deer mice in the Portland, Oregon region, with additional sequences (n=21) from other hantaviruses from GenBank included. Comparison of 617 nucleotides of the G1/G2 glycoprotein precursor gene from the medium (M) segment genomic RNA, to other hantaviruses from around the world, found the Oregon viruses to be 11.2 % divergent from the most closely related described *Hantavirus*, Convict Creek virus, from east-central California, 14.3% divergent from Sin Nombre virus, 21.5% from New York virus, 23.6% from Blue River virus, and 41.4% from Hantaan virus. Maximum Likelihood and Bayesian analyses found the Oregon viruses to be monophyletic with the Convict Creek and Sin Nombre viruses.

These data strongly suggest that the *Hantavirus* found in Oregon minimally constitutes a new strain, and may in fact be a new species. It is proposed here that this new virus be referred to as the Kalapuya virus.

Introduction-

Epizootiology-

In the last few decades there has been what appears to be a significant increase in the emergence of pathogenic infectious diseases such as Sudden Acute Respiratory Syndrome (SARS) (identified SE Asia, 2002), Ebola Virus (sub-Saharan Africa, 1976), Human Immunodeficiency Virus (HIV) (sub-Saharan, 1970's), Marburg Virus (Sub-Saharan Africa, 1970's), and tick-borne diseases such as Lyme disease (NE USA, 1990's). Among these recent discoveries are the hantaviruses, the causative agents of Hantavirus Pulmonary Syndrome (HPS) (Western Hemisphere, 1993) and Hemorrhagic Fever with Renal Syndrome (HFRS) (Eastern Hemisphere, 1950's). The appearance of these diseases is believed to be associated with a range of underlying causal factors including interactions with zoonotic pathogens, that would otherwise normally be contained within a host–parasite relationship, between wildlife and humans (Daszak *et al.*, 2000). The term "emerging infectious disease" (EID) has been coined to describe any of the plethora of pathogens implicated in these recent discoveries, and is specifically used to define diseases that have recently increased in occurrence or geographic range, moved into new host populations, or only recently been discovered (Daszak *et al.*, 2000).

In 1993 in the southwestern United States, an outbreak occurred of a previously unknown disease, now called *Hantavirus* Pulmonary Syndrome (HPS). The subsequent investigation led to the identification of the causative agent—a novel *Hantavirus*— *Sin Nombre* virus (SNV) (Childs *et al.*, 1994; Nichol *et al.*, 1993). In the years since this discovery, the number of *Hantavirus* geno– and serotypes identified in the Western Hemisphere has grown to at least 23 (Johnson *et al.*, 1997; Morzunov *et al.*, 1998; Pini *et al.*, 2003; Rhodes *et al.*, 2000; Sanchez *et al.*, 2001; Schmaljohn *et al.*, 1995; Yates *et al.*, 2002), with this number on the increase as previously unknown hantaviruses are identified. In addition to *Sin Nombre* Virus some of the other most common hantaviruses known to cause HPS include; *New York* virus (NY), *Bayou* virus (BAY), *Black Creek Canal* virus (BCC), and *Andes* virus, with *Sin Nombre* virus being responsible for most of the 465 (Centers for Disease Control [CDC] 2007) known cases in the United States (Monroe *et al.*, 1999; Peters *et al.*, 1998; Schmaljohn *et al.*, 1997). Recent surveys for *Hantavirus* antibodies have revealed *Hantavirus*–infected rodents throughout most of North America (Holmes *et al.*, 2004; Monroe *et al.*, 1999; Rhodes *et al.*, 2000; Sanchez *et al.*, 2001; Schmaljohn *et al.*, 1995; Yates *et al.*, 2002). Hantaviruses are often transmitted among rodents through aggressive encounters—primarily between individuals of the same sex, usually males, and by infectious aerosols generated from contaminated urine, feces, blood, and saliva (Schmaljohn *et al.*, 1997; Olsson *et al.*, 2002).

Description-

Members of the genus *Hantavirus* of the family *Bunyaviridae* (5 genera, 250 species), are spherical, 100 nanometer diameter particles enclosed within a phospholipid bilayer envelope (Elliot *et al.*, 1991; Nichol *et al.*, 2005). Present within and extending above this envelope are two glycoproteins (G1 and G2) that mediate false recognition of the viral particle as benign by the host target cell. The glycoproteins then facilitate cell entry via a clathrin coated pit (Elliot *et al.*, 1991; Nichol *et al.*, 2005). Within this envelope is a protein nucleocapsid that houses a segmented single-stranded negative-sense RNA genome ~12,100 nucleotides (nt) in length (fig. 14). These segments are small (S), medium (M), and large (L) (Plyusnin *et al.*, 1996). The S segment, approximately 2,000nt in length, encodes the genes for the nucleocapsid proteins that encase the RNA genome in daughter viral particles. The medium, or M segment (3700nt), encodes the envelope glycoprotein precursor that is then co-translationally cleaved to yield the G1 and G2 glycoproteins (Elliot, 1990; Vapalahti *et al.*, 1992; Bohlman *et al.*, 2002). The L segment (6,500nt) encodes the RNA-specific polymerase that is used to replicate viral progeny genomes (fig. 14) (Elliott *et al.*, 1991; Chizhikov *et al.*, 1995).

Natural History-

It has been hypothesized by many that for every type of *Hantavirus* there is a specific rodent host species whose members can potentially acquire a chronic, asymptomatic, lifelong viral infection (Kaufman *et al.*, 1994; Morzunov *et al.*, 1998;

Netski *et al.*, 1999). It has been shown through phylogenetic analyses that the topologies of the evolutionary relationships among hantaviruses were closely correlated with those of their known or suspected primary mammal reservoirs (Borucki *et al.*, 2000; Monroe *et al.*, 1999; Plyusnin and Morzunov 2000; Sironen *et al.*, 2001; Yates *et al.*, 2002).

In the Americas, *Peromyscus maniculatus* has been co–evolving with hantaviruses for approximately 12–20 million years, since the first cricetids crossed the Bering Land Bridge, radiating and differentiating into the Rodent subfamilies Neotominae and Sigmodontinae found in the New World today (Yates *et al.*, 2002). While much is known about deer mouse phylogeny, it remains less than fully understood, and as a result of the documented host-parasite specificity among deer mice and their hantaviruses (Yates *et al.*, 2002), the associated viral phylogeny may be unresolved as well. New species of Peromyscus are increasingly being revealed from among these former host conspecifics (Chirhart *et al.*, 2001; Zheng *et al.*, 2003), revealing the potential likelihood of many uncharacterized hantaviruses waiting to be described as well.

For many years it was believed that hantaviruses were maintained exclusively within Order Rodentia. Only very recently has that perception been challenged as genetically distinct hantaviruses have increasingly come to be found residing among members of the Order Soricomorpha (shrews) - family Soricidae (Xiao *et al.*, 1994; Arai *et al.*, 2007, 2008). In the 1980's, in the former Soviet Union, antibodies to *Hantavirus* were found in members of families *Soricidae* and *Talpidae* (Gavrilovskaya *et al.*, 1983; Tkachenko *et al.*, 1983; Gligic *et al.*, 1989). B y that time molecular

techniques were not yet available to delineate genetic identity of potentially hosted viruses to confirm whether these were truly distinct viral evolutionary lineages or merely cases of ecological spillover from a sympatric rodent host. As of yet, no human disease has been associated with shrew–borne hantaviruses (Arai *et al.* 2007).

Worldwide, most hantaviruses have been found in members of the rodent families Cricetidae (Subfamilies Neotominae and Arvicolinae) and Muridae (Subfamily Murinae), with genetically distinct viral lineages found associated with specific members of these taxa (Monroe *et al.*, 1999) (fig. 1). Hantaviruses are believed to have arisen at least 136 million years ago before the split of the Mammalian Orders Soricomorpha and Rodentia, evidenced by the presence of distinct hantaviral lineages found in both Orders (Carey *et al.*, 1971; Plyusnin *et al.*, 1996; Hughes and Friedman, 2000). Among the earliest described are those found in East Asia, including Hantaan virus from the Hantaan River valley, recognized during the Korean War, as well as Seoul virus, also found in Korea (Lee *et al.*, 1978)(fig. 3). These East Asian viral species have been found to be reservoired within members of the family Muridae, Subfamily Murinae, as *Apodemus agrarius* (Hantaan), and *Rattus norvegicus* (Seoul; Lee *et al.*, 1982). Another murine *Hantavirus* is the recently described Sangassou virus, shown to reside within the African wood mouse *Hylomyscus simus*, found in Sangassou, Guinea (Klempa *et al.*, 2006). Reducing the clarity of this strict regional relationship, but upholding the host Subfamily paradigm, is the presence of Dobrava virus found in Northern Europe and hosted by the murine *Apodemus flavicollis*, a congener of the Hantaan virus host (Avsic-Zupanc *et al.*, 1992; 2000). Phylogenetic analyses have supported placement of Dobrava virus in the murine-hosted viral clade

(Avsic-Zupanc *et al.*, 1992) (Figure 1). European and North Asian serotypes such as Tula virus, Topografov virus, and Puumala virus, among others, have been found within arvicoline hosts such as *Microtus* and *Clethrionomys* species (Plyusnin *et al.*, 1994; Vapalahti *et al.*, 1999).

The more recently described members in *Hantavirus* are those found in the new world. In North and South America most of these infections are in species of the Subfamily Neotominae. Only a few Murid-hosted hantaviruses, consisting of Seoul virus in *Rattus norvegicus,* Subfamily Murinae, have been seen in the western hemisphere, primarily in urban environs (Monroe *et al.*, 1999). Cricetid rodents found hosting hantaviruses are many (table 1). In North America most common among these are hosts in the genus *Peromyscus* (Monroe *et al.*, 1999). The deer mouse, *Peromyscus maniculatus,* Subfamily Neotominae, has been identified as the reservoir for Sin Nombre virus (Childs *et al.*, 1994). In depth studies of Sin Nombre virus in North America have shown substantial genetic diversity and geographic structure of genetic variants within the viral quasispecies that may be the result of the genetic diversity in *P. maniculatus* (Monroe *et al.*, 1999; Morzunov *et al.*, 1996; Nichol *et al.*, 1999; Plyusnin *et al.*, 1996; Plyusnin *et al.*, 2000; Salazar-Bravo *et al.*, 2002). The rodent genetic diversity is paralleled by that of the virus (Dragoo *et al.*, 2006).

Scope-

As described above, due to the recognized coevolution between Hantaviruses and their hosts, Hantaviruses are suspected to reside in nearly every (if not every) ecoregion where their potential host species are found. Therefore, the phylogenetic

relationships among members of *Hantavirus* are incomplete, as many Hantaviruses are believed to remain undiscovered and thus undescribed. In light of this, the purpose of this work was to obtain in the field, *Hantavirus* potentially existing in the Portland, Oregon region, and to use molecular data to characterize and test the phylogenetic position of the *Hantavirus* strain found in the local deer mice.

Research Design and Methods-

Field Protocols-

(refer to page 16, Chap. 2)

Molecular Protocols-

Field collected blood samples were tested for the presence of antibodies cross-reactive to Sin Nombre virus (SNV) using Enzyme Linked Immunosorbent Assay (ELISA), performed by L. J. Dizney of the Oregon State Health Laboratory, or Strip Immunoblot Assay (SIA), by B. Hjelle of the University of New Mexico (Kaufman *et al.*, 1994; Mills *et al.*, 1995; Morzunov *et al.*, 1995; Rowe *et al.*, 1995; Vincent *et al.*, 2000).

Lung tissue was extracted from all 86 *Peromyscus* specimens found to be sero-positive for SNV antibodies (tables 2, 3; appx. D).

Approximately 30-50 milligrams of tissue from each individual were used for RNA extraction. Frozen tissues were physically disrupted in liquid nitrogen (lN_2) by grinding with mortar and pestle. Ground tissues were then homogenized using the

"QiaShredder" kit (QIAGEN). RNA was extracted and purified from these tissue samples using the QIAGEN "RNeasy Tissue Kit". Also Hantaviral RNA was recovered from the blood serum of a human HPS patient from the Portland region. The viral RNA was obtained using the QIAGEN "QIAAmp Viral RNA Mini Kit" and protocols contained therein.

Two fragments of the hantaviral M segment (617 nucleotides combined), one each of the G1 (361nt) and G2 (256nt) glycoprotein precursor gene region, were chosen as the targets for analysis (Fig. 14). Viral RNA sequences were amplified in a one step process through primer specific reverse transcription (RT) followed by polymerase chain reaction (PCR) using the QIAGEN OneStep RT-PCR kit. Each reverse transcription and first round PCR reaction was set up in a single 50 µl reaction volume containing 16.0 µl RNase free water, 10.0 µl 5x QIAGEN OneStep RT-PCR buffer, 2.0 µl dNTP mix, 10.0 µl 5x Q-Solution, 2.0 µl QIAGEN OneStep RT-PCR enzyme mix, 1.0 µl RNase inhibitor, 2.0 µl each of first round primers at 10.0 µM concentration, and 5.0 µl of RNA template. Two of each of these reactions were prepared for each specimen, one for the G1 region and one for the G2 region. First round RT-PCR primers are G1 5'-ACAATGGGITCIATGGTITGTGTA-3' (SM1687C) and 5'-TTIAATITIICATCCAATCCA-3' (SM2255R) and G2 5'TGTGAITATCAAGGIAAIAC-3' (SM2779C) and 5'-ACIGTIGCICCATAIACAT-3' (SM3128R) (Johnson *et al.*, 1997). The RT-PCR reactions were set up on ice to prevent or slow any enzymatic catalysis from occurring before samples are placed in the thermocycler.

The RT-PCR was performed by placing the samples in an Eppendorf-Mastercycler 96 well and running the RT-PCR program, defined as follows:

30 min @ 50°C	RT reaction	
15 min @ 95°C	RT inactivated and DNA polymerase activated	
1 min @ 94°C	Template denaturation	25 cycles
1 min @ 62°C	Primer annealing	
1 min @ 72°C	Extension	
10 min @ 72°C	Final extension	

After RT-PCR was complete, reaction products were cleaned using the PCR Purification kit from QIAGEN. To verify successful PCR, the amplified products were evaluated using gel electrophoresis (agarose). 5 µl of amplified DNA product were combined with 12 µl water and mixed. These 17 µl solutions were then placed in each of the wells of an "E-Gel" (Invitrogen) 2% agarose gel. Lane one of the 12-lane gel was left empty to accommodate 10 µl of 80bp-1Kbp DNA ladder (Fermentas MassRuler™ DNA Ladder, Low Range) as well as 7 µl water. The gel was then placed in the Invitrogen E-Base and set to run for 30 minutes. After the run was complete the E-Gel was removed and placed on an ultraviolet viewer to illuminate the fluorescently labeled DNA bands.

When bands were found to be of the correct size (596 nucleotides (nt) for G1 and 350nt for G2), remaining products were then amplified further using hemi-nested primers inside those from RT-PCR. Second round nested primers for G1 (361nt) were 5'-GAITGIGAIACAGCAAAAGA-3' (SM1723C) and 5'-TCIGCACTIGCIGCCCA-

3' (ASM2016R). Hemi-nested primers for the G2 coding region (256nt) were SM2779C (as above) and 5'-CCCCAIGCICCITCAAT-3' (SM3020R) (Johnson *et al.*, 1997).

Second round hemi-nested PCR was set up utilizing Amersham Biosciences "puReTaq ready-To-Go PCR Beads" (each bead contains ~200μM final concentration dATP, dCTP, dGTP, and dTTP, 10mM Tris-HCl, 50mM KCl, 1.5mM $MgCl_2$, 0.4 μl (each) of 10.0 μM primers, and 1.0 μl of template DNA in a 25.0 μl final reaction volume.

Thermocycler protocol (PCR2) was delineated as:

5min @ 95°C	Initial Denaturation	
45sec @ 95°C	Template Denaturation	35 cycles
30sec @ 62°C	Primer Annealing	
90sec @ 72°C	Extension	
10min @ 72°C	Final Extension	
Hold @ 4°C		

Again, to verify successful PCR, the products from the hemi-nested reactions were evaluated using electrophoresis as delineated above. Bands were resolved, as expected, at the range of approximately 361nt and 256nt as designated by the nucleotide ladder.

After confirmation of PCR products the remaining reaction solutions were then subjected to PCR cleanup again to remove excess polymerases, primers, dNTP's, and buffers using the QIAGEN PCR Cleanup Kit and protocols contained therein.

The amplified products from each of these reactions were then utilized as template for sequencing using the modified Sanger chain terminator method. Each primer requires its own sequencing reaction resulting in four sequencing reactions for each original hantaviral sample (G1 set and G2 set). The sequencing reactions were set up with 0.6 ml micro centrifuge tubes recessed in an ice-bath to limit reactivity of constituents until placed in the thermocycler. Each reaction vessel was prepared with 2.0 µl Big Dye Terminator solution (Applied Biosystems), 2.1 µl of 2.5 µM appropriate primer (SM1723C, ASM2016R, SM2779C, SM3020R), 1.0 µl 5x reaction buffer, 4.8 µl water, and 2.1 µl purified PCR product for a final reaction volume of 12 µl. These sequencing reaction vessels were then placed in the Eppendorf thermocycler and exposed to the sequencing thermo protocol (SEQ) as:

	96°C	5min
25 Cycles	96°C	30sec
	50°C	15sec
	60°C	4sec
Hold	4°C	

Upon completion of sequencing cycles, reactant solutions were plated in a 96 well micro titer plate that was then sealed and frozen at -70°C. The sequence reaction products were then shipped over night on dry ice to the Center for Genome Research and Bioinformatics (CGRB) Core Laboratories at Oregon State University, Corvallis, OR. There, sequences were analyzed on an Applied Biosystems (ABI) 3730 Capillary Sequence Machine.

Sequence File Preparation-

After the ABI 3730 generated the representative chromatograms they were downloaded via the internet from the CGRB Core Laboratories web site. Next, the sequence file chromatograms were uploaded into the software program SeqEd (Applied Biosystems v. 1.0.3). Within this program, sequences from corresponding primer pairs are viewed and edited for quality. First, the negative strand sequence is "reverse complimented" where the entire sequence is turned around to orient the last nucleotide first and the first nucleotide last. Then the bases of this reversed sequence are converted to their complementary nucleotide. Next, unidentifiable bases that occur at both the beginning and the end of the sequence were removed. After this is done "comparative alignment" was selected in the program menu that asks the software to analyze and align the two sequences based upon where they are identical. To identify bases mismatched between the two sequences, a shadow sequence was generated that indicates those mismatches with an asterisk. These labeled mismatched bases were then examined based upon their corresponding peak in the sequence chromatogram. In most cases, one of the two opposing sequence peaks was considerably cleaner, or stronger allowing the base to be "called" as the one indicative of the higher quality peak. In this way sequences were edited and aligned to produce a consensus sequence for the target gene group from each hantaviral genomic segment. This task was undertaken twice for each viral sample representing the G1 and G2 coding regions, which were amplified and sequenced separately.

The G1 and G2 consensus sequence fragments from each specimen were concatenated in a text-editing program. The concatenated sequences were imported into MacClade (Maddison and Maddison, 2003) for multiple sequence alignment where sequences from all *Hantavirus* samples were aligned with one another as well as with other out-group species obtained from NCBI GenBank. The multiple sequence alignment (showing coded amino acids) was adjusted as to codon reading frame to represent the natural transcriptional reading frame. To allow separate adjustment of the G1 and G2 reading frames single spaces were inserted between the fragments.

Phylogenetic Analysis-

(refer to pg. 21, Chap. 2)

Results-

Distance Analyses-

In these analyses *Hantavirus* sequences were obtained (n=22; appxs. F, H) from *Peromyscus* in the greater Portland, OR region. In addition, a twenty-third *Hantavirus* sequence was obtained from the blood of a current HPS patient. Based upon a 617 nucleotide fragment of the M segment RNA, glycoprotein precursor gene, Oregon hantaviruses were sequenced for comparison to other hantaviruses (sequences from GenBank, appx. F) from North America and the rest of the world. Genetic divergence (p distance) analysis was conducted using PAUP (Swofford, 1998). Figure 15 and appendix B contain pair-wise genetic distances for the Portland viruses relative to

most other North American (Cricetidae-borne) hantaviruses and others from throughout the world (Muridae-borne). Both uncorrected and corrected genetic distance data are shown. Corrected genetic distances were calculated by application of the general time reversible model of evolution allowing a proportion of sites to be invariant with a gamma distribution of that variance across sites (GTR+I+Γ). Most publications report uncorrected genetic distances, so these will be the focus here for more clarity of comparison.

The Portland area *hantavirus* referred to as Kalapuya virus (KV) here (after the original inhabitants of the Willamette Valley – the Kalapuya tribe), possesses an uncorrected genetic distance of 0.112 (fig. 15) from its nearest known (geographically and genetically) congener, Convict Creek virus (CC) found in the eastern Sierra Nevada Mountains in east-central California (Schmaljohn *et al.*, 1995). Intra-specific average nucleotide genetic distance for the Portland area hantaviruses was 0.017, indicating the lack of diversity expected within a local population (Monroe *et al.*, 1999). Included among these Kalapuya viruses is the sequence recovered from a Washington County, OR human patient serum. This sequence had a genetic distance of 0.014 from Kalapuya virus sequences found in mice from the patients home and 0.016 from the whole of KV. Viral sequences WC7 and WC13 were identical to one another and both most resembled the patient virus at p= 0.008, less than half the distance of the patient virus from the other sequences recovered from the patients home, making it likely that one of the these two mice may have originally possessed the virus(es) that infected the patient (appx. B).

The next nearest (p=0.143) described *Hantavirus* after CC is Sin Nombre virus (SNV) from the four corners region in the American Southwest (Childs *et al.*, 1994). *Peromyscus*-borne hantaviruses in the American west are collectively known as the Sin Nombre-like group (Morzunov *et al.*, 1997). Within this western North American region is El Moro Canyon virus (EMC) from southern California, but as seen in Figs. 16-18, El Moro Canyon virus is not within the Sin Nombre group and is in fact quite divergent with a p=0.278 from the Portland area virus and p=0.269 from Sin Nombre. Fig. 15 also reveals two other hantaviruses from west of the Mississippi River in Blue River virus (BR) hosted by *Peromyscus leucopus* (western haplotype), and Bayou virus (BV) reservoired by *Oryzomys palustrus*. Similar to El Moro Canyon virus, Bayou virus (p=0.273) is quite divergent from Portland and also is not from within the Sin Nombre group (figs. 16-18). Blue River virus (p=0.236) while also significantly divergent from Sin Nombre, is reservoired by a Peromyscine, and therefore is considered part of the Sin Nombre-like group (Morzunov *et al.*, 1997). Of note, Blue River virus has also been described from Indiana (Morzunov *et al.*, 1997) but BR sequences used in these analyses were derived from Oklahoman specimens.

Other more genetically distant hantaviruses seen in Fig. 15 are New York virus (NY) reservoired by the eastern haplotype of *P. leucopus*, and Black Creek Canal virus from south Florida found in *Sigmodon hispidus*. New York virus is shown to possess a genetic distance of 0.215 from Portland virus, similar to the other *P. leucopus* virus, Blue River at 0.236. The final *Hantavirus* seen in Fig. 15 is Prospect Hill virus found in the Northeastern United States and hosted by the arvicoline *Microtus pennsylvanicus*. Not known to cause human disease, Prospect Hill virus is

the most genetically divergent *Hantavirus* in North America with a p=0.331 from Kalapuya virus.

Maximum Likelihood Analysis-

The *Hantavirus* sequences examined with genetic distance methods were also subjected to Maximum Likelihood analysis. Using the GTR+I+Γ model of evolution as chosen by MODELTEST (Posada and Crandall, 1998), maximum likelihood analyses using PAUP (Swofford, 2002) resolved a tree with a score of –lnL=8011.8281 and an Akaike Information Criterion (AIC) of 16043.6562. The likelihood tree was calculated using the tree bisection-reconnection (TBR) swapping algorithm. Nucleotide frequencies were A=0.33470, T=0.30010, C=0.16080, G=0.20440. Among-site rate variation includes an assumed proportion of invariable sites of 0.1364. A gamma distribution of rates across variable sites was implemented with a shape parameter of 0.5469 and four rate categories. Node support for the likelihood tree was generated using 1000 bootstrap replicates.

Similar to the genetic distance tree in Fig. 16, the boot strapped Maximum Likelihood tree in Fig. 17 shows the Portland virus as sister to Convict Creek virus. This same clade is also nested in Sin Nombre virus. Each of these nodes is supported above 90 percent, with the separation of the Portland virus from Convict Creek in 990 of 1000 bootstrap replicates. Differing from the genetic distance tree, the likelihood tree places El Moro Canyon virus outside of the Sin Nombre-like *Hantavirus* clade, more in line with previous research (Hjelle *et al.*, 1994; Morzunov *et al.*, 1997; Vapalahti *et al.*, 1999; Vincent *et al.*, 2000). Supported at 97 percent the three

arvicoline viruses, Prospect Hill, Tula virus, and Puumala virus, were separated in a single clade revealing their genetic similarity with one another but in contrast with their geographic disparity. The node containing these divisions was supported in 1000 of 1000 replicates. Bayou and Black Creek Canal viruses formed their own clade. Although only tepidly supported, all South American hantaviruses were contained within a single clade as well. Fig. 17 shows all of the New World *Hantavirus* clades nested within and monophyletic from Seoul virus. The cricetid (neotomine, sigmodontine, and arvicoline) hantaviruses in Fig. 17 are found nested within the Asian, European, and African murine hantaviruses (Hantaan, Dobrava, and Sangassou viruses).

Bayesian Analysis-

Summarized consensus tree data may be viewed in Fig. 18 with posterior probabilities shown for each bifurcation. The Majority-Rule Bayesian consensus tree yielded a topology very similar to the genetic distance tree (Fig. 16) and similar to the maximum likelihood (Fig. 17) phylogeny. In Fig. 18 the Portland virus is found sister to Convict Creek virus, which in turn is sister to Sin Nombre virus. These western United States hantaviruses are seen sister to the eastern U.S. hantaviruses, New York, and Blue River. These Sin Nombre-like hantaviruses form a single monophyletic clade sister to the clade found to contain the South American hantaviruses and the two southeastern U.S. hantaviruses, Bayou and Black Creek canal. In the same fashion as the likelihood tree in Fig. 17, the Bayesian tree in Fig. 18 also reveals the *R. megalotis* reservoired El Moro Canyon virus outside of each of these clades that are nested

within EMC in the Bayesian tree but not the Neighbor-Joining distance tree (Fig. 16). In the Bayesian analysis the two major clades described above, along with El Moro Canyon virus, are nested in the three arvicoline hantaviruses, Prospect Hill, Puumala, and Tula. Again, as seen in the likelihood tree, the neotomine and arvicoline *Hantavirus* clades are nested in the murine hantaviruses from Europe, Asia, and Africa.

Discussion-

Phylogenetic analyses of Kalapuya virus (KV) were based upon 617 nucleotides of the medium (M) segment genomic RNA. This particular fragment of the genome was selected for these analyses because the envelope glycoproteins are used for host cell entry and quite possibly under the most selective pressure, making it a prime location for divergence in the genome. In addition, most literature on this subject use this region of the genome, making these data directly comparable to the rest of the literature. This fragment codes for two portions of the glycoprotein precursor gene, corresponding to segments of the G1 and G2 coding regions. Figures 17 and 18 have revealed the robustness of these analyses by showing the pair-wise genetic distances among commonly evaluated hantaviruses to be nearly identical to those resolved by Morzunov *et al.* (1998). For example, using M segment data, Morzunov *et al.* (1998) found Sin Nombre virus (SNV) to be at a genetic distance of 0.183 from another Sin Nombre group virus, New York virus, while these data herein show 0.189, also similar is Sin Nombre to Blue River at 0.195 / 0.201, and Sin Nombre to El Moro Canyon at 0.288 / 0.269. This congruity lends strength to the pair-wise genetic distances

resolved by these analyses between the previously un-described Kalapuya virus and Sin Nombre virus (p=0.143), as well as the genetic distances between KV and Convict Creek virus (CC) (p=0.112) and CC and SNV (p=0.130). Convict Creek virus has been characterized as at least a new strain of *Hantavirus* within the Sin Nombre group, if not a new species (Schmaljohn *et al.*, 1995; Li *et al.*, 1995). If Convict Creek virus has been classified as distinct from Sin Nombre, then, so too should Kalapuya virus, found at an even greater genetic distance from SNV than is CC.

Hjelle *et al.* (1995a), and Morzunov *et al.* (1998) have proposed that three lines of evidence be considered when evaluating hantaviruses for possible speciation. First is immunological by using plaque reduction neutralization assays (PRNA), where neutralizing species specific antibodies are bound to viral particles and infection susceptible cells are exposed to the resulting virus-antibody complex. Then speciation is defined by at least a four-fold, two-way difference between putative species, described as the known virus species having four times as much antibody binding (and therefore neutralization) as unknown comparative hantavirus species. The second uses ecological or physiological evidence as found in the viral host. For viral speciation to have occurred, it must be found in a distinct rodent host, known to reservoir no other *Hantavirus*. Morzunov *et al.* (1998) proposed the adoption of the definition of a different rodent host as "a reproductively and/or ecologically and/or geographically separated rodent species *or subspecies*, which carries a phylogenetically distinct *Hantavirus* and which is capable of being the sole carrier of this virus in a rodent community". Third, molecular evidence must reveal significant nucleotide differences from other described hantaviruses. Puthavathana *et al.* (1993) proposed, which has

since been adopted elsewhere, that *Hantavirus* speciation is said to have occurred at more than a 25% nucleotide difference in the glycoprotein precursor gene open reading frame. A nucleotide difference of 15 to 25% was considered a "grey area" where phylogenetic analyses are then required for proper evaluation of speciation (Puthavathana *et al.*, 1993).

In consideration of these criteria, the results of the analyses contained herein are discussed further. In terms of immunological evidence, even though Sin Nombre virus (SNV) has been adapted to cell culture, this examination is not currently possible as the Portland *Hantavirus* has yet to be adapted to cell culture, for which hantaviruses are notoriously difficult, thereby prohibiting the PRNA.

Criterion two, ecological or physiological evidence, is also difficult to evaluate. What is known, is the hosts of SNV and KV are geographically isolated from one another with the SNV host, *P. m. rufinus*, found in the four corners region, some 1,700 kilometers (1,100 miles) from western Oregon. In general terms, the vast difference in the disparate climes occupied by these conspecific hosts (temperate rain forest in western Oregon compared to scrub desert in the four corners region) leads to the logical conclusion that these two hosts, however defined, are also ecologically isolated from one another. Not known is the level of reproductive isolation that may exist between these two hosts, as those examinations have yet to be conducted. Not addressed by Hjelle *et al.* (1995a), but appropriately included in the discussion of different hosts, is the phylogenetic relationship between the two hosts based upon molecular evidence. As has been discussed previously, rodent phylogeny, and especially that among *Peromyscus*, is unresolved. Rodent phylogenies produced in

these analyses, seen in Figs. 11 through 14 reveal the distinct possibility that *Peromyscus maniculatus rubidus*, from which the Kalapuya viruses were obtained, may in fact be a distinct species (along with other nearby allopatric subspecies) from the topo-typical *Peromyscus maniculatus maniculatus*. Making this assessment more difficult is the lack of a comparable sequence (mtDNA ND3, ND4, and ND4L) from the Convict Creek host to have allowed its inclusion in the *Peromyscus* phylogeny. The pair-wise genetic distance between the SNV reservoir, *P. m. rufinus*, and *P. m. rubidus* is seen at 0.025 (figs. 8, 9). While this level of divergence is below the typical speciation threshold for rodents of roughly 4%, Fig. 8 does show that *P. m. rubidus* is, as stated above, quite likely a separate species from *P. m. maniculatus* with a pair-wise genetic distance of 4.1%. Moreover, the Bayesian tree seen in Fig. 13 shows the Pacific Northwest subspecies as a separate clade nested within *P. m. rufinus*.

The lack of complete data for more thorough analyses of the first two criteria has resulted in greater emphasis placed on the third criterion, molecular evidence. Molecular and phylogenetic evidence is the focus of these analyses and has revealed Kalapuya virus with a genetic distance from Sin Nombre virus of 0.143, less than the definitive threshold for speciation as proposed by Puthavathana *et al.* (1993) of 25%, is, however, near the lower limit of the "grey area" that was discussed by the same authors.

Maximum Likelihood and Bayesian phylogenetic analyses contained herein (Figs. 18-19) have strengthened the genetic distance analysis that found Kalapuya virus nested within and monophyletic to Convict Creek and Sin Nombre viruses. As all three are hosted by subspecies of *P. maniculatus*, and considering other North

American hantaviruses, reservoired by the congener *P. leucopus*, are also recognized as part of the Sin Nombre group, this monophyly was expected.

In light of the pair-wise genetic distance as found at the lower limit of the grey area criterion and its relative phylogenetic location strongly within the Sin Nombre group, it may be argued by some that the Kalapuya virus has not yet speciated. That said, the level of genetic divergence from Sin Nombre virus does strongly argue that KV is on a separate evolutionary trajectory and are at the very least nearing speciation, if that level of distinction has not yet been achieved. The findings of the *Peromyscus* phylogenetic, geographic, and ecological relationships discussed above lend themselves to this argument. Further analysis of the complete Kalapuya virus genome, even greater elucidation of the host relationships through further molecular comparison as well as immunological analyses may in fact lead to such a specific classification in the near future. It is therefore concluded that Kalapuya virus – in honor of the first human inhabitants of the Portland, OR region, may in fact be a previously un-described species of *Hantavirus*, and minimally constitutes a new strain.

Chapter 4: *Peromyscus* and *Hantavirus* Coevolution

Abstract-

It has been proposed that hantaviruses are found in a species-specific relationship with their hosts and have experienced a co-evolutionary history. Phylogenetic analyses performed here have been found in support of these studies and revealed the probability of the presence of a new deer mouse species, minimally in Oregon, if not including much of the western United States. As suggested by others, this western deer mouse in Oregon is referred to as *Peromyscus sonoriensis rubidus*. In light of the co-evolutionary relationship, as well as further phylogenetic analyses contained herein, the hantavirus reservoired by *P. s. rubidus* is in fact a new quasi-species of hantavirus, separate from Sin Nombre virus and Convict Creek virus, proposed as Kalapuya virus.

Methods:

Sets of hantavirus and host sequence specimens, as described in chapters 2 and 3, were reduced to a subset of specimens consisting of only those from North America, including from elsewhere only Hantaan virus and its host, *Rattus norvegicus* for out-group comparison. Bayesian analyses were performed on these two sets of data using the same Bayesian protocols as described in chapter 2 (pg. 36). The two resulting majority-rule trees were aligned for comparison after rotating the host tree to its mirror image.

Results:

In addition to the previously discussed observations for individual phylogenies of hantaviruses and hosts a comparative Bayesian double phylogenetic tree of these hantaviruses and hosts is seen in Fig. 19. Included on the left of this figure are most of the hantaviruses from North America, excluding only those found in a reservoir already represented here by another *Hantavirus*, and the other significant mile-post *Hantavirus*, Hantaan virus from Korea, as the out-group. The right side of the figure shows the known reservoirs for these hantaviruses. With consistently strong posterior probabilities (PP>96), the comparative phylogenies are also found to be near perfect mirror images of one another.

Only the location within the tree of El Moro Canyon virus relative to its known host, *Reithrodontomys megalotis*, is in dischord with parallel evolutionary histories. While *R. megalotis* is found more closely allied with other *Peromyscus*, El Moro Canyon virus is associated with hantaviruses (Bayou, Black Creek Canal) hosted by more distantly related Sigmodontines (*O. palustrus*, *S. hispidus*).

Discussion-

Peromyscus speciation-

Recently, Dragoo *et al.* (2006) recognized the hantavirus-host co-evolutionary framework in a more geographically comprehensive study in which the authors recognized six separate *Peromyscus* clades or lineages but, as noted by the authors, missing from their analyses are data from Oregon. Of those lineages found, one that was suggested existed in the Pacific Northwest coastal region. It was also proposed

that an expanding Rocky Mountain clade is overlapping with this coastal clade, said to include *P. keeni*, *P. sejugis*, and *P. maniculatus gambelii* (Dragoo *et al.*, 2006). Conflicting with this proposal is the fact that *Peromyscus* analysed in this study included *P. m. gambelii* from east of the Cascade Mountains in Oregon that were not seen to be significantly different from *P. m. rubidus,* on the west side of the Cascades. Also, these analyses found the Oregonian deer mice to be slightly more distant from the coastal *P. keeni/sejugis* clade (0.0556) than the *P. m. maniculatus* (0.0416) clade from central-northeastern North America, west of the St. Lawrence River, but very closely associated with the Rocky Mountain clade (0.0248). Contrary to Dragoo *et al.* (2006), Washington coastal *P. m. austerus*, which might have been assumed to reside with the coastal clade were not found associated with the coastal clade as hypothesized by those authors, but instead correlated very closely with the other conspecifics *P. m. rubidus*, and *P. m. gambelii* (Figs. 10-13) from Oregon, seen here linked to the Rocky Mountain clade (Figs. 8, 9). Therefore these data in conjunction with those found by Dragoo *et al.* (2006) suggest that there may in fact be several distinct deer mouse lineages in western North America, with those from Oregon, and possibly Washington as well, associating with the Rocky Mountain clade and not the Coastal clade. In addition, the analyses contained herein align with the findings of Hogan *et al.* (1997), and Dragoo *et al.* (2006) in suggesting that a deep genetic division occurs between the greater western North American and the eastern North American deer mouse clades, with this break (as proposed here) along the Mississippi River corridor. It has been proposed by Dragoo *et al.* (2006) that the Rocky Mountain clade may represent the previously described morpho-species *Peromyscus sonoriensis* (Le Conte, 1853).

Hantavirus speciation and Coevolution-

Phylogenetic trees seen in Figs. 17-19 as well as the pair-wise genetic distances in Fig. 15 reveal Kalapuya virus (KV) closely associated with Convict Creek Virus (CC) (p=0.112) and Sin Nombre Virus (SNV) (0.143), all of which are reservoired by putative hosts (*P. m. sonoriensis* and *P. m. rufinus* respectively) found to reside within the Rocky Mountain clade (proposed as *P. sonoriensis*).

The *Hantavirus*/host double phylogeny seen in Fig. 19 displays the suggested co-phylogeny implied by the co-evolution seen between hantaviruses and hosts. The intrigue of this figure is borne-out by the virtually identical topologies of these two trees, only the split between El Moro Canyon virus (EMC) and the nested clade containing Bayou virus (BAY) and Black Creek Canal virus (BCC) differs from the reservoir tree topology for these taxa in that the reservoir tree places the hosts for BAY and BCC (*Oryzomys palustrus* and *Sigmodon hispidus* respectively) as a clade sister to, instead of nested within the EMC host (*Reithrodontomys megalotis*) as is seen for the virus tree. All other hantaviruses examined in Fig. 19, including Kalapuya virus, are found in a perfect mirror-image association with their putative reservoirs, representing mirrored, or co-evolution.

Conclusions-

Peromyscus maniculatus rufinus in the southwestern United States has for the past 14 years been considered to be the reservoir of Sin Nombre *Hantavirus* (Childs *et al.*, 1994). *Peromyscus maniculatus sonoriensis* in eastern California has been recognized

as the host for Convict Creek virus for the last 13 years (Schmaljohn *et al.*, 1995). Armed with the knowledge that species of the genus *Hantavirus* are associated with specific host species, and that both virus and host evolve within this co-evolutionary framework (Monroe *et al.*, 1999; Dragoo *et al.*, 2006), and that the Portland (and likely all western) deer mouse range is composed of what may in actuality be a species distinct from *P. maniculatus sensu stricto*, it is reasonable to hypothesize that hantaviruses found in these reproductively isolated "*P. maniculatus*" populations also will have undergone a similar level of differentiation into a putatively novel viral species distinguishable from Sin Nombre virus at a molecular level. The data contained herein bear that out. It is therefore concluded that Kalapuya virus, found in Oregon deer mice, is a formerly undescribed species of *Hantavirus*, and the Oregon deer mouse, its reservoir, is in fact a separate species of the western deer mouse clade proposed as *Peromyscus sonoriensis*.

Also supported is the hypothesis that coevolution of North American hantaviruses with their hosts is seen in the presence of essentially identical phylogenetic topologies.

Epilogue: Research Significance

In 1993 an outbreak of a previously unrecognized disease occurred in the four corners region of the southwestern United States. Subsequently, phylogenetic analyses of the etiological agent for this disease was identified as a formerly undescribed member of the viral genus *Hantavirus* (Family Bunyaviridae) (Childs *et al.*, 1994). Sin Nombre virus was the moniker given to this new pathogen with the associated pathology described as *Hantavirus* pulmonary syndrome (HPS). With an initial mortality rate of more than 70%, HPS is characterized by bilateral pulmonary infiltrates, resulting in pulmonary deficiency and sometimes, failure. While no direct treatment yet exists, mortality has recently been reduced to 38% through early recognition and subsequent fluid management.

Clouding the understanding of patterns of HPS occurrence is the fact that among the characterized hantaviruses (>40) as many as 20 have not been known to cause disease. Even within the pathogenic group of hantaviruses there exist those with varying degrees of pathogenicity, where some may illicit only minor symptoms instead of the full illness.

The division between pathogenic versus non-pathogenic viral lineage is partially reflected in the reservoir phylogenies. Worldwide, hantaviruses have been recognized in specific mammalian hosts and in the New World, Plyusnin and Morzunov (2001) and others have found a great amount of association among hantaviruses and their hosts. In fact Yates *et al.* (2002) recognized that Sin Nombre virus, and therefore other Sin Nombre-group hantaviruses, were not introduced to the western hemisphere but instead, during the mid-Miocene, migrated and co-evolved in a very close

relationship with their hosts as their reservoirs crossed the Bering land-bridge from Asia to North America, entered the New World, and then radiated and differentiated into the Neotominae and Sigmodontinae currently found there. In the process, those resident hantaviruses differentiated as well into the hantaviral lineages currently seen in the western hemisphere. For many years studies suggested these hosts resided only within Order Rodentia. Recently, however, new viral lineages have been described from Soricid reservoirs (*Blarina spp.* and *Sorex spp.*) (Arai *et al.*, 2006, 2007) but to date, no Soricid-borne *hantavirus* has been associated with human disease. There exist, of course, Murid-borne hantaviruses as well that do not generate disease within humans, especially those found within the Arvicolinae such as one North American *hantavirus*, Prospect Hill virus, reservoired by the Arvicoline *Microtus pennsylvanicus*.

With the knowledge that hantaviruses are associated with specific mammalian hosts, and are not ubiquitously pathogenic, there arises, therefore, the need for a greater understanding of the distribution of hantavirus hosts (potential and recognized) as well as the putative virus strains themselves. The data contained herein contribute to that growing level of clarity of hantaviral-reservoir evolutionary, phylogenetic, and biogeographic associations. The theory espoused by Dragoo *et al.* (2006) that deer mouse phylogenies provide a framework, at least potentially, for the elucidation of the distribution of hantaviruses and their phylogenetic relationships to one another are supported by the findings reported here. In point of fact, Dragoo *et al.* (2006) state that missing from their data are specimens from Oregon of both deer mice and their potential hantaviruses. Again, at the conclusion of this study, those data are now

provided. As acknowledged previously above, these analyses have shown that there exists an extreme likelihood that the deer mice from Oregon, likely in conjunction with other subspecies in the western United States, are in fact a new species separate from *Peromyscus maniculatus sensu-stricto*. In addition, the hantaviruses reservoired by the Oregon deer mice represent a new strain, if not a new species, as well. Taken in consideration with the variability of pathogenicity seen in the various *Hantavirus* strains and species, the new taxonomic designation for Oregon deer mice fills a gap in the current knowledge of those distributions in the Pacific Northwest. This becomes critical when the virulence of the Oregon *Hantavirus* is taken into account. As of this publication, nine cases of HPS have been documented in Oregon with four of those nine (0.44) resulting in death. While rare, any disease that is known to result in a 44% mortality rate warrants efforts to understand as much about its epizootiological, phylogenetic, and biogeographic characteristics as possible. Hantaviruses are referred to as emerging infectious diseases (EID), and as humans expand their environment further into natural habitat and more regularly encounter potential wildlife carriers of disease it is critical that the scientific community endeavor to facilitate the understanding of these disease parameters to gain a greater awareness of all the different quasispecies of hantavirus in nature today and the ranges in which they occur. This knowledge will allow a concentration of management efforts of the associated reservoir species, especially those that carry the most dangerous strains of hantavirus, to raise local community awareness and insofar as possible limit the amount of human exposure to the pathogens potentially carried by the mice.

On a genetic scale, the viral sequences elucidated in these analyses were derived from the envelope glycoprotein-coding region of the viral tripartite genomic RNA. These co-translationally cleaved glycoproteins, G1 and G2, are expressed within and upon the phospholipid bilayer envelope that is procured from the infected cell, which surrounds and encloses the daughter virion. The envelope glycoproteins are believed to play a significant role in cellular recognition, binding of the virus particle to a clathrin coated pit, and subsequent cellular uptake of the virion.

Although attempts have been made, there currently exists no vaccine to inoculate against, or antiviral drug for the treatment of, HPS. Efforts to construct a vaccine to *Hantavirus* have involved utilization of G1 and G2 based upon previously mentioned fact that those glycoproteins play such a large role in the infection process. By focusing sequencing efforts on the envelope glycoprotein precursor coding gene, basal knowledge for the amino acid, and therefore the protein structure, may be extrapolated from those sequences for further application of the study of the interactions involved at the molecular level in the host cell mediated uptake of the virus particle at the clathrin coated pit.

Procurement of pathogens from their sources, in this case, hantaviruses from deer mice, followed by evaluation of their defining characteristics, epizootiology, and distributions are the first steps in working to avoid and/or offset their ultimate pathology. By identifying and characterizing the *Hantavirus* from Oregon, as well as its reservoir species, these analyses have contributed to the greater effort to reduce and understand *Hantavirus* Pulmonary Syndrome.

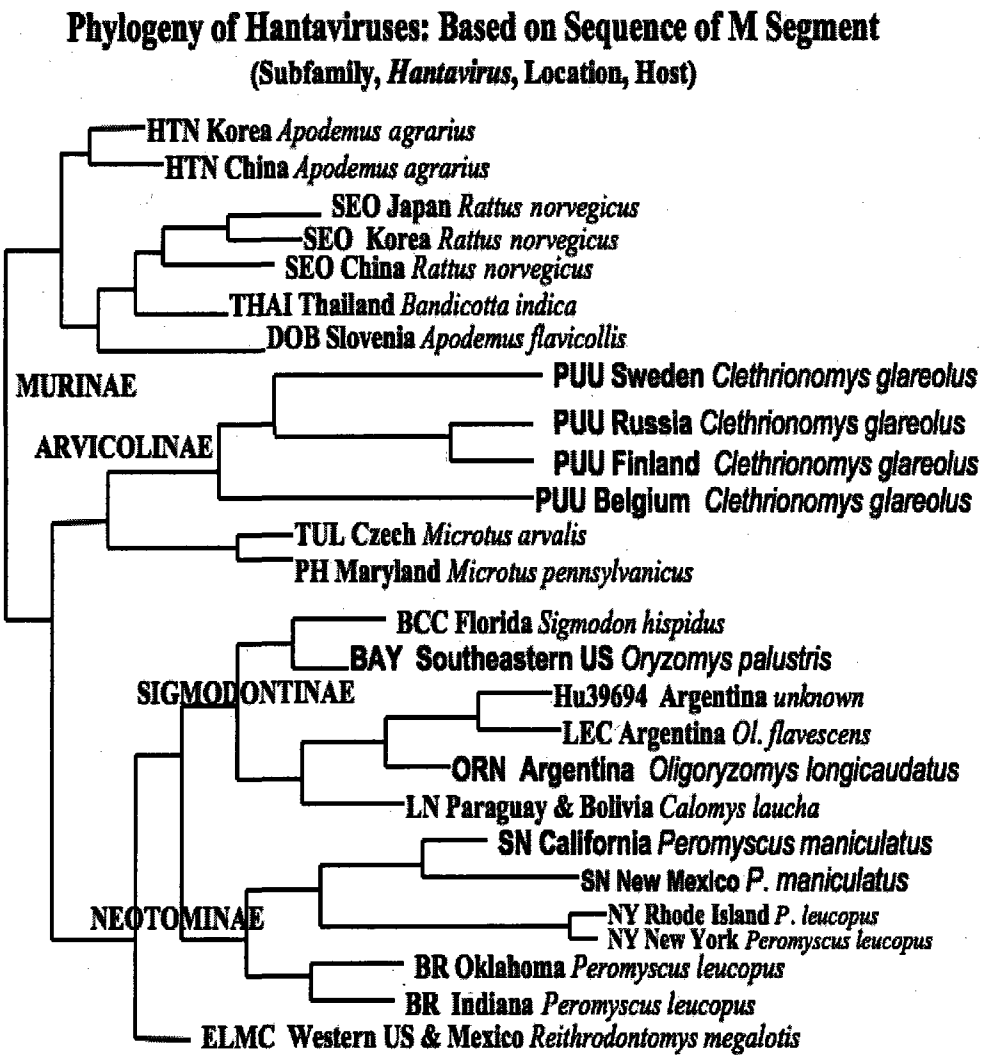


Figure 1: World Wide *Hantavirus* M Segment Phylogeny. SN=Sin Nombre, NY=New York, BR=Blue River, ELMC=El Moro Canyon, LN=Laguna Negra, ORN=Oran, BAY=Bayou, BCC=Black Creek Canal, PH=Prospect Hill, TUL=Tula, PUU=Puumala, DOB=Dobrava, THAI=Thai, SEO=Seoul, HTN=Hantaan. *Reproduced with permission from:* Centers for Disease Control, National Center for Infectious Disease, Special Pathogens Branch, Division of Viral and Rickettsial Diseases – HPS Teaching Slideset.

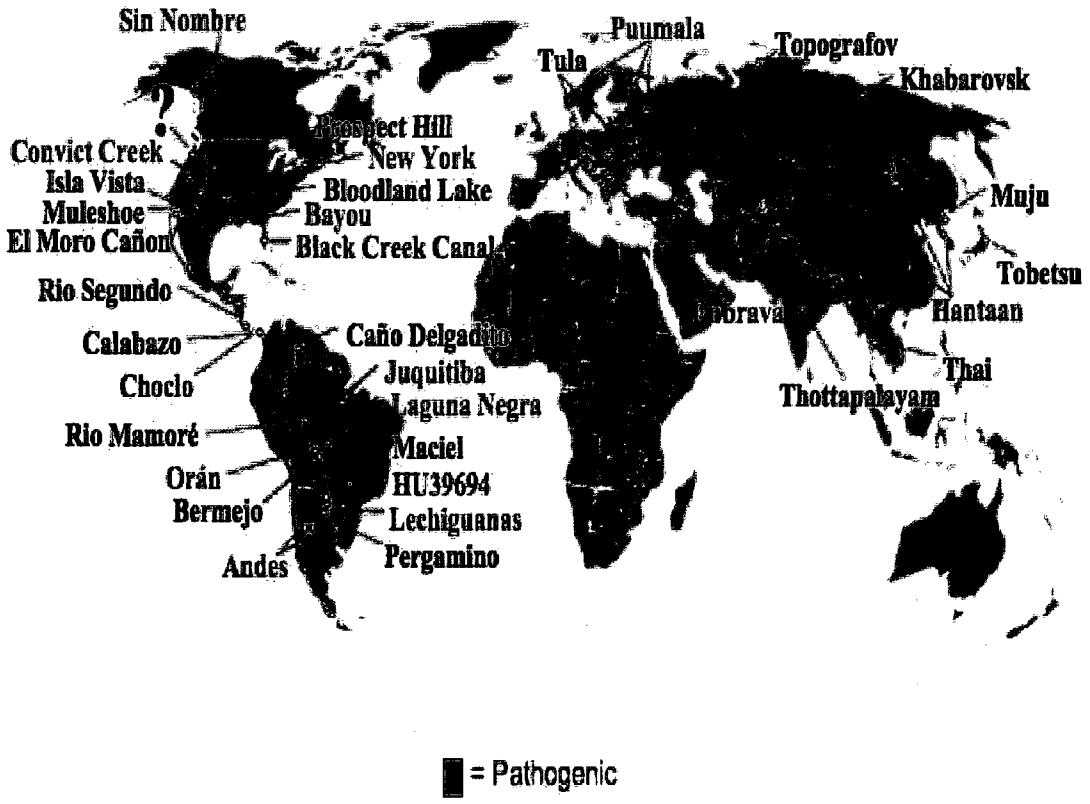


Figure 2: *Hantavirus* Species World Distribution. Known *Hantavirus* species and the regions where they are found. Viruses shown in black are not known to cause Hantavirus Pulmonary Syndrome (HPS) in humans. Viruses in magenta are known causative agents of HPS. Blue question mark represents the undescribed *Hantavirus* in the Portland, OR region.

Figure 3: ***Peromyscus maniculatus*** **Range Map.** The purple overlay indicates the geographic distribution of the deer mouse, *Peromyscus maniculatus*, in North America. Re-drawn from Hall, 1981.

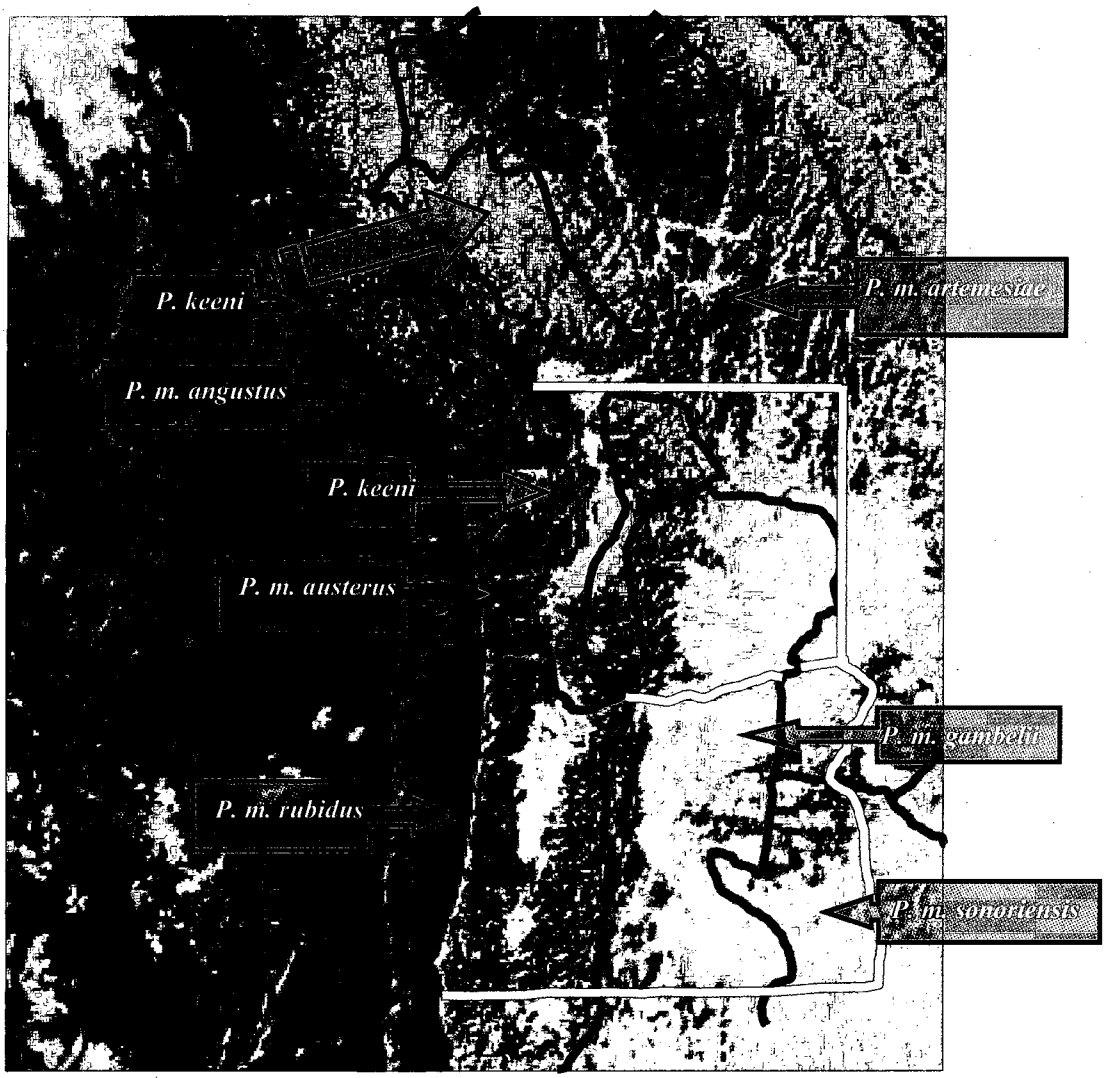
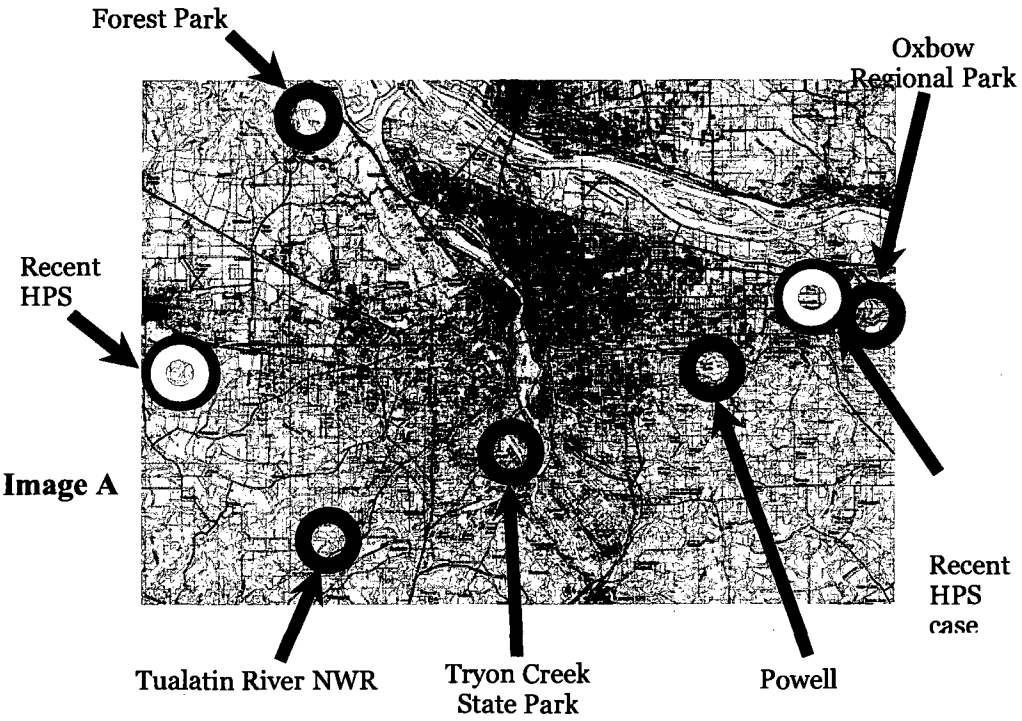
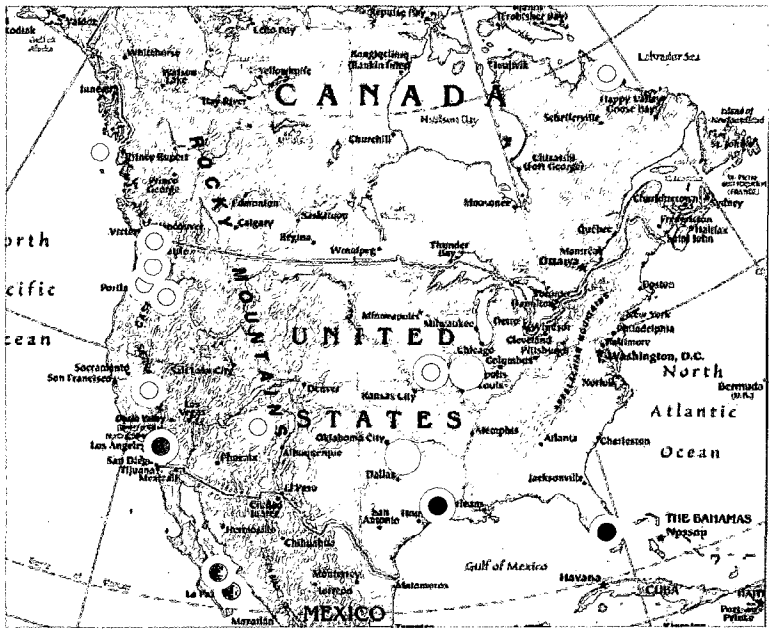


Figure 4: Pacific Northwest Subspecies Map. Distributions of subspecies of *Peromyscus maniculatus* in the Pacific Northwest of the U.S. and Canada, as well as the disjunct ranges of *P. keeni*. Range limits shown by blue lines. Yellow indicates Oregon and Washington state boundaries except where congruent with subspecies range limit.





= *Peromyscus maniculatus* sub spp.
= *Peromyscus keeni*
= *Peromyscus leucopus*
= *Peromyscus sejugis*
= *Reithrodontomys megalotis*
= *Oryzomys palustrus*
= *Sigmodon hispidus*

Figure 5: Specimen Collection Sites. Image A: map of Portland, OR, U.S.A. showing field collection sites of *Peromyscus maniculatus* in the metropolitan area. Concentric blue and light blue rings marks the locations of two recent HPS cases. Image B: locations of specimens from outside Portland, OR. Sequences not from Oregon, Missouri, Illinois, and Labrador were obtained from GenBank.

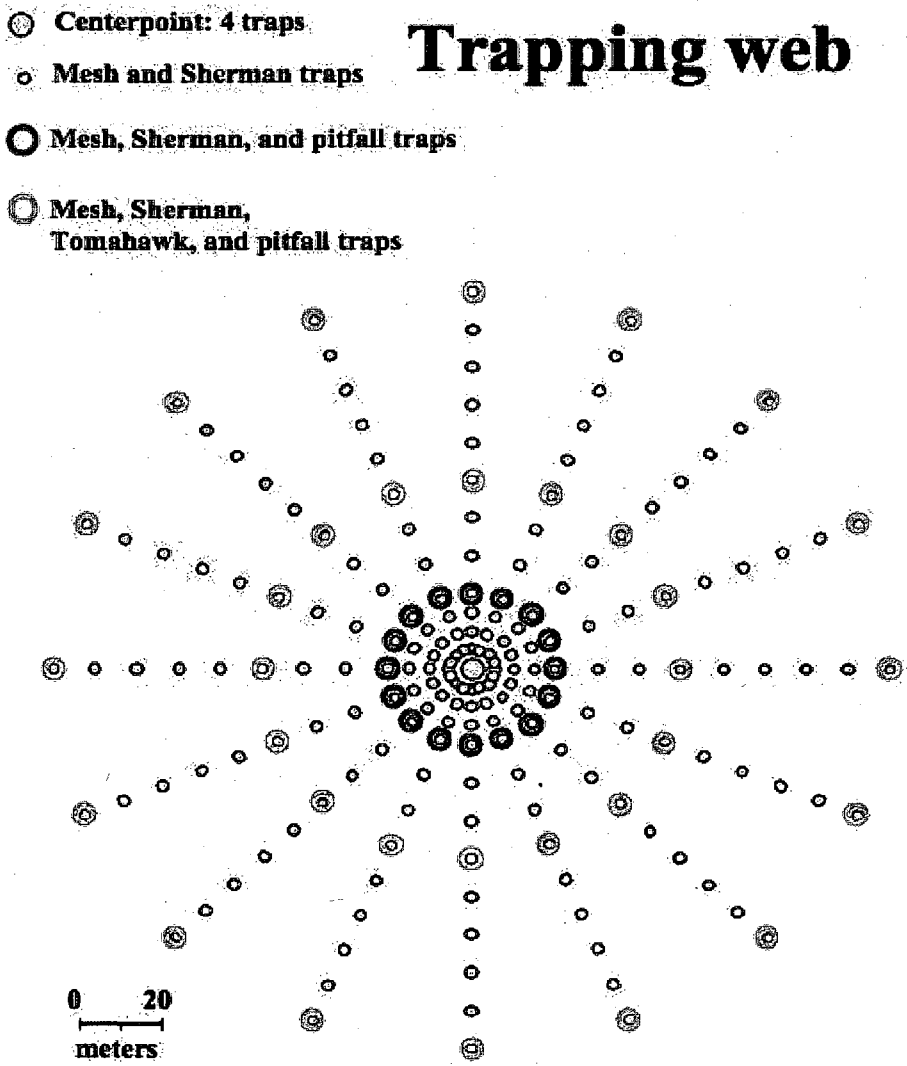
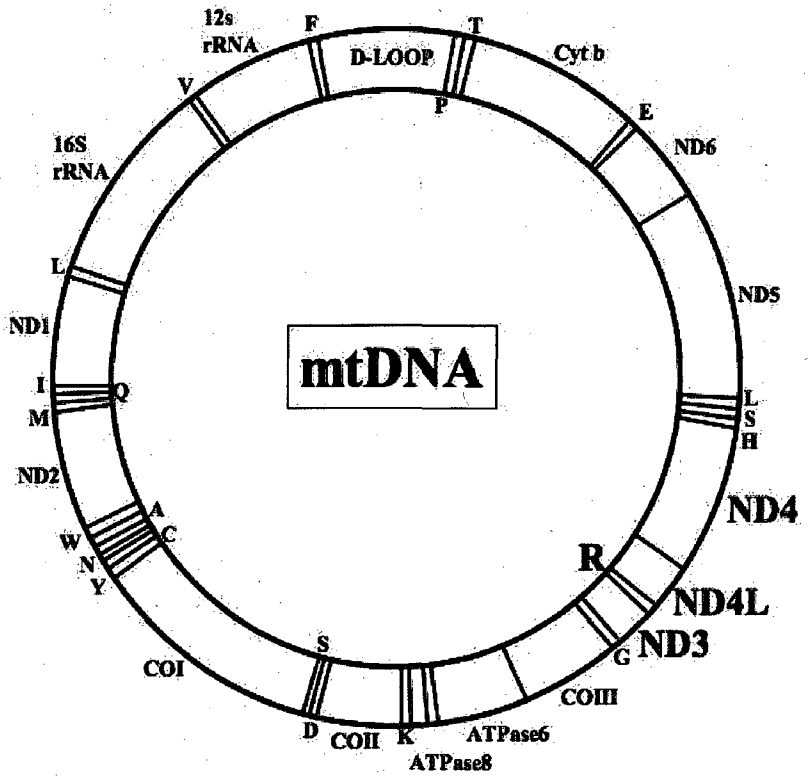
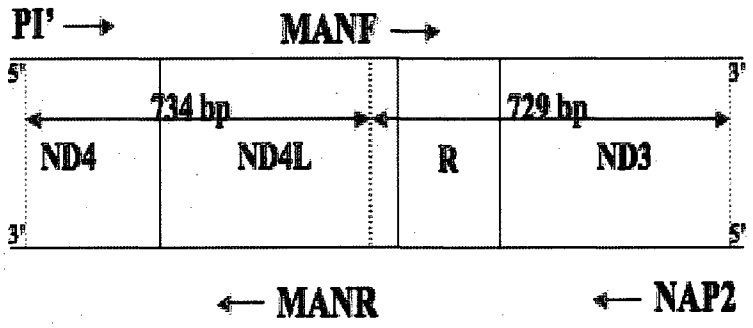


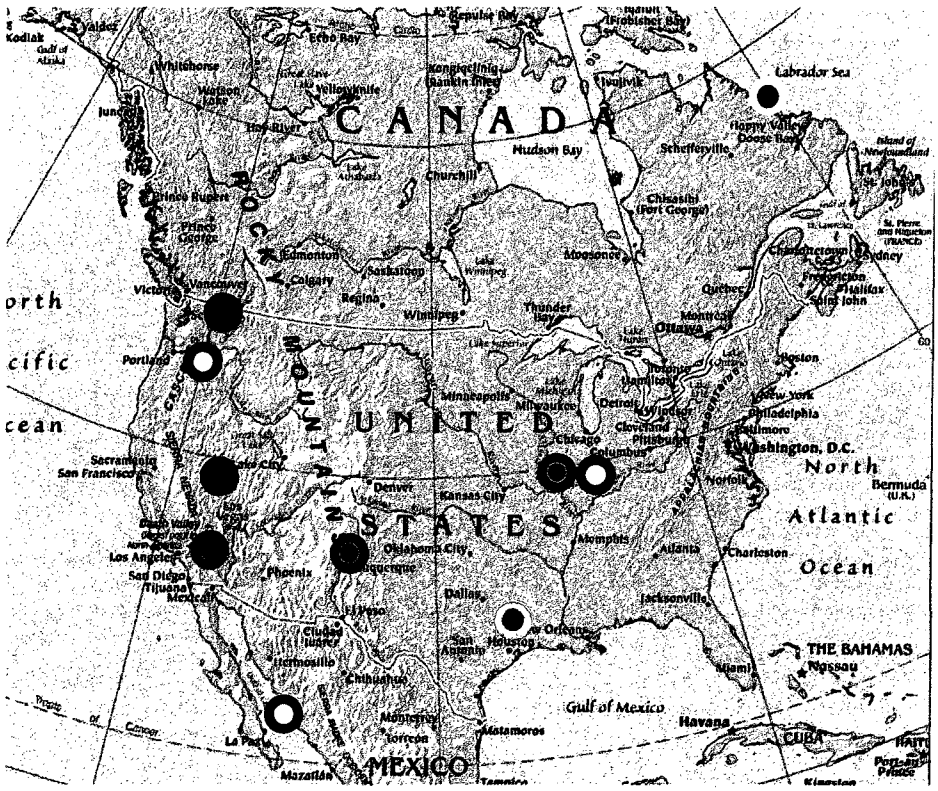
Figure 6: Small Mammal Trapping Web (used for this study). Consists of 12 trap lines radiating and numbered from center at 30° apart, each containing 12 trap stations. Each line is 100m in length from center point with trap stations 1-4 at five-meter intervals on each line. Subsequent stations 5-12 are at 10m. Light blue dots are stations with Sherman and Mesh live traps. Those with dark blue rings include pitfall traps along with the Sherman and mesh live traps. Brown rings add a Tomahawk trap to the other three trap types.





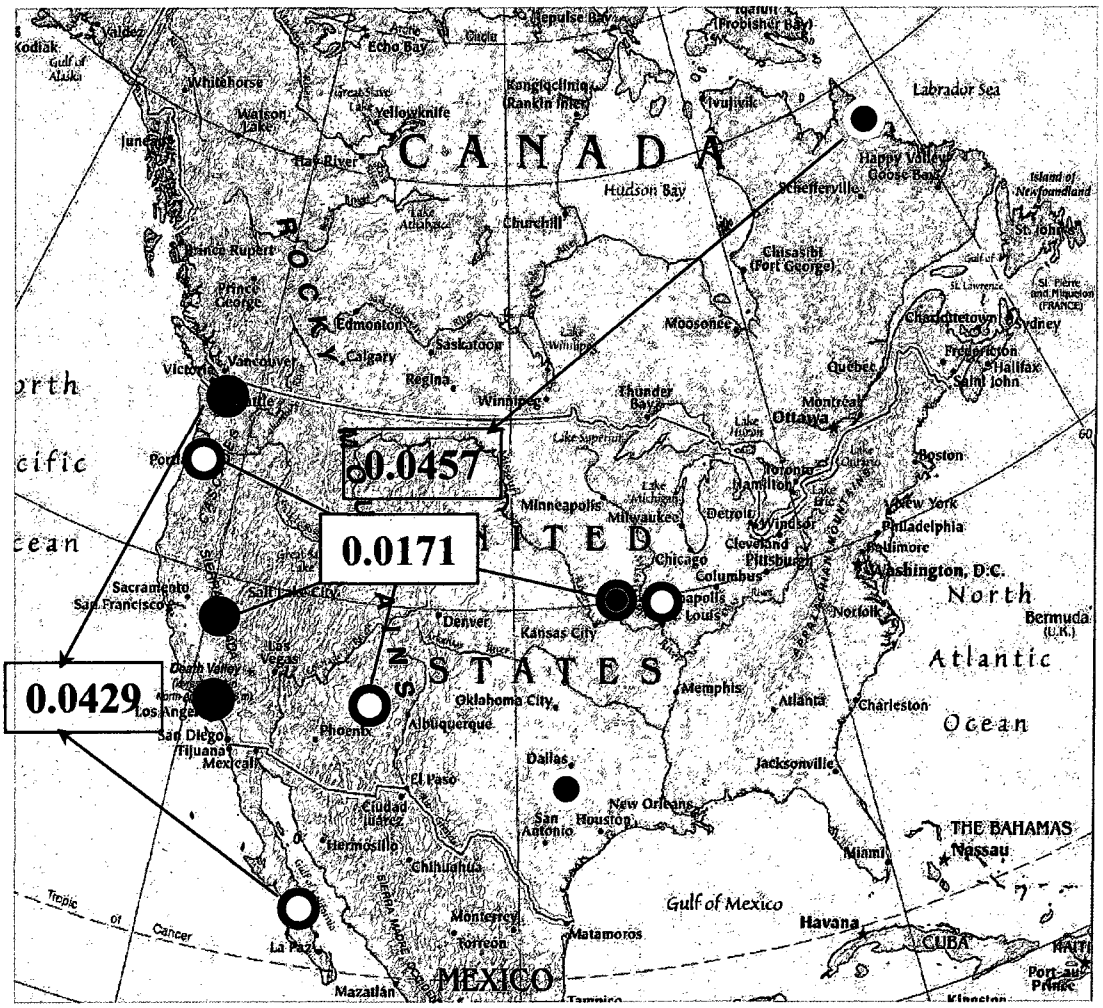
PI': 5' – CGAACTAGTACAGCTGACTTCC – 3'
MANR: 5' – CCGTAGGAGTTTGATAGTTTTGCT – 3' } **Complimentary**
MANF: 5' – AGCAAAACTATCAAACTCCTACGG – 3' } **(indicated by dotted**
NAP2: 5' – TGGAGCTTCTACGTGGGCTTT – 3' **line)**

Figure 7: *Peromyscus* Mitochondrial Genome Map. Upper: Circular mitochondrial genome at top shows locations of ND3, ND4, ND4L, and arginine tRNA (R) genes that were utilized in this study. Middle: Indicates locations of primers used for amplification and the relative size of amplicons (not to scale). Lower: Primer nucleotide sequences.



	Pair-wise Taxa			Avg. Genetic Dist.
	P. m. rubidus	*P. m. maniculatus*		0.0413
○	PNW clade	*P.m.m.*	●	0.0416
	PNW + *P.m.r.* + *P.m.bairdii*	*P.m.m.*		0.0457
●	*P. keeni*	*P. sejugis*		0.0429
	PNW clade	*P.m.b.*		0.0171
	PNW	*P. keeni*		0.0541
○	*P. sejugis*	*P.m.m.*		0.0511
●	*P. m. rufinus*	*P.m.m.*		0.0542
●	*P. m. bairdii*	*P.m.m.*		0.0468
	P. keeni	*P.m.m.*		0.0600
	PNW	*P. m. rufinus*		0.0248
	P.m.m.	*Peromyscus leucopus*	○●	0.2062
	P. keeni	*P. leucopus*		0.2145
	PNW	*R. megalotis*	●	0.5613
	P.m.m.	*R. megalotis*		0.5906
	P. m. bairdii	*R. megalotis*		0.5783

Figure 8: *Peromyscus* Pair-wise Distances. Pair-wise comparison of average percent genetic difference in mitochondrial ND3, ND4, and ND4L genes (1,463bp) between *Peromyscus* (including *R. megalotis*) species and subspecies (n=84). Non-Neotomine sequences not shown – see Appendix A for full pair-wise distance matrix. PNW clade=*P. m. rubidus, P. m. gambelii, P. m. austerus*. Color coded dots correspond to specimen collection locations on map.



● = *Peromyscus maniculatus rubidus/gambeli/austerus*

● = *Peromyscus maniculatus rufinus*

● = *Peromyscus maniculatus sonoriensis*

● = *Peromyscus maniculatus bairdii*

● = *Peromyscus maniculatus maniculatus*

● = *Peromyscus keeni*

● = *Peromyscus sejugis*

● ● = *Peromyscus leucopus*

● = *Reithrodontomys megalotis*

Figure 9: *Peromyscus* Pair-wise Nucleotide Distance Physical Map. Genetic distance of mitochondrial ND3, ND4, ND4L, and arginine tRNA genes of rodents relevant to the phylogenetic position of *Peromyscus* in the Portland, OR region. *P. leucopus* is represented by two separate haplotypes. Data in red indicates average intra-specific distance among western North American clade.

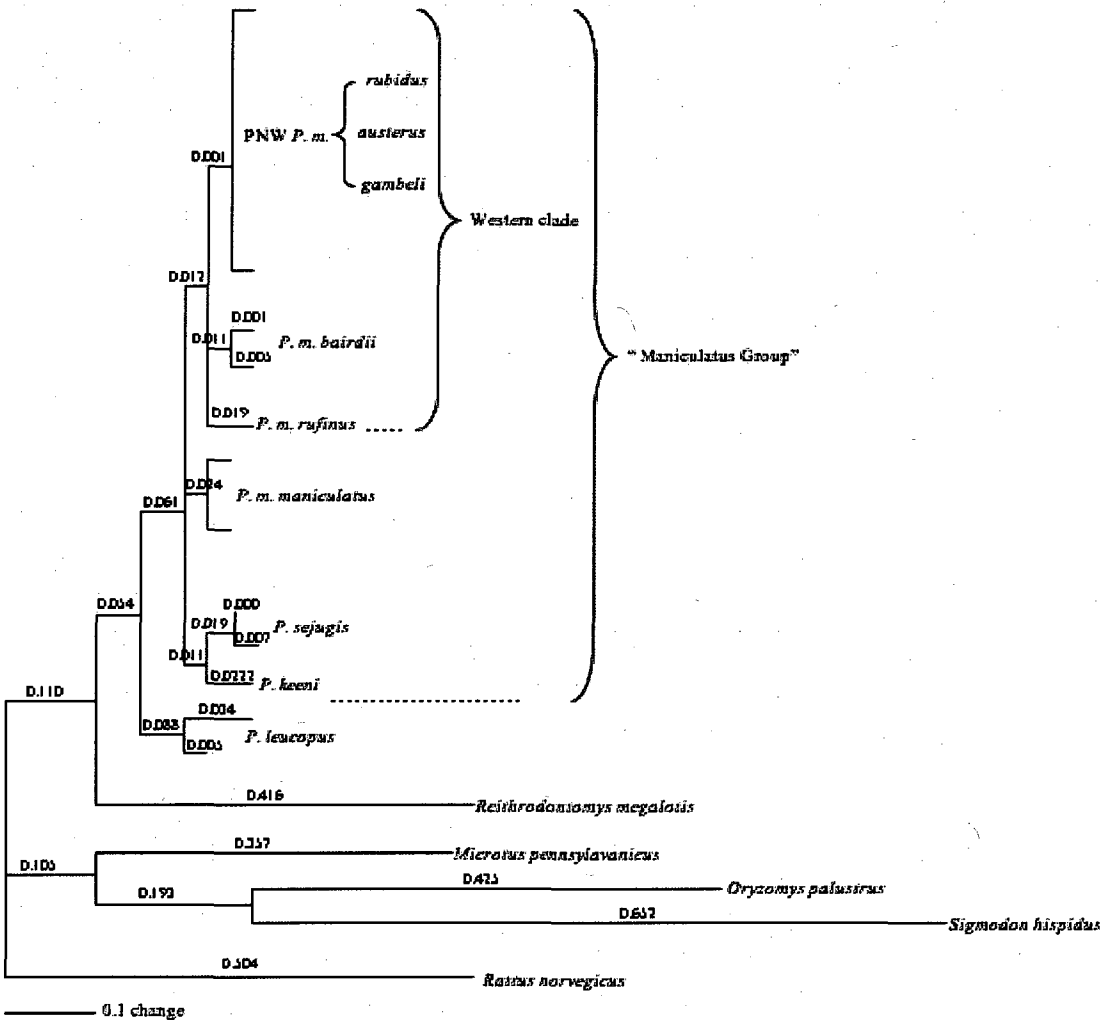


Figure 10: *Peromyscus* Distance Tree. Neighbor-Joining tree of *Peromyscus* and outgroups (n=88) resolved from distance analysis of mitochondrial ND3, ND4, ND4L, and arginine tRNA genes (1,463bp). Numbers represent branch length as changes genetic distance from preceding node. PNW = Pacific Northwest. "Western clade" is west of the Mississippi River. "Maniculatus Group" includes PNW and Western clades.

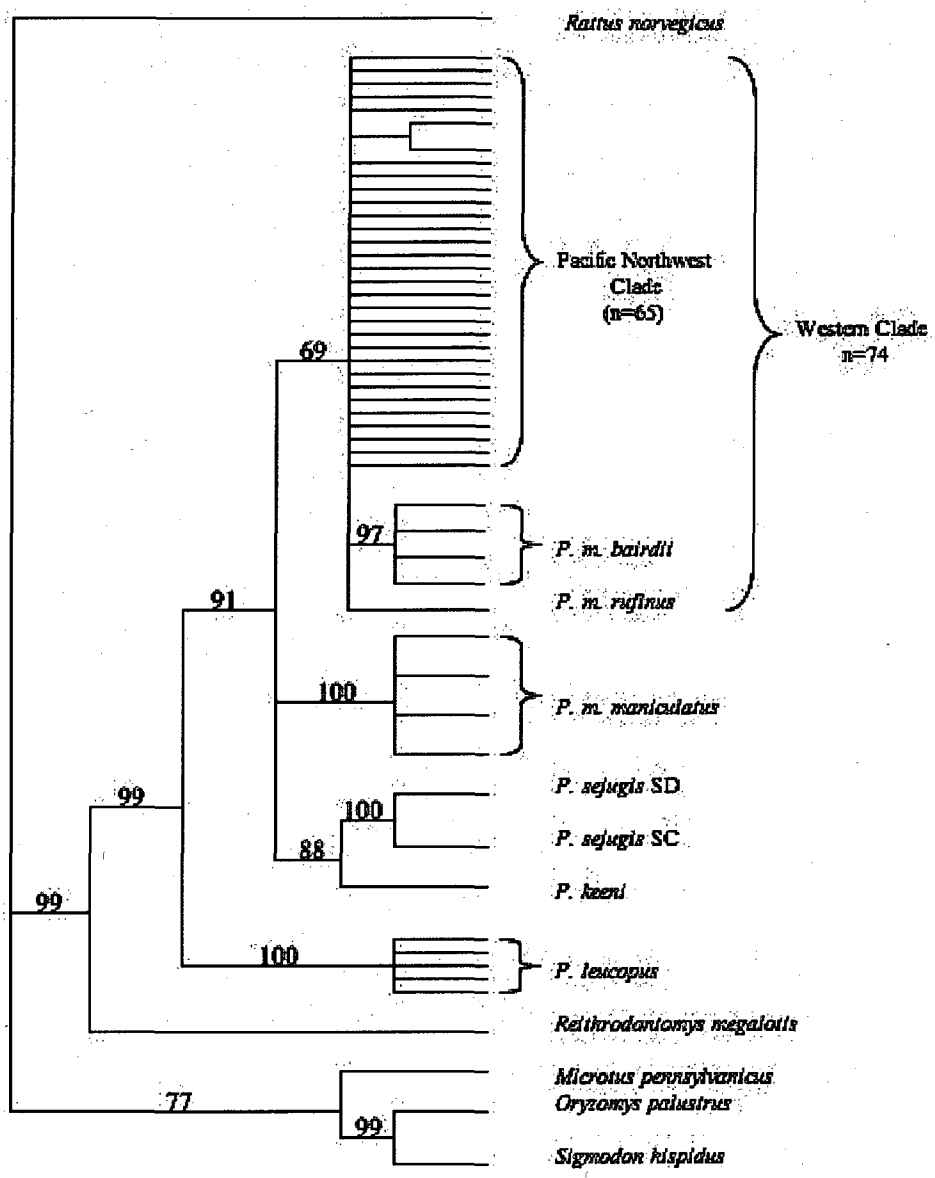


Figure 11: *Peromyscus* Maximum Likelihood Bootstrap Tree. ML tree of *Peromyscus* and outgroups (n=88) using 1,463bp of mitochondrial ND3, ND4, ND4L, and arginine tRNA genes. Numbers represent bootstrap support for nodes after 1000 replicates. –lnL = 8702.95284. Evolutionary model is GTR+I+Γ. SD=San Diego Island. SC=Santa Cruz Island.

Among-site rate variation	
Proportion of invariable sites (I) =	0.2851
Variable sites (G)	
Gamma distribution shape parameter =	0.7693

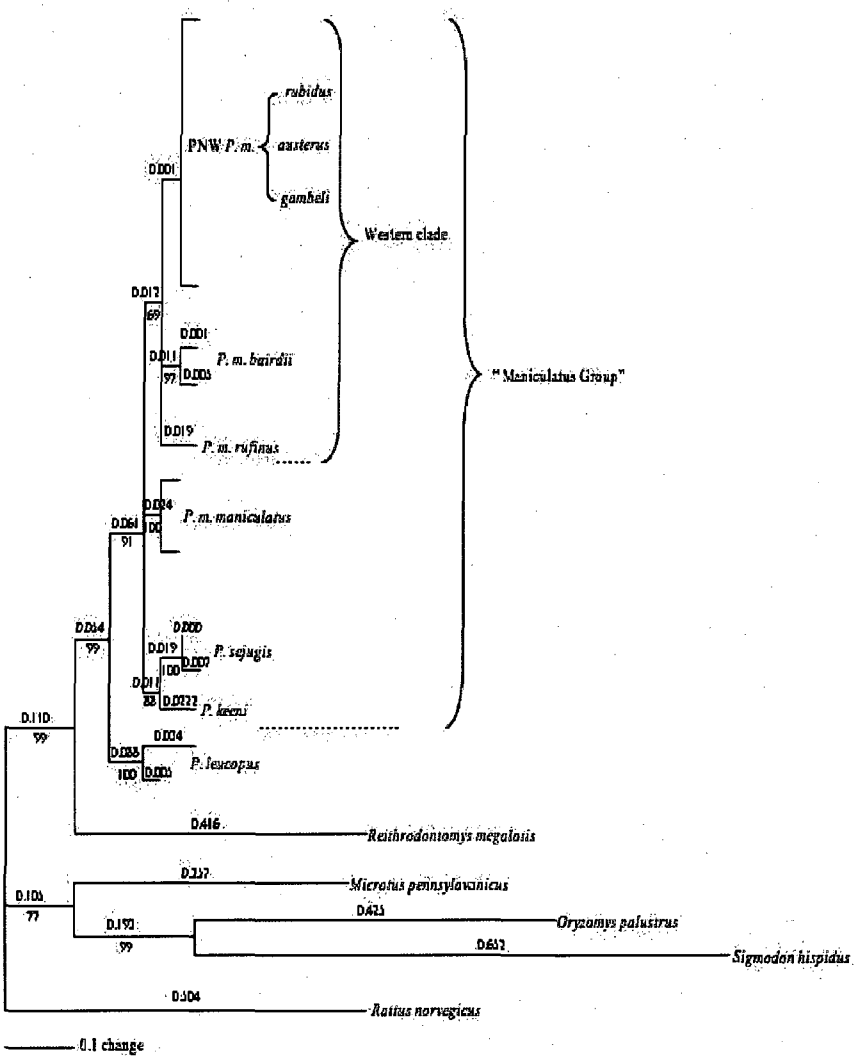


Figure 12: *Peromyscus* Bootstrap/Distance Tree. Combined tree of figures 9 and 10 for direct comparison based upon *Peromyscus* and out-group (n=88) mitochondrial ND3, ND4, ND4L, and arginine tRNA genes (1,463bp). Neighbor-Joining tree (fig. 10) with bootstrap values added from Maximum Likelihood tree (fig. 9) where nodes are identical.

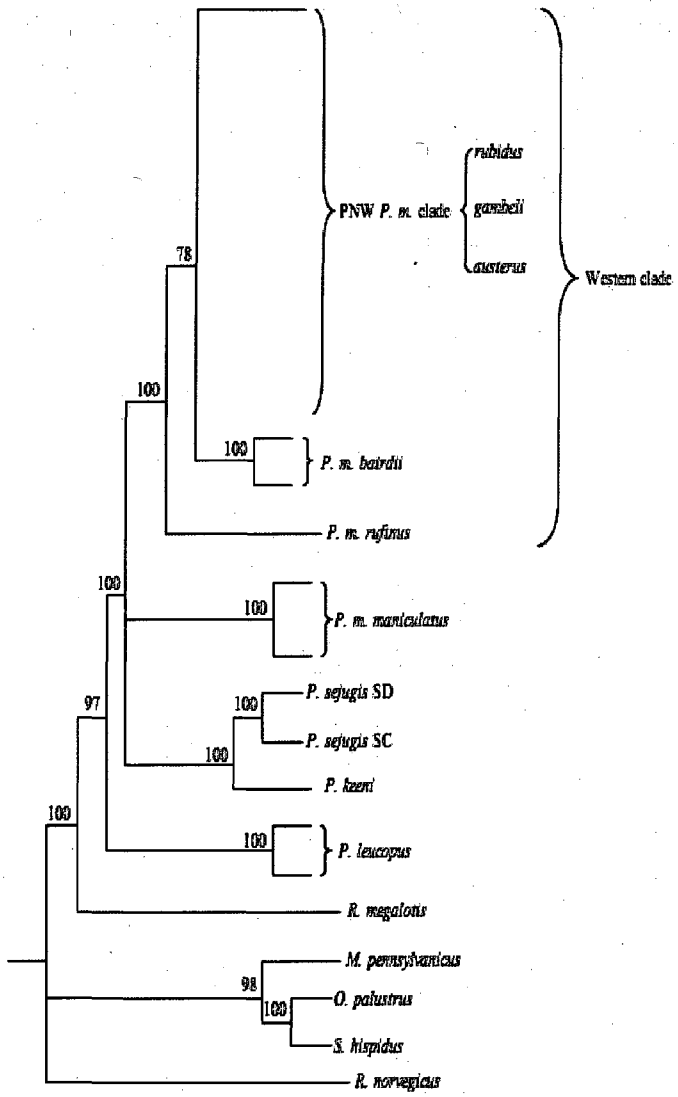


Figure 13: *Peromyscus* Bayesian Majority-Rule Consensus Tree. Based upon *Peromyscus* and outgroups (n=88) mitochondrial ND3, ND4, ND4L, and arginine tRNA genes (1,463bp). Numbers represent bipartition posterior probabilities from 500,000 generations in two runs of four separate Metropolis coupled Markov Chain Monte Carlo computations. Final average standard deviation of split frequencies is 0.0077. Consensus tree derived from majority-rule search of 8,002 sample trees from 800,000 generations.

Component information (consensus fork) = 15 (normalized = 0.652)
Nelson-Platnick term information = 96
Nelson-Platnick total information = 111
Mickevich's consensus information = 0.347
Colless weighted consensus fork (proportion max. information) = 0.371
Schuh-Farris levels sum = 0 (normalized = 0.000)
Rohlf's CI(1) = 0.615
Rohlf's -ln CI(2) = 55.242 (CI(2) = 1.02e-24)

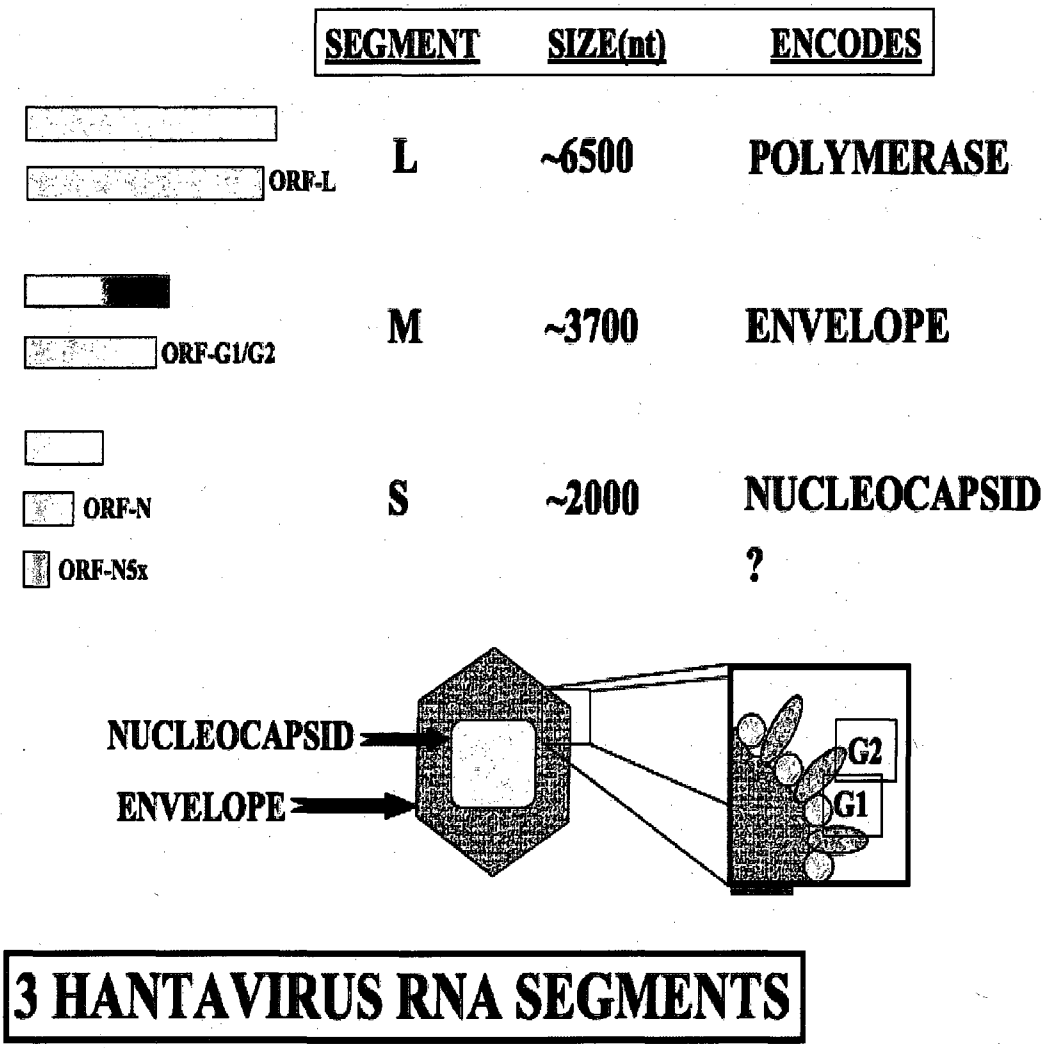
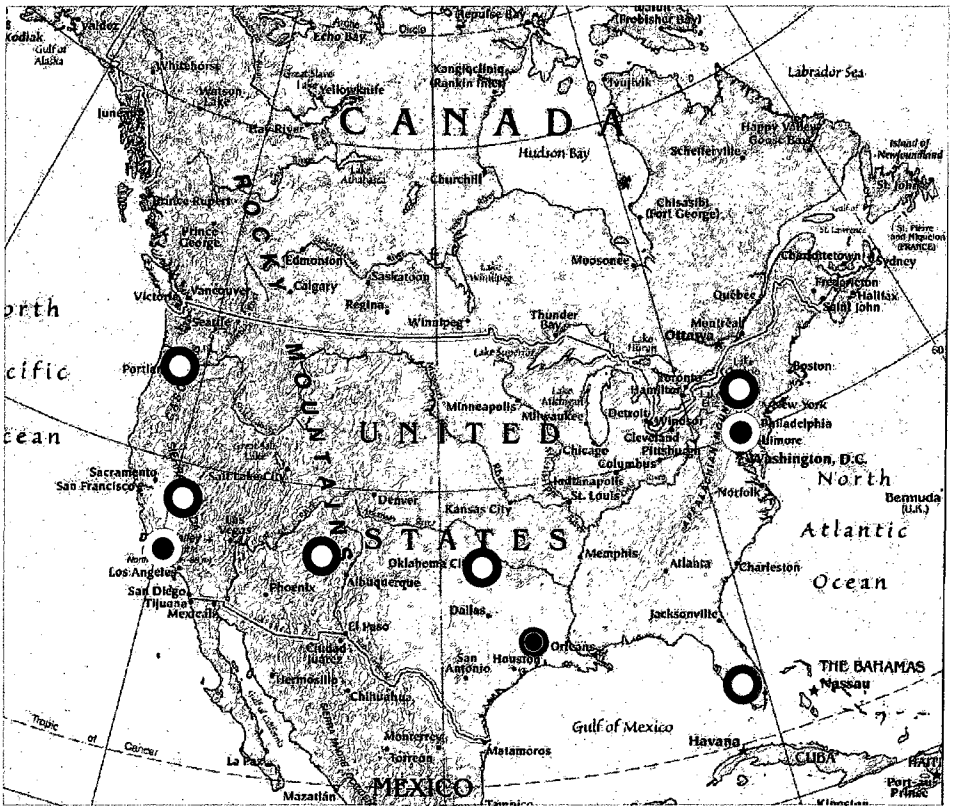


FIGURE 14: ***Hantavirus*** **genome map.** Family Bunyaviridae. Tripartite single-stranded negative sense RNA genome. ~12,200nt total. Targeted G1/G2 glycoprotein precursor gene encoded in M segment.



PAIR-WISE QUASI-SPECIES	UNCORRECTED DISTANCE	CORRECTED DISTANCE (GTR+I+Γ)
KV(OR) / CC	0.112	0.158
KV / SNV	0.143	0.251
KV / NY	0.215	0.441
KV / BR	0.236	0.578
KV / BAY	0.273	0.764
KV / BCC	0.291	0.899
KV / EMC	0.278	0.692
KV / PH	0.331	1.226
SNV / CC	0.130	0.228
SNV / NY	0.189	0.384
SNV / EMC	0.269	0.662

Figure 15: *Hantavirus* Pair-wise Distances: Pair-wise percent genetic distance among North American hantaviruses (n=44) of G1/G2 glycoprotein precursor gene (617nt). KV=Kalapuya virus; CC=Convict Creek virus; SNV=Sin Nombre virus; NY=New York virus; BR=Blue River virus; BAY=Bayou virus; BCC=Black Creek Canal virus; EMC=El Moro Canyon virus; PH=Prospect Hill virus. Corresponding colored dots represent specimen location. Rodent virus hosts: Yellow dot center=*P. maniculatus*, white=*P. leucopus*, aqua=*S. hispidus*, black=*O. palustrus*, red=*R. megalotis*. Corrected Distance derived with General Time Reversible model of evolution with a proportion of sites invariant and gamma distributed variance, as selected by MODELTEST (Posada and Crandall, 1998).

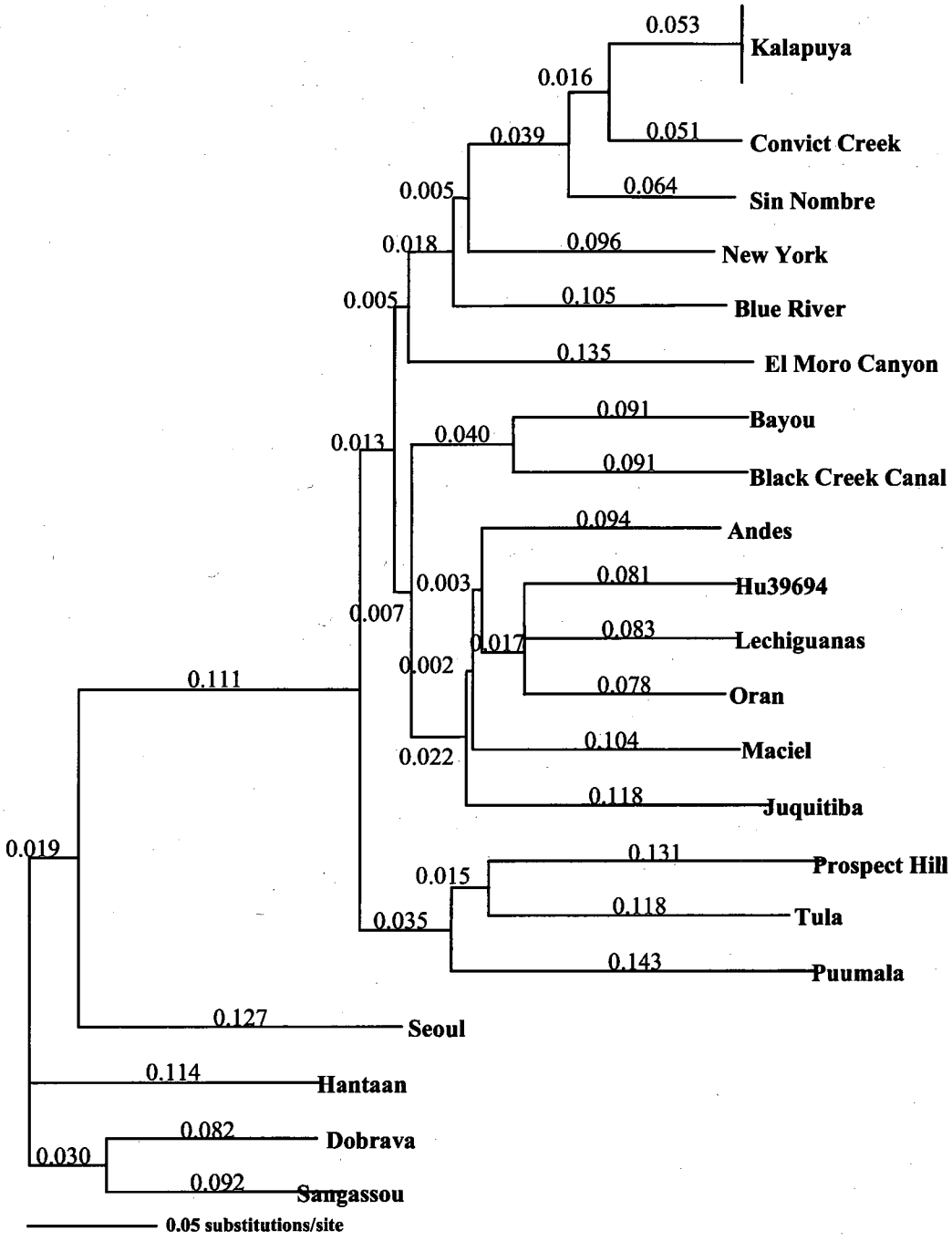


Figure 16: *Hantavirus* Neighbor-Joining Distance Tree. NJ tree of 617nt of *Hantavirus* G1/G2 glycoprotein precursor gene (n=44). Numbers represent branch length as changes from preceding node.

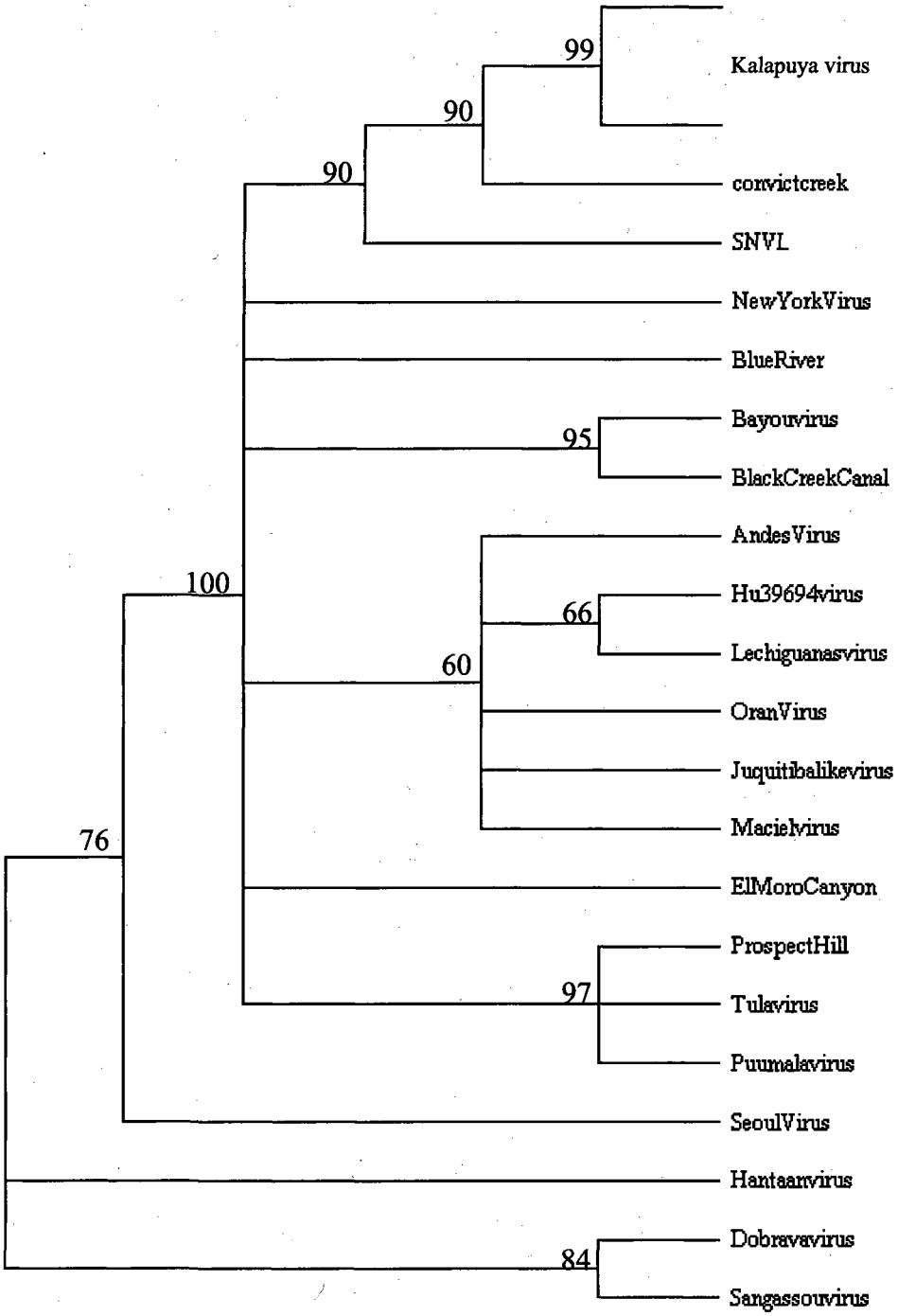


Figure 17: *Hantavirus* Maximum Likelihood Bootstrap Consensus Tree. *Hantavirus* ML tree based upon 617nt of M segment G1/G2 glycoprotein precursor gene (n=44). Numbers represent bootstrap support for nodes after 1000 replicates. Evolutionary model is GTR+I+Γ. –lnL = 8011.8281.

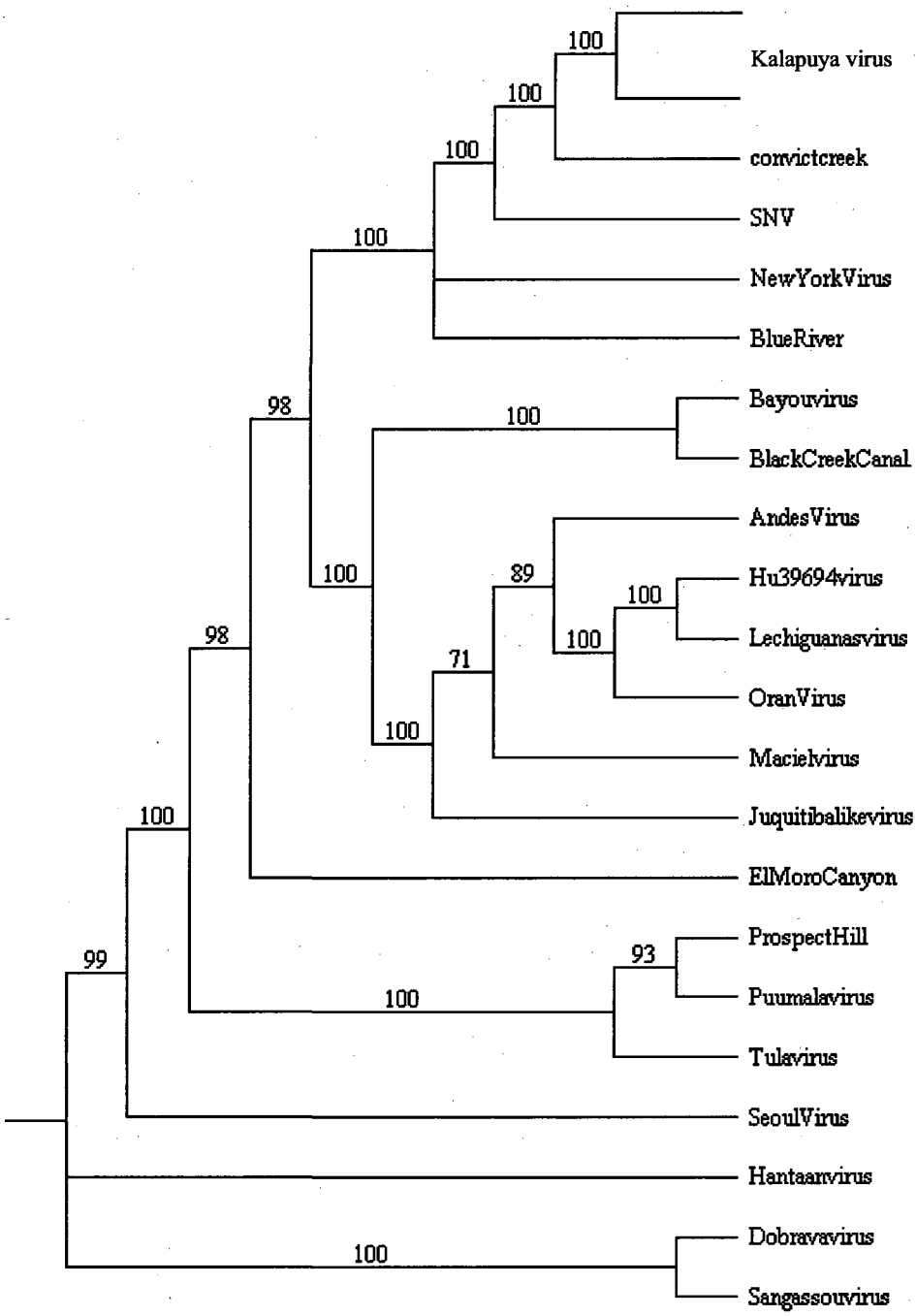


Figure 18: *Hantavirus* Bayesian Majority-Rule Consensus Tree: Tree based upon 617nt of M segment G1/G2 glycoprotein precursor gene (n=44). Numbers represent bipartition posterior probabilities from 500,000 generations in two runs of four separate Metropolis coupled Markov Chain Monte Carlo computations. Final average standard deviation of split frequencies is 0.0023. Consensus tree derived from majority-rule search of 8,002 sample trees from 800,000 generations.

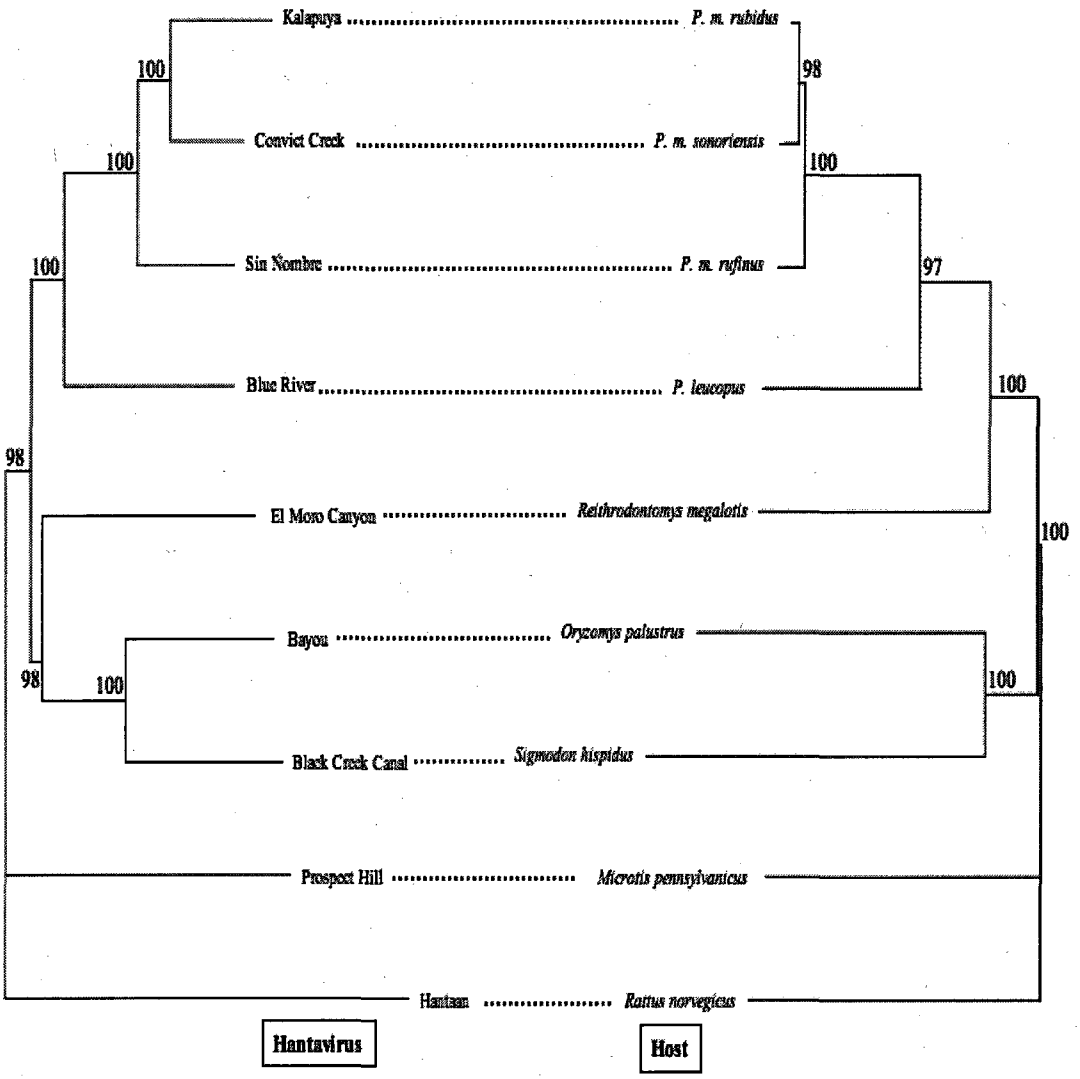


Figure 19: *Hantavirus* / Host Co-Evolutionary Tree. Comparative Bayesian trees of North American hantaviruses (and one Asian) and the rodent hosts for those hantaviruses. *Hantavirus* tree based upon 617nt of M segment G1/G2 glycoprotein precursor gene. Host tree based on 1,463bp of mitochondrial ND3, ND4, ND4L, and arginine tRNA genes. Numbers represent bifurcation posterior probabilities based upon 100,000 generations of Metropolis coupled Markov Chain Monte Carlo computations.

Virus	Disease	Known or suspected host	Location
Cricetidae associated			
Sin Nombre	HPS	*Peromyscus maniculatus* (grassland form)	West & Central U.S. and Canada
Monongahela	HPS	*P. maniculatus* (forest form)	Eastern U.S. and Canada
New York	HPS	*P. leucopus* (eastern haplotype)	Eastern U.S.
Blue River		*P. leucopus* (SW/NW haplotypes)	Central U.S.
Bayou	HPS	*Oryzomys palustris*	Southwestern U.S.
Black Creek Canal	HPS	*Sigmodon hispidus* (eastern form)	Florida
Muleshoe		*S. hispidus* (western form)	Southern U.S.
Caño Delgadito		*S. alstoni*	Venezuela
Andes	HPS	*Oligoryzomys longicaudatus*	Argentina and Chile
Oran	HPS	*O. longicaudatus*	Northwestern Argentina
Lechiguanas	HPS	*O. flavescens*	Central Argentina
Bermejo		*O. chacoensis*	Northwestern Argentina
Hu39694	HPS	Unknown	Central Argentina
Pergamino		*Akadon azarae*	Central Argentina
Maciel		*Bolomys obscurus*	Central Argentina
Laguna Negra	HPS	*Calomys laucha*	Paraguay and Bolivia
Juquitiba	HPS	Unknown	Brazil
Rio Mamore		*O. Microtus*	Bolivia and Peru
El Moro Canyon		*Reithrodontomys megalotis*	Western U.S. and Mexico
Rio Segundo		*R. mexicanus*	Costa Rica

Table 1: Hantaviruses in the New World. Monroe *et al.*, 1999. Western hemisphere Hantaviruses shown with known hosts, status of pathogenicity, and regions of host residence.

Site	**Infected Totals** (M//F)
Forest Park	60 (41//19)
Tryon Creek State Park	10 (8//2)
Oxbow Regional Park	6 (4//2)
Tualatin River NWR	5 (3//2)
Powell Butte Park	5 (4//1)
Total	86 (60//26)

Table 2: Infected Totals by Site. *Hantavirus* antibody sero-positive *Peromyscus maniculatus rubidus* from the Portland, OR region.

Season	**Infected Totals** (M//F)
Fall (Sep-Nov)	18 (14//4)
Winter (Dec-Feb)	11 (9//2)
Spring (Mar-May)	31 (20//11)
Summer (Jun-Aug)	26 (17//9)
Total	86 (60//26)

Table 3: Infected Totals by Season. *Hantavirus* antibody sero-positive *Peromyscus maniculatus rubidus* from the Portland, OR region.

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Centers for Disease Control. Figure 1. HPS Teaching Slideset – Phylogeny of Hantaviruses: Based on Sequence of M Segment. http://www.cdc.gov/ncidod/diseases/hanta/hps/noframes/hpsslideset/hpsslides1-12.htm

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Appendix A: *Peromyscus* Distance Matrix. Pair-wise nucleotide percent difference (distance) of mitochondrial ND3, ND4, ND4L, and arginine tRNA genes (1,463bp) among species and subspecies of *Peromyscus* (Cricetidae) and other out-group Muridae (n=88).

	WC7	WC11	WC12	WC13	ljd3256	ljd3304	ljd3306	ljd3308	ljd3317
WC7									
WC11	0.0014								
WC12	0.0000	0.0014							
WC13	0.0000	0.0014	0.0000						
ljd3256	0.0043	0.0028	0.0043	0.0043					
ljd3304	0.0043	0.0028	0.0043	0.0043	0.0057				
ljd3306	0.0036	0.0021	0.0036	0.0036	0.0050	0.0007			
ljd3308	0.0029	0.0014	0.0029	0.0029	0.0043	0.0043	0.0036		
ljd3317	0.0014	0.0028	0.0014	0.0014	0.0029	0.0028	0.0021	0.0014	
ljd3324	0.0029	0.0014	0.0028	0.0028	0.0028	0.0028	0.0036	0.0029	0.0014
ljd3327	0.0036	0.0036	0.0036	0.0036	0.0050	0.0050	0.0043	0.0007	0.0021
ljd3330	0.0058	0.0050	0.0058	0.0058	0.0073	0.0028	0.0021	0.0058	0.0043
ljd3333	0.0036	0.0021	0.0036	0.0036	0.0050	0.0007	0.0000	0.0036	0.0021
ljd3344	0.0036	0.0028	0.0036	0.0036	0.0050	0.0007	0.0000	0.0036	0.0021
ljd3348	0.0095	0.0080	0.0095	0.0095	0.0110	0.0110	0.0103	0.0081	0.0080
LJD620	0.0058	0.0064	0.0058	0.0058	0.0073	0.0072	0.0065	0.0043	0.0050
LJD774	0.0050	0.0057	0.0050	0.0050	0.0050	0.0065	0.0057	0.0036	0.0042
LJD886	0.0028	0.0035	0.0028	0.0028	0.0028	0.0028	0.0036	0.0029	0.0021
LJD2088	0.0080	0.0079	0.0080	0.0080	0.0079	0.0094	0.0087	0.0065	0.0065
LJD1960	0.0043	0.0086	0.0043	0.0043	0.0043	0.0058	0.0050	0.0029	0.0057
LJD1669	0.0058	0.0101	0.0058	0.0058	0.0057	0.0072	0.0065	0.0043	0.0072
LJD1524	0.0021	0.0021	0.0021	0.0021	0.0036	0.0021	0.0014	0.0021	0.0007
LJD1523	0.0000	0.0014	0.0000	0.0000	0.0043	0.0043	0.0036	0.0029	0.0014
LJD1122	0.0029	0.0014	0.0029	0.0028	0.0043	0.0028	0.0021	0.0029	0.0021
LJD2522	0.0043	0.0050	0.0043	0.0043	0.0028	0.0043	0.0050	0.0043	0.0028
LJD1637	0.0043	0.0043	0.0043	0.0043	0.0072	0.0072	0.0065	0.0043	0.0043
LJD1638	0.0036	0.0036	0.0050	0.0050	0.0065	0.0050	0.0043	0.0036	0.0036
LJD2161	0.0029	0.0014	0.0029	0.0029	0.0029	0.0043	0.0036	0.0029	0.0014
LJD2651	0.0058	0.0043	0.0058	0.0058	0.0072	0.0073	0.0065	0.0043	0.0043
LJD2737	0.0080	0.0087	0.0080	0.0080	0.0095	0.0095	0.0087	0.0065	0.0072
LJD2834	0.0036	0.0021	0.0036	0.0036	0.0050	0.0007	0.0000	0.0036	0.0021
LJD2850	0.0043	0.0029	0.0043	0.0043	0.0058	0.0014	0.0007	0.0043	0.0029
LJD2898	0.0080	0.0065	0.0080	0.0080	0.0095	0.0095	0.0087	0.0065	0.0065
LJD2914	0.0014	0.0000	0.0014	0.0014	0.0029	0.0029	0.0021	0.0014	0.0000
LJD2936	0.0028	0.0021	0.0035	0.0035	0.0028	0.0028	0.0036	0.0029	0.0021
LJD3000	0.0021	0.0007	0.0021	0.0021	0.0036	0.0036	0.0029	0.0014	0.0007
LJD2126	0.0095	0.0095	0.0095	0.0095	0.0110	0.0110	0.0102	0.0080	0.0080
LJD2138	0.0050	0.0043	0.0057	0.0057	0.0072	0.0072	0.0057	0.0050	0.0043
LJD2154	0.0036	0.0021	0.0036	0.0036	0.0050	0.0007	0.0000	0.0036	0.0021
LJD2158	0.0095	0.0087	0.0102	0.0102	0.0117	0.0117	0.0102	0.0080	0.0087
LJD2836	0.0095	0.0080	0.0095	0.0095	0.0110	0.0110	0.0103	0.0080	0.0080

LJD2852	0.0087	0.0073	0.0088	0.0088	0.0103	0.0103	0.0095	0.0073	0.0073
LJD2860	0.0029	0.0014	0.0029	0.0029	0.0028	0.0043	0.0036	0.0029	0.0014
LJD2865	0.0050	0.0036	0.0050	0.0050	0.0050	0.0050	0.0058	0.0043	0.0036
LJD2890	0.0058	0.0043	0.0058	0.0058	0.0073	0.0073	0.0065	0.0043	0.0043
LJD2943	0.0029	0.0014	0.0029	0.0029	0.0029	0.0043	0.0036	0.0029	0.0014
Jefferson3	0.0043	0.0049	0.0043	0.0043	0.0043	0.0043	0.0050	0.0028	0.0035
ADAMS6	0.0050	0.0057	0.0050	0.0050	0.0065	0.0065	0.0058	0.0036	0.0042
clatsop1	0.0029	0.0029	0.0030	0.0029	0.0045	0.0045	0.0037	0.0015	0.0029
clatsop2	0.0029	0.0029	0.0029	0.0029	0.0044	0.0030	0.0022	0.0029	0.0029
clatsop3	0.0029	0.0029	0.0029	0.0029	0.0044	0.0030	0.0022	0.0029	0.0029
clatsop4	0.0029	0.0029	0.0029	0.0029	0.0044	0.0030	0.0022	0.0029	0.0029
LostForest1A	0.0085	0.0084	0.0099	0.0099	0.0082	0.0084	0.0069	0.0069	0.0084
LostForest2	0.0109	0.0100	0.0116	0.0116	0.0124	0.0124	0.0117	0.0087	0.0130
LostForest3	0.0058	0.0107	0.0065	0.0064	0.0057	0.0072	0.0065	0.0043	0.0078
LostForest4	0.0102	0.0115	0.0109	0.0109	0.0117	0.0117	0.0110	0.0087	0.0100
sj1Pmausterus	0.0080	0.0065	0.0080	0.0080	0.0095	0.0095	0.0088	0.0065	0.0065
sj2Pmausterus	0.0080	0.0102	0.0080	0.0087	0.0102	0.0103	0.0095	0.0072	0.0079
sj2aPmausterus	0.0051	0.0036	0.0051	0.0051	0.0066	0.0065	0.0058	0.0036	0.0036
sj3Pmausterus	0.0065	0.0050	0.0065	0.0065	0.0080	0.0080	0.0073	0.0050	0.0050
sj5Pmausterus	0.0058	0.0043	0.0058	0.0058	0.0073	0.0073	0.0065	0.0043	0.0043
sj6Pmausterus	0.0058	0.0043	0.0058	0.0058	0.0073	0.0073	0.0065	0.0043	0.0043
sj7Pmausterus	0.0058	0.0050	0.0058	0.0058	0.0073	0.0072	0.0065	0.0043	0.0043
OSM723Pmman	0.0391	0.0410	0.0389	0.0387	0.0405	0.0424	0.0417	0.0391	0.0391
OSM726Pmman	0.0383	0.0402	0.0380	0.0379	0.0397	0.0416	0.0408	0.0383	0.0383
OSM727Pmman	0.0391	0.0410	0.0389	0.0387	0.0405	0.0424	0.0417	0.0391	0.0391
OSM737Pmman	0.0383	0.0402	0.0380	0.0379	0.0397	0.0416	0.0408	0.0383	0.0383
U40255PsejugSD	0.0498	0.0517	0.0497	0.0496	0.0496	0.0513	0.0505	0.0478	0.0500
U40253PsejugSC	0.0595	0.0613	0.0593	0.0591	0.0591	0.0610	0.0602	0.0573	0.0594
JEB1309APtruei	0.2475	0.2391	0.2439	0.2439	0.2437	0.2391	0.2410	0.2435	0.2391
AF374578PKEEN	0.0542	0.0541	0.0540	0.0538	0.0559	0.0538	0.0529	0.0521	0.0522
U40252Pleuc	0.2439	0.2378	0.2427	0.2418	0.2421	0.2421	0.2447	0.2392	0.2349
JAM160Pleuc	0.1936	0.1923	0.1940	0.1933	0.1935	0.1935	0.1949	0.1894	0.1882
JAM161Pleuc	0.2121	0.2095	0.2116	0.2108	0.2110	0.2110	0.2128	0.2034	0.2053
JAM162Pleuc	0.2027	0.1978	0.2031	0.2024	0.2026	0.2026	0.2040	0.1982	0.1979
JAM163Pleuc	0.2041	0.2027	0.2045	0.2038	0.2039	0.2039	0.2054	0.1952	0.1985
JAM164Pleuc	0.2095	0.2080	0.2099	0.2092	0.2094	0.2094	0.2109	0.2003	0.2039
JAM168Pmbairdii	0.0157	0.0140	0.0156	0.0156	0.0156	0.0171	0.0164	0.0141	0.0140
JAM167Pmbairdii	0.0164	0.0147	0.0163	0.0163	0.0163	0.0179	0.0171	0.0148	0.0148
JAM159Pmbairdii	0.0157	0.0156	0.0157	0.0157	0.0157	0.0172	0.0165	0.0141	0.0141
JAM166Pmbairdii	0.0196	0.0180	0.0196	0.0196	0.0196	0.0212	0.0204	0.0180	0.0180
M.pennsylvanicus	0.6270	0.6193	0.6269	0.6267	0.6331	0.6247	0.6284	0.6334	0.6185
Oryzomyspalustris	0.9310	0.9429	0.9310	0.9309	0.9690	0.9224	0.9283	0.9556	0.9407
Sigmodonhispidus	1.0163	1.0279	1.0164	1.0163	1.0275	1.0370	1.0348	1.0494	1.0251
R.megalotis	0.5375	0.5552	0.5378	0.5381	0.5554	0.5736	0.5733	0.5550	0.5548
Rattusnorvegicus	0.7430	0.7559	0.7469	0.7426	0.7854	0.7527	0.7559	0.7855	0.7507
Pmrufinus	0.0239	0.0244	0.0238	0.0237	0.0237	0.0253	0.0246	0.0223	0.0228

	ljd3324	ljd3327	ljd3330	ljd3333	ljd3344	ljd3348	LJD620	LJD774	LJD886	LJD2088	LJD1960
WC7											
WC11											
WC12											
WC13											
ljd3256											
ljd3304											
ljd3306											
ljd3308											
ljd3317											
ljd3324											
ljd3327	0.0036										
ljd3330	0.0058	0.0065									
ljd3333	0.0036	0.0043	0.0021								
ljd3344	0.0036	0.0043	0.0021	0.0000							
ljd3348	0.0095	0.0088	0.0111	0.0103	0.0102						
LJD620	0.0058	0.0050	0.0087	0.0065	0.0065	0.0110					
LJD774	0.0036	0.0043	0.0065	0.0058	0.0057	0.0087	0.0050				
LJD886	0.0000	0.0036	0.0057	0.0036	0.0035	0.0095	0.0057	0.0035			
LJD2088	0.0080	0.0072	0.0095	0.0087	0.0087	0.0102	0.0094	0.0072	0.0079		
LJD1960	0.0029	0.0036	0.0072	0.0050	0.0050	0.0096	0.0094	0.0072	0.0064	0.0080	
LJD1669	0.0043	0.0051	0.0072	0.0065	0.0065	0.0080	0.0109	0.0071	0.0079	0.0080	0.0014
LJD1524	0.0021	0.0028	0.0036	0.0014	0.0014	0.0088	0.0050	0.0043	0.0021	0.0072	0.0036
LJD1523	0.0028	0.0036	0.0058	0.0036	0.0036	0.0095	0.0058	0.0050	0.0028	0.0080	0.0043
LJD1122	0.0029	0.0043	0.0050	0.0021	0.0028	0.0095	0.0065	0.0057	0.0035	0.0087	0.0050
LJD2522	0.0014	0.0050	0.0072	0.0050	0.0050	0.0110	0.0072	0.0050	0.0014	0.0079	0.0043
LJD1637	0.0058	0.0050	0.0058	0.0065	0.0065	0.0095	0.0072	0.0050	0.0058	0.0080	0.0058
LJD1638	0.0036	0.0043	0.0065	0.0043	0.0057	0.0118	0.0079	0.0072	0.0036	0.0095	0.0050
LJD2161	0.0029	0.0036	0.0059	0.0036	0.0036	0.0096	0.0059	0.0051	0.0029	0.0081	0.0043
LJD2651	0.0058	0.0051	0.0073	0.0065	0.0065	0.0065	0.0073	0.0036	0.0058	0.0080	0.0058
LJD2737	0.0080	0.0073	0.0095	0.0088	0.0087	0.0119	0.0079	0.0057	0.0079	0.0102	0.0116
LJD2834	0.0036	0.0043	0.0021	0.0000	0.0000	0.0103	0.0065	0.0058	0.0036	0.0087	0.0050
LJD2850	0.0043	0.0050	0.0029	0.0007	0.0007	0.0111	0.0073	0.0065	0.0043	0.0095	0.0058
LJD2898	0.0080	0.0073	0.0095	0.0087	0.0087	0.0118	0.0080	0.0058	0.0080	0.0102	0.0080
LJD2914	0.0014	0.0021	0.0043	0.0021	0.0021	0.0080	0.0043	0.0036	0.0014	0.0065	0.0028
LJD2936	0.0007	0.0036	0.0058	0.0036	0.0036	0.0095	0.0057	0.0036	0.0000	0.0079	0.0029
LJD3000	0.0021	0.0021	0.0050	0.0029	0.0029	0.0088	0.0050	0.0043	0.0021	0.0072	0.0036
LJD2126	0.0095	0.0087	0.0110	0.0103	0.0102	0.0029	0.0110	0.0087	0.0095	0.0118	0.0095
LJD2138	0.0057	0.0058	0.0080	0.0058	0.0064	0.0110	0.0087	0.0079	0.0057	0.0094	0.0065
LJD2154	0.0036	0.0043	0.0021	0.0000	0.0000	0.0103	0.0065	0.0058	0.0036	0.0087	0.0050
LJD2158	0.0102	0.0088	0.0110	0.0103	0.0109	0.0036	0.0117	0.0094	0.0102	0.0125	0.0095
LJD2836	0.0095	0.0088	0.0111	0.0103	0.0103	0.0029	0.0110	0.0088	0.0095	0.0118	0.0095
LJD2852	0.0088	0.0081	0.0103	0.0095	0.0095	0.0096	0.0103	0.0080	0.0088	0.0110	0.0088
LJD2860	0.0029	0.0036	0.0058	0.0036	0.0036	0.0096	0.0058	0.0050	0.0028	0.0080	0.0043
LJD2865	0.0021	0.0050	0.0080	0.0057	0.0058	0.0118	0.0080	0.0058	0.0022	0.0102	0.0050
LJD2890	0.0058	0.0051	0.0058	0.0065	0.0065	0.0096	0.0073	0.0051	0.0058	0.0065	0.0058

LJD2943	0.0029	0.0036	0.0058	0.0036	0.0036	0.0096	0.0058	0.0050	0.0029	0.0080	0.0043
Jefferson3	0.0014	0.0036	0.0072	0.0050	0.0050	0.0095	0.0042	0.0021	0.0014	0.0079	0.0064
ADAMS6	0.0050	0.0043	0.0065	0.0058	0.0057	0.0058	0.0050	0.0042	0.0050	0.0072	0.0086
clatsop1	0.0029	0.0022	0.0060	0.0037	0.0037	0.0069	0.0052	0.0044	0.0037	0.0067	0.0074
clatsop2	0.0029	0.0037	0.0045	0.0022	0.0022	0.0099	0.0067	0.0059	0.0037	0.0082	0.0089
clatsop3	0.0029	0.0037	0.0045	0.0022	0.0022	0.0099	0.0067	0.0059	0.0037	0.0082	0.0089
clatsop4	0.0029	0.0037	0.0045	0.0022	0.0022	0.0099	0.0067	0.0059	0.0037	0.0082	0.0089
LostForest1A	0.0099	0.0070	0.0085	0.0069	0.0068	0.0097	0.0097	0.0067	0.0084	0.0052	0.0085
LostForest2	0.0116	0.0110	0.0125	0.0110	0.0123	0.0116	0.0116	0.0108	0.0131	0.0146	0.0169
LostForest3	0.0050	0.0050	0.0072	0.0065	0.0064	0.0095	0.0093	0.0056	0.0078	0.0079	0.0043
LostForest4	0.0109	0.0095	0.0117	0.0110	0.0109	0.0109	0.0086	0.0078	0.0101	0.0124	0.0139
sj1Pmausterus	0.0080	0.0073	0.0095	0.0088	0.0088	0.0043	0.0095	0.0072	0.0080	0.0103	0.0080
sj2Pmausterus	0.0080	0.0080	0.0117	0.0087	0.0095	0.0088	0.0109	0.0102	0.0094	0.0110	0.0109
sj2aPmausterus	0.0050	0.0043	0.0080	0.0058	0.0058	0.0073	0.0065	0.0058	0.0050	0.0088	0.0050
sj3Pmausterus	0.0065	0.0058	0.0095	0.0073	0.0073	0.0088	0.0080	0.0073	0.0065	0.0103	0.0065
sj5Pmausterus	0.0058	0.0051	0.0088	0.0065	0.0065	0.0081	0.0073	0.0065	0.0058	0.0095	0.0058
sj6Pmausterus	0.0058	0.0050	0.0088	0.0065	0.0065	0.0081	0.0073	0.0065	0.0058	0.0095	0.0058
sj7Pmausterus	0.0058	0.0050	0.0087	0.0065	0.0065	0.0081	0.0072	0.0065	0.0058	0.0095	0.0058
OSM723Pmman	0.0389	0.0400	0.0428	0.0419	0.0414	0.0454	0.0419	0.0393	0.0384	0.0452	0.0412
OSM726Pmman	0.0381	0.0392	0.0419	0.0410	0.0406	0.0446	0.0411	0.0384	0.0376	0.0443	0.0403
OSM727Pmman	0.0389	0.0400	0.0428	0.0419	0.0414	0.0454	0.0419	0.0393	0.0384	0.0452	0.0412
OSM737Pmman	0.0381	0.0392	0.0419	0.0410	0.0406	0.0446	0.0411	0.0384	0.0376	0.0443	0.0403
U40255PsejugSD	0.0495	0.0486	0.0515	0.0507	0.0504	0.0543	0.0531	0.0500	0.0490	0.0542	0.0520
U40253PsejugSC	0.0592	0.0582	0.0612	0.0605	0.0600	0.0642	0.0627	0.0595	0.0584	0.0640	0.0617
JEB1309APtruei	0.2393	0.2435	0.2446	0.2427	0.2389	0.2316	0.2436	0.2408	0.2392	0.2363	0.2466
AF374578PKEEN	0.0539	0.0530	0.0520	0.0531	0.0527	0.0550	0.0553	0.0524	0.0533	0.0528	0.0583
U40252Pleuc	0.2387	0.2403	0.2435	0.2458	0.2432	0.2456	0.2454	0.2430	0.2348	0.2267	0.2463
JAM160Pleuc	0.1905	0.1905	0.1932	0.1952	0.1946	0.1948	0.1903	0.1870	0.1891	0.1835	0.1864
JAM161Pleuc	0.2079	0.2045	0.2116	0.2138	0.2122	0.2123	0.2075	0.2040	0.2063	0.2002	0.2039
JAM162Pleuc	0.1995	0.1997	0.2026	0.2043	0.2040	0.2038	0.2000	0.1966	0.1988	0.1924	0.1945
JAM163Pleuc	0.2009	0.1962	0.2036	0.2057	0.2051	0.2052	0.2008	0.1973	0.1995	0.1933	0.1952
JAM164Pleuc	0.2063	0.2014	0.2091	0.2111	0.2105	0.2105	0.2062	0.2027	0.2049	0.1985	0.2005
JAM168Pmbairdii	0.0156	0.0148	0.0173	0.0164	0.0164	0.0164	0.0172	0.0148	0.0155	0.0148	0.0141
JAM167Pmbairdii	0.0163	0.0156	0.0180	0.0171	0.0171	0.0171	0.0179	0.0156	0.0163	0.0155	0.0148
JAM159Pmbairdii	0.0157	0.0149	0.0189	0.0165	0.0165	0.0196	0.0173	0.0164	0.0156	0.0164	0.0141
JAM166Pmbairdii	0.0196	0.0188	0.0213	0.0204	0.0204	0.0188	0.0213	0.0188	0.0196	0.0188	0.0180
M.pennsylvanicus	0.6101	0.6371	0.6183	0.6280	0.6282	0.6317	0.6110	0.6115	0.6099	0.6284	0.6102
Oryzomyspalustris	0.9251	0.9618	0.9381	0.9276	0.9280	0.9341	0.8914	0.9159	0.9251	0.9415	0.9421
Sigmodonhispidus	1.0402	1.0571	1.0263	1.0339	1.0345	0.9834	1.0347	1.0225	1.0402	0.9954	1.0400
R.megalotis	0.5625	0.5571	0.5670	0.5730	0.5734	0.5385	0.5619	0.5825	0.5631	0.5411	0.5769
Rattusnorvegicus	0.7747	0.7857	0.7479	0.7555	0.7538	0.7734	0.7533	0.7521	0.7539	0.7465	0.7872
Pmrufinus	0.0222	0.0231	0.0254	0.0247	0.0245	0.0262	0.0236	0.0197	0.0220	0.0245	0.0260

	LJD1669	LJD1524	LJD1523	LJD1122	LJD2522	LJD1637	LJD1638	LJD2161	LJD2651	LJD2737	LJD2834
WC7											
WC11											
WC12											
WC13											
ljd3256											
ljd3304											
ljd3306											
ljd3308											
ljd3317											
ljd3324											
ljd3327											
ljd3330											
ljd3333											
ljd3344											
ljd3348											
LJD620											
LJD774											
LJD886											
LJD2088											
LJD1960											
LJD1669											
LJD1524	0.0050										
LJD1523	0.0058	0.0021									
LJD1122	0.0065	0.0028	0.0028								
LJD2522	0.0057	0.0036	0.0043	0.0050							
LJD1637	0.0058	0.0050	0.0043	0.0058	0.0072						
LJD1638	0.0065	0.0028	0.0043	0.0036	0.0050	0.0065					
LJD2161	0.0058	0.0022	0.0029	0.0029	0.0043	0.0058	0.0036				
LJD2651	0.0043	0.0050	0.0058	0.0058	0.0072	0.0058	0.0065	0.0058			
LJD2737	0.0116	0.0072	0.0080	0.0087	0.0095	0.0080	0.0088	0.0081	0.0080		
LJD2834	0.0065	0.0014	0.0036	0.0021	0.0050	0.0065	0.0043	0.0036	0.0065	0.0088	
LJD2850	0.0073	0.0021	0.0043	0.0029	0.0057	0.0072	0.0050	0.0036	0.0073	0.0095	0.0007
LJD2898	0.0080	0.0072	0.0080	0.0080	0.0095	0.0080	0.0087	0.0081	0.0080	0.0000	0.0087
LJD2914	0.0043	0.0007	0.0014	0.0014	0.0028	0.0043	0.0021	0.0014	0.0043	0.0065	0.0021
LJD2936	0.0043	0.0021	0.0028	0.0029	0.0014	0.0058	0.0043	0.0029	0.0058	0.0080	0.0036
LJD3000	0.0050	0.0014	0.0021	0.0021	0.0036	0.0050	0.0029	0.0014	0.0050	0.0073	0.0028
LJD2126	0.0080	0.0087	0.0095	0.0102	0.0110	0.0095	0.0103	0.0096	0.0065	0.0118	0.0103
LJD2138	0.0080	0.0043	0.0057	0.0050	0.0072	0.0080	0.0065	0.0051	0.0080	0.0102	0.0057
LJD2154	0.0065	0.0014	0.0036	0.0021	0.0050	0.0065	0.0043	0.0036	0.0065	0.0088	0.0000
LJD2158	0.0080	0.0087	0.0102	0.0095	0.0117	0.0095	0.0110	0.0096	0.0065	0.0118	0.0103
LJD2836	0.0080	0.0088	0.0095	0.0095	0.0110	0.0095	0.0103	0.0096	0.0065	0.0118	0.0103
LJD2852	0.0073	0.0080	0.0088	0.0088	0.0103	0.0072	0.0096	0.0081	0.0058	0.0111	0.0095
LJD2860	0.0058	0.0021	0.0028	0.0029	0.0043	0.0058	0.0036	0.0014	0.0058	0.0080	0.0036
LJD2865	0.0066	0.0043	0.0050	0.0050	0.0036	0.0080	0.0043	0.0029	0.0080	0.0103	0.0057
LJD2890	0.0058	0.0051	0.0058	0.0058	0.0073	0.0043	0.0066	0.0051	0.0058	0.0080	0.0065
LJD2943	0.0058	0.0021	0.0029	0.0029	0.0043	0.0058	0.0036	0.0014	0.0058	0.0080	0.0036

Jefferson3	0.0079	0.0036	0.0043	0.0050	0.0028	0.0057	0.0050	0.0043	0.0058	0.0065	0.0050
ADAMS6	0.0086	0.0043	0.0050	0.0057	0.0064	0.0050	0.0072	0.0051	0.0036	0.0072	0.0058
clatsop1	0.0090	0.0022	0.0029	0.0037	0.0052	0.0045	0.0037	0.0022	0.0030	0.0075	0.0037
clatsop2	0.0105	0.0007	0.0029	0.0037	0.0052	0.0060	0.0037	0.0022	0.0060	0.0090	0.0022
clatsop3	0.0105	0.0007	0.0029	0.0037	0.0052	0.0059	0.0037	0.0022	0.0060	0.0090	0.0022
clatsop4	0.0105	0.0007	0.0029	0.0037	0.0052	0.0060	0.0037	0.0022	0.0060	0.0090	0.0022
LostForest1A	0.0082	0.0069	0.0084	0.0083	0.0084	0.0069	0.0145	0.0101	0.0080	0.0081	0.0069
LostForest2	0.0169	0.0116	0.0109	0.0109	0.0146	0.0109	0.0139	0.0103	0.0110	0.0139	0.0117
LostForest3	0.0043	0.0050	0.0057	0.0064	0.0057	0.0058	0.0087	0.0058	0.0058	0.0101	0.0065
LostForest4	0.0138	0.0094	0.0101	0.0109	0.0116	0.0102	0.0132	0.0103	0.0102	0.0109	0.0110
sj1Pmausterus	0.0065	0.0073	0.0080	0.0080	0.0095	0.0080	0.0088	0.0081	0.0050	0.0103	0.0088
sj2Pmausterus	0.0124	0.0080	0.0080	0.0095	0.0102	0.0095	0.0095	0.0081	0.0081	0.0132	0.0087
sj2aPmausterus	0.0065	0.0043	0.0051	0.0050	0.0065	0.0065	0.0058	0.0051	0.0051	0.0088	0.0058
sj3Pmausterus	0.0080	0.0058	0.0065	0.0065	0.0080	0.0080	0.0073	0.0066	0.0065	0.0103	0.0073
sj5Pmausterus	0.0073	0.0050	0.0058	0.0058	0.0073	0.0072	0.0065	0.0058	0.0058	0.0095	0.0065
sj6Pmausterus	0.0073	0.0050	0.0058	0.0058	0.0072	0.0072	0.0065	0.0058	0.0058	0.0095	0.0065
sj7Pmausterus	0.0073	0.0050	0.0058	0.0065	0.0072	0.0072	0.0065	0.0058	0.0058	0.0095	0.0065
OSM723Pmman	0.0430	0.0398	0.0388	0.0415	0.0404	0.0411	0.0434	0.0416	0.0429	0.0452	0.0419
OSM726Pmman	0.0421	0.0389	0.0380	0.0407	0.0396	0.0402	0.0425	0.0407	0.0421	0.0443	0.0410
OSM727Pmman	0.0430	0.0398	0.0388	0.0415	0.0404	0.0411	0.0434	0.0407	0.0429	0.0452	0.0419
OSM737Pmman	0.0421	0.0389	0.0380	0.0407	0.0396	0.0402	0.0425	0.0407	0.0421	0.0443	0.0410
U40255PsejugSD	0.0536	0.0485	0.0495	0.0522	0.0492	0.0515	0.0523	0.0525	0.0536	0.0523	0.0507
U40253PsejugSC	0.0633	0.0581	0.0591	0.0619	0.0588	0.0594	0.0621	0.0625	0.0635	0.0620	0.0604
JEB1309APtruei	0.2449	0.2411	0.2439	0.2452	0.2392	0.2429	0.2440	0.2598	0.2471	0.2440	0.2424
AF374578PKEEN	0.0580	0.0508	0.0539	0.0546	0.0556	0.0502	0.0547	0.0538	0.0541	0.0547	0.0531
U40252Pleuc	0.2455	0.2400	0.2421	0.2374	0.2370	0.2464	0.2392	0.2502	0.2484	0.2476	0.2457
JAM160Pleuc	0.1863	0.1911	0.1936	0.1897	0.1893	0.1909	0.1913	0.1974	0.1888	0.1930	0.1952
JAM161Pleuc	0.2032	0.2087	0.2111	0.2067	0.2065	0.2092	0.2086	0.2171	0.2068	0.2115	0.2137
JAM162Pleuc	0.1944	0.2004	0.2026	0.1974	0.1989	0.1999	0.2002	0.2069	0.1976	0.2031	0.2043
JAM163Pleuc	0.1951	0.2014	0.2040	0.1997	0.1996	0.2013	0.2016	0.2082	0.1989	0.2056	0.2057
JAM164Pleuc	0.2004	0.2067	0.2095	0.2050	0.2050	0.2067	0.2069	0.2138	0.2041	0.2095	0.2111
JAM168Pmbairdii	0.0141	0.0148	0.0156	0.0156	0.0140	0.0156	0.0163	0.0159	0.0156	0.0181	0.0164
JAM167Pmbairdii	0.0148	0.0155	0.0163	0.0163	0.0147	0.0163	0.0171	0.0166	0.0163	0.0188	0.0171
JAM159Pmbairdii	0.0156	0.0149	0.0157	0.0164	0.0140	0.0172	0.0164	0.0159	0.0172	0.0196	0.0165
JAM166Pmbairdii	0.0180	0.0188	0.0196	0.0196	0.0180	0.0196	0.0204	0.0199	0.0196	0.0221	0.0204
M.pennsylvanicus	0.6172	0.6267	0.6273	0.6174	0.6170	0.6253	0.6256	0.6284	0.6319	0.6120	0.6282
Oryzomyspalustris	0.9542	0.9313	0.9315	0.9309	0.9376	0.9562	0.9205	0.9581	0.9394	0.9764	0.9280
Sigmodonhispidus	1.0412	1.0384	1.0169	1.0152	1.0307	1.0311	1.0290	1.0412	1.0099	1.0380	1.0344
R.megalotis	0.5792	0.5623	0.5376	0.5489	0.5540	0.5572	0.5636	0.5462	0.5623	0.5740	0.5731
Rattusnorvegicus	0.7934	0.7594	0.7437	0.7602	0.7545	0.7577	0.7729	0.7909	0.7576	0.7752	0.7558
Pmrufinus	0.0259	0.0230	0.0237	0.0246	0.0236	0.0223	0.0246	0.0242	0.0239	0.0245	0.0247

	LJD2850	LJD2898	LJD2914	LJD2936	LJD3000	LJD2126	LJD2138	LJD2154	LJD2158	LJD2836	LJD2852
WC7											
WC11											
WC12											
WC13											
ljd3256											
ljd3304											
ljd3306											
ljd3308											
ljd3317											
ljd3324											
ljd3327											
ljd3330											
ljd3333											
ljd3344											
ljd3348											
LJD620											
LJD774											
LJD886											
LJD2088											
LJD1960											
LJD1669											
LJD1524											
LJD1523											
LJD1122											
LJD2522											
LJD1637											
LJD1638											
LJD2161											
LJD2651											
LJD2737											
LJD2834											
LJD2850											
LJD2898	0.0095										
LJD2914	0.0029	0.0065									
LJD2936	0.0043	0.0080	0.0014								
LJD3000	0.0028	0.0072	0.0007	0.0021							
LJD2126	0.0110	0.0118	0.0080	0.0095	0.0087						
LJD2138	0.0065	0.0102	0.0036	0.0057	0.0043	0.0102					
LJD2154	0.0007	0.0087	0.0021	0.0036	0.0028	0.0103	0.0057				
LJD2158	0.0110	0.0118	0.0080	0.0102	0.0087	0.0000	0.0102	0.0103			
LJD2836	0.0110	0.0118	0.0080	0.0095	0.0087	0.0000	0.0102	0.0103	0.0000		
LJD2852	0.0088	0.0110	0.0073	0.0088	0.0073	0.0095	0.0110	0.0095	0.0095	0.0095	
LJD2860	0.0043	0.0080	0.0014	0.0029	0.0021	0.0095	0.0050	0.0036	0.0095	0.0095	0.0088
LJD2865	0.0043	0.0102	0.0036	0.0021	0.0029	0.0117	0.0072	0.0057	0.0117	0.0118	0.0088

LJD2890	0.0065	0.0080	0.0043	0.0058	0.0043	0.0095	0.0065	0.0065	0.0095	0.0095	0.0080
LJD2943	0.0043	0.0080	0.0014	0.0029	0.0021	0.0095	0.0050	0.0036	0.0095	0.0095	0.0088
Jefferson3	0.0057	0.0065	0.0028	0.0014	0.0036	0.0095	0.0072	0.0050	0.0102	0.0095	0.0088
ADAMS6	0.0065	0.0072	0.0036	0.0050	0.0043	0.0072	0.0079	0.0058	0.0079	0.0073	0.0066
clatsop1	0.0037	0.0068	0.0015	0.0029	0.0015	0.0068	0.0052	0.0037	0.0068	0.0068	0.0053
clatsop2	0.0022	0.0083	0.0015	0.0029	0.0015	0.0098	0.0052	0.0022	0.0098	0.0098	0.0083
clatsop3	0.0022	0.0083	0.0015	0.0029	0.0015	0.0098	0.0052	0.0022	0.0098	0.0098	0.0083
clatsop4	0.0022	0.0083	0.0015	0.0029	0.0015	0.0098	0.0052	0.0022	0.0098	0.0098	0.0083
LostForest1A	0.0085	0.0081	0.0069	0.0099	0.0084	0.0099	0.0112	0.0069	0.0113	0.0099	0.0130
LostForest2	0.0118	0.0117	0.0094	0.0116	0.0102	0.0147	0.0139	0.0117	0.0139	0.0132	0.0117
LostForest3	0.0073	0.0065	0.0043	0.0050	0.0050	0.0095	0.0087	0.0065	0.0102	0.0095	0.0088
LostForest4	0.0118	0.0110	0.0087	0.0102	0.0095	0.0125	0.0132	0.0110	0.0132	0.0125	0.0117
sj1Pmausterus	0.0095	0.0103	0.0065	0.0080	0.0072	0.0058	0.0102	0.0088	0.0058	0.0058	0.0080
sj2Pmausterus	0.0095	0.0118	0.0065	0.0080	0.0072	0.0125	0.0102	0.0087	0.0118	0.0118	0.0112
sj2aPmausterus	0.0065	0.0087	0.0036	0.0050	0.0036	0.0088	0.0072	0.0058	0.0088	0.0088	0.0081
sj3Pmausterus	0.0080	0.0103	0.0050	0.0065	0.0050	0.0103	0.0087	0.0073	0.0103	0.0103	0.0096
sj5Pmausterus	0.0073	0.0095	0.0043	0.0058	0.0050	0.0095	0.0080	0.0065	0.0095	0.0095	0.0088
sj6Pmausterus	0.0072	0.0095	0.0043	0.0058	0.0050	0.0095	0.0080	0.0065	0.0095	0.0095	0.0088
sj7Pmausterus	0.0072	0.0095	0.0043	0.0058	0.0050	0.0095	0.0080	0.0065	0.0095	0.0095	0.0089
OSM723Pmman	0.0429	0.0456	0.0391	0.0389	0.0400	0.0474	0.0424	0.0419	0.0482	0.0477	0.0448
OSM726Pmman	0.0420	0.0447	0.0383	0.0380	0.0391	0.0465	0.0415	0.0410	0.0473	0.0468	0.0439
OSM727Pmman	0.0421	0.0456	0.0391	0.0389	0.0400	0.0474	0.0424	0.0419	0.0482	0.0477	0.0441
OSM737Pmman	0.0420	0.0447	0.0383	0.0380	0.0391	0.0465	0.0415	0.0410	0.0473	0.0468	0.0439
U40255PsejugSD	0.0517	0.0528	0.0498	0.0494	0.0507	0.0546	0.0503	0.0507	0.0553	0.0548	0.0554
U40253PsejugSC	0.0615	0.0626	0.0595	0.0591	0.0604	0.0645	0.0599	0.0604	0.0652	0.0648	0.0635
JEB1309APtruei	0.2476	0.2442	0.2425	0.2393	0.2458	0.2348	0.2504	0.2424	0.2354	0.2348	0.2486
AF374578PKEEN	0.0531	0.0552	0.0522	0.0539	0.0530	0.0590	0.0526	0.0531	0.0598	0.0593	0.0531
U40252Pleuc	0.2486	0.2524	0.2387	0.2381	0.2410	0.2517	0.2445	0.2457	0.2526	0.2532	0.2414
JAM160Pleuc	0.1967	0.1952	0.1895	0.1902	0.1899	0.1953	0.1943	0.1952	0.1958	0.1963	0.1868
JAM161Pleuc	0.2162	0.2139	0.2076	0.2075	0.2095	0.2138	0.2117	0.2137	0.2136	0.2150	0.2053
JAM162Pleuc	0.2061	0.2045	0.1983	0.1991	0.1987	0.2048	0.2032	0.2043	0.2050	0.2055	0.1956
JAM163Pleuc	0.2073	0.2060	0.1997	0.2005	0.2001	0.2059	0.2046	0.2057	0.2065	0.2070	0.1967
JAM164Pleuc	0.2128	0.2116	0.2050	0.2058	0.2054	0.2114	0.2100	0.2111	0.2120	0.2125	0.2020
JAM168Pmbairdii	0.0172	0.0180	0.0141	0.0156	0.0148	0.0180	0.0170	0.0164	0.0187	0.0180	0.0187
JAM167Pmbairdii	0.0179	0.0187	0.0148	0.0163	0.0155	0.0187	0.0170	0.0171	0.0187	0.0187	0.0195
JAM159Pmbairdii	0.0173	0.0196	0.0141	0.0157	0.0149	0.0212	0.0180	0.0165	0.0213	0.0213	0.0204
JAM166Pmbairdii	0.0212	0.0221	0.0180	0.0196	0.0188	0.0204	0.0204	0.0204	0.0204	0.0205	0.0212
M.pennsylvanicus	0.6288	0.6094	0.6195	0.6103	0.6203	0.6270	0.6191	0.6282	0.6273	0.6270	0.6204
Oryzomyspalustris	0.9286	0.9702	0.9416	0.9255	0.9430	0.9241	0.9768	0.9280	0.9245	0.9239	0.9671
Sigmodonhispidus	1.0352	1.0318	1.0261	1.0407	1.0279	0.9779	1.0103	1.0344	0.9783	0.9776	1.0357
R.megalotis	0.5728	0.5754	0.5537	0.5626	0.5537	0.5344	0.5523	0.5731	0.5343	0.5343	0.5616
Rattusnorvegicus	0.7565	0.7893	0.7636	0.7721	0.7679	0.7528	0.7508	0.7558	0.7565	0.7597	0.7714
Pmrufinus	0.0256	0.0247	0.0223	0.0222	0.0231	0.0278	0.0270	0.0247	0.0286	0.0279	0.0256

	LJD2860	LJD2865	LJD2890	LJD2943	Jefferson3	ADAMS6	clatsop1	clatsop2	clatsop3	clatsop4	LFst1A
WC7											
WC11											
WC12											
WC13											
ljd3256											
ljd3304											
ljd3306											
ljd3308											
ljd3317											
ljd3324											
ljd3327											
ljd3330											
ljd3333											
ljd3344											
ljd3348											
LJD620											
LJD774											
LJD886											
LJD2088											
LJD1960											
LJD1669											
LJD1524											
LJD1523											
LJD1122											
LJD2522											
LJD1637											
LJD1638											
LJD2161											
LJD2651											
LJD2737											
LJD2834											
LJD2850											
LJD2898											
LJD2914											
LJD2936											
LJD3000											
LJD2126											
LJD2138											
LJD2154											
LJD2158											
LJD2836											
LJD2852											
LJD2860											
LJD2865	0.0050										

LJD2890	0.0058	0.0051									
LJD2943	0.0000	0.0050	0.0058								
Jefferson3	0.0043	0.0036	0.0058	0.0043							
ADAMS6	0.0050	0.0073	0.0051	0.0051	0.0050						
clatsop1	0.0030	0.0029	0.0037	0.0030	0.0037	0.0030					
clatsop2	0.0030	0.0029	0.0052	0.0030	0.0052	0.0059	0.0029				
clatsop3	0.0030	0.0029	0.0052	0.0030	0.0051	0.0059	0.0029	0.0000			
clatsop4	0.0030	0.0029	0.0052	0.0030	0.0052	0.0059	0.0029	0.0000	0.0000		
LostForest1A	0.0097	0.0133	0.0085	0.0097	0.0084	0.0052	0.0075	0.0090	0.0090	0.0090	
LostForest2	0.0110	0.0125	0.0103	0.0110	0.0116	0.0108	0.0105	0.0121	0.0120	0.0121	0.0112
LostForest3	0.0058	0.0065	0.0058	0.0058	0.0064	0.0086	0.0090	0.0105	0.0105	0.0105	0.0068
LostForest4	0.0102	0.0125	0.0102	0.0103	0.0086	0.0078	0.0098	0.0113	0.0113	0.0113	0.0113
sj1Pmausterus	0.0080	0.0102	0.0081	0.0080	0.0080	0.0043	0.0053	0.0083	0.0083	0.0083	0.0098
sj2Pmausterus	0.0080	0.0102	0.0095	0.0080	0.0094	0.0072	0.0052	0.0082	0.0082	0.0082	0.0113
sj2aPmausterus	0.0050	0.0065	0.0065	0.0051	0.0050	0.0029	0.0022	0.0052	0.0052	0.0052	0.0083
sj3Pmausterus	0.0065	0.0080	0.0080	0.0065	0.0065	0.0043	0.0037	0.0067	0.0067	0.0067	0.0083
sj5Pmausterus	0.0058	0.0080	0.0073	0.0058	0.0058	0.0036	0.0030	0.0060	0.0060	0.0060	0.0083
sj6Pmausterus	0.0058	0.0080	0.0073	0.0058	0.0058	0.0036	0.0030	0.0060	0.0060	0.0060	0.0083
sj7Pmausterus	0.0058	0.0080	0.0073	0.0058	0.0058	0.0036	0.0030	0.0059	0.0059	0.0059	0.0083
OSM723Pmman	0.0410	0.0419	0.0413	0.0411	0.0384	0.0392	0.0395	0.0413	0.0412	0.0413	0.0525
OSM726Pmman	0.0401	0.0410	0.0404	0.0402	0.0376	0.0384	0.0395	0.0412	0.0412	0.0412	0.0509
OSM727Pmman	0.0410	0.0419	0.0413	0.0411	0.0384	0.0392	0.0395	0.0413	0.0412	0.0413	0.0525
OSM737Pmman	0.0401	0.0410	0.0404	0.0402	0.0376	0.0384	0.0395	0.0412	0.0412	0.0412	0.0509
U40255PsejugSD	0.0518	0.0523	0.0518	0.0519	0.0490	0.0519	0.0512	0.0510	0.0509	0.0510	0.0704
U40253PsejugSC	0.0615	0.0621	0.0617	0.0617	0.0584	0.0615	0.0612	0.0610	0.0610	0.0610	0.0891
JEB1309APtruei	0.2500	0.2522	0.2439	0.2499	0.2391	0.2364	0.2582	0.2613	0.2613	0.2613	0.2454
AF374578PKEEN	0.0541	0.0549	0.0485	0.0542	0.0533	0.0505	0.0516	0.0515	0.0514	0.0515	0.0613
U40252Pleuc	0.2429	0.2449	0.2523	0.2441	0.2403	0.2414	0.2496	0.2481	0.2481	0.2481	0.2071
JAM160Pleuc	0.1930	0.1903	0.1936	0.1939	0.1891	0.1862	0.1915	0.1948	0.1948	0.1948	0.2018
JAM161Pleuc	0.2113	0.2130	0.2142	0.2123	0.2063	0.2031	0.2110	0.2146	0.2146	0.2146	0.2008
JAM162Pleuc	0.2020	0.2007	0.2042	0.2029	0.1988	0.1957	0.2002	0.2037	0.2036	0.2037	0.2097
JAM163Pleuc	0.2033	0.2007	0.2042	0.2043	0.1995	0.1963	0.2022	0.2057	0.2057	0.2057	0.2018
JAM164Pleuc	0.2087	0.2060	0.2097	0.2097	0.2050	0.2016	0.2076	0.2112	0.2112	0.2112	0.1994
JAM168Pmbairdii	0.0156	0.0179	0.0157	0.0157	0.0155	0.0133	0.0137	0.0153	0.0153	0.0153	0.0129
JAM167Pmbairdii	0.0163	0.0186	0.0164	0.0164	0.0163	0.0140	0.0145	0.0160	0.0160	0.0160	0.0130
JAM159Pmbairdii	0.0157	0.0179	0.0173	0.0157	0.0156	0.0149	0.0137	0.0153	0.0153	0.0153	0.0162
JAM166Pmbairdii	0.0196	0.0219	0.0197	0.0197	0.0196	0.0172	0.0170	0.0186	0.0186	0.0186	0.0130
M.pennsylvanicus	0.6246	0.6103	0.6115	0.6252	0.6105	0.6206	0.6277	0.6291	0.6292	0.6291	0.6628
Oryzomyspalustris	0.9607	0.9251	0.9359	0.9614	0.9149	0.9314	0.9438	0.9340	0.9344	0.9340	0.8696
Sigmodonhispidus	1.0447	1.0401	1.0212	1.0455	1.0415	1.0235	1.0252	1.0339	1.0344	1.0339	1.2549
R.megalotis	0.5489	0.5621	0.5644	0.5486	0.5808	0.5711	0.5621	0.5638	0.5639	0.5638	0.7431
Rattusnorvegicus	0.7773	0.7715	0.7852	0.7852	0.7554	0.7551	0.7479	0.7491	0.7493	0.7491	0.8556
Pmrufinus	0.0239	0.0248	0.0240	0.0239	0.0205	0.0228	0.0238	0.0254	0.0254	0.0254	0.0399

	LostFore st2	LostFore st3	LostFore st4	sj1Pmaust erus	sj2Pmaust erus	sj2aPmaust erus	sj3Pmaust erus	sj5Pmaust erus	sj6Pmauster us	sj7Pmau sterus	OSM723 Pmman
WC7											
WC11											
WC12											
WC13											
ljd3256											
ljd3304											
ljd3306	0.0153										
ljd3308	0.0035	0.0130									
ljd3317	0.0095	0.0080	0.0094								
ljd3324	0.0163	0.0124	0.0140	0.0080							
ljd3327	0.0095	0.0065	0.0095	0.0043	0.0043						
ljd3330	0.0110	0.0080	0.0110	0.0058	0.0043	0.0014					
ljd3333	0.0102	0.0073	0.0102	0.0051	0.0051	0.0007	0.0007				
ljd3344	0.0102	0.0073	0.0102	0.0051	0.0050	0.0007	0.0007	0.0000			
ljd3348	0.0109	0.0072	0.0102	0.0051	0.0058	0.0007	0.0007	0.0000	0.0000		
LJD620	0.0491	0.0446	0.0456	0.0437	0.0451	0.0401	0.0419	0.0410	0.0409	0.0408	
LJD774	0.0483	0.0437	0.0447	0.0428	0.0442	0.0392	0.0410	0.0401	0.0401	0.0400	0.0007
LJD886	0.0491	0.0446	0.0456	0.0437	0.0451	0.0401	0.0419	0.0410	0.0409	0.0408	0.0014
LJD2088	0.0483	0.0437	0.0447	0.0428	0.0442	0.0392	0.0410	0.0401	0.0401	0.0400	0.0007
LJD1960	0.0578	0.0555	0.0544	0.0565	0.0576	0.0529	0.0548	0.0538	0.0537	0.0536	0.0515
LJD1669	0.0678	0.0653	0.0642	0.0666	0.0677	0.0627	0.0648	0.0637	0.0636	0.0634	0.0613
LJD1524	0.2460	0.2433	0.2433	0.2354	0.2487	0.2391	0.2418	0.2408	0.2409	0.2408	0.2634
LJD1523	0.0566	0.0580	0.0531	0.0551	0.0563	0.0533	0.0553	0.0542	0.0542	0.0540	0.0605
LJD1122	0.2529	0.2546	0.2472	0.2521	0.2480	0.2488	0.2475	0.2503	0.2498	0.2491	0.2276
LJD2522	0.2038	0.1939	0.1995	0.1956	0.1982	0.1929	0.1922	0.1947	0.1943	0.1939	0.1962
LJD1637	0.2182	0.2113	0.2127	0.2142	0.2166	0.2117	0.2109	0.2132	0.2128	0.2122	0.2091
LJD1638	0.2051	0.2024	0.2051	0.2047	0.2065	0.2019	0.2010	0.2037	0.2033	0.2031	0.1989
LJD2161	0.2101	0.2031	0.2058	0.2062	0.2070	0.2033	0.2024	0.2051	0.2047	0.2041	0.2023
LJD2651	0.2156	0.2086	0.2113	0.2117	0.2124	0.2086	0.2076	0.2104	0.2100	0.2095	0.2075
LJD2737	0.0194	0.0156	0.0187	0.0165	0.0171	0.0149	0.0149	0.0157	0.0157	0.0157	0.0459
LJD2834	0.0202	0.0163	0.0194	0.0172	0.0171	0.0156	0.0156	0.0164	0.0164	0.0164	0.0477
LJD2850	0.0219	0.0172	0.0203	0.0180	0.0171	0.0150	0.0149	0.0157	0.0157	0.0157	0.0461
LJD2898	0.0212	0.0196	0.0212	0.0204	0.0204	0.0189	0.0188	0.0196	0.0196	0.0196	0.0491
LJD2914	0.6204	0.6221	0.6202	0.6284	0.6251	0.6293	0.6257	0.6326	0.6322	0.6323	0.6798
LJD2936	0.9221	0.9383	0.9217	0.9207	0.9308	0.9307	0.9182	0.9311	0.9306	0.9305	0.9825
LJD3000	1.0125	1.0430	1.0120	0.9802	1.0188	1.0192	1.0271	1.0170	1.0164	1.0162	1.0613
LJD2126	0.5572	0.5932	0.5573	0.5446	0.5416	0.5450	0.5390	0.5471	0.5472	0.5471	0.5907
LJD2138	0.7593	0.8048	0.7496	0.7761	0.7494	0.7612	0.7659	0.7668	0.7634	0.7612	0.7413
LJD2154	0.0300	0.0228	0.0267	0.0263	0.0277	0.0247	0.0263	0.0255	0.0255	0.0255	0.0547

	OSM726Pmman	OSM727Pmman	OSM737Pmman	U40255PsejugSD	U40253PsejugSC	JEB1309APtruei	AF374578PKEEN	U40252Pleuc	JAM160Pleuc	JAM161Pleuc	JAM162Pleuc
LJD2890											
LJD2943											
Jefferson3											
ADAMS6											
clatsop1											
clatsop2											
clatsop3											
clatsop4											
LostForest1A											
LostForest2											
LostForest3											
LostForest4											
sj1Pmausterus											
sj2Pmausterus											
sj2aPmausterus											
sj3Pmausterus											
sj5Pmausterus											
sj6Pmausterus	0.0007										
sj7Pmausterus	0.0000	0.0007									
OSM723Pmman	0.0506	0.0515	0.0506								
OSM726Pmman	0.0603	0.0613	0.0603	0.0071							
OSM727Pmman	0.2655	0.2688	0.2655	0.3065	0.3219						
OSM737Pmman	0.0595	0.0605	0.0595	0.0411	0.0446	0.2605					
U40255PsejugSD	0.2260	0.2276	0.2260	0.2267	0.2336	0.3385	0.2309				
U40253PsejugSC	0.1947	0.1962	0.1947	0.1959	0.2046	0.3338	0.1985	0.0398			
JEB1309APtruei	0.2076	0.2091	0.2076	0.2089	0.2180	0.3274	0.2226	0.0333	0.0087		
AF374578PKEEN	0.1975	0.1989	0.1975	0.2060	0.2152	0.3369	0.2103	0.0404	0.0072	0.0087	
U40252Pleuc	0.2008	0.2023	0.2008	0.2022	0.2112	0.3331	0.2095	0.0366	0.0101	0.0057	0.0087
JAM160Pleuc	0.2060	0.2075	0.2060	0.2076	0.2168	0.3303	0.2150	0.0342	0.0065	0.0036	0.0065
JAM161Pleuc	0.0450	0.0459	0.0450	0.0519	0.0616	0.2538	0.0576	0.2377	0.1830	0.1998	0.1917
JAM162Pleuc	0.0469	0.0477	0.0469	0.0538	0.0636	0.2480	0.0595	0.2422	0.1859	0.2032	0.1946
JAM163Pleuc	0.0453	0.0461	0.0453	0.0544	0.0642	0.2604	0.0598	0.2379	0.1820	0.1996	0.1909
JAM164Pleuc	0.0482	0.0491	0.0482	0.0553	0.0652	0.2576	0.0609	0.2442	0.1872	0.2052	0.1959
JAM168Pmbairdii	0.6794	0.6798	0.6794	0.7243	0.7300	0.7429	0.6985	0.6779	0.6155	0.6317	0.6015
JAM167Pmbairdii	0.9822	0.9825	0.9822	1.0942	1.1110	0.8481	0.9759	1.1452	0.9450	1.0096	0.9628
JAM159Pmbairdii	1.0609	1.0613	1.0609	1.0566	1.0565	0.9196	1.0071	1.1915	1.1053	1.1056	1.0565
JAM166Pmbairdii	0.5906	0.5907	0.5906	0.5643	0.5953	0.6187	0.6225	0.6366	0.6495	0.6171	0.6528
M.pennsylvanicus	0.7407	0.7413	0.7407	0.7561	0.7603	0.9694	0.7486	0.7371	0.7406	0.7492	0.7313
Oryzomyspalustris	0.0538	0.0547	0.0538	0.0595	0.0655	0.3055	0.0594	0.2386	0.2039	0.2215	0.2139

	JAM163Pleuc	JAM164Pleuc	JAM168Pmbairdii	JAM167Pmbairdii	JAM159Pmbairdii	JAM166Pmbairdii	Microtuspennsylvanicus	Oryzomyspalustris	Sigmodonhispidus	Reithrodontomysmegalotis	Rattusnorvegicus
JAM164Pleuc	0.0050										
JAM168Pmbairdii	0.1930	0.1982									
JAM167Pmbairdii	0.1959	0.2012	0.0028								
JAM159Pmbairdii	0.1918	0.1970	0.0043	0.0057							
JAM166Pmbairdii	0.1972	0.2024	0.0050	0.0065	0.0080						
M.pennsylvanicus	0.6286	0.6150	0.6340	0.6218	0.6186	0.6294					
Oryzomyspalustris	0.9927	0.9681	0.9973	0.9941	0.9768	1.0013	0.9124				
Sigmodonhispidus	1.1198	1.0958	1.0335	1.0591	1.0597	1.0370	1.3044	1.0383			
R.megalotis	0.6163	0.6283	0.5736	0.5670	0.5887	0.5836	1.0410	1.2014	1.0315		
Rattusnorvegicus	0.7309	0.7434	0.7605	0.7533	0.7637	0.7285	0.7899	1.0387	1.2793	1.0661	
Pmrufinus	0.2144	0.2200	0.0335	0.0336	0.0353	0.0380	0.6000	0.9950	1.1254	0.5850	0.8446

Appendix B: *Hantavirus* Distance Matrix. Pair-wise percent genetic difference (distance) among hantaviruses (n=44) based upon M segment G1/G2 glycoprotein precursor gene (613nt).

	T7	T8	WC4	WCps
T7				
T8	0			
WC4	0.01689189	0.01689189		
WCps	0.01858108	0.01858108	0.00168919	
WC7	0.01689189	0.01689189	0.00675676	0.00844595
WC12	0.04391892	0.04391892	0.03378378	0.03547297
WC13	0.01689189	0.01689189	0.00675676	0.00844595
LJD1523FP	0.02533784	0.02533784	0.02533784	0.02702703
LJD2126FP	0.0152027	0.0152027	0.01182432	0.01351351
LJD2138FP	0.01182432	0.01182432	0.00844595	0.01013513
LJD2154FP	0.03725455	0.03725455	0.04075247	0.04247823
LJD2493FP	0.0152027	0.0152027	0.00844595	0.01013513
LJD2494FP	0.01689189	0.01689189	0.01013513	0.01182432
LJD2497FP	0.01689189	0.01689189	0.01013513	0.01182432
LJD2499FP	0.03378378	0.03378378	0.02871622	0.03040541
LJD2520FP	0.0152027	0.0152027	0.00844595	0.01013513
LJD2522FP	0.0152027	0.0152027	0.00844595	0.01013513
LJD2737PB	0.00169827	0.00169827	0.01520477	0.01690304
LJD2836FP	0.01351351	0.01351351	0.01013513	0.01182432
LJD2852FP	0.01689189	0.01689189	0.01351351	0.0152027
LJD2860FP	0.0152027	0.0152027	0.00844595	0.01013513
LJD2865FP	0.01858108	0.01858108	0.01182432	0.01351351
LJD2890FP	0.0152027	0.0152027	0.00844595	0.01013513
convict creek	0.11993244	0.11993244	0.1097973	0.11148649
SNVL25783	0.14695945	0.14695945	0.1418919	0.14358108
SNVL37903	0.14695945	0.14695945	0.1418919	0.14358108
NewYorkVirusU36803	0.21452703	0.21452703	0.21621622	0.2179054
BlueRiverAF030552	0.23817568	0.23817568	0.23817568	0.23986487
BayouvirusL36930	0.27364865	0.27364865	0.27533785	0.27702704
BlackCreekCanalL39950	0.2972973	0.2972973	0.28885135	0.29054055
AndesVirusNC003467	0.28378379	0.28378379	0.27702704	0.27871621
Hu39694virusAF028023	0.28547296	0.28547296	0.2804054	0.2820946
OranVirusAF028024	0.28885135	0.28885135	0.28378379	0.28547296
LechiguanasvirusAF028022	0.2668919	0.2668919	0.2652027	0.2668919
Juquitibalikevirus168711	0.3035008	0.3035008	0.29921457	0.29898441
MacielvirusAF028027	0.28885135	0.28885135	0.2804054	0.2820946
ElMoroCanyonU26828	0.28378379	0.28378379	0.27702704	0.27871621
ProspectHillX55129	0.33277026	0.33277026	0.33277026	0.33445945
TulavirusNC005228	0.33277026	0.33277026	0.3277027	0.3293919
PuumalavirusNC005223	0.35135135	0.35135135	0.35304055	0.35472974
HantaanvirusDQ371905	0.41554055	0.41554055	0.41722974	0.41891891
DobravavirusNC005234	0.40202704	0.40202704	0.40202704	0.40371621
SeoulVirusNC005237	0.39864865	0.39864865	0.40202704	0.40371621
SangassouvirusDQ268651	0.40510133	0.40510133	0.40454447	0.40432113

	WC7	WC12	WC13	LJD1523FP	LJD2126FP	LJD2138FP
T7						
T8						
WC4						
WCps						
WC7						
WC12	0.03378378					
WC13	0	0.03378378				
LJD1523FP	0.02533784	0.04898649	0.02533784			
LJD2126FP	0.01182432	0.03885135	0.01182432	0.02027027		
LJD2138FP	0.00844595	0.03547297	0.00844595	0.02364865	0.00337838	
LJD2154FP	0.04075247	0.06115411	0.04075247	0.05596788	0.0356652	0.03230368
LJD2493FP	0.00844595	0.03547297	0.00844595	0.02364865	0.00675676	0.00337838
LJD2494FP	0.01013513	0.03716216	0.01013513	0.02533784	0.00844595	0.00506757
LJD2497FP	0.01013513	0.03716216	0.01013513	0.02195946	0.00506757	0.00506757
LJD2499FP	0.03040541	0.05405406	0.03040541	0.04560811	0.02871622	0.02533784
LJD2520FP	0.00844595	0.03547297	0.00844595	0.02364865	0.00675676	0.00337838
LJD2522FP	0.00844595	0.03547297	0.00844595	0.02364865	0.00675676	0.00337838
LJD2737PB	0.01520477	0.04227104	0.01520477	0.02369345	0.0135065	0.01013055
LJD2836FP	0.01013513	0.03716216	0.01013513	0.02533784	0.00506757	0.00168919
LJD2852FP	0.01351351	0.04054054	0.01351351	0.02871622	0.00844595	0.00506757
LJD2860FP	0.00844595	0.03547297	0.00844595	0.02364865	0.00675676	0.00337838
LJD2865FP	0.01182432	0.03209459	0.01182432	0.02533784	0.01013513	0.00675676
LJD2890FP	0.00844595	0.03547297	0.00844595	0.02364865	0.00675676	0.00337838
convict creek	0.10810811	0.12331081	0.10810811	0.125	0.10810811	0.10810811
SNVL25783	0.1418919	0.1418919	0.1418919	0.15878378	0.1418919	0.13851352
SNVL37903	0.1418919	0.1418919	0.1418919	0.15878378	0.1418919	0.13851352
NewYorkVirusU36803	0.21621622	0.21621622	0.21621622	0.22972973	0.21283785	0.21283785
BlueRiverAF030552	0.23817568	0.23986487	0.23817568	0.2516892	0.2331081	0.2331081
BayouvirusL36930	0.27533785	0.2804054	0.27533785	0.28547296	0.27195945	0.27027026
BlackCreekCanalL39950	0.29054055	0.28547296	0.29054055	0.29898649	0.28885135	0.28716215
AndesVirusNC003467	0.2804054	0.27027026	0.2804054	0.28716215	0.27871621	0.27702704
Hu39694virusAF028023	0.2820946	0.2820946	0.2820946	0.29222974	0.27871621	0.27871621
OranVirusAF028024	0.28547296	0.28716215	0.28547296	0.2956081	0.2804054	0.2820946
LechiguanasvirusAF028022	0.2652027	0.2668919	0.2652027	0.27195945	0.25844595	0.26013514
Juquitibalikevirus168711	0.30200422	0.29626659	0.30200422	0.30796087	0.30351657	0.29905257
MacielvirusAF028027	0.2804054	0.27533785	0.2804054	0.29222974	0.27871621	0.27871621
ElMoroCanyonU26828	0.27702704	0.27533785	0.27702704	0.29222974	0.27702704	0.27533785
ProspectHillX55129	0.33445945	0.33783785	0.33445945	0.3429054	0.3277027	0.3277027
TulavirusNC005228	0.3293919	0.32432431	0.3293919	0.33952704	0.3277027	0.32601351
PuumalavirusNC005223	0.35472974	0.3445946	0.35472974	0.36148649	0.35135135	0.35135135
HantaanvirusDQ371905	0.41722974	0.40371621	0.41722974	0.42398649	0.41554055	0.41385135
DobravavirusNC005234	0.40371621	0.39864865	0.40371621	0.41216215	0.40202704	0.40033785
SeoulVirusNC005237	0.40033785	0.39527026	0.40033785	0.4070946	0.39864865	0.39864865
SangassouvirusDQ268651	0.40454447	0.40356162	0.40454447	0.40474871	0.40480602	0.40467227

	LJD2154FP	LJD2493FP	LJD2494FP	LJD2497FP	LJD2499FP	LJD2520FP
T7						
T8						
WC4						
WCps						
WC7						
WC12						
WC13						
LJD1523FP						
LJD2126FP						
LJD2138FP						
LJD2154FP						
LJD2493FP	0.0356652					
LJD2494FP	0.03736917	0.00168919				
LJD2497FP	0.03736917	0.00337838	0.00506757			
LJD2499FP	0.0542511	0.02533784	0.02702703	0.02702703		
LJD2520FP	0.0356652	0.00337838	0.00506757	0.00506757	0.02533784	
LJD2522FP	0.03569596	0.00337838	0.00506757	0.00506757	0.02533784	0.00337838
LJD2737PB	0.04062414	0.0135065	0.01519001	0.01519001	0.03209038	0.0135065
LJD2836FP	0.03057793	0.00506757	0.00675676	0.00675676	0.02702703	0.00506757
LJD2852FP	0.03736861	0.00844595	0.01013513	0.01013513	0.03040541	0.00844595
LJD2860FP	0.0356652	0.00168919	0.00337838	0.00168919	0.02533784	0.00337838
LJD2865FP	0.03907926	0.00506757	0.00675676	0.00506757	0.02871622	0.00675676
LJD2890FP	0.0356652	0.00168919	0.00337838	0.00168919	0.02533784	0.00337838
convict creek	0.11374537	0.10641892	0.10641892	0.10304054	0.1266892	0.10810811
SNVL25783	0.14770605	0.13851352	0.13682432	0.13851352	0.1570946	0.1402027
SNVL37903	0.14770605	0.13851352	0.13682432	0.13851352	0.1570946	0.1402027
NewYorkVirusU36803	0.21656698	0.21283785	0.21283785	0.21114865	0.22466215	0.21452703
BlueRiverAF030552	0.22702844	0.2331081	0.23141892	0.22972973	0.24662162	0.2347973
BayouvirusL36930	0.27250528	0.27027026	0.27195945	0.26858109	0.27364865	0.27195945
BlackCreekCanalL39950	0.29472989	0.28716215	0.28885135	0.28547296	0.2972973	0.28885135
AndesVirusNC003467	0.28469363	0.27702704	0.27702704	0.27533785	0.28378379	0.27871621
Hu39694virusAF028023	0.27595124	0.27871621	0.2804054	0.27702704	0.29054055	0.2804054
OranVirusAF028024	0.28090265	0.2820946	0.28378379	0.27871621	0.29391891	0.28378379
LechiguanasvirusAF028022	0.26583359	0.26182431	0.26182431	0.25844595	0.27533785	0.26351351
Juquitibalikevirus168711	0.29786795	0.29902834	0.29665294	0.29897928	0.30965298	0.29905257
MacielvirusAF028027	0.27945143	0.27871621	0.2804054	0.27533785	0.29222974	0.2804054
ElMoroCanyonU26828	0.28277552	0.27364865	0.27533785	0.27195945	0.28885135	0.27533785
ProspectHillX55129	0.3277843	0.3277027	0.3277027	0.32432431	0.33277026	0.3293919
TulavirusNC005228	0.32489362	0.32601351	0.32601351	0.32432431	0.33783785	0.3277027
PuumalavirusNC005223	0.35704678	0.35135135	0.35304055	0.34797296	0.3581081	0.35135135
HantaanvirusDQ371905	0.41059139	0.41216215	0.41385135	0.41047296	0.41216215	0.41385135
DobravavirusNC005234	0.39590153	0.40033785	0.40033785	0.39864865	0.4054054	0.40202704
SeoulVirusNC005237	0.40626273	0.39695945	0.39864865	0.39358109	0.40033785	0.39864865
SangassouvirusDQ268651	0.41380125	0.40467227	0.40390712	0.40449309	0.40497798	0.40467227

	LJD2522FP	LJD2737PB	LJD2836FP	LJD2852FP	LJD2860FP	LJD2865FP
T7						
T8						
WC4						
WCps						
WC7						
WC12						
WC13						
LJD1523FP						
LJD2126FP						
LJD2138FP						
LJD2154FP						
LJD2493FP						
LJD2494FP						
LJD2497FP						
LJD2499FP						
LJD2520FP						
LJD2522FP						
LJD2737PB	0.01349755					
LJD2836FP	0.00506757	0.01181405				
LJD2852FP	0.00844595	0.01518105	0.00675676			
LJD2860FP	0.00337838	0.0135065	0.00506757	0.00844595		
LJD2865FP	0.00675676	0.01688827	0.00844595	0.01182432	0.00337838	
LJD2890FP	0.00337838	0.0135065	0.00506757	0.00844595	0	0.00337838
convict creek	0.10810811	0.11831909	0.10641892	0.11317568	0.10472973	0.10810811
SNVL25783	0.1402027	0.14533791	0.1402027	0.14358108	0.13682432	0.13682432
SNVL37903	0.1402027	0.14533791	0.1402027	0.14358108	0.13682432	0.13682432
NewYorkVirusU36803	0.21452703	0.21640176	0.21452703	0.21283785	0.21114865	0.21452703
BlueRiverAF030552	0.2347973	0.23999089	0.2347973	0.23648648	0.23141892	0.2347973
BayouvirusL36930	0.27195945	0.27380687	0.27195945	0.27027026	0.26858109	0.27195945
BlackCreekCanalL39950	0.28885135	0.29755044	0.28885135	0.28885135	0.28547296	0.28885135
AndesVirusNC003467	0.27871621	0.28389847	0.27871621	0.2820946	0.27533785	0.27533785
Hu39694virusAF028023	0.2804054	0.28563884	0.27702704	0.2820946	0.27702704	0.2804054
OranVirusAF028024	0.28378379	0.28903851	0.2804054	0.28716215	0.2804054	0.28378379
LechiguanasvirusAF028022	0.26351351	0.2671409	0.25844595	0.26351351	0.26013514	0.26013514
Juquitibalikevirus168711	0.30135384	0.30143389	0.29941052	0.30393869	0.2968154	0.2964232
MacielvirusAF028027	0.2804054	0.28900537	0.2804054	0.2820946	0.27702704	0.27702704
ElMoroCanyonU26828	0.27533785	0.28219485	0.27702704	0.27871621	0.27195945	0.27533785
ProspectHillX55129	0.3293919	0.331379	0.3293919	0.33277026	0.32601351	0.3293919
TulavirusNC005228	0.3277027	0.33300248	0.3277027	0.33108109	0.32432431	0.3277027
PuumalavirusNC005223	0.35304055	0.35167229	0.35304055	0.35472974	0.34966215	0.34966215
HantaanvirusDQ371905	0.41385135	0.41745156	0.41216215	0.41722974	0.41047296	0.41047296
DobravavirusNC005234	0.40202704	0.40388456	0.39864865	0.40371621	0.39864865	0.39864865
SeoulVirusNC005237	0.39864865	0.40057662	0.40033785	0.40202704	0.39527026	0.39527026
SangassouvirusDQ268651	0.40841582	0.40530401	0.40485737	0.40474808	0.40458268	0.40448716

	LJD2890FP	Convict creek	SNVL25783	SNVL37903	NewYorkVirus	Blue River
T7						
T8						
WC4						
WCps						
WC7						
WC12						
WC13						
LJD1523FP						
LJD2126FP						
LJD2138FP						
LJD2154FP						
LJD2493FP						
LJD2494FP						
LJD2497FP						
LJD2499FP						
LJD2520FP						
LJD2522FP						
LJD2737PB						
LJD2836FP						
LJD2852FP						
LJD2860FP						
LJD2865FP						
LJD2890FP						
convictcreek	0.10472973					
SNVL25783	0.13682432	0.13006757				
SNVL37903	0.13682432	0.13006757	0			
NewYorkVirusU36803	0.21114865	0.21283785	0.1891892	0.1891892		
BlueRiverAF030552	0.23141892	0.21621622	0.20101352	0.20101352	0.19763513	
BayouvirusL36930	0.26858109	0.28547296	0.26013514	0.26013514	0.24155405	0.2804054
BlackCreekCanalL39950	0.28547296	0.27533785	0.2668919	0.2668919	0.25337839	0.27364865
AndesVirusNC003467	0.27533785	0.27702704	0.2516892	0.2516892	0.26351351	0.25
Hu39694virusAF028023	0.27702704	0.25675675	0.2652027	0.2652027	0.25844595	0.2483108
OranVirusAF028024	0.2804054	0.25844595	0.25844595	0.25844595	0.2516892	0.25506756
LechiguanasvirusAF028022	0.26013514	0.23141892	0.25337839	0.25337839	0.25675675	0.27027026
Juquitibalikevirus168711	0.2968154	0.29705411	0.27894211	0.27894211	0.29574701	0.29207158
MacielvirusAF028027	0.27702704	0.25675675	0.25844595	0.25844595	0.26858109	0.26013514
ElMoroCanyonU26828	0.27195945	0.25844595	0.26858109	0.26858109	0.2516892	0.2516892
ProspectHillX55129	0.32601351	0.30405405	0.30743244	0.30743244	0.27871621	0.31756756
TulavirusNC005228	0.32432431	0.30405405	0.30912161	0.30912161	0.2956081	0.30574325
PuumalavirusNC005223	0.34966215	0.32432431	0.3277027	0.3277027	0.33277026	0.31925675
HantaanvirusDQ371905	0.41047296	0.39527026	0.39864865	0.39864865	0.38175675	0.36824325
DobravavirusNC005234	0.39864865	0.39864865	0.3918919	0.3918919	0.38175675	0.3733108
SeoulVirusNC005237	0.39527026	0.41216215	0.40033785	0.40033785	0.38682431	0.3766892
SangassouvirusDQ268651	0.40458268	0.41278094	0.43484983	0.43484983	0.40968382	0.41773394

	Bayou virus	BlackCkCanal	Andes virus	Hu39694	Oran Virus	Lechiguanas
T7						
T8						
WC4						
WCps						
WC7						
WC12						
WC13						
LJD1523FP						
LJD2126FP						
LJD2138FP						
LJD2154FP						
LJD2493FP						
LJD2494FP						
LJD2497FP						
LJD2499FP						
LJD2520FP						
LJD2522FP						
LJD2737PB						
LJD2836FP						
LJD2852FP						
LJD2860FP						
LJD2865FP						
LJD2890FP						
convictcreek						
SNVL25783						
SNVL37903						
NewYorkVirusU36803						
BlueRiverAF030552						
BayouvirusL36930						
BlackCreekCanalL39950	0.18243243					
AndesVirusNC003467	0.26858109	0.24662162				
Hu39694virusAF028023	0.2652027	0.2516892	0.19087838			
OranVirusAF028024	0.26013514	0.2331081	0.17736487	0.1554054		
LechiguanasvirusAF028022	0.2668919	0.25675675	0.20777027	0.16385135	0.16554055	
Juquitibalikevirus168711	0.26260725	0.25545421	0.22389443	0.22706707	0.21387359	0.22467844
MacielvirusAF028027	0.27364865	0.25844595	0.19087838	0.21452703	0.19763513	0.21452703
ElMoroCanyonU26828	0.26013514	0.27364865	0.26182431	0.28378379	0.27702704	0.28716215
ProspectHillX55129	0.33952704	0.3429054	0.33952704	0.33614865	0.3429054	0.33952704
TulavirusNC005228	0.32263514	0.32263514	0.3293919	0.32094595	0.3125	0.3125
PuumalavirusNC005223	0.33614865	0.33952704	0.31756756	0.32263514	0.30405405	0.32432431
HantaanvirusDQ371905	0.39527026	0.4054054	0.38682431	0.37837839	0.39358109	0.40878379
DobravavirusNC005234	0.38513514	0.39695945	0.37837839	0.3902027	0.38344595	0.41722974
SeoulVirusNC005237	0.38175675	0.40202704	0.37837839	0.36824325	0.3766892	0.38344595
SangassouvirusDQ268651	0.40777123	0.38549241	0.34421921	0.38481274	0.38207671	0.38002181

	Juquitiba	Maciel virus	ElMoroCanyon	Prospect Hill	Tula virus	Puumalavirus
T7						
T8						
WC4						
WCps						
WC7						
WC12						
WC13						
LJD1523FP						
LJD2126FP						
LJD2138FP						
LJD2154FP						
LJD2493FP						
LJD2494FP						
LJD2497FP						
LJD2499FP						
LJD2520FP						
LJD2522FP						
LJD2737PB						
LJD2836FP						
LJD2852FP						
LJD2860FP						
LJD2865FP						
LJD2890FP						
convictcreek						
SNVL25783						
SNVL37903						
NewYorkVirusU36803						
BlueRiverAF030552						
BayouvirusL36930						
BlackCreekCanalL39950						
AndesVirusNC003467						
Hu39694virusAF028023						
OranVirusAF028024						
LechiguanasvirusAF028022						
Juquitibalikevirus168711						
MacielvirusAF028027	0.21495967					
ElMoroCanyonU26828	0.30833328	0.28547296				
ProspectHillX55129	0.33723414	0.34628379	0.32263514			
TulavirusNC005228	0.3032096	0.31925675	0.30912161	0.2483108		
PuumalavirusNC005223	0.33232468	0.31925675	0.33614865	0.28547296	0.27871621	
HantaanvirusDQ371905	0.38264218	0.39695945	0.39527026	0.41891891	0.4070946	0.4054054
DobravavirusNC005234	0.40304586	0.3766892	0.38682431	0.42736486	0.40878379	0.40202704
SeoulVirusNC005237	0.38056841	0.37162161	0.38344595	0.41216215	0.4222973	0.39527026
SangassouvirusDQ268651	0.40154818	0.40188473	0.40137625	0.48121792	0.41895321	0.42635861

	Hantaan virus	Dobrava virus	Seoul virus	Sangassou virus
T7				
T8				
WC4				
WCps				
WC7				
WC12				
WC13				
LJD1523FP				
LJD2126FP				
LJD2138FP				
LJD2154FP				
LJD2493FP				
LJD2494FP				
LJD2497FP				
LJD2499FP				
LJD2520FP				
LJD2522FP				
LJD2737PB				
LJD2836FP				
LJD2852FP				
LJD2860FP				
LJD2865FP				
LJD2890FP				
convictcreek				
SNVL25783				
SNVL37903				
NewYorkVirusU36803				
BlueRiverAF030552				
BayouvirusL36930				
BlackCreekCanalL39950				
AndesVirusNC003467				
Hu39694virusAF028023				
OranVirusAF028024				
LechiguanasvirusAF028022				
Juquitibalikevirus168711				
MacielvirusAF028027				
ElMoroCanyonU26828				
ProspectHillX55129				
TulavirusNC005228				
PuumalavirusNC005223				
HantaanvirusDQ371905				
DobravavirusNC005234	0.23817568			
SeoulVirusNC005237	0.24155405	0.25337839		
SangassouvirusDQ268651	0.22419307	0.17467813	0.28966558	

Appendix C: Specimen Capture Data. Small mammal field captures in the Portland, OR region during the period October, 2002 through October, 2005.

PM = *Peromyscus maniculatus*
ST = *Sorex trowbridgii*
SV = *Sorex vagrans*
NG = *Neurotrichus gibsii*
MO = *Microtis oregoni*
SB = *Sorex bendirii*
PL = *Procyon lotor*
MT = *Microtus townsendii*
SN = *Sciurus niger*
TD = *Tamiasciurus douglasii*
TT = *Tamias townsendii*
ST = *Scapanus townsendii*
DV = *Didelphis virginianus*
MM = *Mephitis mephitis*
ME = *Mustela erminea*
SG = *Spilogale gracilis*

Specimen #	Trap	G/S	Sex	Mass	ELISA/Notes
Forest Park					
31		PM			
70		PM			
71		PM			
72		PM			
73		PM			trace
74		PM			positive
76		PM			
77		PM			
78		PM			
79		PM			
80		PM			positive
81		PM			
82		PM			
83		PM			
84		PM			
85		PM			
86		PM			positive
87		PM			
88		PM			
89		PM			
90		PM			
91		PM			
92		PM			
93		PM			
94		PM			
95		PM			
Tryon Creek	10/02				
201	m108	PM	F	18	
202	m	PM	F	18.5	
203	m45	PM	M	18	
204	m	PM	M	16	
205	p28	PM	M	14.5	
206	p96	PM	M	18.5	
207	s12	PM	F	17	
208	p12	MO	F	12	

209	s6	PM	F	17.5	
210	p48	PM	M	16	
211	s78	PM	M	16	
212	p76	PM	M	16.5	
213	s23	PM	M	18	
214	s24	PM	M	15	trace
215	p96	PM	F	21.5	
216	s129	PM	F	22.5	
217	s125	PM	F	17.5	
218	s117	PM	F	25	
219	s116	PM	F	21	
220	s114	PM	M	18.5	
221	s14	PM	F	16.5	
222	t112	SN	F	~600	
223	s14	ME	M	62	
224	m23	SV-NBS		5	
225	s128	PM	F	19	
226	s12	PM	M	17	
227	t24	SN	M	500+	
228	p115	PM	M	7	
229	p115	PM	M	7.5	
230	m8	PM	M	7	
231	p103	PM	M	7.5	
232	s47	PM	F	17	
233	s101	PM	M	17	
234	s33	PM	M	18.5	
235	s98	PM	F	16	
236	s101	PM	F	14	
237	s131	SV-NBS		6	
238	s96	TT	M	130	
239	t116	SN	F?		
240	p115	PM-LS	M	19.5	clotted
241	p48	PM	M	19	
242	p127	PM	M	6	
243	s24	TT	M	65	
244	s89	PM	M	11	
245	s129	PM	M	13	
246	?	PM-LS	M	14	clotted
247	s101	PM	M	18	
248	s100	PM	M	17	trace
249	s45	TT	M	68	
250	t84	SN	M		
251	p40	SV-NBS		6	
252	s44	SV-NBS		6	
Forest	Park 10/02				
253	m108	PM	F	21	
254	m72	PM	M	18	

255	s95	PM	F	17	
256	s74	PM	M	19	
257	s127	PM	M	14.5	
258	m54	PM	F	15.5	trace
259	m118	PM	M	9	
260	s21	PM	M	18	positive
261	m83	PM	F	16.5	
262	s83	SV-NBS		5	
263	s64	SV-NBS		5	
264	s6	PM	M	18	
265	s39	PM	M	12	
266	s130	PM	F	17	
267	s14	PM	M	14	trace
268	s119	PM	M	20	positive
269	s117	PM	F	18	
270	s83	PM	M	16	
271	s95	PM	F	16	
272	s80	PM	F	19	
273	p76	SV-NBS		5	
274	m74	PM-NBS	F	15	
275	m132	PM-NBS	F	50	
276	s89	SV-NBS		4.5	
277	s76	SV-NBS		5	
278	s45	SV-NBS		5.5	
279	m72	PM	F	24	positive
280	s142	PM	M	20	
281	p112	PM	F	20	
282	s59	PM	M	11.5	
283	s83	PM	M	13.5	
284	p76	PM	F	16	
285	s119	PM	M	10	
286	s29	PM	M	11.5	
287	s63	SV-NBS		5	
288	s85	SV-NBS		4	
289	s9	SV-NBS		5	
290	m72	PM	M	12	
291	m19	PM	M	12	
292	t79	TT	M	160	
293	s23	PM	M	9	
294	s130	PM	M	10	
295	s127	PM	M	10	
296	s80	PM	M	15	
297	s47	PM	M	15	
298	s44	PM	F	11	
299	s22	PM	M	14.5	trace
300	m90	PM	F	9	
301	m118	PM	M	16	
302	m	PM	M	17	
303	s119	PM	M	19	

304	p24	PM	M	16	
305	s32	SV-NBS		4.5	
306	p76	SV-NBS		4.5	
307	m18	SV-NBS		4	
308	s67	SV-NBS		4.5	
309	s73	SV-NBS		4.5	
PowellButteA	11/02				
310	s142	M	M	16.5	
311	s47	PM	F	15	
312	s41	PM	M	14.5	
313	s80	PM	M	18	
314	s107	PM	F	16	
315	s143	PM	M	17	
316	s8	PM	F	12.5	
317	m60	PM	M	16	
318	m7	PM	M	14	
319	m132	PM	F	17	
320	s117	PM	M	14	
321	s54	PM	M	15	
322	s83	PM	F	13	
323	s141	PM	M	16	
324	m95	PM	F	16	
325	p120	PM	M	17	
326	s122	PM	F	11	
327	p96	PM	M	15	
328	m45	PM-NBS	F	10	
329	s118	PM-NBS	F	11	
330	s11	PM-NBS	M	11	
331	m58	PM-NBS	M	17	
332	s26	E	M	75	
	m26	G-ESC			
	s89	E-ESC			
333	m141	PM	M	17	
334	s105	PM	F	11	
335	s107	PM	M	18	
336	s77	PM	F	17	
337	s39	PM-NBS	F	9	
338	t12	SC-NBS	M?	500+	
339	p96	SV-NBS		3.5	
340	s93	E	M	60	
341	s143	M-NBS	M?	13	
342	s20	PM-NBS	F	14	
343	s1	E-NBS	M?	70	
344	m96	PM	M	15	
345	s23	PM	M	15	
346	s47	PM	M	20.5	
347	s143	PM	M	14	
348	s139	E-NBS	M	70	

349	s94	SV-NBS		4	
PowellButteB	11/02				
350	s6	PM	F	14	
351	s47	PM	F	14	
352	s18	PM	F	15	
353	m97	PM	M	11.5	
354	s104	PM	F	10.5	
355	s112	PM	F	14	
356	s18	PM	M	19	
357	p115	PM	M	17	
358	s59	PM	F	12	
359	s112	PM	F	15	
360	s20	PM	M	15	
361	m60	PM-NBS	M	10.5	
362	p100	PM-NBS	M	13	
363	s32	PM	M	17	
364	s73	PM	F	11.5	
365	s104	PM	M	14	
366	s20	PM	M	13	
367	s118	PM	F	22.5	
368	s59	PM	F	15.5	
369	p60	PM	F	14	
370	m60	PM	M	18	
371	s57	PM	F	10	
Tryon Creek	12/02				
372	s29	PM	M	19	
373	s18	PM	F	12.5	
374	s108	PM	F	22	
375	s113	PM	F	19	
376	s117	PM	M	14	
377	s55	PM	F	17	
378	s57	PM	F	20	
379	s47	PM	F	14	
380	s45	PM	M	14	
381	m45	PM	F	25.5	
382	s95	PM	M	18	
383	s90	PM	F	8	
384	s142	PM	F	16.5	
385	s141	PM	F	16.5	
386	s78	PM	M	11	
387	s55	PM	F	18	
388	s47	PM	M	17	
389	s11	PM	F	20	
390	s119	PM	M	11	
391	s111	PM	M	15.5	
392	s108	PM	M	18	
393	s21	PM	M	15	
394	m103	PM	F	17.5	
395	t120	SN			

396	m90	PM-NBS	F	16	
397	s29	PM-NBS	F	11.5	
	s5	SV-ESC			
398	s94	PM	F	13	
399	p55	PM	F	7.5	
400	s45	PM	F	12	
401	s42	PM	M	7.5	
402	s70	PM	M	9	
403	s91	PM	F	13	trace
404	t84	SN	F		
405	p55	PM-NBS	F	6	
406	p55	PM-NBS	M	7	
407	s1	PM	M	13	
408	s7	PM	M	11	
409	s90	PM	M	10	
410	s94	PM	F	10	
411	m67	MO	F	15	
Oxbow	12/02				
412	s22	PM	M	13	
413	s120	PM	F	16	
414	s56	PM	M	13.5	
415	s103	PM	F	12	
416	s116	PM	F	16.5	
417	s68	PM	F	16	
418	s94	PM	F	13	
419	m59	PM	M	17	
420	s60	PM	F	14	
421	s108	PM	M	15	
422	s90	PM	M	19	
423	s80	PM	M	14	
424	s141	GS	F	94	
425	s137	GS	F	141	
426	p144	S-NBS		4	
427	s136	PM-NBS	M	12	
428	p60	S-NBS		5	
429	p43	PM-NBS	M	19	
430	p120	S-NBS		5	
431	p100	S-NBS		4.5	
432	p120	PM-NBS	M	14	
433	p120	PM-NBS	M	17.5	
434	p112	S-NBS		6	
435	p112	S-NBS		5	
436	p112	S-NBS		6	
	t84	Sp			
437	m66	PM	F	15	
438	s108	PM	M	12.5	
439	p76	PM	M	13	
440	s142	PM	M	15.5	
441	s82	PM	M	15	

442	s79	PM	M	17	
443	p127	S-NBS		5	
444	p7	S-NBS		5.5	
445	p16	S-NBS		6	
446	p16	S-NBS		7	
447	s92	PM-NBS	F	11	
448	s100	S-NBS		5	
449	p100	S-NBS		5	
450	p100	S-NBS		6	
451	p48	S-NBS		5	
452	p110	S-NBS		4.5	
453	p124	S-NBS		5	
454	p12	S-NBS		4	
455	p12	S-NBS		6	
456	p60	PM-NBS	M	16	
457	p60	S-NBS		6	
458	p60	S-NBS		5	
459	p96	S-NBS		6	
	t91	Sp			
460	m60	PM	F	17	
461	s108	PM	F	17	
462	p64	S-NBS		6	
463	p64	NG		11	
464	p7	MO	F	16	
465	p132	S-NBS		5	
466	p132	S-NBS		6.5	
467	p144	S-NBS		5	
468	p28	S-NBS		5	
469	p108	S-NBS		5.5	
470	p79	S-NBS		4	
471	p79	S-NBS		6	
472	p79	S-NBS		5.5	
473	p60	PM-NBS	M	14	
	t67	Sp			
474	s60	PM	M	16	
475	s144	PM	M	12	trace
476	p12	PM-NBS	F	11	
477	p12	S-NBS		5	
478	p12	S-NBS		6	
479	p144	S-NBS		6	
480	p144	S-NBS		6	
481	p127	S-NBS		5	
482	p76	S-NBS		5	
483	p100	S-NBS		5	
484	p96	S-NBS		5	
485	p103	S-NBS		5	
486	p32	S-NBS		5	
487	p108	S-NBS		5.5	
488	p108	S-NBS		5	

489	s113	PM-NBS	?		Half eaten
Forest Park	1.18.03				
490	s52	PM	M	11	
491	s60	PM	M	18	positive
492	s104	PM	M	15	
493	s117	PM	F	14	
494	s18	PM	F	11	
495	s33	PM	F	12	
496	s88	PM	M	14	
497	s120	PM	F	14.5	
498	s130	PM	F	11	
499	s126	PM	M	12	
500	s47	PM	M	9.5	
501	s33	PM	M	12	
502	s120	PM	M	11	
503	s24	PM	M	14	
504	s72	PM	F	14.5	
505	s73	PM	F	12	
506	s144	PM	F	13	
507	s82	PM	M	9.5	
508	s91	PM	M	12.5	
509	s113	PM	M	13	
510	s140	PM	F	13	
TRNWR	2.8.03				
511	s84	PM	M	15	
512	s82	PM	M	12	
513	m68	PM	F	14	
514	s68	PM	M	15	
515	s65	PM	M	12.5	
516	p103	PM	F	16	
517	s32	PM	M	16	
518	s45	PM	M	17	
519	s143	PM	M	17	
520	p84	PM	F	12.5	
521	s33	PM	F	12	
522	s131	PM	M	13	
TRNWR	2.9.03				
523	s32	PM	F	13	
524	s46	PM	M	14	
525	s143	PM	M	15	
526	s105	PM	M	16	
527	s72	PM	F	16	
528	s68	PM	F	14	
TRNWR	2.10.03				
529	s72	PM	F	13	
530	s129	GS	M?	82	
TRNWR	2.11.03				
531	s131	PM	F	12	
532	p139	S	?	5	

533	p119	S	?	4.5	
Powell Butte	2.15.03				
534	p60	PM	M	11	
535	s124	PM	M	13.5	
536	s131	PM	M	18	
537	s142	PM	M	14	
538	s143	PM	M	11	
P. B. 2.16.03					
539	s21	PM	M	13	
540	s20	PM	M	14	
541	s46	PM	M	13	
542	s78	PM	M	13	
543	s30	PM	M	13	
544	s108	PM	F	19	
545	s119	PM	F	15	
546	s116	PM	F	16	
547	s56	PM	F	17	
P.B. 2.17.03					
548	s143	PM	F	13	
549	s6	PM	M	14	
550	s104	PM	F	11	
551	p108	PM	M	13	
552	s108	PM	M	14	
553	s30	PM	F	17	
554	s90	S	?	4	
P.B. 2.18.03					
555	s120	PM	F	13	
556	m117	PM	M	14	
557	p31	S	?	4	
Tryon Creek	3.1.03				
558	s91	PM	F	14	
559	m31	PM	F	17	
560	s102	PM	M	19.5	
561	s108	PM	M	15	
562	s33	PM	M	16	
563	s103	PM	M	17	
564	s117	PM	M	16.5	
565	s114	PM	M	18	
566	s22	PM	M	16	
567	s10	PM	M	12.5	
568	s12	PM	F	12	
569	s6	PM	M	13	
570	m39	PM	M	14	
571	p60	PM	F	15	
572	s93	PM	M	15.5	
573	p24	PM	F	11	
574	s60	PM	M	20.5	
T.C. 3.2.03					

575	s125	PM	F	18	
576	s104	PM	F	16.5	
577	p139	PM	M	13.5	
578	s24	PM	M	20	
579	s84	PM	M	15	
580	s93	PM	M	15.5	
581	s58	PM	F	19	
582	s20	PM	F	14	
583	s107	PM	F	13.5	
584	s19	PM	M	13.5	
585	s119	PM	F	14	
586	s6	PM	M	13	
587	p60	PM	M	13	
588	m113	PM	F	14	
589	s118	PM	F	11	
590	s129	S	?	5	
591	s12	S	?	5	
T.C. 3.3.03					
592	s58	PM	M	19.5	
593	s71	PM	F	12	
594	s78	GS	M	131	
595	p76	PM	F	12	
596	m18	PM	F	13	
597	p103	S	?	7	
598	p103	S	?	8	
T.C. 3.4.03					
599	s12	MO	M	16	
600	s46	PM	?	?	
601	s71	PM	F	19	
602	p7	S	?	6	
Oxbow	3.22.03				
603	s117	PM	M	13	
604	s96	PM	M	16	
605	s37	PM	M	14	
606	s11	PM	M	16	
607	s2	PM	M	17	
608	s123	PM	F	12	
609	m23	TT	M	71	
610	s10	TT	F	65	
611	s72	TT	F	72	
612	p144	GS	M	180	
613	p79	S	?	4	
614	p79	MO	M	17	
615	?	S	?	4.5	
616	p76	S	?	4	
617	p76	MO	M	14	
	t84	SP			
	t120	SP			
Oxbow	3.23.03				

618	s11	PM	F	8	
619	s98	PM	M	15.5	
620	s56	PM	F	14	
621	p12	S	?	6.5	
622	p67	S	?	7	
623	p67	S	?	7	
624	s35	PM	F	14	
625	p4	MO	M	14.5	
626	p79	S	?	6.5	
627	p24	PM	F	13.5	
	T48	SP			
Oxbow 3.24.03					
628	s72	PM	M	13	
629	p24	S	?	5.5	
630	s69	TT	M	65	
631	s38	TT	M	85	
632	p28	S	?	5.5	
633	p60	S	?	5	
634	p31	S	?	7	
635	s119	TT	M	68	
636	s96	S	?	6.5	
	t103	SP			
Oxbow 3.25.03					
637	s119	S	?	6.5	
638	s143	TT	M	69	
639	p55	S	?	6	
640	p12	S	?	7.5	
641	s131	MO	M	13.5	
642	p92	S	?	6	
643	p108	S	?	7.5	
644	s65	TT	M	74	
Forest Park 4.12.03					
645	s130	PM	M	22	
646	s82	PM	F	13	
647	s10	PM	M	20.5	
648	p120	PM	M	20.5	
649	s53	PM	M	19	
650	s41	PM	F	13	
651	s19	PM	M	17	
652	s46	PM	M	20	
653	s21	PM	F	14	
654	p36	PM	M	15	
655	p84	ST	?	6	
F.P. 4.13.03					
656	m84	PM	M	17	
657	s92	PM	M	21	
658	s95	PM	F	14	

659	s71	PM	M	17	
660	p139	PM	M	19	
F.P. 4.14.03					
661	s95	PM	M	16	
662	s48	PM	F	14	
663	s126	PM	F	17	
664	s96	T	M	79	
665	s138	T	M	71	
666	p84	ST	?	5	
F.P. 4.15.03					
667	s82	T	M	82	
668	s87	T	M	73	
669	s83	T	M	75	
670	m4	T	M	71	
671	s60	T	F	76	
672	s71	T	M	72	
673	s77	T	M	70	
674	p96	ME	F	45	
675	p96	SV	?	6	
676	p84	ST	?	5	
677	m60	PM	M	16.5	
TRNWR 4.26.03					
678	m113	T	F	70	
679	s126	PM	M	16	
680	s20	PM	F	24	
681	s33	PM	M	19	
682	m20	PM	F	15	
683	m143	PM	M	24.5	
684	s141	PM	M	18	
685	s84	PM	M	22	
686	s34	PM	F	18	
687	s60	PM	F	20.5	
688	p55	ST	?	4.5	
689	S31	T	M	75	
690	S34	PM	M	22.5	
691	s114	PM	M	19	
692	s118	PM	M	21.5	
693	m120	PM	F	19	
694	s60	PM	M	19	
695	s55	PM	F	17	
696	s48	PM	M	19.5	
697	p28	ST	F	7	
698	p28	ST	?	4.5	
699	p112	ST	?	6	
700	m101	PM	F	16	
701	m131	PM	M	21	
702	p144	PM	M	19	
703	p72	ST	?	4	

704	p112	ST	?	8	
705	p112	ST	?	8	
706	p112	ST	?	7.5	
707	p112	ST	?	7.5	
708	p112	ST	?	7	
709	p112	ST	?	8	
710	p112	ST	?	10	
711	p112	ST	?	5	
712	m30	T	M	65	
713	s22	T	M	68	
714	s142	T	M	75	
715	s118	T	F	82	
716	s52	T	M	71	
717	t115	SN	M	>500	
718	p52	ST	?	6	
719	p112	ST	?	7.5	
720	m144	PM	F	17	
721	t60	T	F	68	
722	s52	T	M	66	
723	s117	T	M	63	
724	s116	T	F	75	
725	s68	T	F	76	
726	s69	T	M	76	
727	s18	T	M	72	
728	s32	T	M	71	
729	s12	T	M	74	
730	s115	PM	M	13	
731	p144	PM	M	15	
732	s9	PM	F	25	
733	s20	PM	M	21	
734	s106	PM	M	11	
735	s48	PM	F	19.5	
736	s30	ST	?	4.5	
737	p120	ST	?	4.5	
Powell Butte 5.10.03					
738	s47	PM	M	16.5	
739	s60	PM	F	13.5	
740	s50	PM	F	17.5	
741	s47	PM	M	16	
742	p40	ST?	?	4.5	
P.B. 5.11.03					
743	s72	PM	F	16	
744	s120	PM	F	17	
745	m104	PM	M	19.5	
746	s119	PM	M	23	
747	s44	PM	M	19.5	
748	s128	PM	F	15.5	
P.B. 5.12.03					

749	s130	PM	M	20.5	
750	s23	PM	M	22.5	
751	s31	PM	F	15.5	
752	s20	PM	-	-	
753	s120	PM	M	19	
754	s43	PM	F	16.5	
755	m66	TT	M	61	

P.B. 5.13.03

756	s108	PM	M	14	
757	s70	PM	M	19	
758	s9	PM	M	16	
759	s6	PM	F	14	
760	p4	ST	?	3.5	

Oxbow 5.17.03

761	m68	TT	M	79	
762	s80	TT	M	77	
763	s97	TT	M	88	
764	s66	PM	F	17.5	
765	m102	PM	F	19.5	
766	p108	PM	M	13	
767	s127	PM	M	17	
768	s142	PM	F	15.5	
769	p4	ST	?	4	
770	p48	SB	F	17.5	

Ox 5.18.03

771	s53	TT	M	80	
772	s89	TT	M	72	
773	s27	TT	M	78	
774	s45	PM	F	11	
775	p4	ST	?	4.5	
776	p12	ST	?	4.5	
777	p112	ST	?	4.5	

OX 5.19.03

778	p28	ST	?	3.5	
779	s65	TT	F	70	
780	s117	TT	F	74	
781	s74	TT	M	79	
782	s92	TT	M	69	
783	s127	TT	M	71	
784	s131	TT	F	73	
785	s24	TT	M	64	

OX 5.20.03

786	s44	TDm	F	203	
787	m114	TT	M	68	
788	m103	TT	M	82	
789	s63	TT	F	74	
790	s67	TT	M	80	
791	s141	GS	M	98	
792	s32	TT	M	72	

793	s17	TT	M	71	
794	s108	TT	M	80	
795	s66	PM	M	18	
796	m128	TT	M	63	
797	m124	TT	M	64	
798	s8	ST	?	5	
799	p12	ST	?	4	
800	p67	ST	?	4	
801	p64	ST	?	4	
802	p99	ST	?	5	
TRYON CREEK 5.24.03					
803	S12	PM	F	26.5	
804	S114	PM	M	18.5	
805	S113	PM	M	16.5	
806	S26	PM	M	22	
807	M36	PM	F	20.5	
808	S45	PM	F	19	
809	S24	PM	M	19.5	
810	S116	PM	M	24	
811	S48	PM	M	20	
812	S144	PM	M	23	
813	M13	PM	F	16	
814	S129	PM	M	10	EARS DAMAGED
815	S?	ST	?	4.7	DIT/NBS
816	P115	ST	?	6.8	DIT/NBS
817	?	ST	?	5.6	DIT/NBS not from today
818	S116	ST	?	5.4	NBS/REL
TC 5.25.03					
819	m106	MO	F	7.5	JUV
820	s108	PM	F	21	
821	m76	PM	M	21.5	
822	p67	PM	F	17.5	
836	s137	PM	M	19.5	
823	s23	PM	M	12.5	JUV
825	S8	PM	F	25	PREG?
826	S114	PM	F	21	
827	M48	PM	M	17.5	
828	S112	PM	M	17	JUV
829	P100	PM	M	14	
830	S47	PM	M	19	
830	S58	PM	F	21	
832	P91	SCAT	F?	101	NBS/REL
833	P84	ST	?	4.6	NBS/REL
834	P84	ST	?	4.0	DIT/NBS
835	P103	SCAT	?	119	DIT/NBS
824	S118	PM	M	19	
837	P52	SCAT	?	100	DIT/NBS

838	P124	MT	?	70	DIT/NBS
839	P136	MT	?	61	DIT/NBS
840	P96	PM	M	19.5	DIT/NBS
841	P76	ST	?	3.8	DIT/NBS
842	P19	ST	?	4.4	DIT/NBS
843	P72	ST	?	4.3	DIT/NBS
844	P108	SCAT	?	137	DIT/NBS
	P7	ST	?	?	ESC
TC 5.26.03					
845	S70	PM	F	24	
846	P112	PM	M	10.5	JUV
847	S120	PM	M	6.5	JUV
848	S108	PM	M	24	
849	S118	PM	F	14.5	
850	S35	PM	F	23	
851	S32	PM	M	21	
852	S27	PM	M	20	
853	S48	PM	F	20.5	
854	S130	PM	F	28	
855	M9	PM	M	18	
856	S68	PM	M	26	
857	S106	TT	M	70	REL
858	S94	TT	M	68	REL
859	M69	TT	F	81	REL
860	S101	ST	?	4.2	NBS/REL
861	P48	ST	?	4	DIT/NBS
862	P7	ST	?	4.6	DIT/NBS
863	P48	ST	?	4.2	NBS/REL
864	P115	ST	?	7.6	DIT/NBS
865	P84	ST	?	4.6	DIT/NBS
866	P144	PM	M	10.5	DIT/NBS
867	P144	ST	?	5.6	DIT/NBS
TC 5.27.03					
868	S10	PM	F	27.5	PREG?
869	S108	PM	F	21	
870	P144	PM	F	17.5	
871	S134	PM	M	17	SUBA
872	S129	PM	M	7	JUV
873	S101	PM	M	8	JUV
874	S27	PM	F	11.5	JUV
875	S70	TT	M	61	
876	S71	TT	M	73	
877	S65	TT	M	79	EARTAG R640
878	P19	SV	?	5.5	
879	P115	ST	?	4.1	
880	P16	ST	?	4.0	
881	P108	SCAT	F	81	
882	S91	TT	M	63	DIT/NBS
883	S61	ST	F	11	DIT/NBS/PREG?

884	S58	TT	M	69	DIT/NBS
	P91	SCAT	?	?	ESC

Forest Park
6.6.03

885	s24	PM	M	17.5	
886	p96	PM	M	19	
887	s80	PM	F	17	
888	s96	PM	F	22	
889	s11	PM	F	15	
890	s132	PM	M	16.5	
891	s107	PM	M	19.5	
892	s60	PM	M	21.5	
893	s116	PM	F	25	
894	m96	TT	F	80	

F.P. 6.7.03

895	s82	TT	F	79	
896	s106	TT	M	72	
897	s108	TT	M	62	
898	s117	TT	M	60	
899	s116	PM	M	17	
900	s60	PM	F	14.5	
901	s71	PM	M	12	
902	p60	ST	?	8	

F.P. 6.8.03

903	m75	TT	M	71	
904	s22	TT	M	70	
905	s120	TT	M	62	
906	s88	TT	M	72	
907	m114	TT	M	74	
908	s106	PM	F	18	
909	p60	ST	?	4	
910	p60	ST	?	5	
911	p40	SB	M	19.5	

F.P. 6.9.03

912	s74	TT	M	73	
913	s83	TT	M	68	
914	p60	ST	?	4.8	
915	p60	ST	?	4.2	
916	s20	ST	?	7	
197	m126	ST	?	4	
918	m118	TT	M	61	
919	m63	TT	F	66	
920	s75	TT	M	58	
921	s19	ST	?	4.4	

TRNWR
6.11.03

922	s82	PM	M	17	
923	s84	PM	M	17.5	
924	s32	PM	M	19	
925	s24	PM	F	19.5	positive

926	s107	PM	M	14	
927	m9	PM	M	14.5	
928	s128	PM	F	16	
929	s64	PM	M	13	
930	s12	PM	M	18	
931	s21	TT	F	74	
932	s56	TT	F	70	
933	s92	TT	M	75	
934	s72	TT	F	89	
935	s81	TT	F	85	
936	s118	TT	M	62	
937	p67	ST	?	3.8	
938	s67	ST	?	5.4	

TRNWR
6.12.03

939	s82	PM	M	19.5	
940	s12	PM	F	16.5	
941	s107	PM	F	14	
942	m9	PM	M	18	
943	m101	TT	M	80	
944	s119	TT	F	88	
945	s91	TT	F	84	
946	s93	ST	?	4.3	
947	s100	ST	?	?	
948	p4	ST	?	3.5	
949	p4	ST	?	2.8	
950	p84	PM	M	23	
951	p144	ST	?	5.4	
952	s9	ST	?	3.9	

TRNWR
6.13.03

953	s117	PM	M	18	
954	m34	TT	F	80	
955	s82	PM	M	13.5	
956	p88	ST	?	4.5	
957	p96	ST	?	6.2	
958	p144	ST	?	6	
959	s99	ST	?	3.6	
960	s107	ST	?	5.6	
961	s72	TT	F	82	
962	s81	ST	?	3.8	

TRNWR
6.14.03

963	S117	PM	M	17	
964	S80	ST	?	3.9	
965	S48	ST	?	4.2	
966	S10	TT	M	70	
967	S8	NG	?	11	
968	S120	ST	?	4.2	
969	S35	ST	?	4.2	

970	S96	ST	?	6	
971	S19	ST	?	4.3	
972	S115	TT	F	75	

POWELL BUTTE 6.28.03

973	s3	TT	F	81	
974	s66	PM	F	14.5	
975	s56	PM	F	16	
976	s129	PM	M	17.5	
977	s127	PM	F	19	
978	s131	PM	M	18.5	
979	s116	PM	M	17.5	
980	s8	PM	M	15.5	
981	s15	PM	M	15.5	
982	s23	PM	F	19.5	
983	s68	PM	M	15	
984	p112	ST	?	3.6	
985	p16	ST	?	3.8	

P.B. 6.29.03

986	s17	GS	F	156	
987	s18	PM	M	?	
988	s35	PM	M	13	
989	s47	PM	M	20	
990	s3	ST	?	5.5	

P.B. 6.30.03

991	s94	TT	F	71	
992	m57	PM	M	15.5	
993	s21	PM	F	18.5	
994	s22	PM	M	18.5	
995	s125	ST	?	2.8	
996	p64	ST	?	?	
997	p64	ST	?	3.0	

P.B. 7.1.03

998	s90	TT	M	31	
999	s95	GS	F	115	
1000	s104	ST	?	4.8	
1001	s32	M	F	20	
1002	s76	ST	?	6.2	
1003	s54	ST	?	3.0	
1004	s110	ST	?	4.7	
1005	s66	ST	?	5.3	

OXBOW 7.4.03

1006	s71	PM	F	19	
1007	s72	PM	F	16	
1008	m104	PM	F	26	positive
1009	s24	PM	M	16.5	positive
1010	s143	PM	F	8	
1011	s23	PM	F	18.5	
1012	s52	PM	M	8	

1013	s12	TT	M	79	
1014	s118	TT	F	84	
1015	s36	TT			
1016	s69	TT	F	74	
1017	s59	TT	F	89	
1018	s34	TT	M	72	
1019	p76	ST	?	2.0	
1020	p79	ST	?	4.2	
1021	p64	ST	?	3.7	
1022	p136	ST	?	4.5	
1023	p28	ST	?	4.2	
1024	p139	ST	?	4.4	
1025	p91	ST	?	4.6	
1026	p88	ST	?	4.0	
1027	p16	ST	?	4.3	
1028	s41	ST	?	4.5	
1029	s129	ST	?	4.5	
1030	p127	ST	?	4.8	
1031	p103	ST	?	4.2	
1032	p32	ST	?	4.0	
1033	p31	ST	?	4.2	
1034	p7	ST	?	3.9	
1035	m40	MO	F	15.5	
1036	p40	MO	M	21	
1037	p40	MO	M	18.5	
1038	p76	ST	?	4.0	
1039	s10	ST	?	4.2	
1040	p132	ST	?	4.6	
1041	p144	ST	ESCAPED		

OX 7.5.03

1042	s68	TT	M	62	
1043	s124	TT	M	32	
1044	s27	TT	M	30	
1045	s112	TT	M	68	
1046	m45	TT	M	72	
1047	m8	TT	M	37	
1048	s103	TT	M	61	
1049	s115	TT	F	74	
1050	m115	MO	F	13	
1051	s79	PM	F	17	
1052	s81	PM	M	14.5	
1053	s127	PM	M	16	
1054	s131	PM	M	15	
1055	s83	TT	M	70	
1056	p115	ST	?	7.2	
1057	p120	ST	?	4.5	

1058	p132	ST	?	3.5	
1059	p100	ST	?	4.4	
1060	p67	ST	?	4.3	
1061	p96	NG	?	8.1	
1062	m121	TT	M	31	

OX 7.6.03

1063	s108	PM	F	23.5	
1064	s96	PM	F	18	
1065	s1	PM	M	15	
1066	s72	TT	F	72	
1067	s44	TT	M	67	
1068	s18	TT	M	70	
1069	s47	TT	F	83	
1070	s15	TT	M	33	
1071	m110	TT	F	77	
1072	s27	TT	M	31	
1073	s13	TT	M	30	
1074	s119	TT	F	ESC	
1075	s61	TT	M	70	
1076	m115	MO	?		
1077	p67	SB	M	14	
1078	s143	SV	?	ESC	
1079	p79	SV	?	7.1	
1080	s144	ST	?	4.5	

OX 7.7.03

1081	p91	PM	M	7.5	
1082	s19	TT	M	68	
1083	s26	TT	M	30	
1084	s120	TT	F	80	
1085	s50	TT	M	30	
1086	p144	NG	?	7.3	
1087	p144	NG	?	5.9	
1088	p67	ST	?	3.9	
1089	p67	ST	?	3.3	
1090	s46	SV	?	5.3	
1091	s17	SV	?	4.5	
1092	p12	ST	?	4.1	
1093	p108	ST	?	4.7	
1094	p132	ST	?	4.2	
1095	p132	ST	?	0.6	
1096	p37	ST	?	3.8	
1097	s114	ST	?	4.0	
1098	p52	ST	?	3.5	
1099	p24	ST	?	4.3	
1100	s139	ME	M	31	
1101	m29	TT	M	31	
1102	s55	SV	?	4.6	
1103	s56	TT	M	64	

Tryon Creek 7.11.03 (skip 1104-1109)

1110	s95	TT	F	72	
1111	s94	TT	F	74	
1112	m105	TT	M	71	
1113	s130	TT	M	78	
1114	p12	PM	M	15.5	
1115	s143	PM	M	20	
1116	s20	PM	F	7.5	
1117	m58	PM	M	19	
1118	s59	PM	F	16.5	
1119	s24	PM	F	20.5	
1120	s64	PM	M	19.5	
1121	s44	PM	M	20.5	
1122	s46	PM	F	19.5	positive
1123	s114	PM	M	13.5	
1124	s108	PM	M	16	
1125	s106	PM	M	15	
1126	p100	PM	F	15	
1127	s107	PM	F	18	
1128	s11	PM	F	15	
1129	p48	PM	F	15	
1130	s68	PM	M	18.5	
1131	p19	ST	?	4.3	
1132	p118	ST	?	4.2	
1133	s131	ST	?	5	
1134	p40	ST	?	4.1	
1135	s144	ST	?	4	
1136	s118	ST	?	4.3	
1137	p144	ST	?	4.8	
1138	p19	ST	?	4.2	
1139	s32	SV	?	9.6	
1140	p76	ST	?	3.4	
1141	s136	ST	?	4.1	
1142	p124	ST	?	4.2	
1143	p127	ST	?	3.9	
1144	p88	ST	?	5.1	
1145	p88	ST	?	4.3	
1146	t60	TT	M	69	

T.C. 7.12.03

1147	m94	TT	M	69	
1148	s96	TT	M	70	
1149	s115	TT	F	71	
1150	s94	TT	F	68	
1151	s72	PM	F	16	
1152	m108	PM	M	16	
1153	s71	PM	F	20	
1154	s106	PM	M	23.5	
1155	m113	PM	F	22	
1156	m132	PM	M	14.5	
1157	s24	PM	M	18	

1158	s11	PM	F	6.5	
1159	s33	PM	M	14.5	
1160	s95	ST	?	5	
1161	p118	ST	?	3.8	
1162	p19	SV	?	5	
1163	p55	ST	?	4	
1164	s112	SV	?	7.9	
1165	p24	ST	?	3.8	
1166	s87	ST	?	4.5	
1167	p7	ST	?	4.5	
1168	p7	NG	?	8.6	
1169	p103	ST	?	3.9	
1170	s129	ST	?	5.2	
1171	p119	ST	?	4	
1172	p119	ST	?	3.9	
1173	s143	SV	?	8.5	
1174	p144	ST	?	4.3	
1175	s69	ST	?	4	
1176	s57	ST	?	4	
1177	s142	PM	F	18	

T.C. 7.13.03

1178	m107	TT	M	62	
1179	s11	PM	F	18.5	
1180	s107	PM	M	19.5	
1181	s108	PM	F	15	
1182	s33	PM	M	8	
1183	s113	PM	M	16	
1184	s23	PM	M	20	
1185	s58	PM	F	9	
1186	s72	PM	M	17	
1187	p40	SV	?	7.4	
1188	p144	ST	?	4.5	
1189	s144	ST	?	4.2	
1190	s124	ST	?	1.6	
1191	s20	SV	?	7.5	
1192	s96	TT	F	61	

T.C. 7.14.03

1193	p60	PM	M	16	
1194	p12	ST	?	3.9	
1195	p64	ST	?	3.9	
1196	p64	ST	?	1.1	
1197	s11	ST	?	4.4	
1198	s140	ST	?	4.3	
1199	p144	ST	?	?	
1200	s108	SV	?	4.8	
1201	s127	ST	?	4.9	
1202	s127	ST	?	5.5	
1203	p112	ST	?	4.0	
1204	p112	ST	?	4.6	

1205	p112	ST	?	2.3	

FOREST PARK 7.16.03

1206	p60	PM	F	24.5	
1207	p72	PM	M	16.5	
1208	s72	PM	F	12.5	
1209	s87	PM	F	19.5	
1210	s95	PM	M	22	
1211	s116	PM	M	20	
1212	s60	PM	M	20	
1213	s82	PM	F	13	
1214	p24	PM	M	15	
1215	s133	PM	M	17	
1216	m107	TT	M	60	
1217	s83	ST	?	4.2	
1218	s34	ST	?	?	

F.P. 7.17.03

1219	s131	PM	M	15	
1220	s92	PM	M	18.5	
1221	s94	PM	M	16.5	
1222	s72	PM	F	12	
1223	p36	ST	?	4.2	
1224	p60	ST	?	7	
1225	p54	SV	?	6.2	
1226	p12	ST	?	4.5	
1227	p12	ST	?	4.3	
1228	s10	SV	?	5.9	
1229	p96	SV	?	5.6	
1230	s86	ST	?	4.0	
1231	s47	ST	?	3.8	
1232	m119	TT	M	60	

F.P. 7.18.03

1233	s46	PM	M	15	
1234	s143	PM	M	15	
1235	s119	PM	M	13.5	
1236	s82	PM	M	18	
1237	s72	PM	F	9	
1238	s44	PM	F	17	
1239	s108	TT	F	79	
1240	s83	TT	M	60	
1241	s144	ST	?	4.5	
1242	s6	ST	?	4	
1243	s114	ST	?	4.2	
1244	p55	ST	?	3.9	
1245	m73	TT	M	71	

F.P. 7.19.03

1246	m72	PM	M	16.5	
1247	s21	PM	M	18	
1248	s132	TT	F	81	
1249	s72	TT	M	60	

1250	s82	TT	F	89	
1251	s49	TT	M	56	
1252	s143	PM	F	13	
1253	s32	ST	?	4.5	
1254	s95	SV	?	6.1	
1255	p96	S?	?	?	
1256	s126	ST	?	4.5	
1257	p96	ST	?	3.1	
1258	s139	ST	?	0.4	
1259	s23	ST	?	5.2	
1260	s18	SV	?	4	
1261	p31	ST	?	4.5	
1262	p84	ST	?	3.9	
1263	s54	SV	?	4	

TRNWR 8.5.03 (1264-1289 SKIPPED)

1290	s132	PM	F	18	
1291	s144	PM	F	18	
1292	s125	PM	M	16	
1293	s141	PM	F	18	
1294	s116	PM	F	23	
1295	s117	PM	M	19	
1296	s101	PM	F	22.5	
1297	s92	PM	F	20.5	
1298	s77	PM	M	18	
1299	s83	PM	M	13	
1300	s72	PM	?	?	
1301	s65	PM	F	21	
1302	s53	PM	M	14	
1303	m12	TT	M	61	
1304	p67	ZT	M	8	
1305	t31	DV	M	220	
1306	p79	ST	?	4.6	
1307	p79	ST	?	4	
1308	p79	ST	?	?	
1309	p67	ST	?	3.4	
1310	s140	ST	?	4.3	
1311	p139	ST	?	4.9	
1312	s22	ST	?	4	
1313	s18	ST	?	4	
1314	m88	PM	M	18.5	
1315	p28	PM	F	24.5	
1316	p12	PM	F	22	

TRNWR 8.6.03

1317	p84	PM	F	23	
1318	s56	PM	M	16	
1319	s78	PM	M	7	
1320	s78	PM	F	6.5	
1321	s78	PM	M	6.5	
1322	p72	PM	M	10	

1323	s72	PM	F	22	
1324	p60	ZT	M	8	
1325	s82	TT	F	62	
1326	s91	TT	M	62	
1327	s65	NG	?	8.7	
1328	s119	ST	?	4	
1329	p79	ST	?	4.5	
1330	p84	PM	?	?	

TRNWR 8.7.03

1331	p84	MO	M	21.5	
1332	s82	PM	F	30	
1333	s67	PM	F	15	
1334	s69	PM	F	11.5	
1335	m28	PM	M	18	positive
1336	s10	PM	M	17.5	
1337	s35	PM	M	5.5	
1338	s101	PM	M	9.5	
1339	s141	PM	M	15.5	
1340	p79	ST	?	4.6	
1341	p79	ST	?	4.8	
1342	m24	TT	M	62	
1343	s106	NG	?	8.5	
1344	s116	ST	?	4.2	
1345	s142	ST	?	4.5	
1346	s80	NG	?	7.9	

TRNWR 8.8.03

1347	m88	PM	M	13	
1348	s129	PM	M	13.5	
1349	s89	PM	M	17	
1350	s44	PM	F	15.5	
1351	s69	PM	M	16	positive
1352	s128	PM	F	?	
1353	s49	DV	M	?	
1354	p88	MO	M	36	
1355	m123	MO	M	28	
1356	p36	MO	F	48	
1357	m39	ST	?	5.	
1358	s47	ST	?	4	
1359	s58	ST	?	3.9	
1360	s11	ST	?	5.2	
1361	s132	ST	?	3.9	
1362	p103	ST	?	5.	
1363	p115	ST	?	4.8	
1364	p120	ST	?	6	
1365	p120	PM	M	21.5	
1366	p88	PM	F	11	
1367	p100	ST	?	6	

POWELL BUTTE 8.19.03

1368	P84	PM	M	14.5	

1369	S78	PM	M	14	
1370	P144	PM	M	19	
1371	S118	PM	M	13.5	
1372	S98	SV	?	3	
1373	P72	ST	?	4	

POWELL BUTTE 8.20.03

1374	S15	PM	F	12	
1375	T96	DV	?	?	

P.B. 8.21.03

1376	S15	PM	M	14	
1377	S134	PM	M	12	
1378	S96	PM	M	10.5	
1379	P144	PM	F	15	
1380	P144	PM	F	12	
1381	S115	SV	?	4.7	
1382	S126	SV	?	3	

P.B. 8.22.03

1383	s144	PM	M	16	
1384	s139	PM	M	12	
1385	s127	PM	F	15	
1386	s83	MO	F	15.5	
1387	s134	MO	F	17.5	
1388	s75	GS	F	130	
1389	s39	ST	?	3.2	

TILLY JANE 9.2.03

1390	s90	PM	M	18	
1391	p28	MO?	F	23.5	

TILLY JANE 9.3, 9.4.03 - NA

TJ 9.5.03

1392	m36	PM	M	10.3	
1393	s7	PM	F	19.2	
1394	s141	PM	M	10.0	
1395	p139	PM	F	13.2	
1396	t60	TA	M	70	
1397	s81	GS	F	154	

OXBOW 9.9.03

1398	p12	PM	M	6	
1399	s12	PM	F	9	
1400	s115	PM	M	11	
1401	s28	PM	F	6	
1402	m108	PM	F	10	
1403	s93	PM	F	7	
1404	s71	PM	F	10.5	
1405	s69	PM	M	13	
1406	s63	PM	M	9	
1407	m80	TT	M	79	
1408	s132	TT	M	72	
1409	s144	TT	F	62	
1410	p7	SV	?	8	

1411	p132	ST	?	4.5	
1412	p100	SV	?	5.4	
1413	p103	ST	?	4.9	
1414	p120	PM	F	6.4	
1415	p124	ST	?	5.2	
1416	p67	ST	?	3.9	
1417	p64	ST	?	3.9	
1418	p28	NG	?	6.9	
1419	p76	SV	?	7.2	
1420	p76	SV	?	5.8	
1421	m33	GS	M	141	
1422	m11	TT	M	71	
1423	s91				escaped
1424	s127				escaped

OX 9.10.03

1425	s94	PM	M	8.5	
1426	s84	PM	M	6	
1427	p108	PM	F	9.5	
1428	s137	PM	M	9	
1429	s38	TT	M	81	
1430	s58	TT	F	73	
1431	s68	TT			
1432	s130	MO	F	23	
1433	p132	MO	F	9.5	
1434	s126	NG	?	8	
1435	p40	MO	F	20.5	
1436	s11	NG	?	7.5	
1437	s23	NG	?	9.5	
1438	p144	ST	?	7.5	
1439	p144	ST	?	6.5	

OX 9.11.03

1440	s130	MO	F	10	
1441	p84	PM	F	6.5	
1442	s84	PM	F	13.5	
1443	s12	PM	M	17.5	
1444	s100	TT	M	72	
1445	s86	TT	F	42	
1446	s114	TT	F	40	
1447	s79	NG	?	10	
1448	s67	NG	?	9	
1449	p64	NG	?	9.5	
1450	p60	SV	?	5.6	
1451	p67	ST	?	4.0	
1452	p67	NG	?	6.5	
1453	s23	NG	?	8.2	
1454	p79	ST	?	6.7	
1455	s47	NG	?	7.6	
1456	s118	NG	?	9.6	
1457	m119	TT	F	59	

1458	m91	TT	F	67	
1459	m50	TT	M	59	

OX 9.12.03

1460	s106	TT	M	79	
1461	s80	TT	F	78	
1462	s24	MO	F	19.5	
1463	s30	MO	F	20.5	
1464	p120	PM	F	5.5	
1465	s72	NG	M ?	7.5	
1466	s10	SV	?	4.3	
1467	s118	NG	?	8.6	
1468	s83	NG	?	7.4	
1469	s96	TT	M	58	
1470	m130	TT	M	64	

TRYON CREEK 9.16.03

1471	s129	PM	F	20	
1472	s68	PM	F	?	
1473	s58	PM	M	26	
1474	s59	PM	F	24.5	
1475	s70	PM	M	14.5	
1476	s89	PM	M	18.5	
1477	s106	PM	F	18	
1478	s118	PM	F	13.5	
1479	s140	PM	M	15	
1480	s125	PM	M	21.5	
1481	m120	PM	M	16	
1482	p28	ST	?	5.0	
1483	s11	ST	?	5.4	
1484	s102	ST	?	4.4	
1485	m117	PM	M	17	
1486	p79	ST	?	5.2	
1487	p144	ST	?	4.5	
1488	s142	SV	?	5.2	

TC 9.17.03

1489	s11	PM	F	15.5	
1490	s130	PM	M	14.5	
1491	p144	PM	M	16.5	
1492	m128	PM	M	14.5	
1493	s140	PM	M	16	
1494	m47	PM	M	18	
1495	s26	PM	F	17	
1496	s106	PM	M	14	
1497	s107	PM	F	17	
1498	s96	PM	F	26	
1499	s70	PM	F	19	
1500	p19	ST	?	4.9	
1501	p4	ST	?	4.5	
1502	s93	ST	?	4.2	

1503	p55	SV	?	5.3	
1504	p144	ST	?	5.4	
1505	p144	ST	?	5.8	

TC 9.18.03

1506	s120	PM	M	23.5	
1507	s107	PM	F	10	
1508	s47	PM	F	14	
1509	p108	PM	F	21.5	
1510	s129	PM	M	17.5	
1511	s144	PM	M	10	
1512	s22	PM	F	19.5	
1513	p19	MO	F	11	
1514	p60	MO	?	?	
1515	s143	PM	F	11	
1516	s11	ST	?	5.6	
1517	s79	ST	?	4.7	

TC 9.19.03

1518	s11	PM	M	19.5	
1519	s119	ST	?	4.0	
1520	m50	ME	F?	70	
1521	p24	SV	?	4.3	
1522	s96	ST	?	4.4	

FOREST PARK 9.23.03

1523	p144	PM	M	16	positive
1524	s142	PM	M	17.5	positive
1525	s143	PM	M	15	
1526	p126	PM	M	15.5	
1527	s112	PM	F	16.5	
1528	p24	PM	F	15.5	
1529	p55	PM	F	15	
1530	m78	PM	F	22.5	

FP 9.24.03

1531	s127	PM	F	22	
1532	m105	PM	M	15	
1533	m7	PM	M	16	
1534	s35	PM	M	14.5	
1535	m60	PM	F	18	
1536	t43	TD	M	?	
1537	m84	TT	M	66	
1538	t96	TD	F	220	
1539	p48	ST	?	4.2	
1540	m22	ME	F	34	
1541	s43	SV	?	?	

FP 9.25.03

1542	s35	PM	M	15	
1543	s118	PM	M	16.5	
1544	s135	MO	F	16	
1545	t43	TD	F	?	

FP 9.26.03

1546	s96	PM	M	17.5	
1547	m95	PM	F	13.5	
1548	s144	PM	F	14	
1549	s3	MO	M	6.5	
1550	s143	PM	M	16.5	positive
1551	s106	PM	F	11.5	
1552	s115	PM	M	13	
1553	s107	PM	M	18.5	
1554	s138	ST	?	5.0	
1555	s11	PM	F	16	
1556	s82	ST	?	4.4	
1557	s5	MO	M	5.6	
1558	p136	SV	?	3.1	
1559	s133	PM	M	15	

TRNWR 9.30.03

1560	s10	PM	M	15	
1561	s127	PM	F	15.5	
1562	s131	PM	M	11.5	
1563	s130	PM	M	14.5	
1564	s128	PM	M	15	
1565	p76	PM	F	16.5	
1566	s82	PM	F	19	
1567	s92	PM	M	19	
1568	s45	PM	M	16.5	
1569	s31	PM	M	18.5	
1570	s106	PM	M	13.5	
1571	s23	PM	F	17.5	
1572	p28	PM	F	15	
1573	s117	PM	M	15.5	
1574	s101	PM	F	18.5	
1575	s118	PM	F	21.5	
1576	s51	PM	F	19	
1577	s9	PM	F	15.5	
1578	p91	PM	M	9	
1579	s80	SV	?	3.5	
1580	p144	ST	?	4.6	
1581	s140	NG	F	8.5	
1582	s129	ST	?	4.5	
1583	t120	MM	?	?	

TRNWR 10.1.03

1584	s117	PM	M	14	
1585	s46	PM	F	20.5	
1586	p76	PM	F	6	
1587	s113	PM	M	17	
1588	s48	PM	M	15	
1589	s131	PM	F	13	
1590	s45	PM	F	19	
1591	s35	PM	F	15	
1592	s68	PM	M	19.5	

1593	s70	PM	F	18	
1594	m69	PM	F	18	
1595	m70	PM	M	20	
1596	s105	ST	?	4.7	
1597	s27	ST	?	4.0	
1598	s142	NG	M ?	7.5	
1599	s11	SV	?	4.6	
1600	s32	PM	F	13.5	
1601	p7	PM	M	21	
1602	p7	PM	F	17.5	
1603	p7	PM	F	21.5	
TRNWR 10.2.03					
1604	s80	PM	F	18.5	
1605	s21	PM	M	16.5	
1606	s45	PM	M	16.5	
1607	s32	PM	M	13	
1608	s113	PM	F	15	
1609	m23	PM	M	13.5	
1610	s120	PM	M	17	
1611	s12	PM	F	16	
1612	m42	PM	F	17	
1613	p72	PM	M	15.5	
1614	p127	PM	F	14	
1615	s25	PM	M	14.5	
1616	p48	PM	M	13	
1617	s74	PM	M	13	
1618	s141	PM	M	11	
1619	s144	PM	F	6.5	
1620	p40	PM	F	5	
1621	p40	PM	M	5	
1622	s96	SV	?	4.0	
1623	s11	NG	M ?	9	
1624	p43	ST	?	5	
1625	s35	ST	?	4.6	
1626	s84	ST	?	3.8	
1627	t72	DV	?	?	
TRNWR 10.3.03					
1628	p107	PM	F	11.5	
1629	p102	PM	F	19	
1630	m30	PM	M	12	
1631	s141	PM	F	11	
1632	s16	PM	M	6	
1633	s101	PM	M	16.5	
1634	s103	PM	F	9	
1635	s96	PM	M	19	
1636	s33	PM	F	12	
1637	s84	PM	M	19.5	positive
1638	s116	PM	F	18.5	positive

1639	s120	PM	F	14	
1640	s113	PM			
1641	s115	PM	F	16	
1642	s87	PM	F	7	
1643	s35	ST		4.5	
1644	s31	PM	M	12.5	
1645	t7	TT	M	62	

Powell Butte 10.14.03

1646	s94	PM	M	17	
1647	m116	PM	F	19	
1648	s78	PM	F	20	
1649	s69	PM	M	15.5	
1650	s8	PM	F	23	
1651	s106	MO	F	15.5	
1652	s56	MO	F	17	
1653	s3	MO	F	21	
1654	s111	MO	M	17	
1655	s45	SV	?	4.0	
1656	p40	SV	?	4.2	
1657	p120	ST	?	5.6	
1658	s126	SV	?	4.0	

P.B. 10.15.03

1659	s129	PM	F	21.5	
1660	s84	PM	F	13.5	
1661	s23	PM	F	20.5	
1662	s104	MO	F	13	
1663	s2	MO	M	18.5	
1664	s119	SV	?	4.3	
1665	s21	PM	?	?	
1666	s18	S?	?	?	

P.B. 10.16.03

1667	s41	PM	F	20	
1668	p28	PM	F	12	
1669	s28	PM	M	18	positive
1670	s47	PM	M	17	
1671	s110	PM	M	19	
1672	s18	PM	F	9	
1673	s20	PM	F	18	
1674	s4	PM	F	8	
1675	s78	PM	M	18	
1676	s137	PM	M	20	
1677	m141	PM	F	26	
1678	s84	MO	F	17	
1679	s112	MO	M	11	
1680	s56	MO	M	13	
1681	s55	MO	M	13	
1682	s134	MO	M	13	
1683	s126	MO	M	17.5	
1684	s106	MO	M	16	

1685	s144	PM	F	17	
1686	s3	MO	F	19	
1687	s104	MO	M	15	
1688	p28	PM	M	21	
1689	p124	PM	M	17	
1690	t144	DV	?	?	

P.B. 10.17.03

1691	s47	PM	F	?	
1692	s44	PM	M	14.5	
1693	s70	PM	M	17	
1694	s23	PM	M	17	
1695	s115	GS	M	85	positive
1696	p3	PM	M	11.5	
1697	s7	PM	M	22	
1698	s118	PM	M	16.5	positive
1699	p88	MO	M	16	
1700	p91	MO	M	13	
1701	p108	MO	M	13	
1702	s105	MO	M	18	
1703	s122	MO	M	14	
1704	s124	MO	M	14	
1705	s79	MO	M	13	
1706	s85	MO	M	14	
1707	s76	MO	M	11	
1708	p7	PM	M	7	
1709	s56	MO	M	13	
1710	s4	SV	?	4.5	

OXBOW 10.21.03

1711	s65	PM	M	13.5	
1712	s24	PM	F	18.5	
1713	p36	PM	M	13.5	
1714	s7	PM	M	15.5	positive
1715	s88	PM	M	15	positive
1716	m24	TT	F	71	
1717	m75	TT	M	70	
1718	s129	TT	M	79	
1719	s118	TT	M	69	
1720	s4	ST	?	5.0	
1721	s19	ST	?	3.8	

OX 10.22.03

1722	s59	PM	F	16.5	
1723	s24	PM	M	13	
1724	m126	PM	F	20	positive
1725	s44	PM	M	18	
1726	s22	TT	M	74	
1727	s80	TT	M	71	
1728	s107	TT	M	71	
1729	s8	MO	F	13	
1730	s130	MO	M	20	

1731	p112	ST	?	3.8	
Oxbow 10.23.03					
1732	s85	PM	F	22.5	
1733	s79	PM	M	17	
1734	s72	PM	M	14	
1735	s12	PM	M	13	
1736	s90	PM	F	16.5	
1737	s91	TT	M	66	
1738	s144	TT			
1739	s114	TT	F	71	
1740	s130	MO	M	18	
1741	p16	SB	?	16.5	
1742	s82	ST	?	5.4	
1743	s119	ST	?	5.2	
Oxbow 10.24.03					
1744	s33	GS	F	150	
1745	m106	TT	M	68	
1746	m51	TT	F	62	
1747	s112	TT	F	70	
1748	s8	SV	?	7.0	
1749	s59	ST	?	6.0	
TRYON CREEK 10.28.03					
1750	s30	PM	F	20	
1751	s6	PM	M	21	
T.C. 10.29.03					
1752	s60	PM	F	18.5	
1753	s116	PM	F	18	
1754	s102	MO	M	12.5	
1755	s23	ST	?	5.2	
1756	p14	ST	?	6.0	
T.C. 10.30.03					
1757	s91	PM	F	20	
1758	s47	PM	M	14	
1759	s99	PM	F	16.5	
1760	s41	PM	F	8.4	
1761	s57	PM	F	18	
1762	s19	PM	M	17	
1763	s4	MO	F	16	
1764	s83	SV	?	6	
1765	m90	PM	M	17	
1766	s84	PM	F	18	
1767	s118	PM	F	17	
1768	s60	PM	M	17.5	
1769	s49	PM	F	19	
1770	s23	SV	?	7	
T.C. 10.31.03					
1771	s92	PM	M	18.5	
1772	s40	PM	F	20	
1773	s118	PM	M	10	

1774	p4	MO	M	16	
1775	s120	PM	M	16.5	
1776	s75	ST	?	5.5	

FOREST PARK 11.4.03

1777	s71	PM	M	20.5	
1778	p24	ST	?	3.8	
1779	s119	ST	?	4.3	

F.P. 11.5.03

1780	s82	PM	M	19	
1781	s40	PM	F	17.5	
1782	s130	PM	F	19	
1783	m55	PM	F	24	positive
1784	s96	PM	M	20	
1785	s117	PM	F	16	
1786	s55	ST	?	3.7	
1787	p60	SV	?	5.0	
1788	p24	SV	?	4.6	
1789	s22	ST	?	4.0	

F.P. 11.6.03

1790	s119	PM	M	19.5	
1791	m71	PM	M	19	
1792	s112	PM	M	16	
1793	s104	SV	?	5.0	
1794	s90	SV	?	?	

F.P. 11.7.03

1795	p96	PM	F	22.5	
1796	p40	PM	M	17	
1797	m143	PM	M	26	positive
1798	s106	PM	M	15.5	
1799	s112	PM	M	21.5	
1800	s18	PM	M	19.5	
1801	p36	ST	?	3.8	
1802	s12	PM	M	15	
1803	s4	ST	?	3.9	
1804	s140	ST	?	4.5	
1805	?	ST	?	4	

TUALATIN RIVER NWR 11.11.03

1806	s67	PM	M	16	
1807	s0	PM	M	12	
1808	s117	PM	F	14	
1809	s18	PM	F	16.5	
1810	s65	PM	M	18	
1811	s106	PM	M	13	
1812	s119	ST	?	3.8	
1813	s80	SV	?	?	
1814	p48	ST	?	5.5	

TRNWR 11.12.03

1815	s113	PM	M	15	

1816	s102	PM	M	21	
1817	s67	PM	F	12.5	
1818	s66	PM	M	15	
1819	s99	PM	M	13	
1820	s18	PM	M	14	
1821	s60	ST	?	4.2	
1822	t31	DV	?	?	

TRNWR 11.13.03

1823	s32	PM	M	15	
1824	s83	PM	M	18	
1825	s23	PM	M	15	
1826	s102	PM	F	11	
1827	m53	PM	F	16	
1828	t31	DV	M	?	
1829	s107	SV	?	3.5	
1830	s96	SV	?	3.5	

TRNWR 11.14.03

1831	m81	PM	F	14	
1832	m141	PM	M	17	
1833	s92	PM	F	13	
1834	s96	PM	M	20	
1835	s32	PM	M	16	
1836	s107	PM	M	16	
1837	s68	PM	M	12	
1838	s33	ST	?	4.8	

POWELL BUTTE 11.18.03

1839	s21	PM	F	22.5	
1840	s105	PM	M	18	
1841	s31	PM	F	18.5	
1842	s6	PM	F	15	
1843	s103	MO	F	15	
1844	s139	GS	F	140	
1845	m41	GS	M	65	
1846	p31	ST	?	3.5	

P.B. 11.19.03

1847	p92	PM	F	14	
1848	s102	MO	F	14	
1849	s111	GS	F	132	

P.B. 11.20.03

1850	m108	PM	F	22	
1851	s92	GS	M	132	
1852	s0	GS	M	74	

P.B. 11.21.03

1853	s83	GS	M	92	
1854	s110	SV	?	3.5	

OXBOW 12.2.03

1855	s96	PM	M	18	
1856	s24	PM	F	16	

1857	s48	PM	F	19	
1858	s21	PM	M	18	
1859	s117	PM	M	17	
1860	s51	PM	M	16	
1861	s130	PM	M	18	
1862	s129	PM	F	13	
1863	s136	MO	F	18	
1864	p40	MO	F	19	
1865	p19	ST	?	4.4	

OX 12.3.03

1866	m88	PM	F	23	
1867	s106	PM	F	18	
1868	s134	PM	M	15	
1869	s129	PM	M	18	
1870	s131	PM	M	17.5	
1871	s119	PM	F	17.5	
1872	s31	PM	M	16.5	
1873	s44	PM	F	20.5	
1874	s98	PM	M	19	
1875	s80	GS	M	110	
1876	s141	GS	M		
1877	s10	GS	F	150	
1878	p120	PM	M	16	
1879	p19	SV	?	5.4	

OX 12.4.03

1880	s93	PM	F	17	
1881	s96	PM	M	15.5	
1882	s47	GS	F	140	
1883	s33	GS	F	110	
1884	s44	MO	F	16	
1885	s22	PM	F	16	
1886	s28	PM	F	11.5	
1887	p36	PM	M	16	
1888	p103	ST	?	4.6	
1889	p79	SV	?	5.0	

OX 12.5.03

1890	s12	PM	F	20	
1891	s57	PM	F	11	
1892	s123	PM	M	19.5	
1893	s107	PM	M	18.5	
1894	p100	SB	?	14	
1895	s119	PM	F	14.5	
1896	s64	ST	?	6.0	
1897	p12	SV	?	4.2	
1898	p89	ST	?	5.3	
1899	m22	SV	?	5.4	

Tryon Creek 12.9.03

1900	s78	PM	F	19	
1901	s83	PM	F	17	

1902	s105	PM	F	25	
1903	s42	PM	M	21	
1904	p91	PM	M	18	
1905	p91	PM	M	20.5	
1906	s116	PM	F	23	
1907	s95	PM	F	24.5	
1908	m93	PM	M	20	

Tryon Creek 12.10.03

1909	s83	PM	F	23	
1910	s91	PM	F	21	
1911	s119	PM	F	21	
1912	s5	PM	M	18.5	
1913	s82	PM	M	15	

TC 12.11.03

1914	s15	PM	F	19.5	
1915	s112	PM	F	19	
1916	s117	PM	M	20	
1917	s5	PM	M	21.5	
1918	p91	PM	F	17	
1919	p36	PM	M	23	
1920	m30	PM	F	19	

TC12.12.03

1921	s117	PM	F	22.5	
1922	m127	PM	M	20	
1923	s42	PM	M	19	
1924	s108	PM	F	22	
1925	s141	PM	F	16.5	
1926	s102	PM	M	22	
1927	p102	ST	?	5.5	
1928	p96	PM	M	18	
1929	s93	PM	M	17	

FOREST PARK 12.16.03

1930	s4	PM	M	17.5	
1931	s116	PM	M	20	
1932	t55	TD	F	179	
1933	t132	PL	?	?	RELEASED

FP 12.17.03

1934	s144	PM	F	16	
1935	s105	PM	M	22	
1936	s108	PM	F	23	
1937	s117	PM	M	26	
1938	s120	PM	F	28.5	
1939	s19	PM	M	20.5	
1940	s96	PM	F	20	
1941	s42	PM	F	17.5	
1942	s44	PM	F	20	
1943	s50	PM	M	19	
1944	s140	PM	F	22.5	
1945	p104	PM	F	21	

1946	p124	PM	M	14	
1947	p72	PM	M	16.5	
1948	s91	SV	?	7.9	
1949	p12	SV	?	4.7	
1950	s90	S?	?	?	

FP 12.18.03

1951	s98	PM	M	23.5	
1952	s21	PM	M	18	
1953	s44	PM	M	19	
1954	s72	PM	F	18.5	
1955	p36	PM	M	16	

FP 12.19.03

1956	s11	PM	F	24.5	
1957	s82	PM	M	18.5	
1958	s139	PM	M	22	
1959	s106	PM	M	18.5	
1960	s131	PM	M	21.5	positive
1961	s104	PM	M	21	
1962	s72	PM	F	22.5	
1963	s18	PM	M	20	
1964	p112	PM	F	6.5	
1965	t72	MM	?	?	

Tualatin River National Wildlife Refuge 1.13.04

1966	s93	PM	F	18.5	
1967	s33	PM	M	14	
1968	s104	PM	M	16	
1969	s118	PM	M	16	
1970	s53	PM	F	13	
1971	p91	PM	F	14	
1972	s24	PM	M	13	
1973	s54	PM	M	15	
1974	s103	PM	F	14.5	
1975	s131	PM	F	12.5	
1976	s134	PM	F	13.5	
1977	s117	PM	F	10	

TRNWR 1.14.04

1978	s132	PM	M	16	
1979	s131	PM	M	15	
1980	s11	PM	F	13.5	
1981	p67	PM	F	13	
1982	p67	PM	F	13	
1983	s21	PM	F	13.5	
1984	s33	PM	F	13	

TRNWR 1.15.04

1985	s34	PM	F	15	
1986	s60	PM	M	13	
1987	s6	PM	M	16.5	
1988	s78	PM	F	12.5	
1989	s33	PM	M	12	

1990	s141	PM	?	?	

TRNWR 1.16.04

1991	s80	PM	M	12.5	
1992	p84	PM	F	13	
1993	s76	PM	M	13.5	
1994	s122	PM	M	15.5	
1995	s72	PM	F	16	
1996	s21	PM	M	17	
1997	s83	PM	F	15	
1998	m83	PM	M	13	
1999	p84	PM	F	12	
2000	s?	SV	?	5.2	
2001	p16	PM	?	?	
2002	s105	ME	?	?	

Powell Butte 1.20.04

2003	m8	PM	M	17	
2004	s5	PM	M	18.5	
2005	s144	PM	M	16.5	
2006	s32	PM	M	19	
2007	s98	PM	M	18.5	
2008	s105	PM	M	21	
2009	p84	PM	F	16	
2010	s143	PM	F	18	
2011	s27	PM	M	16.5	
2012	p72	PM	F	19.5	

P.B. 1.21.04

2013	s104	PM	M	19	
2014	s126	PM	M	15.5	
2015	s32	PM	F	13.5	
2016	s18	PM	M	17	
2017	s3	PM	M	18.5	
2018	m16	GS	F	125	
2019	s116	PM	M	16.5	
2020	s105	PM	F	17.5	
2021	s22	PM	?	?	escaped

P.B. 1.22.04

2022	s90	MO	M	16	NBS
2023	s3	PM	F	14	
2024	s144	PM	M	18	1 SAMPLE
2025	s126	MO	M	14.5	NBS
2026	s18	PM	F	16.5	
2027	s5	PM	M	15	
2028	s132	PM	M	18	
2029	s22	PM	M	15	
2030	p84	PM	F	12.5	
2031	s116	PM	M	16	

P.B. 1.23.04

2032	s13	GS	F	145	
2033	p68	PM	M	14.8	

2034	s132	PM	M	15.0	
2035	s136	PM	M	12.5	
2036	s103	PM	F	18.5	
2037	s78	PM	M	17	
2038	s26	PM	M	13	
2039	s3	PM	F	16.5	
2040	m120	GS	M	115	DIT/NBS
2041	s116	PM	M	10.8	
2042	s137	SV	?	4.0	NBS
2043	s87	SV	?	4.5	NBS

Oxbow 2.3.04

2044	s70	PM	M	18	
2045	s53	PM	M	17.5	
2046	s139	PM	F	16	
2047	s132	PM	M	17	
2048	s144	PM	F	19.5	
2049	m69	PM	F	17	
2050	m43	PM	F	16	
2051	s32	PM	F	15.5	
2052	s43	MO	F	17	
2053	p64	ST	F	4.5	
2054	s135	ST	F	4.5	
2055	s130	PM	?	?	
2056	m87	PM	?	?	

OX 2.4.04

2057	s94	PM	F	21	
2058	m90	PM	F	18.5	
2059	s118	PM	F	24	
2060	s108	PM	M	16.5	
2061	p79	PM	M	14.5	
2062	s126	PM	F	22.5	
2063	s2	PM	M	18.5	
2064	s133	PM	F	10.5	
2065	s123	PM	M	23	
2066	s32	PM	M	17	
2067	m69	PM	M	18	
2068	p24	PM	M	15	
2069	s23	PM	F	19.5	
2070	s139	PM	M	17.5	
2071	s75	PM	M	17	
2072	s124	PM	F	15	
2073	p60	PM	M	16	
2074	s100	PM	F	17	
2075	s116	PM	M	15	
2076	p40	ST	?	4.4	
2077	p64	SV	?	5.4	
2078	s66	ST	?	4.6	
2079	p100	ST	?	4.3	
2080	p100	PM	?	?	

2081	s11	NG	?	9.5	
2082	s103	DV	?	?	
2083	t67	SG	?	?	
2084	s92	TD	?	?	

OX 2.5.04

2085	s36	PM	M	17	
2086	s51	PM	F	27	
2087	s118	PM	M	18	
2088	s113	PM	M	21.5	
2089	s72	PM	M	16	
2090	s9	PM	M	10	
2091	p31	MO	M	16.5	
2092	m115	PM	M	16	

OX 2.6.04

2093	T103	TD	F	180	
2094	S114	TD	F	170	
2095	S32	MO	M	14	
2096	S86	PM	F	21	
2097	S118	PM	F	19	
2098	S75	PM	F	18	
2099	S60	PM	F	21	
2100	S90	PM	M	17.5	
2101	S144	PM	M	18.5	
2102	S106	PM	M	16.5	
2103	S33	GS	M	105	
2104	P120	ST	?	5.5	
2105	S130	ST	?	6.0	
2106	S29	SV	?	5.5	

FOREST PARK 2.10.04

2107	s132	PM	F	23	PREG
2108	s117	PM	F	24.5	PREG
2109	s45	PM	F	27	PREG
2110	s118	PM	M	18	
2111	s120	PM	F	20	PREG
2112	s71	PM	F	19	PREG
2113	s60	PM	F	26.5	PREG
2114	s69	PM	F	20	PREG
2115	s8	PM	M	19	
2116	s77	PM	M	21	
2117	s67	PM	F	17	
2118	m24	PM	F	20.5	PREG
2119	s105	PM	F	20	PREG
2120	s97	PM	F	22	PREG
2121	s8	PM	F	25	PREG
2122	p36	ST	M	4.8	
2123	p4	SV	F	5.2	SUB A
2124	p19	ST	?	?	ESCAPED

F.P. 2.11.04

2125	s64	PM	F	23	

2126	s3	PM	M	18	
2127	s58	PM	F	21	
2128	s67	PM	M	20	
2129	p127	PM	F	21	
2130	s130	PM	F	22	PREG
2131	s127	PM	F	23	
2132	s131	PM	F	22.5	PREG
2133	s45	PM	M	17.5	
2134	s95	PM	F	20.5	
2135	s10	PM	M	17.5	
2136	m24	PM	M	24	
2137	s118	PM	F	16.5	
2138	s97	PM	M	21	
2139	s60	PM	F	29	PREG
2140	s77	PM	M	19.5	
2141	s144	PM	M	21	
2142	s120	PM	F	17.5	
2143	p127	ST	?	?	ESCAPED
2144	s22	ST	?	5.4	RELEASED
2145	s33	PM	F	19.5	
2146	s34	PM	F	17	
2147	s87	PM	F	19	
2148	s24	PM	F	20.5	PREG
2149	s8	PM	F	29	PREG
2150	p88	SV	?	4.6	

F.P. 2.12.04

2151	s95	PM	M	20.5	
2152	s84	PM	F	20	PREG
2153	s106	PM	M	21	
2154	p100	PM	F	13.5	SUB A
2155	p100	PM	M	14.5	SUB A
2156	s103	PM	F	17	
2157	s5	PM	M	12	JUV
2158	m105	PM	M	23.5	
2159	s127	PM	M	20.5	
2160	s117	PM	F	11	JUV
2161	m24	PM	M	16	
2162	s131	PM	M	22	
2163	s43	PM	F	22	
2164	s109	PM	M	19	
2165	s22	PM	M	15.5	
2166	s83	PM	F	18	
2167	s130	PM	F	20	PREG
2168	s59	PM	M	15.5	
2169	s139	PM	F	24	
2170	s3	PM	F	15.5	SUB A
2171	s60	PM	M	22.5	
2172	p100	PM	M	15	DIT/NBS
2173	p100	PM	M	12	DIT/NBS

2174	s19	PM	F	20.5	DIT/NBS
2175	m108	PM	F	12	DIT/NBS
2176	m108	PM	M	16	DIT/NBS
2177	p64	PM	M	19	DIT/NBS
2178	s33	PM	M	17.5	DIT/NBS
2179	p72	ST	?	4.6	DIT/NBS
2180	p19	ST	?	4.5	DIT/NBS
2181	p12	ST	?	4.6	DIT/NBS
2182	p24	ST	?	4.4	DIT/NBS

F.P. 2.13.04

2183	s35	PM	M	20	
2184	s80	PM	M	14	JUV
2185	s92	PM	F	20	
2186	s77	PM	M	19.5	
2187	s117	PM	F	15	
2188	s10	PM	M	20.5	
2189	s103	PM	M	16.5	
2190	s130	PM	F	23	
2191	s21	PM	M	18	
2192	m8	PM	M	12.5	
2193	m10	PM	F	21	
2194	s22	PM	M	10	DIT/NBS
2195	p126	PM	M	10	DIT/NBS
2196	s83	SV	?	3.8	DIT/NBS
2197	s60	PM	F	27	DIT/NBS
2198	s61	SV	?	3.2	DIT/NBS
2199	p144	PM	F	20	DIT/NBS
2200	p96	ST	?	5.4	DIT/NBS

TRYON CREEK 2.17.04

2201	s94	PM	M	18.5	
2202	s93	PM	F	20	
2203	s90	PM	M	20.5	
2204	s84	PM	F	18.5	
2205	s82	PM	F	26	
2206	s48	PM	F	22.5	
2207	s8	PM	M	19	
2208	s19	PM	M	12.5	
2209	s129	PM	M	15	
2210	s137	PM	M	14	
2211	s128	PM	M	19	
2212	s33	PM	F	19.5	
2213	s28	PM	M	17	
2214	s72	PM	F	22	
2215	m108	PM	F	22	
2216	s26	PM	F	22.5	
2217	s4	PM	M	13	
2218	s103	PM	M	23	
2219	s139	PM	M	21.5	
2220	s136	PM	F	21.5	DIB/NBS

2221	s126	PM	F	27	DIB/NBS
2222	p139	SV	?	5.6	DIB/NBS
2223	s117	PM	?	?	ESCAPED

T.C. 2.18.04

2224	p43	PM	M	18	
2225	p96	PM	M	17.5	
2226	s118	PM	M	15	
2227	s138	PM	M	14	
2228	s92	PM	F	20	
2229	s81	PM	M	21	
2230	s142	PM	F	21	
2231	s131	PM	F	18	
2232	s137	PM	F	18.5	
2233	s93	PM	F	14	
2234	s79	PM	M	20	
2235	p10	PM	F	13	
2236	s11	PM	F	25	
2237	p24	PM	M	15	
2238	p108	PM	M	14	DIT/NBS
2239	p76	PM	F	17	DIT/NBS
2240	p24	PM	M	13	DIT/NBS
2241	p4	PM	M	23.5	DIT/NBS
2242	s18	PM	F	15	DIT/NBS
2243	p79	PM	F	30	DIT/NBS
2244	p79	PM	F	24.5	DIT/NBS
2245	p55	PM	M	23.5	DIT/NBS
2246	p84	PM	M	21	DIT/NBS
2247	p84	ST	?	7.5	DIT/NBS
2248	p84	ST	?	7.4	DIT/NBS
2249	p84	ST	?	7.0	DIT/NBS
2250	p67	SV	?	6.0	DIT/NBS

T.C. 2.19.04

2251	p12	PM	M	17.5	
2252	s19	PM	M	18	
2253	s10	PM	M	20.5	
2254	s4	PM	M	21	
2255	s18	PM	F	15.5	
2256	p43	PM	M	16	
2257	s94	PM	M	20	
2258	s77	PM	M	19	
2259	s84	PM	F	30.5	
2260	s83	PM	M	22	
2261	s139	PM	F	16	
2262	s138	PM	F	23	
2263	s24	PM	M	19	
2264	s43	PM	M	22.5	
2265	s99	PM	F	22.5	
2266	s118	PM	F	12	
2267	p64	PM	F	24	

2268	s138	PM	M	21.5	
2269	s127	PM	F	21	
2270	s72	PM	M	20.5	
2271	p72	PM	F	19	DIT/NBS
2272	p84	PM	F	24.5	DIT/NBS
2273	s6	PM	M	17.5	DIT/NBS
2274	p43	PM	M	15.5	DIT/NBS
2275	s65	PM	M	17	DIT/NBS
2276	p24	PM	F	17.5	DIT/NBS
2277	p91	PM	F	19	DIT/NBS
2278	p96	PM	M	21	DIT/NBS
2279	p96	PM	F	23.5	DIT/NBS
2280	p79	PM	F	21.5	DIT/NBS
2281	p79	PM	F	19	DIT/NBS
2282	p79	ST	?	7.5	DIT/NBS
2283	p115	ST	?	6.8	DIT/NBS
2284	p115	PM	F	13	DIT/NBS
2285	s142	ST	?	5.6	DIT/NBS
2286	p36	ST	?	6.1	DIT/NBS
2287	p36	ST	?	7.6	DIT/NBS
2288	p36	ST	?	6.7	DIT/NBS
2289	p36	ST	?	6.2	DIT/NBS
2290	p36	ST	?	6.9	DIT/NBS
2291	p36	ST	?	4.6	DIT/NBS
2292	p139	ST	?	5.3	DIT/NBS

T.C. 2.20.04

2293	s69	PM	M	18.5	
2294	s129	PM	M	17.5	
2295	s118	PM	F	11	
2296	s140	PM	F	13.5	
2297	s105	PM	M	17.5	
2298	s10	PM	F	18	
2299	s107	PM	F	14	
2300	s92	PM	M	15	
2301	s43	PM	M	19	
2302	s66	PM	M	18	
2303	s71	PM	M	14	
2304	s26	PM	M	15.5	
2305	s109	PM	M	14	
2306	s39	PM	F	17	
2307	s93	PM	F	11.5	
2308	s79	PM	M	21	
2309	p36	PM	F	15	DIT/NBS
2310	p31	PM	F	13	DIT/NBS
2311	p31	PM	F	14.5	DIT/NBS
2312	p12	PM	F	16	DIT/NBS
2313	p115	PM	F	13	DIT/NBS
2314	s69	PM	F	20	DIT/NBS
2315	m43	SV	?	4.8	DIT/NBS

2316	s44	PM	F	20.5	DIT/NBS
2317	s107	PM	F	18	DIT/NBS
2318	s92	ST	?	5.6	DIT/NBS

Tualatin River NWR 2.24.04

2319	s32	PM	M	15	
2320	p84	PM	F	13.5	
2321	p84	PM	F	20.5	
2322	s89	PM	M	16	
2323	s80	PM	M	17.5	
2324	s72	PM	F	15.5	
2325	s10	PM	F	13	
2326	s59	PM	F	17	
2327	s51	PM	M	16	
2328	s107	PM	M	12.5	DIT/NBS
2329	t120	MM	?	?	RELEASED

TRNWR 2.25.04

2330	s102	PM	F	11.5	SUB A
2331	s41	PM	F	16	
2332	s31	PM	M	15	
2333	s9	PM	M	14.5	
2334	m34	PM	F	16	
2335	s45	PM	F	21.5	
2336	s20	PM	M	14.5	
2337	s79	ST	F	4.6	NBS RELEASED
2338	s117	ST	M	4.4	NBS RELEASED
2339	s51	ST	?	?	NBS ESCAPED
2340	t84	MM	?	?	NBS RELEASED

TRNWR 2.26.04

2341	s144	PM	F	16	
2342	s106	PM	M	14	
2343	s20	PM	M	16	
2344	s82	PM	M	20.5	
2345	s129	PM	F	16	
2346	p132	PM	M	13	
2347	s45	PM	F	16.5	
2348	p28	PM	F	14	SUB A
2349	p28	PM	F	13.5	SUB A
2350	s10	PM	F	16	
2351	s59	PM	M	15.5	
2352	p124	PM	M	17	DIT/NBS
2353	p48	PM	F	17	DIT/NBS
2354	s53	ST	F	5.0	RELEASED
2355	t139	MM	?	?	RELEASED

TRNWR 2.27.04

2356	s134	PM	F	13.5	
2357	s140	PM	F	16	
2358	s120	PM	M	19.5	
2359	p43	PM	F	17.5	
2360	p60	PM	M	20.5	DIT/NBS

2361	p52	ST	?	7.7	DIT/NBS
2362	s11	ST	?	6.0	DIT/NBS
2363	s103	SV	?	6.2	DIT/NBS
2364	s129	ST	?	6.0	DIT/NBS

Powell Butte 3.9.04

2365	s48	PM	F	16	PREG
2366	s0	MO	F	15.5	NBS RELEASED

POWELL BUTTE 3.10.04

2367	m129	PM	F	21	PREG
2368	s117	PM	F	22	PREG
2369	m101	GS	M	143	RELEASED
2370	s56	PM	F	16.5	DIT/NBS
2371	s116	PM	M	16	DIT/NBS

PB 3.11.04

2372	s105	GS	M	123	RELEASED
2373	s32	PM	F	20.5	
2374	p144	PM	M	20.5	
2375	s124	PM	M	19	
2376	s3	PM	M	18.5	
2377	s83	PM	F	20	
2378	s93	PM	F	24	
2379	s0	PM	F	22	
2380	s4	SV	?	5.5	DIT/NBS

PB 3.12.04

2381	t120	TD	M	?	NBS
2382	s0	PM	M	13.5	
2383	s32	PM	F	19.0	
2384	s73	PM	M	15.5	
2385	s72	PM	M	15.0	ONE BLOOD SAMPLE
2386	s21	PM	M	16.0	
2387	s21	PM	F	17.5	PRG.
2388	s88	ST	?	4.2	
2389	s0	SV	?	6.5	
2390	p48	PM	?	12	DIT/NBS
2391	?	SV	?	4.3	

Oxbow 3.16.04

2392	m106	TD	M	170	
2393	s75	TD	?	?	
2394	s71	TT	M	78	
2395	p144	MO	F	13	
2396	s68	PM	F	15	
2397	s70	PM	F	16.5	
2398	m129	PM	F	12	
2399	m94	PM	M	15	
2400	s113	PM	M	18.5	
2401	s108	PM	M	15	
2402	s72	PM	M	18	
2403	s74	PM	M	15.5	

2404	s132	PM	M	16	
2405	s19	PM	M	16	
2406	p96	ST	?	6.2	
2407	p24	SV	?	4.7	
2408	s129	ST	M	5.0	
2409	s53	SV	?	6.4	
2410	s33	ST	?	4.8	
2411	p96	ST	?	4.4	
2412	p96	ST	?	3.9	

Ox 3.17.04

2413	s118	TT	M	72	Tag G472
2414	p108	PM	F	7	
2415	m92	TD	F	130	Tag G701
2416	s52	PM	M	15	
2417	s88	PM	M	12.5	
2418	s79	PM	F	13.5	
2419	s95	PM	M	17	
2420	s139	PM	M	16.5	
2421	s32	MO	M	20	
2422	s33	PM	F	14.5	
2423	p29	PM	M	13	
2424	s134	PM	F	19	
2425	p7	ST	?	5.0	
2426	p64	SV	?	5.0	
2427	s128	ST	F	5.9	
2428	s128	ST	F	4.7	
2429	s59	PM	F	13	
2430	p19	PM	F	11	
2431	p144	PM	F	12.5	
2432	s97	ST	?	4.0	
2433	p36	ST	?	6.1	
2434	?	ST	?	4.9	
2435	s96	ST	M	5.8	

OX 3.18.04

2436	s34	TT	M	69	Tag# G702
2437	s71	PM	M	15	
2438	s96	PM	M	15	
2439	s120	PM	M	13.5	
2440	s117	PM	M	15	
2441	s118	PM	M	15.5	
2442	s24	PM	F	14	
2443	s128	PM	F	14.5	
2444	s108	PM	M	18	
2445	s94	PM	M	17.5	
2446	s83	PM	F	14.5	
2447	p132	PM	?	?	
2448	s70	ST	?	4.5	
2449	s69	ST	?	5.0	

OX 3.19.04

2450	s142	PM	F	20	
2451	p132	PM	F	12	
2452	s63	PM	F	15	
2453	p60	PM	F	12	
2454	s11	PM	F	16.5	
2455	s103	PM	M	16.5	
2456	s36	PM	F	11	
2457	s70	PM	F	20	
2458	s33	PM	M	19	
2459	s106	PM	F	16	
2460	s117	PM	F	15	
2461	m89	PM	F	17.5	
2462	s94	PM	M	16	
RECAP	m116	TT	M		G472
2463	p67	SV	?	4.8	
2464	s134	SV	?	4.9	
2465	s96	ST	?	5.8	

FOREST PARK 3.30.04

2466	s139	PM	M	13.5	
2467	p55	PM	F	16	
2468	s137	PM	M	18.5	
2469	s126	PM	M	15.5	
2470	s144	PM	M	22	
2471	s86	PM	M	17	
2472	s101	PM	M	18	
2473	m118	PM	F	14.5	
2474	s102	PM	M	12.5	
2475	s82	PM	M	16	
2476	s119	PM	M	15.5	
2477	s130	PM	F	16.5	
2478	s21	PM	F	17	
2479	s45	PM	F	17.5	
2480	s44	PM	M	16	
2481	s99	PM	F	14.5	
2482	s25	PM	F	14	
2483	s8	TT	M	75	TAG G704
2484	s84	TT	M	80	G703
	s119	TT	M	80	959
2486	t144	TD	M	225	G705
2487	s86	ST	F	5..0	
2488	s63	PM	M	18.5	

F.P. 3.31.04

2490	s137	PM	F	14	
2491	s44	PM	M	20	
2492	s119	PM	M	20.5	
2493	s45	PM	F	17.5	
2494	m18	PM	F	21.5	
2495	p120	PM	F	24	
2496	s117	PM	M	20.5	

2497	s130	PM	M	20.5	
2498	s86	PM	M	16.5	
2499	s144	PM	F	17.5	
2500	s80	PM	M	19	
2501	s64	PM	F	15.5	
2502	s118	PM	F	12.5	
2503	p120	PM	F	7	
2504	s55	PM	M	8	
2505	p55	PM	F	7	
2506	p55	PM	M	7.5	
2507	s104	ST	?	5.2	
2508	s102	PM	?	?	

F.P. 4.1.04

2510	s79	TT	M	79	G706
2511	s12	PM	M	22.5	
2512	s119	PM	M	14.5	
2513	s21	PM	M	19.5	
2514	s117	PM	F	21.5	
2515	s102	PM	M	15	
2516	s103	PM	M	13.5	
2517	s104	PM	M	13.5	
2518	s120	PM	F	7	
2519	s5	PM	M	19	
2520	m10	PM	F	26.5	
2521	s137	PM	M	16	
2522	s31	PM	M	17.5	
2523	s83	PM	M	20	
2524	s75	PM	F	15.5	
2525	s70	PM	F	19.5	
2526	s40	PM	F	16	
2527	p120	PM	M	6.5	
2528	s142	PM	M	19.5	
2529	p24	PM	M	18.5	
2530	s101	SV	F	4.7	
2531	p12	ST	?	5.9	

F.P. 4.2.04

2532	p120	PM	M	8.5	
2533	p120	PM	M	7.5	
2534	s7	PM	M	16	
2535	s97	PM	F	19	
2536	s69	PM	M	11	
2537	s122	PM	M	19	
2538	p91	PM	M	13	
2539	p19	PM	M	20	
2540	s32	PM	F	14	
2541	s80	PM	F	13	
2542	s89	PM	M	13	
2543	s113	PM	M	16	
2544	p120	PM	M	11.5	

2546	s118	PM	F	12.5	
2547	s117	SV	?	6.9	
2548	s73	ST	M	5.6	

Tryon Creek 4.6.04

2549	s89	TT	M	100	
2550	p84	ST	M	5.5	
2551	s34	PM	F	17	
2552	p24	PM	M	12	
2553	p115	PM	M	14.5	
2554	s120	PM	F	15.5	
2555	s132	PM	M	15.5	
2556	s83	PM	M	16.5	
2557	s141	PM	F	15	
2558	s138	PM	M	15	
2559	s137	PM	F	9	
2560	s129	PM	M	14	
2561	s91	PM	F	12	
2562	s101	PM	M	14.5	
2563	s87	PM	F	14	
2564	s21	PM	M	14	
2565	s6	PM	F	15	
2566	s7	PM	M	15	
2567	s4	PM	M	16	
2568	s95	PM	M	16.5	
2569	s24	PM	M	16	
2570	s108	PM	F	13	
2571	s81	PM	F	15	
2572	s144	PM	M	14.5	
2573	s59	PM	M	15.5	
2574	s60	PM	M	16.5	
2575	s28	PM	F	18	
2576	s125	PM	M	18	
2577	s27	PM	M	17	
2578	s48	PM	M	16.5	
2579	s47	PM	F	12	
2580	s15	PM	M	11	
2581	s45	PM	M	20.5	
2582	s98	PM	M	16	
2583	s68	PM	M	15	DIB/NBS
2584	s9	PM	M	17	DIB/NBS
2585	s51	PM	M	19.5	DIB/NBS
2586	p115	PM	F	14.5	DIT/NBS
2587	p115	PM	M	13	DIT/NBS
2588	m101	PM	M	16	DIT/NBS
2589	s117	PM	M	17.5	DIT/NBS
2590	s44	ST	?	5.5	DIT/NBS
2591	p84	ST	?	3.5	DIT/NBS
2592	s142	ST	F	5.7	DIT/NBS

T.C. 4.7.04

2593	s9	PM	M	18.5	
2594	s88	PM	M	21.5	
2595	s96	PM	F	19.5	
2596	s80	PM	M	17.5	BROKEN TAIL
2597	s72	PM	F	19	
2598	s4	PM	F	17	
2599	s144	PM	F	11.5	JUVY
2600	s101	PM	M	14	SUB A
2601	s51	PM	F	22.5	PREG
2602	s117	PM	M	13	SUB A
2603	s103	PM	M	21	
2604	s115	PM	F	20	
2605	s107	PM	M	17.5	
2606	s118	PM	F	13.5	SUB A
2607	s130	PM	F	14.5	SUB A
2608	s128	PM	F	18.5	
2609	s142	PM	F	13	JUVY
2610	s33	PM	F	14	
2611	s132	PM	F	19	
2612	p48	PM	F	17	
2613	s48	PM	M	21	DIB/NBS
2614	s44	PM	F	14	DIB/NBS
2615	s42	PM	F	19.5	DIB/NBS
2616	s12	PM	M	16	DIT/NBS
2617	s141	PM	F	12	DIT/NBS
2618	s135	PM	F	10	DIT/NBS
2619	s22	MO	F	20	DIT/NBS
2620	s81	ST	?	6	DIT/NBS
2621	s35	PM	?	?	ESCAPED

T.C. 4.8.04

2622	s105	TT	M	75	RELEASED
2623	m105	TT			RELEASED
2624	m113	TT	M	80	RELEASED
2625	s142	PM	M	11.5	
2626	s36	PM	F	15.5	
2627	s36	PM	M	11.5	
2628	s130	PM	M	14.5	
2629	s64	PM	M	13.5	
2630	s26	PM	M	18	
2631	s33	PM	M	16.5	
2632	m119	PM	M	13.5	
2633	s11	PM	M	13.5	
2634	s132	PM	M	14	
2635	s109	PM	F	14	
2636	s120	PM	F	11	
2637	s12	PM	F	11	
2638	s34	PM	M	13.5	
2639	s113	PM	M	11.5	DIT/NBS
2640	s117	PM	F	20	DIB/NBS

2641	s57	PM	M	16	DIB/NBS
2642	s107	TT	M	70	DIT/NBS
2643	p79	ST	F	4.9	DIT/NBS
2644	p31	PM	M	6.5	DIT/NBS
2645	s137	ST	?	5.6	DIT/NBS

T.C. 4.9.04

2646	s125	TT	M	78	
2647	s129	PM	M	16	
2648	s22	PM	F	14	
2649	s132	PM	M	14.5	
2650	s47	PM	F	13	
2651	s12	PM	M	17	
2652	s11	PM	M	14	
2653	s57	PM	F	23	PREG
2654	s121	PM	F	12	
2655	s45	PM	M	20	
2656	s?	PM	M	21	
2657	s137	ST	?	4.5	DIB/NBS
2658	p132	NG	?	7.6	DIB/NBS
2659	p96	ST	?	4.6	DIT/NBS
2660	s88	TT	-	-	DIT/NBS
	s105	TT	-	-	RELEASED

TRNWR 4.20.04

2661	s36	PM	F	15	
2662	s18	PM	F	16	
2663	s14	PM	F	17	
2664	s124	PM	M	16	
2665	s126	PM	M	19.5	
2666	s120	PM	M	28	
2667	p127	PM	M	16	
2668	s105	PM	F	21	PREG
2669	s67	PM	M	18	
2670	s53	PM	M	18.5	
2671	s131	PM	M	18	
2672	p132	PM	F	16.5	
2673	s23	PM	F	17.5	
2674	s45	PM	F	18	
2675	s44	PM	M	17	
2676	s48	PM	F	19.5	
2677	s32	PM	M	14.5	
2678	s34	ST	F	6.2	RECAP
2679	t19	SN	F	550	TAGGED G711 RELEASED
2680	p91	ST	F	4.6	DIT
2681	p88	SV	F	3.6	DIT
2682	p64	SV	?	4.2	DIT
2683	p64	ST	F	5.9	DIT
2684	p64	SV	?	4.8	DIT
2685	p127	PM	F	12	DIT
2686	s84	ME	M	75	DIT

TRNWR 4.21.04

2687	s113	PM	F	14.5	
2688	s131	PM	F	13	
2689	s80	PM	M	13.5	
2690	s23	PM	M	17.5	
2691	s142	PM	M	17.5	
2692	p48	PM	M	17.5	DIT/NBS
2693	s83	SV	F	5.7	DIT/NBS
2694	s117	SV	M	6.2	RELEASED/NBS

TRNWR 4.22.04

2695	s17	PM	M	17.5	
2696	s97	SV	M	6.2	DIT/NBS
2697	s16	ST	F	6.1	RELEASED

TRNWR 4.23.04

2698	s116	PM	F	18	
2699	s107	SV	?	3.8	DIT/NBS
2700	s105	SV	M	6.4	DIT/NBS
2701	?	ST	F	5.8	DIT/NBS

Powell Butte 4.27.04

2702	p144	PM	F	13.5	
2703	s6	PM	M	16.5	
2704	s126	PM	M	15	
2705	s56	PM	M	16.5	
2706	s79	PM	F	15	
2707	s82	PM	M	19	
2708	s116	PM	M	14.5	
2709	s84	PM	M		
2710	s43	PM	F	13	
2711	t24	SN	F	700	TAG G712
2712	p136	SV	?		
2713	p136	SV	?	3.2	

P.B. 4.28.04

2714	m122	PM	F	15	
2715	s134	PM	M	18	
2716	s139	PM	F	13.5	
2717	s130	PM	M	15.5	
2718	s5	PM	M	15	
2719	p144	PM	M	15	
2720	p144	PM	M	16	
2721	s117	PM	F	9	
2722	s85	PM	M	16	
2723	p84	PM	F	14.5	
2724	s56	PM	M	15.5	
2725	s6	PM	F	13	
2726	s126	MO	F	17	
2728	p139	SV	M	4.4	
2729	s136	SV	M	6.0	
2730	p136	MO	F	17.5	
2731	p57	MO	M	24	

2732	p139	SV	M	5.0	
2733	p139	SV	?	6.0	

P.B. 4.29.04

2734	S133	PM	M	16	
2735	S11	PM	M	17	
2736	S8	PM	M	16	
2737	P20	PM	F	15.5	
2738	S17	PM	M	14	
2739	S80	PM	M	16	
2740	S11	PM	M	15	
2741	S79	PM	F	12	
2742	S44	PM	M	17	
2743	P31	PM	M	17	
2744	S118	PM	M	16.5	
2745	P4	ST	?	3.5	
2746	S108	PM	?		
2747	P108	SV	?		
2748	P20	SV	?	3.5	
2750	T144	Sba	?		

P.B. 4.30.04

2751	p96	PM	M	16.5	
2752	s36	PM	?	?	
2753	s35	PM	M	14	
2754	s128	PM	M	14.5	
2755	p144	PM	F	13	
2756	s80	PM	M	17.5	
2757	p14	PM	F	13.5	
2758	p115	PM	M	14.5	
2759	s7	PM	F	17.5	
2760	s39	PM	F	18	
2761	s77	PM	F	12	
2762	p76	SV	?	4.5	
2763	p139	SV	M	6.0	
2764	p20	SV	?	3.4	
2765	s2	ST	F	5.3	
2766	t72	DV	M	?	

OXBOW 5.11.04

2767	s72	TT	M	80	TAG G722 RELEASED
2768	m141	GS	F	118	TAG G726 RELEASED
2769	t84	NF	M	100	TAG G723
2770	m17	TD	F	228	TAG G719
2771	s107	PM	F	19.5	
2772	s68	PM	M	14.5	
2773	s71	PM	M	14	
2774	s116	PM	M	16.5	
2775	s118	PM	M	17	
2776	s60	PM	M	16	
2777	s19	PM	F	15.5	
2778	p109	PM	M	18	

2779	s27	PM	M	18	
2780	s119	PM	M	17	
2781	s144	PM	F	14.5	
2782	s22	PM	M	19	
2783	s84	PM	M	14.5	
2784	s82	PM	F	15	
2785	p64	PM	F	15.5	
2786	p91	PM	M	13.5	
2787	s93	PM	M	12	
2788	s55	ST	?	4.0	
2789	p60	SV	F	5.5	
2790	s28	ST	?	4.6	
2791	p126	ST	F	5.5	
2792	p1332	ST	F	6	
2793	p96	ST	F	6.2	
2794	p96	ST	M	4.6	
2795	p64	NG	?	11	
2796	p40	SB	M	21	
2797	s81	SV	M	7.5	

OXBOW 5.12.04

2798	S66	TT	M	85	TAG G728
2799	S31	TT	M	70	TAG G720
2800	S115	GS	M	130	TAG G727
2801	S95	GS	M	175	TAG G729
2802	S12	TT	F	71	TAG G 730
2803	S70	PM	F	16.5	
2804	S107	PM	M	17	
2805	S69	PM	M	20	
2806	S141	PM	M	16	
2807	S23	PM	F	15	
2808	S8	PM	F	17	
2809	P52	ST	M	4.5	
2810	P24	ST	?	4.0	
2811	P96	ST	?	4.5	

OX 5.13.04

2812	s14	GS	F	13.5	TAG G731
2813	s107	PM	M	18.5	
2814	s106	PM	M	16	
2815	s24	PM	M	18.5	
2816	s53	SV	M	7.6	
2817	p84	ST	F	4.6	
2818	p112	ST	M	4.7	
2819	p115	ST	?	4.0	
2820	p127	ST	F	4.6	
2821	p88	ST	F	3.8	
2822	p28	MO	F	23.5	

OX 5.14.04

2823	M110	GS	F	150	TAG G732
2824	s67	TT	M	70	TAG G733

2826	t48	TD	M	190	
2827	s5	PM	F	17	
2828	s48	PM	M	17	
2829		TT	M	70	
2830	p64	ST	?	4	
2831	p127	NG	?	7	
2832	s48	MO	M	10	

FOREST PARK 5.18.04

2833	s79	TT	m	63	TAG G734 RELEASED
2834	s5	PM	m	19.5	
2835	m12	PM	m	16.5	
2836	s90	PM	f	15	
2837	s83	PM	m	21	
2838	m83	PM	f	16.5	
2839	s91	PM	f	15	
2840	s81	PM	f	19.5	
2841	m131	PM	f	16	
2842	s23	PM	m	13	
2843	s80	PM	m	15.5	
2844	s84	PM	m	15	
2845	s96	PM	m	14.5	
2846	s24	PM	f	13.5	
2847	s70	PM	m	16	
2848	s19	PM	m	17.5	
2849	s125	PM	m	19.5	
2850	s58	PM	f	14	
2851	s53	PM	f	12	
2852	s71	PM	m	20	
2853	s44	PM	m	16	
2854	s46	PM	f	16.5	
2855	s95	PM	m	14.5	
2856	p84	PM	f	14.5	
2857	s34	PM	f	17	
2858	s103	PM	f	18.5	
2859	p120	PM	m	18.5	
2860	s78	PM	m	17.5	
2861	s107	PM	m	15	
2862	s115	PM	m	14.5	
2863	s119	PM	m	17.5	
2864	s141	PM	f	14.5	
2865	s144	PM	m	17.5	
2866	p115	PM	m	14.5	
2867	p120	PM	m	15.5	
2868	m115	PM	f	16	
2869	p120	PM	m	17.5	
2870	s67	PM	f	15.5	
2871	s104	PM	m	18	
2872	s125	MO	m	14.5	
2873	s31	PM	m	15.5	

2874	p12	PM	f	12.5	
		TT	f	75	G703

F.P. 5.19.04

2875	s71	PM	M	18	
2876	s117	PM	F	15	
2877	s115	PM	F	16	
2878	s99	PM	M	13	
2879	s107	PM	F	14	
2880	s105	PM	F	16	
2881	s108	PM	M	17	
2882	p60	PM	M	18	
2883	s127	PM	F	18	
2884	s23	PM	F	13	
2885	s36	PM	M	15	
2886	s125	PM	F	19	
2887	s31	PM	F	18	
2888	s46	PM	F	15	
2889	s19	PM	M	15	
2890	s24	PM	M	22	
2891	s5	PM	M	15	
2892	p139	PM	F	17	
2893	s144	PM	F	14	
2894	s74	PM	M	16	
2895	s82	PM	M	22	
2896	s39	PM	M	17	
2897	p90	PM	M	18	
2898	s96	PM	F	17	
2899	s92	PM	M	19	
2900	s76	MO	M	6.5	
2901	p112	ST	F	5	
2902	p28	PM	F	14	
2903	s8	PM	F	14	
2904	s10	PM	M	17	
2905	p7	SV	F	7.5	
2906	s23	TT	F		

F.P. 5.20.04

2907	s141	PM	M	17.5	
2908	s121	PM	F	15	
2909	s23	PM	F	14.5	
2910	s46	PM	F	13	
2911	s8	PM	M	16.5	
2912	s95	PM	F	20	
2913	p96	PM	F	12	
2914	s31	PM	M	15.5	
2915	s101	PM	M	17.5	
2916	s108	PM	F	15	
2917	s115	PM	F	17	
2918	s24	PM	F	18.5	
2919	s119	PM	F	20	

2920	s79	PM	F	20	
2921	m80	PM	F	18	
2922	s36	PM	M	16.5	
2923	s45	PM	M	17	
2924	p64	PM	M	13	
2925	p60	PM	F	13	
2926	s71	PM	F	15	
2927	p55	PM	F	15	
2928	s80	PM	M	17.5	
2929	s78	ST	?	5.4	
2930	s76	MO	?	6.5	
2931	p19	ST	?	4.5	
2932	p31	SV	?	4.9	
2933	p43	SV	?	6.7	
2934	s131	PM	F	15.5	

F.P. 5.21.04

2935	s58	PM	M	15	
2936	s24	PM	F	14.5	
2937	s104	PM	F	13.5	
2938	s108	PM	M	16.5	
2939	s74	PM	F	19.5	
2940	s51	PM	F	14	
2941	s35	PM	F	13.5	
2942	s135	PM	F	12	
2943	s8	PM	M	17.5	
2944	s132	PM	M	18	
2945	s124	ST	?	4.4	
2946	p115	SV	F	7.9	

6.8.04 TRYON CREEK

2947	m82	PM	M	19	WET
2948	m127	PM	M	23.5	WET
2949	p72	PM	F	17.5	
2950	s69	PM	F	18.5	
2951	s88	PM	M	19.5	
2952	s96	PM	M	20.5	
2953	s77	PM	M	24	
2954	s39	PM	M	20.5	
2955	s6	PM	M	16.5	
2956	s48	PM	F	15	
2957	s24	PM	M	23	
2958	s23	PM	F	17.5	
2959	m118	PM	F	20	
2960	s132	PM	M	20	
2961	s130	PM	M	19	
2962	m12	PM	M	20.5	
2963	s107	TT	F	92	TAGGED G735
2964	s76	GS	M	135	TAGGED G736
2965	s59	ST	?	6.4	DIT/NBS
2966	p136	SV	?	6.6	DIT/NBS

2967	p132	PM	M	23	DIT/NBS
2968	m47	PM	M	21	DIT/NBS
2969	m113	TT	M	82	DIT/NBS
2970	p144	ScT	?	110	DIT/NBS

T.C. 6.9.04

2971	S12	PM	M	19	
2972	S18	PM	M	18.5	
2973	S66	PM	M	20	
2974	M59	PM	M	18	
2975	S70	PM	M	15	
2976	S117	PM	M	16.5	
2977	S106	PM	F	21	
2978	S139	PM	F	14.5	
2979	S143	PM	M	24	
2980	S142	PM	M	20	
2981	S107	PM	M	22	
2982	S118	PM	M	19	
2983	S47	PM	F	13	
2984	S32	PM	F	15	
2985	P137	MO	M	26	DIT/NBS
2986	P96	PM	M	24	DIT/NBS
2987	P31	ST	?	5.2	DIT/NBS
2988	P31	ST	?	5.4	DIT/NBS
2989	P124	SV	?	6.5	DIT/NBS
2990	P127	ST	?	5.3	DIT/NBS
2991	P48	ST	?	4.7	DIT/NBS
2992	P48	ST	?	6.5	DIT/NBS
2993	P48	ST	?	6.2	DIT/NBS
	S108	TT	-		RECAP G735

T.C. 6.10.04

2994	p132	PM	M	18	
2995	m58	PM	F	17	
2996	s106	PM	F	18	
2997	s114	PM	F	24.5	PREG
2998	s45	PM	F	22.5	
2999	s4	PM	F	16.5	
3000	s24	PM	M	19	
3001	s129	PM	F	15	
3002	s75	PM	F	20.5	
3003	s107	TT	M	43	TAGGED G737
3004	t72	SN	F	570	TAGGED G739
3005	s80	SV	?	6.1	RELEASED
3006	s108	MT	M	28.5	DIT/NBS
3007	s33	PM	M	19	DIT/NBS
3008	p100	NG	?	13.5	DIT/NBS
3009	p100	NG	?	12.5	DIT/NBS
3010	p100	ST	?	6.6	DIT/NBS

T.C. 6.11.04

3011	s22	PM	M	18.5	

3012	s80	PM	M	18	
3013	s56	PM	M	18.5	
3014	s92	PM	M	16.5	
3015	p96	PM	M	19.5	
3016	s45	PM	M	17.5	
3017	s14	PM	M	18	
3018	s132	PM	M	19.5	DIT/NBS
3019	p144	ST	?	5.4	DIT/NBS
3020	p100	ST	?	5.0	DIT/NBS
3021	p91	ST	?	4.5	DIT/NBS

Tualatin River National Wildlife Refuge 6.22.04

3022	s82	TT	M	62	TAG G751
3023	s77	PM	M	13.5	
3024	s80	PM	M	25	
3025	p143	PM	M	14	
3026	s32	PM	F	23.5	
3027	s136	PM	F	15.5	
3028	m24	PM	M	14.5	
3029	s118	PM	M	16	
3030	s4	PM	M	14	
3031	p139	PM	M	19	
3032	s24	ST	?	5.0	
3033	p84	PM	F	20	
3034	p76	ST	?	5.3	
3035	p67	ST	?	5.4	
3036	p124	ST	?	5.9	

TRNWR 6.23.04

3037	s114	TT	F	68	TAG G749
3038	p40	MT	M	45	
3039	s80	PM	F	15	
3040	s60	TT	M	60	
3041	s20	PM	F	23..5	
3042	s95	PM	M	16	
3043	s87	PM	M	14	
3044	s140	PM	M	24	
3045	s116	PM	M	23.5	
3046	s36	PM	F	20	
3047	s9	PM	F	23.5	
3048	s95	ME	M	73	
3049	s32	ME	M	70	
3050	s117	ME	M	72	TAG G740
3051	p120	PM	F	10.5	

TRNWR 6.24.04

3052	s103	PM	F	13.5	
3053	s88	PM	M	19	
3054	s118	PM	F	23	
3055	s47	PM	M	17	
3056	s87	PM	F	17	

3057	s78	PM	F	21	
3058	s20	PM	M	10	
3059	p79	SV	?	8.6	
3060	p76	ST	?	4.3	
	t36	PL	?	?	

TRNWR 6.25.04

3061	m29	PM	M	15	
3062	s141	PM	M	18	
3063	s80	SV	?	4	
3064	p79	ST	?	5.5	
3065	p79	SV	?	3.5	
3066	*7	PM	M	4.5	
3067	s116	ME	M	65	
	t120	DV	F		
	t48	DV	M		

Powell Butte 6.29.04

3068	s46	MO	F	16.5	
3069	p64	PM	F	11.5	
3070	p119	PM	M	15	
3071	s69	PM	M	15.5	
3072	s60	PM	F	19	
3073	s68	PM	F	17	
3074	?	PM	M	19.5	
3075	s48	PM	M	16.5	
3076	s84	PM	M	12	
3077	s89	PM	M	21	
3078	s21	PM	F	18	
3079	m117	PM	F	14	
3080	p28	PM	F	17	
3081	s28	PM	F	17.5	
3082	s142	PM	M	20	
3083	s63	PM	M	17	
3084	s129	PM	F	15	
3085	s128	PM	F	16	
3086	p64	NG	M	8.5	
3087	p4	SV	?	3.5	
3088	p124	SV	?	3.6	
3089	p64	SV	?	4.1	
3090	s33	PM	M	18.5	
3091	p7	MO	M	6.9	
3092	p20	SV	F	4.7	
	m5	SV	?		

P.B. 6.30.04

3093	p144	PM	M	19	
3094	s144	PM	F	16.5	
3095	m129	PM	F	14.5	
3096	s129	PM	M	17.5	
3097	s128	PM	F	10	
3098	s57	PM	M	20.5	

3099	s72	PM	M	16	
3100	s24	PM	M	18.5	
3101	s21	PM	F	10	
3102	s78	PM	F	11	
3103	p84	PM	M	13.5	
3104	p89	PM	M	16	
3105	s35	PM	M	19	
3106	s0	PM	F	18	
3107	p52	SV	?	4.2	
3108	p24	MO	M	13.5	
3109	s117	PM	M	132	
3110	s127	PM	F	8	
3111	s31	SV	?	5.2	

P.B. 7.1.04

3112	p67	MT	M	34	
3113	s143	PM	M	17	
3114	s144	PM	M	18	
3115	s46	PM	M	15.5	
3116	s22	PM	F	15.5	
3117	s131	PM	M	18	
3118	s31	PM	F	15	
3119	p72	PM	M	18.5	
3120	s118	ST	F	4.6	
3121	p108	ST	M	4.3	
3122	s72	PM	F	16	
3123	s14	PM	M	18.5	
3124	s21	PM	M	11	
3125	p92	ST	F	5.2	
3126	s135	SV	F	3.5	

P.B. 7.2.04

3127	s21	PM	M	17	
3128	s68	PM	M	17	
3129	s85	PM	M	19	
3130	s140	PM	M	18.5	
3131	s23	PM	M	9.5	
3132	s143	PM	M	13	
3133	s82	PM	M	19	
3134	s68	PM	F	11	
3135	s22	PM	F	16	
3136	p7	ST	?	3	
3137	s4	SV	?	5	
3138	s34	SV	?	3.3	
3139	p36	SV	F	5.4	
3140	s2	ST	?	3.5	
3141	s14	SV	?	5	
3142	p92	ST	?	3	
3143	p84	ST	?	4.3	
3144	p84	ST	?	4.7	
3145	s41	SV	?	4.21	

OXBOW 7.6.04

3146	S81	MO	F	20.5	
3147	S86	MO	M	20	
3148	S93	TT	F	73	TAG G724
3149	S72	TT	M	70	G738
3150	S21	TT	F	84	G740
3151	M129	TT	M	60	G741
3152	S92	NG	M	7.4	
3153	P132	PM	F	18	
3154	S18	PM	M	14	
3155	S96	PM	F	15	
3156	S94	PM	M	15	
3157	S136	PM	M	18	
3158	S47	PM	F	19.5	
3159	S105	PM	M	16	
3160	s119	PM	F	20.5	
3161	p52	PM	F	14.5	
3162	s59	PM	M	16	
3163	p40	ST	F	4.1	
3164	p48	ST	F	4.5	
3165	s144	ST	M	4.6	
3166	s130	ST	M	4.6	
3167	p24	ST	F	3.8	
3168	p4	ST	F	5.4	
3169	p7	ST	F	4.0	
3170	p12	ST	M	4.3	
3171	p79	SV	M	5.0	
3172	p88	ST	F	3.9	
3173	p91	NG	?	7.9	
3174	p115	ST	M	3.9	
3175	p67	ST	?	4.2	
3176	p132	ST	M	4.5	
3177	p132	ST	M	4.6	
	p144	ST	?	?	
	p60	ST	?	?	
	p131	ST	?	?	

OXBOW 7.7.04

3178	m72	TT	F	95	TAG G742
3179	s54	TT	M	50	G743
3180	s144	TT	F	90	G744
3181	s33	TT	M	64	G745
3182	s95	GS	F	155	G754
3183	s59	PM	F	16.5	
3184	s115	PM	M	21	
3185	s84	PM	M	17	
3186	s17	PM	M	14	
3187	s141	PM	F	13	
3188	p43	SCAT	M	48	
3189	s72	ME	M	60	

3190	p128	SV	M	4.2	
3191	p28	SV	M	5.0	
3192	p12	SV	F	5.3	
3193	s36	TT	F	69	
3194	s80	SV	?	4.5	
3195	p112	ST	?	4.5	
3196	p88	ST	?	4.3	
3197	p91	ST	?	3.9	
3198	p96	ST	?	4.6	
3199	p128	ST	?	3.5	

Oxbow 7.8.04

3200	s96	TT	M	68	TAG G757
3201	s81	MO	M	15.5	
3202	s83	MO	M	18.5	
3203	m21	TT	F	74	G750
3204	s4	GS	M	125	G729
3205	s32	TT	M	74	
3206	p124	TT	M	41	G759
3207	m132	TT	M	50	
3208	s1112	TT	M	?	
3209	s100	GS	F	130	G732
3211	p67	PM	F	15.5	
3212	s143	PM	F	13	
3213	s117	PM	F	20	
3214	s119	PM	M	15	
3215	s66	PM	F	19	
3216	p144	ST	?	4.2	
3217	p79	ST	?	4.4	
3218	p96	SV	?	5.0	
3219	p24	ST	F	4.4	
3220	p36	ST	?	4.0	
3221	s48	SV	?	7.1	

OXBOW 7.9.04

3222	s42	TT	M	49	TAG G755
3223	s45	TT	M	60	G756
3225	s81	MO	F	19	
3226	m132	GS	F	130	G760
3227	s117	MO	F	15	
3228	s137	TT	M	54	G761
3229	s108	TT	M	71	G762
3230	s72	PM	M	18	
3231	s49	PM	F	16	
3232	p84	ST	M	4.2	
3234	s116	MO	M	15	
3235	s104	TT	M	51	
3236	m104	TT	F	62	
3237	p31	ST	?	4.6	
3238	p103	ST	?	5.0	
3239	s79	SV	M	7.1	

3240	p79	NG	?	8	
3241	s128	ST	?	4.0	
	P84	SV			

FOREST PARK 7.13.04

3242	s75	MO	M	11	
3243	p67	MT	F	28.5	
3244	s108	TT	F	34	TAG G763
3245	s84	TT	M	65	G764
3246	s24	PM	F	15	
3247	m46	PM	F	18	
3248	s89	PM	M	18.5	
3249	s56	PM	F	14	
3250	s66	PM	M	18	
3251	p36	PM	F	17.5	
3252	p36	PM	M	17	
3253	m115	PM	M	19.5	
3254	s11	PM	M	23	
3255	s115	PM	F	19	
3256	s12	PM	M	18.5	
3257	s10	PM	M	15	
3258	s33	PM	F	21.5	
3259	p19	PM	F	17	
3260	s131	PM	F	23	
3261	s96	PM	F	18	
3262	s79	PM	M	18.5	
3263	s118	PM	F	17	
3264	s42	PM	M	17.5	
3265	s144	PM	F	15	
3266	s130	PM	F	16	
3267	s119	PM	M	21	
3268	s82	PM	F	15.5	
3269	s118	PM	M	16	
3270	s29	PM	M	16.5	
3271	s54	PM	F	15	
3272	s64	PM	M	15.5	
3273	s72	PM	M	17.5	
3274	m131	PM	M	18	
3275	s36	PM	M	19.5	
3276	m143	PM	M	19	
3277	s92	PM	M	17	
3278	s71	PM	M	18.5	
3279	m19	PM	F	23	
3280	s139	PM	M	20	
3281	p72	PM	F	19	
3282	p72	PM	F	14	
3283	s127	PM	F	16	
3284	m102	PM	M	18.5	
3285	s107	PM	M	17.5	
3286	s81	PM	F	13	

3287	s126	PM	M	20.5	
3288	s143	PM	M	17.5	
3289	s125	PM	F	15	
3290	s46	PM	M	20.5	
3291	s60	PM	M	19	
3292	s103	PM	F	15.5	
3293	s9	PM	F	22	
3294	s116	ST	?	4.5	
3295	p36	ST	M	4.1	
3296	p28	ST	?	4.8	

FOREST PARK 7.14.04

3297	s22	TT	M	65	TAG G766
3298	s84	TT	M	60	G763
3299	s140	PM	M	14	
3300	s143	PM	M	16	
3301	s92	PM	F	17.5	
3302	p132	PM	M	21.5	
3303	s12	PM	M	18	
3304	s132	PM	M	16.5	
3305	s130	PM	F	15	
3306	s89	PM	F	17	
3307	s24	PM	F	14	
3308	s60	PM	F	16	
3309	p82	PM	F	12.5	
3310	s33	PM	F	17	
3311	s96	PM	M	17	
3312	s120	PM	F	15	
3313	s107	PM	M	16	
3314	s118	PM	M	19	
3315	s102	PM	F	20.5	
3316	s108	PM	F	16	
3317	s115	PM	M	16	
3318	p28	SV	F	4.1	
3319	p115	SV	?	?	
3320	p76	ST	?	3.8	
	p91	SCAT	?	?	

FOREST PARK 7.15.04

3321	s81	PM	M	18	
3322	s104	PM	M	15.5	
3323	s33	PM	M	17	
3324	m60	PM	F	16.5	
3325	s107	PM	F	16	
3326	s60	PM	M	16.5	
3327	s59	PM	F	17	
3328	s19	PM	M	16	
3329	s143	PM	F	26	
3330	s120	PM	M	17.5	
3331	s48	PM	M	17	
3332	s108	PM	M	18	

3333	s24	PM	M	19	
3334	p78	PM	M	15	
3335	p91	SCAT	F	86	
3336	s82	ST	?	4.5	
3337	s101	SV	F	5.2	
3338	s9	ST	F	4.2	
3339	s91	SV	?	5.6	

FOREST PARK 7.16.04

3340	s109	MO	F	17	
3341	s35	PM	M	14	
3342	s69	PM	M	15	
3343	s66	PM	M	16	
3344	s72	PM	M	19	
3345	s42	PM	M	17	
3346	s120	PM	F	15.5	
3347	p48	PM	F	13.5	
3348	s81	PM	M	15	
3349	p91	MT	M	28	
3350	s117	ST	?	4.3	
3351	s8	MO	F	17.5	
3352	s139	ST	?	4.0	
3353	s140	ST	?	4.8	
3354	s9	ST	?	3.7	
3355	s103	ST	?	4.7	
3356	s89	ST	?	4.7	
3357	s18	MO	M	8	
3358	p28	SV	M	4.0	

TRYON CREEK 7.20.04

3359	s117	TT	F	75	G73?
3360	s24	PM	M	21.5	
3361	s41	PM	F	12	JUVY
3362	s12	PM	F	16.5	
3363	s44	PM	M	17	
3364	p36	PM	M	14	
3365	s125	PM	M	17	
3366	s73	PM	M	16.5	
3367	p91	PM	F	19	PREG
3368	p96	PM	F	18	
3369	m54	PM	F	15.5	
3370	s23	PM	M	17	
3371	m24	PM	F	20	PREG
3372	s118	PM	F	15	
3373	?	PM	M	21	
3374	s132	PM	M	19	
3375	s124	PM	F	16	
3376	s57	PM	F	20.5	PREG
3377	s108	PM	M	19	
3378	s72	PM	F	15.5	DIB/NBS
3379	s32	PM	M	21	DIB/NBS

3380	p43	ST	?	5.2	DIT/NBS
3381	s140	ST	?	4.5	RELEASED

TRYON CREEK 7.21.04

3382	s5	MO	F	20	RELEASED
3383	s77	PM	F	16.5	
3384	p43	PM	M	19.5	
3385	s117	PM	F	18	
3386	m59	PM	M	16	
3387	s108	PM	M	19	
3388	s78	PM	M	19	
3389	s32	PM	F	12.5	JUVY
3390	s57	PM	M	19.5	
3391	s144	PM	F	19	
3392	s130	PM	F	18.5	
3393	s45	PM	F	16	
3394	s47	PM	F	13	JUVY
3395	s117	PM	F	18	
3396	s24	PM	F	17.5	
3397	s113	SV	F	8.5	RELEASED
3398	p24	ST	?	4.6	DIT/NBS
3399	s93	ST	?	3.8	DIT/NBS
3400	s114	ST	?	4.6	DIT/NBS
3401	s100	ST	?	4.8	DIT/NBS
	s118	SV	?	?	ESCAPED

TC 7.22.04

3402	S66	PM	M	18.5	
3403	S83	PM	M	16.5	SUBA
3404	S75	PM	F	16.5	
3405	M10	PM	F	15.5	
3406	S108	PM	F	14.5	
3407	S45	PM	M	19.5	
3408	S47	PM	M	15	
3409	T84	SN	F	520	TAGGED G777 RELEASED
3410	P91	ST	?	4.7	DIT/NBS
3411	S116	ST	?	4.9	DIT/NBS
3412	S93	SV	?	5.1	DIT/NBS
3413	S86	ST	?	4.2	DIT/NBS
3414	P88	ST	?	4.3	
3415	S19	ST	?	5.0	

TC 7.23.04

3416	S4	MO	F	15.5	DIT/NBS
3417	S142	PM	M	17	
3418	S105	PM	F	21.5	
3419	S45	PM	F	15.5	
3420	S60	PM	M	15.5	
3421	S22	NG	F	9	NBS/RELEASED
3422	S104	SV	?	4.6	DIT/NBS
3423	P127	ST	?	4.2	DIT/NBS
3424	P72	SV	?	4.7	DIT/NBS

3425	S5	MO	M	23	DIT/NBS
3426	P12	ST	?	4.2	DIT/NBS
3427	S128	ST	?	3.8	DIT/NBS
3428	S127	SV	?	5.5	DIT/NBS

TUALATIN RIVER NWR 7.27.04

3429	M51	PM	M	16.5	
3430	s84	PM	F	20	PREG
3431	p115	PM	M	14	SUBA
3432	s125	PM	M	15	
3433	s89	PM	F	17	PREG
3434	s82	PM	M	14	
3435	p76	ST	M	4.8	DIT/NBS
3436	S142	ST	?	4.4	DIT/NBS
3437	P12	SV	F	4.0	DIT/NBS
3438	S26	PM	M	14	DIT/NBS
3439	S91	SV	?	3.7	RELEASED

TRNWR 7.28.04

3440	s24	PM	F	20	
3441	S141	PM	M	17	
3442	s9	PM	M	14	SUBA/A
3443	S40	PM	M	12.5	SUBA
3444	P103	PM	F	15.5	GROWTH ON POST VENTER/1 BS
3445	S10	ME	M	73	G771 RELEASED
3446	S142	ST	F	4.0	
3447	s81	SV	?	3.8	RELEASED
3448	T48	MM	?	?	RELEASED

TRNWR 7.29.04

3449	S142	TT	M	73	G774 REL
3450	S34	PM	F	20	
3451	S141	PM	F	19.5	PREG
3452	S51	ST	?	5.5	DIT/NBS
3453	s108	SV	F	4.2	RELEASED
	S127	ME			G771 RECAP/DIT
	T72	MM	?		RELEASED
	T144	DV	?		RELEASED

TRNWR 7.30.04

3454	S141	PM	M	14.5	
3455	S105	PM	F	19	PREG
3456	M36	PM	F	10.5	JUVY
3457	s114	SN	F	600	G770 REL
3458	S80	SV	?	4	RELEASED

Powell Butte 8.24.04

3459	m47	PM	M	17.5	G768
3460	s120	PM	F	25	G713
3461	p31	PM	M	12.5	G714
3462	s108	PM	M	17	G716
3463	s24	PM	F	21.5	G717
3464	s11	PM	F	12.5	G718

3465	s66	PM	M	15	G779
3466	s58	PM	M	18.5	G775
3467	s71	PM	F	20	G776
3468	s50	PM	M	13	G773
3469	s94	PM	F	27.5	G772
3470	s141	PM	M	15	G769
3471	s32	PM	F	13	G790
3472	s34	PM	M	20	G791
3473	s36	PM	F	22	G792
3474	s40	PM	M	15	G793
3475	s139	PM	M	14.5	G794
3476	s136	PM	F	14.5	G795
3477	s131	PM	M	16	G796
3478	s128	PM	F	17	G797
3479	s102	SV	M	4.1	DIT/NBS
3480	p112	SV	?	?	ESCAPED
3481	p79	SV	?	3.8	DIT/NBS
3482	p84	MO	M	7.1	DIT/NBS
3483	p64	MO	F	16	DIT/NBS
3484	p64	MO	M	8.9	RELEASED
3485	p64	MO	M	8.6	RELEASED

P.B. 8.25.04

3486	p40	MO	F	14.5	
3487	p64	MO	F	13.5	
3488	s110	MO	M	13	
3489	s58	PM	M	22.5	TAG G798
3490	s141	PM	M	15.5	TAG G799
3491	s96	PM	M	16.5	TAG G800
3492	s35	PM	M	16	TAG G601
3493	s23	PM	F	12	TAG G602
3494	s84	PM	M	21	TAG G603
3495	s2	PM	M	16	TAG G604
3496	p84	SV	?	4.2	
3497	p115	SV	?	?	
3498	s22	PM	M	18	
3499	p136	SV	?	4.2	

P.B. 8.26.04

3500	s59	MO	M	15	TAG G605
3501	s97	MO	F	13	TAG G607
3502	s66	MO	M	14	TAG G608
3503	s118	PM	M	16	TAG G609
3504	s10	PM	M	15	TAG G610
3505	s42	SV	?	3.5	
3506	s123	MO	F	16	
3507	p36	SV	?	4.7	
3508	p144	PM	F	16.5	
3509	p7	SV	?	4.9	
3510	p7	SV	?	4.5	
3511	p7	SV	?	?	

3512	s78	MO	M	10.0	
3513	p84	ST	?	5.1	
3514	p84	ST	?	5.3	

P.B. 8.27.04

3515	S59	MO	M	11	TAG G611
3516	S25	MO	F	14	TAG G612
3517	S127	MO	M	7	G613
3518	S11	MO	M	10	G614
3519	S129	PM	M	17	G615
3520	S108	PM	M	18	G616
3521	S119	PM	F	17.5	G617
3522	S11	PM	F	19	G618
3523	S84	PM	M	16	G619
3524	P84	MO	M	15	
3525	P64	PM	F	19	
3526	P28	PM	M	19	

OXBOW 8.31.04

3527	T115	TT	M	64	G620
3528	M82	TT	M	80	G621
3529	S111	TT	F	70	G622
3530	S107	TT	M	68	G623
3531	M17	TT	M	62	G624
3532	M94	TT	M	64	G626
3533	M15	TT	F	63	G627
3534	S24	TT	F	73	G628
3535	S142	TT	M	74	G629
3536	S44	TT	M	79	G756
3537	M23	TT	F	83	G740
3538	S84	PM	F	14.5	G630
3539	S7	PM	M	13.5	G632
3540	S88	PM	M	14.5	G633
3541	S65	PM	M	13.5	G634
3542	S58	PM	M	15	G635
3543	S52	PM	M	13	G636
3544	S83	PM	M	15	G637
3545	S60	PM	M	13.5	G638
3546	S101	PM	F	16	G639
3547	S125	PM	M	11.5	G640
3548	S49	PM	M	14	G641
3549	S23	PM	M	14	G642
3550	S140	PM	F	18	G643
3551	S103	PM	M	16.5	G644
3552	S129	PM	F	15	G645
3553	S17	PM	M	13	G646
3554	S110	PM	F	18	G647
3555	S106	S?	?	5.7	
3556	P136	S?	?	5.4	
3557	P84	S?	?	3.8	
3558	P24	S?	?	5.2	

3559	P136	S?	?	3.9	
3560	T67	TD	M	172	
OX 9.1.04					
3561	m47	TT	M	68	G648
3562	s72	TT	M	61	G649
3563	s55	TT	F	73	G743
3564	s48	TT	M	61	G650
3565	s10	TT	M	70	G651
3566	s93	TT	M	79	G621
3567	s70	TT	M	60	G653
3568	s139	TT	M	69	G654
3569	s144	TT	M	72	G655
3570	m23	TT	M	54	G656
3571	m116	TT	?	?	
3572	s80	PM	M	15	G657
3573	s132	PM	F	10	G658
3574	s36	PM	F	14	G659
3575	s71	PM	F	12.5	G660
3576	p7	PM	M	12.5	G661
3577	p24	PM	M	8.5	G662
3578	s21	PM	M	15	G663
3579	s41	PM	F	11	G664
3580	s120	PM	M	18.5	G665
3581	p88	S?	?	?	
3582	p115	PM	M	14	
3583	m53	TT	F	59	G627
OX 9.2.04					
3584	S132	TT	M	72	G667
3585	S34	TT	M	70	G668
3586	S58	TT	F	69	G669
3587	S120	TT	M	78	G670
3588	S46	TT	M	60	G671
3589	S116	TT	M	73	G672
3590	s91	TT	M	71	G673
3591	m87	TT	M	79	G674
3592	s141	PM	F	6.5	G675
3593	m116	PM	F	15.5	G676
3594	s6	PM	F	12	G677
3595	s130	PM	F	13.5	G678
3596	s89	PM	M	14	G679
3597	p52	SV	?	4.5	
3598	s87	SV	?	6.1	
3599	s81	SV	?	6.6	
3600	s16	ME	M	54	G666
3601	s87	SB	?	17	
OX 9.3.04					
3602	S81	SV	M	5.8	
3603	S42	TT	M	69	G680
3604	s69	TT	M	73	G681

3605	s47	PM	M	15.5	G682
3606	m47	PM	F	10	
3607	s127	PM	F	16.5	G683
3608	s15	PM	M	17.5	G684
3609	s116	PM	M	18	
3610	s89	MO	F	15.5	
3611	s122	TT	M	68	
3612	s56	MO	F	18	
3613	t60	TD	M	191	
3614	s117	MO	F	14.5	G685

FOREST PARK 9.14.04

3615	s77	PM	M	15.5	G686
3616	s90	PM	M	18	G687
3617	s118	PM	M	18.5	G688
3618	s105	PM	M	20	G689
3619	s108	PM	F	20	G690
3620	s105	PM	M	20.5	G691
3621	s81	PM	F	16	G692
3622	s144	PM	M	21	G693
3623	s140	PM	M	18.5	G694
3624	s130	PM	F	17	G695
3625	s83	PM	M	18	G783
3626	s127	PM	F	19	G785
3627	s84	PM	F	16.5	G780
3628	s92	PM	?	?	
3629	s51	PM	M	15	G696
3630	s35	PM	F	18	G697
3631	s36	PM	M	16	G698
3632	s72	PM	M	16.5	G699
3633	s66	PM	F	22.5	G700
3634	s69	PM	F	17	TAG 1
3635	s31	PM	M	20	2
3636	s47	PM	F	10.5	3
3637	s45	PM	F	20.5	4
3638	s12	PM	M	20.5	5
3639	s11	PM	F	18	6
3640	s17	PM	F	18.5	7
3641	s143	PM	F	15.5	G784
3642	s8	SV	?	5.5	

F.P. 9.15.04

3643	s72	PM	F	21.5	TAG 8
3644	s70	PM	M	17	9
3645	s43	PM	M	15	10
3646	s60	PM	F	24	11
3647	m23	PM	M	19	12
3648	s48	PM	M	18	13
3649	s32	PM	F	7.5	14
3650	s36	PM	M	18.5	15
3651	s132	PM	M	19.5	16

3652	s134	PM	F	11	17
3653	s144	PM	F	19.5	18
3654	s115	PM	M	19	19
3655	s102	PM	F	19.5	20
3656	s118	PM	F	22	21
3657	s107	PM	M	19	22
3658	s82	PM	M	16	23
3659	s75	PM	M	20.5	24
3660	s77	PM	F	15	25
3661	s140	PM	F	18	26
3662	s130	PM	M	14.5	27
3663	s90	MO	M	10	
3664	s8	SV	?	7.8	

F.P. 9.16.04

3665	p72	PM	M	15	TAG 28
3666	s54	PM	M	18	29
3667	s60	PM	F	21	30
3668	s144	PM	F	18	31
3670	s130	PM	F	19	32
3671	s139	PM	M	19	G707?
3672	s140	SV	?	5.1	
3674	t132	TD	M	141	
3675	t12	MM	?	?	

F.P. 9.17.04

3676	p96	PM	F	15	TAG 33
3677	s103	PM	M	14	34
3678	s98	PM	M	12.5	35
3679	s109	PM	M	21	36
3680	s144	PM	M	7	37
3681	s144	PM	F	6.5	38
3682	s42	PM	F	9	39
3683	s65	PM	F	19	40
3684	t120	TD	F	196	
3685	p67	SV	?	3.5	
3686	s123	SV	M	8.2	
3687	s81	PM	F	14	

TRNWR 9.22.04

3688	s44	PM	F	17.5	TAG 41
3689	m138	PM	M	19	43
3690	s79	PM	F	16	44
3691	s87	PM	M	17	45
3692	s118	PM	F	19.5	46
3693	s68	PM	F	18	47
3694	s77	PM	F	14.5	48
3695	s82	PM	M	14.5	49
3696	p127	PM	M	14.5	DIT/NBS
3697	s43	PM	M	14	DIT/NBS
3698	s11	SV	?	4	DIT/NBS
3699	s7	SV	F?	4.9	DIT/NBS

3700	s127	ST	?	4.3	DIT/NBS
3701	S101	SV	?	3.7	DIT/NBS
3702	s117	SV	?	4.0	DIT/NBS
	t72	DV	M		

TRNWR 9.23.04

3703	s9	PM	F	16	TAG 51
3704	s12	PM	F	18	52
3705	s118	PM	M	12	53
3706	m23	PM	M	17	54
3707	s38	PM	F	16.5	55
3708	s113	PM	F	14	56
3709	s130	PM	F	15	57
3710	s95	PM	F	20	58
3711	s93	PM	F	18.5	59
3712	s68	PM	M	15.5	60
3713	s77	PM	F	12.5	61
3714	m138	PM	M	14	62
3715	p7	ST	F	4.5	
3716	s33	ST	?	4.7	
	t132	DV			

TRNWR 9.24.04

3717	S21	PM	M	8.5	TAG 63
3718	S7	PM	M	15	64
3719	S127	PM	M	8	65
3720	s113	PM	M	15	66
3721	S30	PM	M	13.5	67
3722	S70	PM	M	16	68
3723	S81	PM	F	21	69
3724	S106	PM	M	15	74
3725	M125	PM	F	22	70
3726	S89	ST	F	3.7	DIT/NBS
3727	S8	ST	?	4	DIT/NBS
3728	P139	ST	?	5	DIT/NBS

TRNWR 9.25.04

3729	s106	PM	F	13	TAG 71
3730	s12	PM	M	15	72
3731	s69	PM	F	18.5	73
3732	s53	PM	M	12.5	75
3733	t24	MM	?		

TRYON CREEK 9.28.04

3734	s54	PM	F	19	TAG 76
3735	s82	PM	M	16.5	77
3736	s117	PM	F	20	78
3737	s42	PM	M	16.5	79
3738	m106	PM	F	19.5	80
3739	s6	PM	M	18	82
3740	s142	PM	F	17	83
3741	s125	PM	M	17	84
3742	s118	PM	M	17.5	DIT/NBS

3743	p64	ST	?	6	
TC 9.29.04					
3744	p67	PM	M	13	TAG 86
3745	s114	PM	M	21	87
3746	s108	PM	F	15	88
3747	s14	PM	F	17	89
3748	s118	PM	F	13	90
3749	s126	PM	F	15.5	91
3750	s58	PM	M	21	92
TC 9.30.04					
3751	s79	PM	M	17	TAG 93
3752	s33	PM	F	27	94
3753	s9	PM	F	13	95
3754	s142	PM	M	20	96
3755	s108	PM	M	21	97
TC 10.1.04					
3756	s2	PM	F	16	TAG 98
3757	s106	PM	M	15.5	99
3758	s108	PM	M	19	100
3759	s100	PM	F	15	101
3760	p72	ST	?	5.3	DIT/NBS
3761	p40	PM			Esc/NBS
POWELL BUTTE 10.5.04					
3762	s58	MO	F	17	TAG 102
3763	s56	PM	M	15	103
	s5	PM	F	15.5	G795
3765	s127	PM	M	17	104
3766	s68	PM	M	20.5	105
3767	s130	PM	F	15	106
3768	s29	PM	M	16.5	107
3769	s110	MO	F	10.5	
	s128	PM	F	17.5	G797
3771	s21	PM	F	17.5	108
3772	s144	PM	F	16	109
	s33	PM	M	15	G768
3774	s46	PM	F	15.5	110
3775	m60	PM	M	17	111
3776	s84	PM	F	16	112
3777	s69	ST	?	4.2	
3778	s84	PM	M	15.5	G619
PB 10.06.04					
3779	s14	PM	F	17	TAG 113
3780	s22	PM	F	20.5	114
3781	s23	PM	M	14	115
3782	s33	PM	M	15.5	116
3783	s63	PM	F	8	117
3784	s68	PM	F	14	118
3785	s103	PM	M	16	119
3786	s105	PM	M	16.5	120

3787	s101	MO	F	13	122
3788	s108	PM	M	12	123
3789	p100	PM	F	13	124
3790	s29	SV	?	4.9	

PB 10.7.04

3791	s58	PM	F	20	TAG 125
3792	s104	PM	F	14.5	126
3793	s130	PM	F	19	127
3794	s32	PM	M	14	128
3795	s39	PM	F	14.5	129
3796	s114	PM	M	13.5	130
3797	s109	PM	F	8	131
3798	s84	PM	M	15	132
3799	p96	PM	F	19	133
3800	m96	PM	F	13	134
3801	s67	MO	F	14	
3802	s66	ST	?	5.0	
3803	p120	MO	M	18	

PB 10.8.04

3804	m96	PM	F	12.5	TAG 135
3805	s58	PM	M	15.35	136
3806	s144	PM	M	16	137
	t72	DV			

OXBOW 10.12.04

3807	s95	TT	M	80	TAG 138
3808	s61	TT	F	72	139
3809	s96	PM	M	16	140
	s131	PM	F	19	G678
	s126	PM	F	17.5	G683
3812	s142	PM	M	14	141
3813	s130	PM	M	15	143
3814	s83	PM	M	?	
3815	s113	PM	M	14	144
3816	s119	PM	M	16	145
	s59	PM	M	13	G638
3818	s60	PM	F	17.5	146
3819	s46	PM	F	11	147
	s55	PM	M	18	G684
3821	s44	PM	F	17	148
3822	s41	PM	F	15	G664
3823	s7	PM	F	15.5	149
	s23	PM	F	13.5	150
3825	s22	PM	F	19.5	151
3826	s119	SV	M	5.2	
3827	p7	ST	?	3.5	
3828	s70	PM	F	19	
3829	t24	TD	M	192	

Ox 10.13.04

3830	s62	TT	M	78	TAG 152
3831	s116	PM	M	9.5	153
3832	m116	PM	F	20	154
3833	m68	PM	M	17	155
3834	s41	PM	M	7.5	156
3835	s69	PM	M	16	157
3836	s35	PM	F	16	158
3837	s49	PM	M	16	159
3838	s143	PM	F	13.5	160
3839	s23	PM	M	17.5	161
3840	s26	PM	M	14.5	162
3841	s24	PM	M	17	163
3842	s5	PM	M	13.5	164
3843	m21	PM	M	16	166
3844	p40	ST	F	4.4	
3845	s66	SV	M	7.5	
3846	s108	PM	M	11	
3847	m100	PM	F	17	
3848	t84	TD	F	176	
3849	p84	ST	F	4.5	

OX 10.14.04

3850	p95	PM	F	8.5	TAG 167
3851	s90	TT	M	?	
3852	s130	TT	F	69	168
3853	s93	TT	F	68	169
3854	s49	ME	M	64	170
3856	t24	TD	F	139	

OX 10.15.04

3857	s68	TT	M	70	TAG 171
3858	s71	PM	M	10.5	172
3859	s84	TT	F	72	173
3860	s66	PM	F	11	174
3861	s46	TT	M	75	176
3862	s27	PM	M	11	177
3863	s30	PM	F	13.5	178
3864	s119	PM	F	14	
3865	s125	TT	F	70	
3866	p139	PM	M	13.5	
3867	p139	PM	F	9.5	
3868	p7	ST	F	4	
3869	p28	ST	F	3.5	
3870	p31	ST	F	2.5	
3871	p40	ST	?	4	
3872	t84	TD	F	122	
3873	t144	TD	M	150	
3874	p4	ST	F	4.25	

Forest Park 10.26.04

3874	s46	TT	F	75	TAG 179

3875	s43	PM	F	14.5	180
3876	s50	PM	F	14.5	181
3877	s102	PM	M	14	182
3879	s38	PM	M	19.5	183
3880	s95	PM	M	19	184
3883	s59	PM	F	22	185
3884	s72	PM	F	16.5	186
3885	s67	PM	F	12	187
3886	s119	PM	F	19	188
3893	s120	PM	F	18.5	
3894	s69	ST	?	4.8	
3895	s144	PM	F	15.5	
3896	s84	PM	M	16.5	
3897	p144	PM	F	16.5	
3898	p144	PM	M	15	
3666	s65	PM	M	18	29
3646	s60	PM	F	21.5	11
3656	m120	PM	F	20	21
3629	s61	PM	M	16.5	696
3639	s70	PM	M	16	6
3650	s9	PM	M	16.5	15
3670	s132	PM	F	17	32
3659	s91	PM	M	17.5	24
3679	s89	PM	M	17	36

FP 10.27.04

3899	s69	PM	F	14.5	TAG 190
3900	s44	TT	F	80	191
3901	s22	PM	F	13	192
3902	s24	PM	F	14	193
3903	s95	PM	F	19.5	194
3904	s96	PM	F	18	195
3905	s85	PM	F	17.5	197
3906	s12	PM	M	18	
3907	s96s	PM	F	10.5	
3645	s32	PM	M	15	10
3671	s138	PM	M	18	787
3660	s78	PM	F	15.5	25

FP 10.28.04

3908	p55	PM	F	16	TAG 198
3909	s105	PM	F	19.5	200
3910	s71	PM	M	17.5	201
3911	s90	PM	M	13	202
3913	s46	PM	M	18.5	203
3914	s47	PM	M	13	204
3915	s55	PM	M	15	205
3916	m117	TT	F	71	
3626	s139	PM	F	15.5	785
3617	p96	PM	M	16.5	688

FP 10.29.04

3917	s72	PM	F	17.5	TAG 206
3918	s47	PM	M	20	207
3919	s0	PM	M	14	208
3920	s46	PM	M	18	209
3921	s78	PM	M	17	210
3922	s9	PM	M	10	
3923	t7	TD	M	180	
3615	s78	PM	M	17	G686
3621	s90	PM	F	15	G692
3618	s105	PM	M	17	G689

TRNWR 11.2.04

3924	s10	PM	M	13	TAG 210
3925	s83	PM	M	17	211
3926	s11	PM	M	14	212
3928	s23	PM	F	13	213
3929	s140	PM	M	15.5	214
3930	s102	PM	M	15	215
3931	s24	PM	F	15	217
3932	s30	PM	F	11.5	218
3933	s46	PM	M	14	219
3934	m8	PM	F	18	220
3935	m81	PM	F	13	221
3936	p84	PM	F	14	222
3937	p31	PM	M	14.5	223
3938	p48	PM	M	13	224
3940	p43	PM	F	13.5	225
3941	p84	PM	F	18	226
3942	p48	PM	F	15.5	
3943	?	PM	F	15	
3725	s126	PM	M	15.5	70
3709	s128	PM	F	14.5	57
3691	s123	PM	M	16	45
3706	s33	PM	M	18	54
3705	s118	PM	M	14	53

TRNWR 11.3.04

3944	s131	PM	M	11.5	TAG 227
3945	s125	PM	F	13	228
3946	s47	PM	F	20.5	229
3947	s83	PM	M	16	230
3948	s118	PM	F	11.5	231
3949	s4	PM	F	15	232
3950	s45	PM	?	5.7	
3951	s32	PM	M	54	
3690	s7	PM	F	16	44

TRNWR 11.4.04

3952	p48	PM	M	16	TAG 233
3953	s144	PM	F	17	234
3954	s128	PM	M	17	235
3955	s7	PM	F	15	236

3956	s46	PM	M	12	237
3957	s96	PM	M	17	
3958	s103	PM	F	21	
3959	s83	MT	F	38	

TRNWR 11.5.04

3960	s33	PM	F	11.5	TAG 238
3961	s134	PM	M	17.5	239
3962	s128	PM	F	12.5	240

TRYON CREEK 11.9.04

3963	s68	PM	M	16.5	TAG 242
3964	s55	PM	F	15.5	243
3965	s83	PM	M	16	245
3966	s108	PM	M	20	244
3967	s14	PM	F	21.5	246
3968	s128	PM	F	18	247
3969	s119	PM	F	15.5	248
3970	s96	PM	M	18	249
3971	s102	PM	F	18.5	250
3972	m140	PM	F	28.5	251
3973	p91	PM	F	14	
3974	p67	PM	F	4.4	
3975	p115	PM	F	5	
3736	s116	PM	F	19.5	78
3756	s97	PM	F	17.5	98
3745	m112	PM	M	17.5	87

TC 11.10.04

3976	s89	PM	F	18	TAG 252
3977	s92	PM	F	21	253
3978	s114	PM	F	18	254
3979	s99	PM	M	17	255
3980	s137	PM	M		
3981	s43	TT	F	68	
3982	p40	PM	M	11	
3758	S108	PM	M	18	100

TC 11.11.04

3983	s45	PM	F	24	TAG 256
3984	s137	PM	M	20.5	257
3985	s58	PM	M	22	258
3986	s48	PM	F	22	259
3987	s116	PM	M	10	260
3988	s59	PM	F	17.5	261
3989	p79	PM	F	17.5	262
3990	s81	PM	F	13	
3991	s102	SV	M	8.5	
3753	s8	PM	F	20	95
3754	s128	PM	M	19	96
3746	s108	PM	F	13	88
	s60	PM	?	?	

TC 11.12.04

3992	P115	PM	M	12	TAG 263
3993	S66	PM	F	22.5	264
3994	S9	PM	M	17.5	265
3995	S8	PM	F	14.5	267
3996	S20	PM	F	19	268
3997	S60	PM	M	13.5	269
3998	P60	PM	M	19	270
3999	P60	PM	M	15	271
4000	S21	PM	F	12	272
4001	P24	SV	M	8.5	
4002	S132	PM	F	17	
4003	S89	PM	M	16	
4004	P76	ST	?	5.2	
4005	T36	SN	M		
3739	S16	PM	F		82

POWELL BUTTE 11.16.04

4007	s142	PM	F	16	TAG 273
4008	s143	PM	F	18	274
4009	s116	PM	M	17	275
4010	s45	PM	M	15	276
4011	s3	PM	F	17.5	277
3765	s127	PM		15.5	104
3478	s128	PM		15.5	797
3796	s123	PM		15	130
3784	s56	PM		14	118
3466	s60	PM		21.5	775
3782	s33	PM		16.5	116
3797	s26	PM		13.5	131

PB 11.17.04

4012	s25	PM	F	13.5	TAG 279
4013	s111	PM	M	15	280
4014	s104	PM	M	16	281
4015	s57	PM	M	14	282
4016	s5	PM	M	13	283
4017	s33	PM	M	12.5	284
4018	s48	PM	M	17	285
4019	p108	PM	F	13	
4020	p144	PM	F	14	
3491	m96	PM		20	800
3492	s36	PM		16	601

PB 11.18.04

4021	s69	MO	F	15	TAG 286
4022	s142	PM	M	16	287
4023	p84	PM	M	14	288
4024	s77	PM	M	13.5	289
4025	m77	PM	M	16.5	290

PB 11.19.04

4026	s95	GS	F	120	TAG 291
4027	s142	PM	M	13	292

4028	s5	PM	M	13	293
4029	s81	PM	M	17.5	294
4030	s7	PM	F	15	
4031	s139	PM	F	12	
4032	s108	PM	F	18.5	

OXBOW 11.30.04

4033	s78	PM	M	16.5	TAG 295
4034	s77	PM	F	14	296
4035	S108	PM	F	13	297
4036	s128	PM	F	18	298
4037	s134	TT	M	82	300
4038	s28	TT	M	78	301
4039	s32	PM	F	15	302
4040	s59	PM	M	13.5	303
4041	s33	PM	M	14	304
4042	p55	PM	M	13	305
4043	s59	ST	F	4.2	
4044	p48	ST	F	5.0	
4045	p100	ST	F	6.3	
4046	s119	ST	F	5.5	
4047	p144	ST	?	4.3	
4048	p60	ST	?	3.8	
4049	m114	MO	F	17.5	
4050	s68	PM	M	14	
4051	p84	SV	?		
4052	p112	ST	?		
3859	s105	TT	F	72	173
3592	s143	PM	F	14.5	675
3843	s72	PM	M	15	166
3835	s69	PM	M	16	157
3840	s66	PM	M	16	162
3580	s120	PM	M	14	665

OX 12.1.04

4054	s14	PM	F	17	306
4055	m127	PM	F	12	307
4056	p120	PM	F	11	308
4057	s59	PM	F	13	309
4058	s126	PM	F	13	310
4059	s98	PM	M	14	311
4060	s49	PM	M	12	
4061	p64	SV	?	8.4	
4062	s41	ST	?	4.8	
4063	p48	ST	?	4.4	
4064	p31	ST	?	5.7	
2768	s1	GS	F	120	G726
3816	m115	PM	M	17	145
3545	s58	PM	M	11.5	G638
3579	m65	PM	F	12	G664
3819	s45	PM	F	11	147

3841	s24	PM	M	14	163
OX 12.2.04					
4065	S95	GS	M	?	ESC
4066	S118	GS	F	134	312
4067	S114	PM	F	15.5	313
4068	P120	PM	F	10	314
4069	P96	PM	F	14.5	315
4070	P55	SV	M	8.5	
4071	T144	DV	?	?	
3839	s23	PM	M		
3825	s33	PM	F		
OX 12.3.04					
4072	t60	TD	?	?	ESC
4073	s126	TT	M	102	316
4074	s96	PM	M	14	317
4075	s95	PM	M	16.5	318
4076	s23	PM	F	12	
4077	s1	PM	F	10	319
4078	s134	PM	F	8	320
4079	s58	PM	F	10	321
4080	p76	SV	?	6.2	
4081	s96	SV	?	5.4	
4082	p67	SV	?	5.2	
4083	p60	MO	F	12.5	
FOREST PARK 12.7.04					
4084	s12	PM	M	14.5	TAG 323
4085	s120	PM	M	15	324
4086	s144	PM	M	13	325
4087	s107	PM	M	16.5	326
4088	s115	PM	M	15	327
4089	m95	PM	F	11	328
4090	s119	PM	F	13.5	329
4091	s97	PM	F	12	330
4092	p136	PM	F	11	331
4093	s102	PM	M	15	332
4094	p115	PM	F	16	
3615	s82	PM	M	16	G686
3618	s116	PM	M	15	G689
3633	s84	PM	F	15.5	G700
3874	s35	TT	F	73	179
3920	m46	PM	M	16	209
3883	s46	PM	F	16.5	185
3915	s54	PM	M	15	205
3666	s56	PM	M	16.5	29
3639	s47	PM	M	17	6
3647	s23	PM	M	17.5	12
3879	s34	PM	M	17.5	183
FP 12.8.04					
4095	p120	PM	M	13	333

4096	s51	PM	M	15	335
4097	s70	PM	F	13	336
4098	s5	PM	F	13	337
4099	p100	PM	F	12.5	338
4100	p72	PM	F	19	
3649	p36	PM	F	12.5	14
3657	s89	PM	M	20	22

FP 12.9.04

4101	s42	PM	F	14	339
4102	s70	PM	F	12.5	340
4103	p144	PM	M	18	
4104	p115	PM	F	17.5	
3913	s46	PM	M	17.5	203
3875	s44	PM	F	13.5	180

FP 12.10.04

4105	s41	PM	F	18	341
4106	s101	PM	F	14	342
4107	s59	PM	F	15	343
4108	p79	SV	F?	5.6	
4109	p28	ST	?	5	
4110	p127	ME	M	80	
4111	p55	PM	F	11	
3671	?	PM	M		G787

TRNWR 12.14.04

4112	s72	PM	F	17.5	344
4113	s23	PM	M	17.0	345
4114	s118	PM	F	15.0	347
4115	s71	PM	M	13.5	348
4116	s93	PM	F	13.5	349
4117	s141	PM	M	16.0	351
4118	s82	PM	F	13.0	352
4119	s112	PM	F	15.5	353
4120	s9	PM	M	16.5	354
3706	s20	PM	M	16.5	54
3725	s128	PM	F	17.5	70
3931	s23	PM	F	21.0	217
3694	s26	PM	F	16.0	48
3713	s49	PM	F	12.5	61
3707	s35	PM	F	14.5	55
3932	s29	PM	F	14.5	218
3730	s24	PM	M	15.0	72
3937	s32	PM	F	14.0	223
	s119	PM			
	m80	PM			

TRNWR 12.15.04

4121	s130	PM	F	17.5	355
4122	s131	PM	M	15.0	356
4123	s47	PM	F	16.0	357?

3941	s21	PM	F	13.0	226
3955	s126	PM	M	13.5	236
3928	s21	PM	F	13.0	213

TRNWR 12.16.04

4124	s132	PM	M	13.5	359
4125	s9	PM	F	13.5	360
3705	s128	PM	M	13.5	53
3719	s12	PM	M	16.5	65
3707	s36	PM	F	9.0	55
3729	s102	PM	F	13.0	71
3712	m68	PM	M	16.0	60

TRNWR 12.17.04

4126	s68	PM	M	15	361
4127	p141	PM	M	11	362
4128	s53	PM	F	13.5	363
4129	s7	GS	F	148	364
4130	s25	NG	F	13	
4131	p139	ST	F	5.8	
3961	s143	PM	M	17	239

TRYON CREEK 1.11.05

4132	S44	PM	M	19	366
4134	S93	PM	M	16.0	367
4135	S91	PM	M	17	368
4136	S89	PM	F	14	369
4137	S106	PM	M	18	370
4138	S87	PM	F	20	371
4139	S114	PM	M	18	372
4140	S60	PM	F	14	373
4141	S115	PM	F	16	374
4142	S32	ST	?	5	
4143	S44	PM	F	15	
4144	S117	PM	F	19	
4145	S43	PM	F	18	
4146	S9	ST	?	6	
3994	S17	PM	M	21	
3971	S90	PM	F	18	

TC 1.12.05

4147	S6	PM	M	16	376
4148	S24	PM	M	18.5	377
4149	S116	ST	F?	5	
4150	S8	ST	F	5.5	
4151	S20	PM	F	14	
4152	S67	PM	M	17	
4153	S12	PM	F	18	
4154	S35	PM	F	14	
4155	P28	ST	?	5.5	
4156	S130	ST	F	5.3	
	T127	SN	M		
3744	S68	PM	M	20	86

TC 1.13.05

4157	S95	PM	F	20	378
4158	S44	PM	M	?	ESC/NBS
4159	S70	PM	M	16	379
4160	S89	PM	M	17	381
4161	P120	PM	M	14.5	
4162	S105	PM	?	6.0	
	T139	SN	F		

TC 1.14.05

4163	S32	PM	M	17	382
4164	S47	ST	?	5.4	
4165	S96	ST	?	6.0	
4166	S119	PM	F	14	
4167	S66	ST	?	4.4	
4168	P40	ST	?	4.5	
4169	P40	ST	?	4.7	
3993	S65	PM	F	22	264

POWELL BUTTE 1.18.05

4170	S105	PM	M	13	383
4171	S11	PM	F	14	384
4172	S29	PM	M	15	385
4173	S4	PM	F	14	386
4174	S56	ST	?	5.0	
3792	P120	PM	M	12.5	126
4018	S46	PM	M	17.5	285
4009	S117	PM	M	18	275
3776	S84	PM	F	16	112
3796	S115	PM	M	15.5	130
4010	S58	PM	M	16.5	276
4022	S143	PM	M	15	287

PB 1.19.05

4175	S10	PM	M	16	387
4176	S58	PM	F	15.5	388
4177	S84	PM	M	16	389
3784	S65	PM	F	14.5	118

PB 1.20.05

4179	S31	PM	M	11	390
4180	S47	PM	M	16.0	391
3797	S2	PM	F	13.5	131

PB 1.21.05

4181	S22	PM	M	151 6	392
3796	S85	PM	M		130

OXBOW 1.25.05

4182	S36	PM	M	17	393
4183	S54	PM	M	13.5	395
4184	S57	PM	F	15	396
4185	S143	PM	M	15	397
4186	S3	SV	?	7	

4186.5	S87	PM	F	12	DIT/NBS
4187	S125	SV	?	7.4	DIT/NBS
4041	S43	PM	M	16.5	304
4033	S62	PM	M	?	295
3809	S106	PM	M	?	140
3824	S24	PM	F	16.5	150
3840	S59	PM	M	15	162
3816	S117	PM	M	15	145

OX 1.26.05

4188	P120	PM	M	13	398
4189	S81	PM	F	15.5	400
4190	S15	GS	F	150	402
4191	S24	PM	M	15.5	394
4192	S117	SV	F	5.7	
4193	S9	SV	F	6.5	
4194	S60	SV	?	5.1	
4195	S47	SV	?	5.3	
4196	S62	MO	M	14	
	P120	PM			
3578	S36	PM	M	15.5	
4033	S87	PM	M	16.5	
4059	S111	PM	M	15	
4069	S106	PM	F	14.5	

OX 1.27.05

4197	S5	PM	F	12	
4198	S128	ST	F	4.5	
4199	S80	PM	M	16	403
4200	P84	ST	F	4.4	
4048	S93	PM	M	14.0	303
4056	S128	PM	F	15.0	308

OX 1.28.05

4201	S22	ST	F	5.3	
4202	S41	ST	M	5.7	
4203	S29	ST	?	5.5	
4204	S59	PM	M	14.5	
4205	S102	PM	F	14.0	
3862	P60	PM	M	14.5	177

FOREST PARK 2.1.05

4206	S132	PM	M	14.5	404
4207	S75	PM	F	15.5	405
4208	S20	PM	M	14	406
4209	S99	PM	F	6.0	
4210	T103	SN	M	510	
4089	S95	PM	F	12.5	328
4085	S120	PM	M	16.0	324
4106	S117	PM	F	16.0	342
4090	S119	PM	M	13.5	329

FP 2.2.05

4211	S133	PM	M	15	407

4212	S108	PM	M	19	408
4213	S130	PM	F	4.5	
4214	S119	PM	F	11	
4215	S127	PM	M	12	
4216	P31	ST	F?	4.0	
4217	S82	SV	F?	4.5	
4218	P4	ST	?	4.5	
4219	P48	ST	?	4.5	
3626	S125	PM	M	18	785
3909	S105	PM	F	17	200
4088	S117	PM	M	13	327

FP 2.3.05

4220	S80	PM	M	15	410
4221	S24	PM	F	13	411
4222	S132	ST	?	4.5	
4223	S140	ST	?	4.5	
4224	P31	ST	?	4.5	

FP 2.4.05

4225	P72	PM	F	13.5	421
4226	P55	PM	M	16	414
4227	P55	ST	F	3.4	
4228	P124	ST	M	5.0	
4229	P84	ST	?	4.7	
4230	S133	ST	M ?	5.1	
3908	S140	PM	F	15	198

TRNWR 2.8.05

4231	S46	PM	M	15	417
4232	S47	PM	M	17	416
4233	S103	PM	F	13	415
4234	S35	ST	F?	5.5	
3929	S140	PM	M		
3725	S126	PM	F	16	
3705	S128	PM	M	16.5	
3713	S53	PM	F	15.5	
4115	S69	PM	M	16	
3718	S21	PM	M	16	
4120	S9	PM	F	17	
4112	S72	PM	F	12.5	
	S143	PM			
	S119	PM			

TRNWR 2.9.05

4235	S95	PM	M	16.5	418
4236	S86	ST	F	4.5	
4237	S140	ST	F?	4.8	
4238	P48	ST	F	11.5	
3706	S31	PM	M	16.5	54
4126	S105	PM	M	15	361
3929	S37	PM	M	17.5	214

3961	S122	PM	M	14.5	239
	S128	PM			
	S48	MM			

TRNWR 2.10.05

4239	S72	PM	M	14	419
4241	S118	ST	M ?	5.5	
4242	S8	ST	F	4.8	
4243	P76	ST	M ?	6.1	
4244	S144	ST	F	5.5	
4245	S29	ST	M	5.5	
4246	S25	ST	M	12	
	T96	SYB			
3948	S130	PM			231
3932	S18	PM	M	13	218

TRNWR 2.11.05

4247	S78	ST	?	5.7	
4248	S81	PM	M	14.5	
	T31	DV			

TRYON CREEK 2.15.05

4249	S32	PM	F	21	421
4250	S35	PM	F	21	422
4251	S31	PM	F	19	423
4252	S7	PM	M	17	424
4253	S22	PM	M	19	425
4254	S91	PM	M	17	426
4255	S72	PM	F	15	427
4256	S92	PM	F	14	428
4257	S90	PM	M	17	429
4258	S106	PM	F	17	430
4259	S117	PM	M	15	431
4260	P84	ST	?	7.0	
4261	S119	TT	F	75	432
4262	S61	ST	?	6.3	
4263	S75	ST	M ?	5.2	
4264	S118	ST	M ?	5.2	
4265	S40	ST	M/	6.0	
4266	S142	PM	M	18	
4267	S67	ST	F?	6.5	
4268	S71	PM	M	17	
3744	S77	PM	M	20	86
3983	S68	PM	F	24	256
3994	S5	PM	M	21	265

TC 2.16.05

4269	S17	PM	M	8.5	433

4270	S8	PM	F	14.5	434
4271	S96	PM	M	18	435
4272	S36	PM	M	20	436
4273	S47	PM	F	14.5	437
4274	S21	PM	F	15.5	438
4275	P4	PM	M	8.5	
4276	P120	PM	M	13.5	
4277	P72	ST	?	5.2	
4278	S116	ST	F?	6.2	
4279	P108	ST	M	5.8	
4280	S103	ST	M	5.6	

TC 2.17.05

4281	S10	PM	M	17	439
4282	P68	PM	F	16	440
4283	S101	PM	M	19	441
4284	S94	PM	F	15	442
4285	S107	PM	M	?	
4286	S127	PM	M	16.5	443
4287	S104	ST	M ?	5.5	
4288	P144	ST	?	4.5	
4289	S90	ST	M	5.5	
4290	S72	ST	M/	5.0	
4291	S120	ST	M	5.0	
4292	S118	ST	?	5.0	
4293	P84	ST	M	4.5	
4294	S32	PM	M	13	
4295	S84	PM	F	17	
4296	S137	PM	M	16	
4297	S15	PM	M	10	
	P31	ST	?		
	P31	ST	?		
	P31	ST	?		
	P31	ST	?		
	P31	ST	?		

TC 2.18.05

4298	S0	PM	M	16	444
4299	S90	PM	M	17	445
4300	S77	PM	F	13.5	446
4301	S130	PM	F	13.5	447
4302	S120	PM	M	17	448
3969	S107	PM	F	19	248
4157	S94	PM	F	15.5	378
	P4	ST			

POWELL BUTTE 3.1.05

4303	S23	PM	F	13	449
4304	S116	PM	M	15	450
4305	S104	ST	F?		
	T12	SYB			

4176	S72	PM	F	17	388
4173	S3	PM	F	18	386
3478	S129	PM	F	18	797
4175	S22	PM	M	15	387
3792	S108	PM	F	16	126
3796	S114	PM	M	20	130
3784	S56	PM	F	13	118
PB 3.2.05					
4306	S56	PM	F	14	451
4307	S104	ST	?	5.5	
4170	S91	PM	M	15	383
4172	S25	PM	M	17	385
PB 3.3.05					
4308	P108	ST	?	4.9	
PB 3.04.05					
4309	S128	SV	?	4.7	
4310	S84	PM	M	15	452
OXBOW 3.8.05					
4311	S144	PM	M	14.5	453
4312	S72	PM	F	22	454
4313	S82	PM	M	18	456
4314	S88	PM	M	16.5	457
4315	S107	PM	M	13.5	458
4316	S24	PM	M	16.5	459
4317	P19	SV	M ?	7.0	
4318	P96	ST	F?	4.5	
4319	P96	ST	F?	5.0	
4058	S115	PM	F	16	310
4079	S87	PM	F	13.5	321
4034	S59	PM	F	20	296
2768	M41	GS	F	105	726
4189	S95	PM	F	14.5	400
OX 3.9.05					
4320	P60	PM	M	15.5	460
4321	S106	PM	M	16	461
4322	S23	PM	F	14.5	462
4323	S96	GS	M		
4324	S128	ST	M	4.8	
4325	P96	ST	M	5.4	
4326	S115	ST	F	5.3	
4327	S35	ST	M	6.4	
4328	P36	SV	F	5.2	
4057	M58	PM	F	13.5	
OX 3.10.05					
4329	S94	ST	F	6.0	
4330	S46	ST	F	5.0	
4331	P144	ST	M	4.6	
4332	S5	SV	M	5.5	

OX 3.11.05

4333	S60	TT	M	52	463
4334	S54	SV	M	6.4	
4335	S43	SV	F	5.8	
4336	P120	SV	F	6.3	
4337	P108	ST	F	6.2	
4338	P80	ST	F	6.5	
4339	S55	ST	M	4.5	
4034	S66	PM	F	15	296

FOREST PARK 3.15.05

4340	S72	PM	F	13.5	464
4341	S99	PM	M	17	465
4342	S83	PM	M	13.5	466
4343	M132	PM	M	13	467
4344	S116	PM	M	16	468
4345	M96	PM	M	12	
3920	S46	PM	M	17	209
4085	S120	PM	M	16.5	324
4207	S90	PM	F	15.5	405

FP 3.16.05

4346	S83	PM	M	14	469
4347	S22	PM	M	12.5	470
4348	S116	PM	M	15	471
4349	S126	SV	M	5.0	
4350	S120	ST?	M	7.0	
3908	M140	PM	M	15	198

FP 3.17.05

4351	S96	PM	M	16	472
4352	S120	PM	M	14	473
4353	S58	ST	F	4.3	
4354	S131	ST	F	4.5	
4220	S82	PM	M	17	
4089	S92	PM	F	13	

FP 3.18.05

4355	S131	PM	M		

Tualatin River NWR 4.5.05

4356	S12	PM	F	22	475
4357	S82	PM	F	14	476
4358	S83	PM	M	15	477
4359	S139	PM	M	20	478
4360	S84	ST	F	6.6	
4361	P127	ST	F	5.6	
4362	P127	ST	F	5.6	
3932	S20	PM	F	23	218
3706	S9	PM	M	20	54
3708	S127	PM	M	17	56
3713	S114	PM	F	17	61
3948	S118	PM	F	17	231

TRNWR 4.6.05

4363	S35	PM	F	80	479
4364	S53	ST	F	7.0	DIT/NBS
4365	S66	ST	F	5.4	DIT/NBS
4366	S87	ST	F	6.2	DIT/NBS
	S80	PM			
3705	S65	PM	M	18.5	53

TRNWR 4.7.05

4367	S23	PM	M	15	480
4368	S92	PM	M	13	481
4369	S46	ST	F	6.0	
4370	S80	SV	F	6.5	
	T96	DV			

TRNWR 4.8.05

4371	S117	PM	M		482
4372	S128	ST	M ?		
4373	S141	ST	F		
	T120	MM			REL

TRYON CREEK STATE PARK 4.12.05

4374	S127	PM	M	19	483
4375	S23	PM	F	12	484
4376	S58	PM	F	20	486
4377	S55	PM	M	17	487
4378	S59	PM	M	17	
4379	S48	PM	F	15	488
4380	S104	PM	M	19	489
4381	S107	PM	F	21	490
4382	S120	TT	M	75	491
4383	S72	TT	F	80	492
4384	S68	TT	M	70	493
4386	S45	PM	M	19	494
4387	S48	PM	M	18	495
4388	S122	PM	M	17	496
4389	S128	PM	M	18	497
4390	S132	PM	M	22	498
4391	S20	PM	F	15	499
4392	S30	PM	F	19	500
4393	S46	PM	M	19	501
4394	S24	PM	M	18	502
4395	S36	ST	F	7.5	
4396	P124	ST	F	5.5	
4301	S129	PM	F	22	447
4300	S62	PM	F	24	446
3477	S19	PM	M	18	86
4141	S115	PM	F	25	374
4299	S102	PM	M	19	445
4284	S91	PM	F	17	442
3969	S106	PM	F	26	248
4270	S6	PM	F	16	434

4272	S33	PM	M	17	436
4253	S10	PM	M	17	425
4274	S22	PM	F	17	438
4147	S11	PM	M	18	376
4271	M105	PM	M	18	435

TC 4.13.05

4397	S104	PM	F	17.5	504
4398	S108	PM	M	22.5	506
4399	S129	PM	F	24.5	507
4400	S126	PM	F	27	508
4401	S7	PM	M	18.5	511
4402	S144	PM	M	20.5	512
4403	S140	PM	F	20	513
4404	S143	PM	F	16	514
4405	S118	PM	M	21.5	515
4406	S79	PM	M	15	516
4407	S77	PM	M	18	517
4408	S33	PM	M	19.5	518
4409	S54	PM	M	19	519
4410	S63	PM	M	20	520
4411	P36	PM	M	18	521
4412	P96	ST	F	3.9	
4413	S48	PM	M	13.5	
4414	P64	SCAT	F	99	
4415	P108	ST	M	10	
4416	P108	ST	M	12.5	
4287	S89	PM	M	20.5	429
	S130	PM			
	S6	PM			
	S29	PM			

TC 4.14.05

4417	S141	PM	F	17	521
4418	S140	PM	F	15	522
4419	S114	PM	M	19.5	523
4420	S132	PM	F	16.5	524
4421	S117	PM	M	20	525
4422	S37	PM	F	20	526
4423	S69	PM	F	16.5	527
4424	S23	PM	F	16	528
4425	S2	PM	F	19	529
4426	S15	PM	F	15.5	530
4427	S22	PM	F	17.5	531
4428	M93	PM	F	13.5	532
4429	P84	ST	F?	4.3	
4430	P36	PM	M	19.5	533
4431	S81	PM	M	16	
4432	P72	ST	F	4.0	
4433	S36	PM	M	17	
4434	P40	ST	F	5.3	

4435	S31	PM	F	18.5	
4257	S89	PM	M	20.5	429
4255	S72	PM	F	16	427
	P4	ST	?	5.4	
	P28	ST	?	5.8	

TC 4.15.05

4436	S94	PM	M	20	535
4437	S114	PM	M	17	536
4438	S81	PM	F	17.5	537
4439	S106	PM	M	15	538
4440	S92	ST	F	3.7	
4441	S84	SV	F	9.3	
4442	S43	ST	F	4.5	
4443	P67	ST	M	4.3	
4444	P67	ST	F	4.6	
4445	S46	ST	F	4.6	
4446	S57	PM	M	18	
	S72	PM			

POWELL BUTTE 4.26.05

4447	P16	MT	M	40	539
4448	S20	PM	M	20	540
4449	S144	PM	M	20	542
4450	S23	PM	F	20	543
4451	M130	PM	F	18	544
4452	S11	PM	F	20	545
4454	S29	PM	M	20	546
4455	S101	PM	M	20	549
4456	S119	PM	M	20	550
4457	S56	PM	M	19	551
4458	S42	PM	F	16	552
3792	M88	PM	F	19	126
3796	S114	PM	M	17	130

PB 4.27.05

4459	S56	PM	M	22.5	554
4460	S33	PM	M	19.5	555
4461	S22	PM	F	20.5	556
4462	P72	PM	M	18.5	558
4463	S91	MO	M	17.5	

PB 4.28.05

4464	P72	PM	F	15.5	559
4465	P72	PM	F	14.0	560
4466	S25	PM	M	17	561
4467	S69	PM	F	17	562
4468	P124	ST	M	5.5	
4469	P55	ST	F	5.7	
	S141	PM			

PB 4.29.05

4469	P43	MO	M	21	563
4470	P84	PM	F	14	564

4471	M56	PM	F	21	565
4472	S10	PM	M	21	566
4473	S51	PM	M	20	567
4474	P115	MT	F	26	
4475	S111	SV	F	6	
4476	P48	MT	M	21	
	S1	PM			

OXBOW 5.3.05

4477	M89	TT	M	75	568
4478	S18	TT	M	80	569
4479	S93	TT	F	85	570
4480	S21	TT	F	85	571
4481	S106	TT	M	85	572
4482	S111	TT	M	95	573
4483	S108	TT	M	85	574
4484	S117	TT	F	100	575
4485	S104	TT	M	90	576
4486	S60	PM	M	19	577
4487	S69	PM	M	16	578
4488	S61	PM	M	14	579
4489	S115	PM	M	20	580
4490	P52	ST	F	4.4	
4491	P84	ST	F	4.4	
4492	P127	ST	F	4.4	
4493	P31	SV	F	7.9	
4494	P136	ST	M	4.2	
4495	P136	SV	F	4.0	
3859	S116	TT	F	90	173
4058	S131	TT	F	85	316
4073	S127	PM	F	19	310

OXBOW 5.4.05

4496	P108	PM	F	17.5	581
4497	S83	TT	F	70	582
4498	S65	PM	M	18.5	583
4499	S106	TT	M	78	584
4500	S90	PM	M	19.5	585
4501	S36	TT	M	85	586
4502	S68	PM	F	14	587
4503	S128	TT	M	78	588
4504	S131	PM	M	17.5	589
4505	S142	PM	F	23	590
4506	S21	PM	F	15	591
4507	S60	PM	F	22	592
4508	S24	TT	F	72	593
4509	P64	ST	F	4.2	
4510	P64	NG	?	?	
4511	S31	SV	F	7.2	
4512	P24	ST	F	3.8	
4513	P96	SV	F	8.5	

4514	P144	ST	F	4.3	
4515	S126	NG	F	9.0	
4516	P136	ST	F	4.0	
4517	P7	ST	F	3.7	
4190	S140	GS	F	130	402
4312	S80	PM	F	17	454
4333	M129	TT	M	82	463

OXBOW 5.5.05

4518	M65	TT	F	90	594
4519	S19	PM	M	17	595
4520	P36	ST	M	5.5	
4521	S125	SV	F	5.5	
	S72	SV			

OXBOW 5.6.05

4522	P64	NG	F	8	
4523	S35	PM	M	22	596
4524	S82	TT	F	70	597
4525	S72	ST	M	5.6	
4526	P144	ST	F	4.5	
4527	S119	MO	F	19	
4528	S32	SV	M	8.9	
4311	M7	PM	M	18.0	453

FOREST PARK 5.17.05

4529	M82	PM	F	21	598
4530	S71	PM	M	22	599
4531	S83	PM	M	23.5	601
4532	S141	PM	M	18.5	602
4533	S96	PM	M	18.5	603
4534	S119	PM	F	16	604
4535	S107	PM	F	18.5	605
4536	S116	PM	F	16	606
4537	P139	ST	F	5.6	
4086	S143	PM	M	19.5	325
4220	S25	PM	M	20	410
4089	S95	PM	F	15	328
4208	S137	PM	M	19	406

FP 5.18.05

4538	S96	PM	F	16	608
4539	S117	PM	M	18.5	609
4540	S34	ST	F	6.6	
4541	P84	ST?	F	4.2	
4542	P60	SV	M	9.5	
4543	P12	ST	F	6.8	
4544	T127	TD	F	204	
4085	S107	PM	M	24.5	324

FP 5.19.05

4545	S30	PM	M	18.5	610
4546	S36	PM	F	19	611
4547	S46	PM	M	24	612

4548	S7	PM	F	18	614
4549	S83	PM	M	20	615
4550	S127	PM	F	17.5	616
4551	T127	TD	M	220	617
4552	P7	PM	M	21.5	
4553	P120	SV?	F	7.5	

FP 5.20.05

4554	P60	PM	F	19.5	618
4555	S107	PM	F	14	619
4556	P84	PM	M	22.5	621
4557	S30	PM	F	17	622
4558	S141	PM	F	16	
4559	P36	ST	F	4.0	
4560	S58	ST	F	3.7	

TRYON CREEK STATE PARK 5.24.05

4561	S113	PM	M	16	600
4562	S115	PM	M	17	626
4563	S141	PM	M	18	627
4564	S138	TT	M	100	628
4565	S143	PM	F	16	629
4566	S140	PM	M	17	630
4567	S131	PM	F	20	632
4568	S83	PM	M	21	633
4569	S57	PM	F	26	634
4570	S36	PM	F	22	635
4571	S19	PM	M	20	636
4572	M30	PM	M	15	637
4573	S31	PM	F	16	638
4574	S12	PM	M	20	639
4575	S20	PM	M	18	640
4576	S33	PM	M	22	641
4577	S21	SV	F	9	
4578	P84	ST	?	4	
4579	P67	ST	F	4.4	
4580	P4	ST	F?	3.8	
4581	P84	ST			
4582	P67	ST			
4583	P55	ST	F?	6.0	
4584	P110	ST		4.4	
4585	P124	ST		4.8	
4586	P19	SV		4.4	
4390	S132	PM	M	21	498
4588	P96	ST			
4589	P96	ST		4.9	
4300	S97	PM	F	28	446
4418	S142	PM	F	15	522
4388	S134	PM	M	21	496
4399	S128	PM	F	27	507
4427	S80	PM	F	21	531

3744	S77	PM	M	21	86
4299	S112	PM	M	20	445
4407	S67	PM	M	21	517
4250	S35	PM	F	22	422
3969	S95	PM	F	28	248
4425	S17	PM	F	20	529
4394	M36	PM	M	19	502
	T60	SN	F		

TC 5.25.05

4590	S58	PM	F	18.5	624
4591	S99	PM	F	22.5	642
4592	S54	PM	F	21.5	643
4594	S45	PM	M	21	644
4595	S24	PM	M	22	645
4596	S89	PM			
4596.1	P84	ST		4.1	
4597	P76	SV	F	4.4	
4598	P64	ST	F	4.6	
4598.1	P79	SV	F	3.9	
4599	P12	ST		5.0	
4600	S8	SV	M	6.0	
4601	S109	ST	M	4.7	
4602	S107	TT		70	
4602.1	P4	ST	F	4.8	
4603	P7	SV	F	6.1	
4604	P16	ST	F	4.4	
4605	P16	ST	F	5.8	
4605	S53	TT	M	75	482

TC 5.26.05

4606	P40	PM	F	26	646
4607	S120	PM	F	18.5	647
4608	S93	PM	M	22	648
4609	S33	PM	M	19	650
4610	S26	PM	F	17	651
4611	S80	PM	M	20	652
4612	S0	PM	F	21.5	653
4613	S48	PM	F	19.5	654
4614	P24	SV	F?	4.4	
4615	P139	ST	F?	5.1	
4616	P12	ST	F	5.5	
4617	P12	ST	F	4.7	
4618	S117	PM	F	25.5	
4619	P115	ST	F	5.8	
4620	P115	ST	F	6	
4621	P4	SV?	F	4	
4622	S20	ST	F	4.4	
4623	P55	SV	F	4.6	
4624	P96	ST	F	4.9	
4625	P72	SCAT	F?	88	

	P72	SCAT	F?		
189	S105	PM	M	20	
TC 5.27.05					
4626	S47	PM	M	18	655
4627	S41	PM	M	21.5	656
4928	S81	PM	F	13.5	657
4629	S121	PM	M	20	658
4630	S116	PM	F	19.5	659
4631	S0	PM	F	20	660
4632	S59	PM	M	20.5	661
4633	P96	ST	F?	4.5	
4634	P96	ST	F	5.8	
4635	P55	SV		3.9	
4637	P124	SV		4.3	
4638	S14	SV	M	8	
4639	S15	PM	F	13.5	
4640	P136	SV	F	5	
4641	P31	SV		3.5	
4642	S23	ST	F	4.2	
4643	P48	SV		4.6	
4644	T79	SN	F	425	
Tualatin River NWR 5.31.05					
4645	S83	PM	F	24	662
4646	S103	PM	F	17	663
4647	S91	PM	M	19	666
4648	S118	PM	M	14.5	
4649	S116	PM	F	21	667
4650	S68	PM	M	21	668
4651	P139	ST	M	5	
4652	P139	ST		5.5	
4653	P139	ST		7	
4654	P36	SV	F	4.5	
4655	P55	ST		5	
4656	P64	SV		5	
4657	P76	SV		4.3	
4658	P100	ST		3.9	
4659	P112	ST		4.2	
4660	P115	ST		4.5	
4661	P132	ST	M	5	
4662	P7	ST		5.7	
4663	P7	ST		4.9	
4664	P79	ST		5.8	
4358	S106	PM	M	17	
3706	S42	PM	M	21	
	T103	DV			
	P31	DV			
	S46	PM			
	S105	TT			
	P139	ST			

	P139	ST			
	P55	ST			
	P79	ST			

TRNWR 6.1.05

4665	S117	TT	M	70	675 DIED
4666	S114	TT	M	75	670
4667	S115	PM	M	24	671
4668	P48	PM	F	18.5	672
4669	P36	MT	F	40	
4670	P36	MT	F	35	
4671	P36	MT	M	50	
4672	P28	MT	F	40	
4673	P64	ST	F	4.1	
4674	P7	ST	F	5.3	
4675	P40	ST	F	4.5	
4676	S144	ST	F	5.6	
4677	P36	MT	M	37	
4678	P36	MT	M	46	
	S92	TT	F		
	T96	DV			
	P79	SV			

TRNWR 6.2.05

4679	S128	PM	M	19.5	625
4680	S106	TT	F	75	655
4681	S6	TT	M	85	631
4682	S87	TT		85	
4683	S92	TT	F	80	
4684	P136	ST	M	6.5	
4685	S31	MT	F?	40	
4686	P36	ST		5.2	
4687	S140	PM	F	21	
4371	S102	PM	M	21.5	482
	S80	DV			
	P115	SCAT			
	S43	TT			

TRNWR 6.3.05

4688	S2	PM	M	17	674
4689	S141	PM	F	17	675
4690	S115	TT	F	52.5	676
4691	S69	TT	F	56.5	DIT/NBS
4692	S78	ST	M	4.6	DIT/NBS
4693	P112	ST	F	4.1	DIT/NBS
4694	S96	ST	F	6.8	DIT/NBS
	T12	SV			REL/NBS
	T48	DV			REL/NBS
	T108	MM			REL/NBS

POWELL BUTTE 6.7.05

4695	S117	PM	M	21	677
4696	S50	PM	M	15	678

4697	S48	PM	M	20	679
4698	S12	PM	M	22	680
4699	M120	PM	F	27	681
4700	P60	NG	?	9	
4701	P144	ST	?	4.4	
4702	P12	SV	?	4.4	
4703	P52	MO	F	20	
	T108	DV	?		
4457	S71	PM	M	20	551
4464	S95	PM	F	20	559
4473	S143	PM	M	18	567

PB 6.8.05

4704	S46	PM	M	15	682
4705	S128	PM	F	17.5	683
4706	P144	PM	M	19	684
4707	P48	SV		3.4	
4708	P108	ST		3.7	
4709	P76	SV		3.6	
4710	M31	TT	F	75	
4711	P31	SV		3.6	
4712	P52	MO	M	20	
4713	P60	ST	F	7.9	
4714	P60	SV		5.3	
4715	P64	SV	M	4.1	

PB 6.9.05

4717	S143	PM	F	17.5	685
4718	S56	PM	F	18	686
4719	P64	SV	F	3.8	
4720	P52	SV	F	6	
4721	P24	SV	F	6.7	
4722	P19	SV	F	6.5	
4456	S118	PM	M	20.5	550

PB 6.10.05

4723	S71	PM	F	16.5	687
4724	S7	PM	M	15.5	688
4725	P60	MO		20	
4726	S100	SV	F	7.3	
4727	P120	PM	F	18	
4728	P31	ST	F?	4.0	
4729	P40	SV	F	6.4	
4730	P126	ST	F?	4.3	
	P144	ST			
	P124	SV			

OXBOW 7.05.05

4731	S18	ME	F	52	689
4732	S84	TT	M	72	690
4733	S29	TT	F	100	691
4734	S33	PM	M	20	692
4735	S30	TT	F	90	693

4736	S42	PM	M	15.5	694
4737	S131	ST	F	5.4	
4738	P52	NG	M	9.5	
4739	P12	PM	F	10.5	695
4740	S104	SV	M	9.0	
4741	P7	ST	?	4.4	
4742	P55	ST	?	4.5	
4743	S130	ST	?	4.9	
4744	T144	SB	?	?	
4519	S127	PM	M	16.5	595
4190	S132	GS	F	96	402
4504	S120	PM	M	21	589
4312	P67	PM	F	22	454

OXBOW 7.06.05

4746	S120	TT	M	75	696
4747	S125	TT	M	?	
4748	S66	PM	F	20.5	697
4749	S103	PM	F	10	698
4750	S105	PM	M	16.5	699
4751	S93	PM	M	15	700
4752	S130	PM	M	9.5	701
4753	P67	PM	M	6.5	702
4754	P36	ST	F	4.6	
4755	P144	NG	F	9.5	
4756	P88	ST	F	4.4	
4757	P52	SV	M	7.7	
4758	P126	ST	F	4.0	
4759	P84	ST	F	3.8	
4760	P96	ST	F	4.0	
4761	P4	ST	M	5.0	
4508	S23	TT	M	72	593
4500	S105	PM	M	20.5	585

OXBOW 7.07.05

4762	S120	PM	F	22	703
4763	S91	PM	M	17	704
4764	P16	SV	?	7	
4765	S85	SV	?	7.5	
4766	S118	SV	M	5	
4767	P76	ST	M	5.5	
4768	S117	SV	M	9.5	
4499	S106	TT	M	76	584
4506	P12	PM	F	18	591
	S111	PM			

OXBOW 7.08.05

4769	S114	TT	F	95	705
4770	S135	PM	F	9	708
4771	S117	PM	M	20	710
4772	S59	PM	M	17.5	711
4773	S27	PM	M	15	712

4774	S108	PM	F	17	714
4775	S14	SV	F	7	
4776	S13	SV	F	6	
4777	P52	MO	M	19	
4778	P76	ST	?	4.3	
4779	P132	SV	F	4.8	
4780	P144	SV	M	7.7	
4781	S107	ST	?	4.5	

FOREST PARK 7.13.05

4782	S83	PM	M	20	715
4783	S30	PM	M	20.5	716
4784	S59	PM	F	19.5	717
4785	S46	PM	M	15.5	718
4786	P36	SV	?	3.1	
4532	S139	PM	M	18	602
4536	S127	PM	F	22	606
4550	S116	PM	F	20	616
4547	S47	PM	M	21	612
4530	S69	PM	M	24	599
4548	S24	PM	F	20.5	614
4529	S107	PM	F	20.5	598
4533	S81	PM	M	19.5	603
4085	S118	PM	M	23.5	324
	S19	PM			

FOREST PARK 7.14.05

4787	M70	PM	F	21	719
4788	S120	PM	M	25	720
4789	S0	PM	M	18	721
4790	S24	PM	M	19	722
4791	S139	PM	F	21	723
4792	S47	PM	F	16	724
4793	P96	SV	F	4.8	
4794	S90	ST	F	4.3	
4556	S99	PM	M	23	621

FOREST PARK 7.15.05

4795	S34	PM	M	17	725
4796	S39	PM	M	15.5	726
4797	S2	PM	F	18	727
4798	S104	ST		4	
4799	P7	SV		4.5	
4801	S143	ST		4	
4802	S86	SV	F	4.5	
3632	S69	PM	M	18	

FOREST PARK 7.16.05

4803	S29	ST		4.0	
4804	S44	PM	M	14.5	728
4805	P72	ST	F	4.5	
4806	P40	ST	F	5.0	
4807	S107	SV	M	3.5	

4808	P7	SV	F	5.0	
4531	S83	PM	M	21.5	601

TRNWR 7.19.05

4809	S143	PM	F	16	729
4810	S118	TT	M	65	730
4811	S24	TT			
4812	P139	ST	F	4.6	
4813	S19	ST	F	4.1	
4814	S119	ST	F	4.3	
4815	P48	ST	F	3.7	
4816	P48	ST	F	4.3	
4817	T144	DV			
4647	S90	PM	M	17	666
4667	S30	PM	M	20	671
4359	S9	PM	M	21.5	478
4688	S29	PM	M	18.5	674

TRNWR 7.20.05

4818	S31	PM	F	23.5	731
4819	P36	ST	F	4.4	
4820	P88	ST	M	5.0	
4821	P76	ST	F	5.1	
4822	P79	ST	M	5.3	
4679	S131	PM	M	20	625

TRNWR 7.21.05

4823	S89	PM	M	15	732
4824	S33	TT	M	65	733
4825	S7	ST	F	3.9	
4826	P55	SV		4.0	
4827	S10	ST		3.7	
	P48	ST			

TRNWR 7.22.05

4823	P42	PM	M	17	734
4824	P79	MT	M	35	735
4825	P79	MT	F	17	736
4826	P36	MT		47	
4827	P28	ST	F	5.3	
4528	P136	ST	F	6.2	
4829	S3	NG		14	
48300	S141	ST	F	4.4	
4831	S3	ST	F	4.8	
	T60	MM			

TRYON CREEK 8.16.05

4832	S82	PM	M	22.5	738
4833	S36	PM	F	24	739
4834	S33	PM	M	19.	740
4835	S10	PM	F	520.5	741
4836	S142	PM	M	19	742
4837	M142	PM	M	20.5	743

4838	S115	PM	F	16	744
4839	S118	PM	M	19..5	745
4840	S84	PM	M	23	746
4841	S117	PM	F	20	747
4842	S97	PM	M	22	748
4843	S102	ST	F	4.4	
4844	P100	ST	M	5.4	
4845	S83	ST	F	4.4	
4846	S82	ST	F	4.5	
	P67	SV			
4569	S43	PM	F	27	634
4425	S41	PM	F	22.5	529
4380	S105	PM	M	20.5	489
4424	S23	PM	F	19	528
4571	S7	PM	M	20.5	636
4572	M7	PM	M	18	637
4403	S139	PM	F	23	513
4567	S129	PM	F	19.5	632
4631	S66	PM	F	19.5	660
4409	S65	PM	M	20	519
4423	S69	PM	F	18	527
4607	S119	PM	F	17	647
4422	S117	PM	F	17.5	526
4438	S81	PM	F	20	537

TC 8.17.05

4847	S59	PM	M	18.5	749
4848	S72	PM			
4849	S48	PM	M	18.5	750
4850	S108	PM	M	22	751
4851	S93	PM	M	20	752
4852	S7	SV		7	
4853	P140	ST		4.5	
4854	P31	ST		5.0	
4855	S82	ST	F	3.9	
4856	P79	ST	M	4.8	
4857	S83	ST	M	5.0	
4858	P40	ST	F	4.3	
4859	P67	ST	F	2.4	
4860	S118	ST	F	5.1	
3966?	S107	PM	M	28.5	244?

TC 8.18.05

4861	S23	PM	F	13.5	753
4862	S108	PM	F	24	754
4863	S103	PM	M	15.5	755
4864	S77	PM	F	11.5	756
4865	S59	PM	M	18.5	758
4866	S123	PM	F	22	759
4867	S93	PM	F	22	760

4868	S70	PM	F	22.5	761
4869	S47	PM	M	23	762
4870	S129	PM	F	16	763
4871	S143	PM	M	17	764
4872	P124	ST	F	4.1	
4873	S140	SV	F	8.7	
4874	S32	SV	F	5.7	
4875	P40	SV	F	5.4	

TC 8.19.05

4876	P136	PM	M	14	765
4877	S85	PM	M	14.5	766
4878	S53	PM	M	16	767
4879	S98	PM	M	19	768
4880	S103	PM			
4881	P96	ST	F	4.2	
4883	S93	ST	F	4.3	
4885	S12	PM	F	16.5	
3984	P7	PM	M	19	257
4887	S84	PM	F	11.5	
4888	P24	SV	F	3.3	
4889	P115	SV		4.1	
4890	P120	SV	F	3.9	
4611	S72	PM	M	19.5	652

POWELL BUTTE 8.30.05

4891	S24	TT	M	80	
4892	S34	PM	M	19	769
4893	S29	PM	F	16	770
4894	S140	PM	M	19.5	771
4895	S11	PM	M	20	772
4896	S8	PM	M	17.5	773
4897	P48	PM	M	15	774
4898	P60	MO	M	19.5	
4899	P60	ST	M	4.9	
4900	P60	ST	F	5.3	
4901	P144	ST	F	4.0	
4902	S139	ST	F	4.3	
4903	P36	MO	M	16.5	
4904	P36	ST	F	5.2	
	T60	DV			
4697	S48	PM	M	26.5	679
	S39	PM	M	22.5	210
4696	S6	PM	M	22.5	678
	S10	PM	F	26.5	225
	M93	PM	F	24.5	94
4699	S119	PM	F	23.5	681
4695	S116	PM	M	26	677

PB 8.31.05

4905	S34	PM	F	14	775
4906	S104	PM	F	13	776

4907	P72	PM	F	16	777
4908	S27	PM	M	16	778
4909	S91	TT	F	70	779
4910	S47	PM	M	15.5	780
4911	P12	ST	F	3.8	
4912	P100	SV	F	3.4	
4913	P108	ST	F	3.7	
4914	S55	TT	M	60	
	S23	PM	M	25.5	92
4473	S143	PM	M	21.5	567

PB 9.1.05

4915	P100	MO	M	35	
4916	S66	PM	F	19.5	782
4917	S68	MO	F	14.5	783
4918	S108	ST	M	4.7	
4919	S105	ST	F	4.6	
4920	S69	TT	M	68	
4921	S67	ST	F	3.7	
4922	S20	PM			
4923	T48	DV			
	P127	ST	F	4.5	
	P84	MO	M	20.5	
	S23	PM	M	23	217

PB 9.2.05

4925	S77	MO	M	15	784
4926	S55	PM	M	13.5	785
4947	S16	PM	M	17	786
4928	S108	MO	M	17	787
4929	S117	PM	M	14	788
4930	S139	PM	F	26	789
4931	S144	PM	F	21.5	790
4932	S130	MO		13	
4933	S95	ST		2.5	

OXBOW 10.11.05

4934	S23	PM	M	19	791
4935	S74	PM	F	12	792
4936	S120	PM	F	13	793
4937	S20	PM	F	19	794
4938	S67	PM	M	15	795
4939	S34	PM	F	16.5	796
4940	S9	PM	F	17	797
4941	S84	TT	M	66	798
4942	S144	TT	M	82	799
4943	S108	TT	F	72	800
4944	S129	TT	F	60	801
4945	P120	SB	M	13	
4946	P120	SB	M	15	
4947	P108	ST	F	4.7	
4948	P31	ST	?	5.0	

4949	P40	MO	F	12	
4950	P52	MO	M	15	
4951	P52	MO	M	13	
4952	P84	ST	?	4.4	
3831	P96	PM	M	17.5	
4058	S107	PM	F	19.5	
4312	S92	PM	F	20	
4333	M47	TT	M	79	
	P108	SV			
	P76	ST			

OX 10.12.05

4953	S117	PM	M	14	801
4954	S92	PM	M	12	803
4955	S66	PM	F	12	804
4956	P52	MO	M	13	
	S126	SV			
	S17	SV			
	P28	ST			
	P36	ST			
	P64	SV			

OX 10.13.05

4957	P91	PM	M	14	805
4958	S55	PM	F	16	806
4959	P76	ST	F	6.8	
4960	P96	SV	F	6.6	
4961	S96	SV	M	5.5	
	S79	SV			
	S139	SV			
	S141	ST			
	S132	MO			

OX 10.14.05

4962	S111	TT	M	61	807
4963	S117	TT	M	86	808
4964	M16	TT	M	70	809
4965	P136	ST	M	4.9	
	P108	SV			
	S90	SV			
	S6	SV			
	S11	ST			

TRNWR 10.18.05

4966	S142	TT	M	69	810
4967	S10	TT	M	72	811
4968	S10	PM	M	13	812
4969	S127	PM	M	14	813
4970	S118	PM	F	13	814
4971	S32	PM	F	13	815
4972	P103	PM	M	10	816
4973	P40	PM	F	15	817
4979	S130	PM	M	20	625

4667	S30	PM	M	18	671
TRNWR 10.19.05					
4974	S138	PM	M	18	818
4975	S43	PM	M	16	819
4976	S8	PM	F	16	820
4977	S31	PM	M	18	821
4978	S40	PM	M	16	822
4979	P103	PM	F	12	823
4980	S102	PM	F	14	824
4981	P139	ST			
TRNWR 10.20.05					
4982	S114	PM	M	15	NO TAG
4983	S106	PM	M	18	NO TAG
4984	S142	PM	F	18	NO TAG
4985	S19	PM	M	20	NO TAG
4986	S95	PM	F	18	NO TAG
4987	S84	PM	M	18	NO TAG
4988	P48	PM	M	18	NO TAG
4989	S95	PM	M	20	NO TAG
4990	T12	DV			NO TAG
TRNWR 10.21.05					
4991	S127	PM	M	12	NO TAG
4992	S8	PM	M	18	NO TAG
4993	S142	PM	F	15	NO TAG
4994	S33	PM	M	14	NO TAG
4995	S86	PM	M	83	NO TAG
4996	S113	PM	M	13	NO TAG
4997	S31	PM	M	10	NO TAG
4998	T24	DV			
4999	S143	ST		6.6	

Appendix D: *Hantavirus* Antibody-Positive Specimens. Small mammals found infected with *Hantavirus* during the period October, 2002 through October, 2005. The positive *Glaucomys sabrinus* (likely due to a spill-over event) was unable to be confirmed after release of the specimen.

Specimen #	Species
260	*Peromyscus maniculatus*
268	*P. maniculatus*
279	*P. maniculatus*
491	*P. maniculatus*
925	*P. maniculatus*
1008	*P. maniculatus*
1009	*P. maniculatus*
1122	*P. maniculatus*
1335	*P. maniculatus*
1351	*P. maniculatus*
1523	*P. maniculatus*
1524	*P. maniculatus*
1550	*P. maniculatus*
1637	*P. maniculatus*
1638	*P. maniculatus*
1669	*P. maniculatus*
1695	*Glaucomys sabrinus*
1698	*P. maniculatus*
1714	*P. maniculatus*
1715	*P. maniculatus*
1724	*P. maniculatus*
1783	*P. maniculatus*
1797	*P. maniculatus*
1960	*P. maniculatus*
2059	*P. maniculatus*
2063	*P. maniculatus*
2067	*P. maniculatus*
2126	*P. maniculatus*
2138	*P. maniculatus*
2154	*P. maniculatus*
2161	*P. maniculatus*
2293	*P. maniculatus*
2468	*P. maniculatus*
2470	*P. maniculatus*
2471	*P. maniculatus*
2472	*P. maniculatus*
2479	*P. maniculatus*
2491	*P. maniculatus*
2493	*P. maniculatus*
2494	*P. maniculatus*
2497	*P. maniculatus*
2499	*P. maniculatus*

2511	*P. maniculatus*
2520	*P. maniculatus*
2522	*P. maniculatus*
2525	*P. maniculatus*
2630	*P. maniculatus*
2651	*P. maniculatus*
2722	*P. maniculatus*
2737	*P. maniculatus*
2834	*P. maniculatus*
2836	*P. maniculatus*
2850	*P. maniculatus*
2852	*P. maniculatus*
2860	*P. maniculatus*
2865	*P. maniculatus*
2890	*P. maniculatus*
2891	*P. maniculatus*
2892	*P. maniculatus*
2898	*P. maniculatus*
2900	*Microtus oregoni*
2914	*P. maniculatus*
2936	*P. maniculatus*
2940	*P. maniculatus*
2943	*P. maniculatus*
2947	*P. maniculatus*
3000	*P. maniculatus*
LAR 9	*P. maniculatus*
LAR 10	*P. maniculatus*
3254	*P. maniculatus*
3268	*P. maniculatus*
3277	*P. maniculatus*
3278	*P. maniculatus*
3279	*P. maniculatus*
3304	*P. maniculatus*
3306	*P. maniculatus*
3308	*P. maniculatus*
3314	*P. maniculatus*
3317	*P. maniculatus*
3321	*P. maniculatus*
3323	*P. maniculatus*
3324	*P. maniculatus*
3327	*P. maniculatus*
3330	*P. maniculatus*
3333	*P. maniculatus*
3344	*P. maniculatus*
3348	*P. maniculatus*
MT HOOD 114	*P. maniculatus*
MT HOOD 116	*P. maniculatus*

3617	*P. maniculatus*
3621	*P. maniculatus*
3622	*P. maniculatus*
3626	*P. maniculatus*
3627	*P. maniculatus*
3631	*P. maniculatus*
3644	*P. maniculatus*
3645	*P. maniculatus*
3651	*P. maniculatus*
3654	*P. maniculatus*
3656	*P. maniculatus*
3662	*P. maniculatus*
3665	*P. maniculatus*
3666	*P. maniculatus*
3671	*P. maniculatus*
3676	*P. maniculatus*
3679	*P. maniculatus*
3782	*P. maniculatus*
3822	*P. maniculatus*
3834	*P. maniculatus*
3877	*P. maniculatus*
3879	*P. maniculatus*
3659	*P. maniculatus*
3629	*P. maniculatus*
3639	*P. maniculatus*
3666	*P. maniculatus*
3656	*P. maniculatus*
3902	*P. maniculatus*
3903	*P. maniculatus*
3905	*P. maniculatus*
3909	*P. maniculatus*
3910	*P. maniculatus*
3911	*P. maniculatus*
3645	*P. maniculatus*
3621	*P. maniculatus*
3639	*P. maniculatus*
3666	*P. maniculatus*
3879	*P. maniculatus*
3883	*P. maniculatus*
3913	*P. maniculatus*
3920	*P. maniculatus*
4087	*P. maniculatus*
4091	*P. maniculatus*
4096	*P. maniculatus*
4148	*P. maniculatus*
4207	*P. maniculatus*
3909	*P. maniculatus*

4250	*P. maniculatus*
4298	*P. maniculatus*
4306	*P. maniculatus*
3920	*P. maniculatus*
4207	*P. maniculatus*
4341	*P. maniculatus*
4449	*P. maniculatus*
4451	*P. maniculatus*
4549	*P. maniculatus*
4086	*P. maniculatus*
4539	*P. maniculatus*
4570	*P. maniculatus*
4576	*P. maniculatus*
422	*P. maniculatus*
4627	*P. maniculatus*
4631	*P. maniculatus*
4667	*P. maniculatus*
4688	*P. maniculatus*
4717	*P. maniculatus*
589	*P. maniculatus*
4782	*P. maniculatus*
4783	*P. maniculatus*
4784	*P. maniculatus*
602	*P. maniculatus*
612	*P. maniculatus*
621	*P. maniculatus*
4788	*P. maniculatus*
4789	*P. maniculatus*
MH 353	*P. maniculatus*
671	*P. maniculatus*
674	*P. maniculatus*
4818	*P. maniculatus*
MH346	*P. maniculatus*
660	*P. maniculatus*
652	*P. maniculatus*
4851	*P. maniculatus*
4861	*P. maniculatus*
4870	*P. maniculatus*
217	*P. maniculatus*
4907	*P. maniculatus*
4992	*P. maniculatus*

Appendix E: Rodent Specimen mtDNA Sequences. Resolved sequences of mitochondrial ND3, ND4, ND4L, and arginine tRNA genes (1,463bp). N=88.

WC7

ACAGCTGACTTCCAATCAGTTAGATCTAGACCTAACCTAGAAGAAAGTAA
TAAATATACTAACAGCCCTATTAGTAAATATTACGCTATCAATACTCCTAA
TCATCATTGCCTTCTGACTACCCCAACTTAATTTATACACTGAAAAAGCAA
ACCCGTATGAGTGCGGATTTGACCCCATAGGCTCTGCTCGCCTCCCATTCT
CAATAAAATTTTTCCTAGTAGCAATCACTTTCTTACTATTTGACCTAGAAAT
TGCACTTCTACTTCCACTACCATGAGCTATCCAAATATATAATATTAACAT
CATAATATTAACAGCTTTCATCCTAGTCTCCGTATTAGCATTAGGCTTAGC
CTACGAGTGACTACAAAAAGGACTAGAATGAACTGAA-
TAACTGGTAATTAGTTTAATTAAAACAAATGATTTCGACTCATTAGATTAT
GATATACATTATAATTACCAAAA----
ATGTCATCTGTAACCTCCAATATTATATTAGCATTCTCATTCTCATTTCTAG
GAACACTAGTATTTCGATCCCACCTAATATCAACTCTCCTATGCCTTGAAG
GAATAATACTATCACTGTTTATTATAACCACAATTACATCCCTTAATTCCC
ACTCAATAATTATATACCCTCTACCCATTGTTATTCTAGTATTCGCAGCATG
TGAAGCAGCCATTGGCTTAGCCCTATTAGCAAAACTATCAAACTCCTACGG
AACAGATTATGTGCAAAATCTAAACCTACTTCAATGT-
TAAAAATTATTTTTCCCTCTATCATATTACTCCCACTCACCTGATTATCAAA
CAAAAAAAACCTATGAGTCAATGTTACCTCCTACAGCTTTATAATCAGCTT
GACTTCAGCTATGTTTTTATGACAAAACGACATAAATAACCTAAACTTCTC
ACTACTATTCTCAACTGACTCCCTATCCTCCCCTCTTATCATTCTAACAACA
TGACTTCTACCACTCATACTGCTAGCCAGCCAAAACCACATAAAAAAGGA
AACAGAGTCAAACAAAAAAACATACATTTCAATACTAGTCTTACTACAAA
TTCTTCTAATCATAACATTTTCTGCAAACGAACTAATTATATTTTACATCTT
ATTTGAAGCCACCCTAATCCCCACCCTTATTATCATCACCCGATGGGGTAA
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WC11

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WC12
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WC13

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ljd3256 --

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ljd3304 --
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ljd3306 --------
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ljd3308 ----------
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ljd3317 -
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ljd3324 -
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ljd3327 ----------
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ljd3330 ----------
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ljd3333 ----------
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ljd3344 --
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ljd3348 --
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LJD620 --
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CTCCA--

LJD774 --
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CTCCA--

LJD886 --
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CTCCA--

LJD2088 ---
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LJD1960 ----------
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LJD1669 -------
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LJD1524 --------
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LJD1523 ---
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LJD1122 -------
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LJD2522 --
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LJD1637 ----------
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LJD1638 -
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LJD2161 ----------
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LJD2651 ----------
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LJD2737 ----------
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CTCCAA-

LJD2834 ----------
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LJD2850 ----------
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LJD2898 ----------
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LJD2914 ----------
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LJD2936 -
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LJD3000 ----------
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LJD2126 ----------
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-

LJD2138 ------
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LJD2154 ----------
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LJD2158 ------
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LJD2852 ----------
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LJD2860 ----------
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LJD2865 ----------
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LJD2890 ----------
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LJD2943 ----------
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Jefferson3 --
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CTCCA--

ADAMS6 --
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CTCCA--

clatsop1 ----------
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CTCCA--

clatsop2 ----------
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CTCCA--

clatsop3 ----------
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CTCCAA-

clatsop4 ----------
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CTCCA--

LostForest1A
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LostForest2
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CTCCAA-

LostForest3

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GCTCCAA

LostForest4 -
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CTCCA--

sj1Pmausterus ----------
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sj2Pmausterus ----------
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TCC---

sj2aPmausterus ----------
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<u>sj6Pmausterus</u> ----------
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sj7Pmausterus ----------
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OSM723Pmman --
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OSM726Pmman --
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OSM727Pmman --
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OSM737Pmman --
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U40255PsejugSD (GenBank) ----
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U40253PsejugSC (GenBank) ----
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JEB1309APtruei (GenBank) ----
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CTCCA--

U40252Pleuc (GenBank) ----
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JAM160Pleuc ----------
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JAM161Pleuc -------
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JAM162Pleuc ----------
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JAM163Pleuc ----------
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JAM164Pleuc ----------
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JAM168Pmbairdii -----
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JAM167Pmbairdii ---------
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JAM159Pmbairdii ----------
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JAM166Pmbairdii ----------
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Microtus pennsylvanicus (GenBank)

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Oryzomys palustris (GenBank)

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Sigmodon hispidus (GenBank)

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C----------

Reithrodontomys megalotis (GenBank)

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Rattus norvegicus (GenBank)

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CCA--

Pmrufinus ----

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CTCCA--

Appendix F: *Hantavirus* Specimen Sequences. Resolved sequences M segment G1/G2 glycoprotein precursor gene (617nt). N=44.

T7

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T8

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WC4

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WCps

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WC7

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WC12

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WC13

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LJD2522FP

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GGGCTTCACATTAGTATGTACGGAGGCGCTCATAGCACATC

LJD2737PB

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AACA----------
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LJD2836FP

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ATGGTTTTAAATAGAGATGTTTCCTTTCAAGATCTAAGTGATAACCCATGT
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GGGCTTCACATTAGTATGTACGGAGGCGCTCATAGCACATC

LJD2852FP

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AA----------
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LJD2860FP

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LJD2865FP

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LJD2890FP

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GGGCTTCACATTAGTATGTACGGTGGCGCTCATAGCACATC

Convict Creek

ATGAATGTGAGACGGCAAAAGAGCTCGAAACACATAAGAAAAGTT
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AT----------
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ATGGTTTTGAATAGAGATGTTTCCTTCCAAGATCTAAGTGATAATCCATGT
AAGGTTGATTTGCATACACAATCTATTGATGGGGCTTGGGGATCAGGAGT
GGGCTTTACATTAGTATGTACTGTAGGTCTTACAGAGTGTG

SNV (GenBank L25783)

ACGAATGCGAAACAGCAAAAGAACTTGAAACACATAAGAAAAGCT
GTCCAGAAGGTCAATGCCCGTATTGTATGACAATAACTGAATCCACTGAG
AGTGCTCTCCAAGCCCATTTTGCAATCTGTAAGCTAACAAACAGGTTTCAG
GAAAACTTAAAAAAGTCATTGAAACGCCCAGAAGTACGGAAAGGTTGTTA
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AC----------
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CTCGAGATTCTTTCCAGTCATTCAATGTGACAGAACCACATATCACTAGCA
ACCGACTTGAGTGGATTGATCCAGATAGCAGTATCAAAGATCACATTAAT
ATGGTTTTAAATCGAGATGTTTCCTTTCAGGATCTAAGTGATAACCCATGC
AAGGTTGACCTGCATACACAATCAATTGACGGGGCCTGGGGTTCAGGAGT
AGGTTTTACGTTGGTATGTACTGTGGGGCTTACAGAGTGTG

SNV (GenBank L37903)

ACGAATGCGAAACAGCAAAAGAACTTGAAACACATAAGAAAAGCT
GTCCAGAAGGTCAATGCCCGTATTGTATGACAATAACTGAATCCACTGAG
AGTGCTCTCCAAGCCCATTTTGCAATCTGTAAGCTAACAAACAGGTTTCAG
GAAAACTTAAAAAAGTCATTGAAACGCCCAGAAGTACGGAAAGGTTGTTA
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ATGGTTTTAAATCGAGATGTTTCCTTTCAGGATCTAAGTGATAACCCATGC
AAGGTTGACCTGCATACACAATCAATTGACGGGGCCTGGGGTTCAGGAGT
AGGTTTTACGTTGGTATGTACTGTGGGGCTTACAGAGTGTG

New York Virus (GenBank U36803)

ATGAGTGTGAAACAGCAAAAGAGCTAGAAACTCATAAGAAAAGCT
GTCCTGAAGGTCAGTGTCCATACTGCATGACAATGACAGAATCCACAGAG
AGTGCTCTTCAGGCTCATTTTTCAATTTGTAAGCTTACAAATAGGTTTCAG
GAAAATCTAAAAAAAATCACTTAAACGCCCTGAAGTTAAACAAGGATGCTA
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GTGGGGGGTCCTTCTTACAACTGAACTCATAGTTTGGGCAGCTAGTGCTGA
C----------
CTGTGAGTATCAAGGTAATACTATCTCGGGATTTCAGAGAATGATGGCTAC
AAGAGACTCTTTTCAGTCATTCAATGTAACAGAACCGCACATTACCAGTAA
TCGTCTTGAATGGATTGATCCTGATAGCAGTATAAAAGATCATATTAATAT

GGTCTTAAACCGAGATGTTTCATTTCAGGATTTGAGTGATAATCCCTGTAA
AGTGGATCTACATACGCAGTCAATTGATGGAGCTTGGGGCTCTGGGGTAG
GTTTCACTCTGGTATGTACAGTGGGACTGACTGAATGTG

Blue River (GenBank AF030552)

ATGATTGTGAGACAGCTAAAGAGCTTGATACACACAAAAAGAGTTG
TCCAGAGGGTCAATGCCCTTACTGTATGACCATGACTGAATCAACAGAAA
GTGCTCTCCAGGCCCATTTTTCAGTCTGCAAACTTACAAATAGATTTCAAG
AAAATTTAAAAAAAATCCTTAAAGCACCCAGAAGTAAAACAGGGCTGTTAT
AGGACATTAGGAGTATTTAGGTATAAAAGTAGATGTTATGTAGGCCTTGTG
TGGGGTTTGCTTCTGACAACTGAACTTATCATCTGGGCAGCTAGTGCAGAA

TTGCGAATATCAGGGCAATACAATTTCAGGATTTAAAAGAATGATGGCCA
CAAGAGATTCTTTCCAGTCATTCAATGTTACAGAACCTCATATAACTAGTA
ACCGACTAGAATGGATTGACCCTGACAGTAGTATTAAAGACCATATAAAT
GTAGTGCTAAATCGTGATGTGTCTTTTCAAGATTTAAGTGATAATCCCTAC
AAAGTAGATTTGCACACACAATCTATAGACGGTGCATGGGGTTCTGGGGT
AGGTTTTACTCTAGTATGTATTGTGGGTCTTACAGAGTGTG

Bayou virus (GenBank L36930)

ATGAGTGTGAAACAGCAAAAGAACTTGAGGGACATAAAAAAAGCT
GTGCTGAAGGGCAGTGCCCTTACTGCATGACTCTTACAGAAGCAACAGAG
AGTGCCCTCCAGGCCCATTATGCAGTCTGTAAATTAACTGGGCGGTTTCAA
GAGGCATTAAAAAAATCACTTAAGAAGCCAGAAGTCAAGAGAGGCTGTTA
TAGAACACTTGGTGTTTTTCGTTACAAGAGTAGGTGTTATGTCGGTCTAGT
CTGGTCATTTTTACTGACACTTGAATTAATAGTCTGGGCTGCCAGTGCTGA
C----------
CTGTGAGTATCAAGGGAATACTGTCTCTGGATTTAAGCGGCTAATGGCAAC
TAAAGACTCATTTCAATCATTTAATGTCTCTGAGGCACACATAACAACAAA
CAGTCTAGAGTGGGTAGATCCAGACAATAACATAAAAGATCATATCAATC
TGGTTCTTAACCGGGATATTTCATTTCAAGATCTGAGTGACAATCCATGTA
AGGTGGACCTGTCAACACAATCGATTGATGGTGCATGGGGCTCGGGTGTT
GGTTTCACATTGACATGTGTAGTTGGCCTGACAGAATGCC

Black Creek Canal (GenBank L39950)

ATGAATGTGAAACAGCAAAAGAACTTGAAAGCCATAAAAAAAGTT
GTGCTGATGGGCAGTGCCCATACTGTATGACTATTACCGAGGCAACTGAG
AGTGCTTTACAGGCCCATTATGCTGTATGTAAATTAACAGGGCGCTTTCAT
GAGGCTTTAAAAAAATCATTAAAAAAACCAGAGGTTCAGAGGGGTTGTTA
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T----------
TTGTGAGTATCAAGGGAATACAGTCTCTGGTTTTAAAAGATTGATGGCTAC
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CAAGCTAGAATGGAGTGATCCTGATAGTAACATCAAAGATCATATAAATT

TGATTTTAAACCGAGATGTATCATTTCAAGACTTAAGTGACAATCCGTGCA
AAGTGGACCTTTCAACACAGGCAATTGATGGTGCATGGGGCTCTGGTGTA
GGTTTTACATTGACATGTATAGTGGGATTAACAGAATGCT

Andes Virus (GenBank NC003467)

ATGAGTGTGAAACAGCAAAAGAACTTGAATCACATAGACAGAGTT
GTATCAATGGACAATGTCCTTATTGCATGACAATAACTGAAGCAACTGAA
AGTGCCTTGCAAGCCCATTATTCCATTTGTAAATTGACAGGAAGATTTCAG
GAGGCACTGAAAAAGTCACTTAAAAAGCCAGAGGTAAAAAAAGGTTGTTA
CAGAACACTCGGGGTATTTAGATATAAAAGTAGATGTTATGTGGGTTTGGT
ATGGTGCCTATTGTTGACATGTGAAATTGTTATTTGGGCCGCAAGTGCAGA
G----------
TTGTGAATATCAAGGAAATACCATTTCTGGATATAAAAGAATGATGGCAA
CAAAAGATTCATTCCAATCATTTAACTTAACAGAACCTCACATCACAACAA
ACAAGCTTGAATGGATCGACCCAGATGGGAATACAAGAGACCACGTAAAC
CTTGTCTTAAATAGAGATGTCTCATTTCAGGATTTAAGTGATAACCCCTGT
AAAGTAGACCTACACACACAAGCAATAGAAGGGGCATGGGGTTCTGGTGT
AGGGTTTACACTCACATGTACTGTCGGATTAACAGAGTGCC

Hu39694virus (GenBank AF028023)

ATGAGTGTGAAACAGCAAAAGAATTAGAATCCCATAAACAAAGCT
GCATCAACGGGCAATGCCCTTACTGTATGACCATGACAGAGGCAACAGAA
AGTGCCTTACAGGCTCATTACTCTATTTGTAAATTAACAGGCAGATTCCAG
GAAGCTTTAAAGAAATCACTGAAGAGACCAGAAGTCAAAAAGGGTTGTTA
TCGTACATTAGGGGTATTTAGGTACAAGAGTAGATGCTATGTTGGGCTGGT
GTGGTGTGTGCTCTTAACATGTGAACTTATCGTATGGGCTGCTAGTGCAGA
G----------
TTGTGAGTACCAAGGGAACACAATCTCAGGATATAAAAGAATGATGGCCA
CAAAGGATTCATTCCAATCTTTCAATTTGACTGATCCACATATTACAACAA
ATAAACTTGAATGGATTGACCCTGATGGTAACACACGCGATCATGTAAATT
TAGTATTGAATAGAGATGTTTCATTTCAGGATCTAAGTGATAACCCATGTA
AGGTTGATCTACACACACAAGCTATAGAAGGAGCATGGGGTTCAGGTGTT
GGATTTACATTAACTTGTACTGTCGGATTGACTGAGTGCC

Oran Virus (GenBank AF028024)

ATGAATGTGAGACAGCAAAAGTGTTAGAATCACATAAACAAAGCT
GCATTAATGGACAGTGCCCGTACTGCATGACTATGACTGAGGCAACTGAA
AGTGCTCTACAAGCTCATTATTCTATCTGCAAATTGACAGGGAGGTTTCAG
GAGGCTTTAAAAAAATCATTAAAAAAACCAGAGGTAAAAAGGGGTTGTTA
CCGTACCTTAGGTGTATTTAGATACAAGAGTAGATGTTATGTTGGATTAGT
TTGGTGTGTGCTTTTAACATGTGAGCTTATTGTCTGGGCAGCTAGTGCGGA
A----------
ATGTGAGTATCAAGGGAATACCATCTCAGGCTATAAACGAATGATGGCAA
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ACAAACTTGAATGGATTGACCCTGATGGCAATACAAGGGATCATGTAAAT

CTCGTTTTAAATAGAGACGTCTCATTTCAGGATTTAAGTGACAACCCGTGT
AAGGTTGATTTACATACACAGGCAATAGAAGGGGCATGGGGTTCTGGTGT
TGGATTTACACTTACATGTACAGTTGGTTTGACTGAGTGTC

Lechiguanas virus (GenBank AF028022)

ATGAGTGTGAGACAGCCAAAGAATTGGAATCTCATAAGCAAAGTTG
CATAAATGGTCAATGTCCATATTGTATGACTATGACTGAGGCAACAGAAA
GTGCGCTACAAGCTCATTTTGCTATTTGTAAGCTTACAGGGAGATTCCAGG
AAGCCTTAAAAAAATCATTGAAGAAACCAGAAGTCAGAAAGGGCTGTTAC
CGTACTCTAGGAGTTTTTAGATACAAGAGCAGGTGCTATGTTGGCTTAGTT
TGGTGTGTGTTATTGACATGTGAGCTCATTGTATGGGCTGCTAGTGCAGAG

ATGTGAGTACCAAGGTAACACTATATCTGGATACAAGAGAATGATGGCTA
CAAAGGATTCTTTTCAATCATTTAATCTTACTGACCCTCACATAACTACAA
ATAAGCTTGAATGGATCGATCCAGATGGCAATACACGAGATCATGTCAAT
CTTGTATTGAATAGAGATGTGTCATTTCAAGATTTAAGTGACAATCCTTGT
AAGGTTGATTTGCATACACAAGCTATTGAAGGGGCTTGGGGTTCTGGTGTT
GGGTTTACATTGACTTGCACTGTTGGTTTAACTGAATGCC

Juquitiba virus (GenBank 168711) ----------

TCTTTAAAGAAACCAGAGATTAAAAGGGGTTGCTATCGCACCATCGGTGTT
TTTAGATATAAAAGTAGATGTTATGTGGGGTTAGTATGGTGTTTATTGTTA
ACTTTCGAATTGATAGTTTGGGCAGCAAGTGCAGAG----------
ATGTGAGTACCAAGGCAATACTGTGTCAGGGTATAAGAGGATGATGGCAA
CCAAGGATTCTTTTCAGTCTTTTAATCTAACAGATCCACATATAACAACCA
ACAAATTGGAGTGGATAGACCCTGATGGGAATACAAGGGATCATGTCAAC
CTTGTATTGAATCGTGATGTGTCTTTCCAGGACCTAAGTGATAACCCTTGT
AAGGTAGACCTTCATACACAGGCTATTGAGGGGGCATGGGGCTCAGGTGT
TGGTTTCACATTAACATGTGGGGTTGGGCTAACAGAATGCC

Maciel virus (GenBank AF028027)

ACGAATGTGAAACAGCTAAAGAGCTAGAATCACATAGACAGAGTT
GTCTTAATGGGCAATGCCCATATTGTATGACAATGACAGAGGCAACAGAA
AGTGCTTTGCAAGCTCACTATTCCATTTGCAAGTTAACTAATAGGTTTCAG
GAAGCACTAAAGAAGTCATTGAAGAAACCAGAGGTAAGAAGAGGTTGTT
ACAAAACATTAGGTGTGTTTAGATACAAAAGTAGATGCTATGTGGGCTTA
GTCTGGTGTATATTGCTAACCTTTGAATTGATCATTTGGGCTGTGAGTGCA
GAA----------
ATGCGAGTATCAAGGGAATACTGTCTCTGGCTATAAAAGATTGATGGGCA
CAAAAGGTTCTTTCCAATCATTTAACCTTACAGAACCACATATCACCACAA
ATAAACTTGAATGGATTGACCCAGATGGTAATACCCGTGATCATGTAAATC
TCATCTTAAATAGAGATGTGTCATTCCAGGATCTGAGTGACAACCCTTGTA
AAGTAGATTTGCATACACAAGCAATTGAAGGGGCTTGGGGATCGGGGGTT
GGTTTCACACTCACATGTGTTGTCGGTCTCACAGAATGCC

El Moro Canyon (GenBank U26828)

ATGAATGTGAAACAGCAAAAGAACTCGATTGTCATAAAAAGAGCT
GTGCTGAAGGACAATGCCCTTACTGCATGACATTGACAGAATCTACAGAA
AGTGCACTTCAAGCACATTTTGCAATCTGCAAACTAACTTCAAGATTTCAG
GAGAATTTGAAGAAATCTTTGAAAAGGCAGGATGTTAAACCTGGCTGTTA
CAGAACTCTAGGTGTATTTAGATACAAGAGCCGTTGTTATGTCGGGCTTGT
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T----------
TTGTGAGTATCAAGGGAATACAGTTTCAGGATATCAAAGGATGATGGCTA
CAAAAGATTCTTTTCAGTCATTTAATGTCACGCAACCGCACTTAACAGCCA
ATCTACTGGAATGGGTGGACCCAGATAGTACCATCAAAGACCACATTAAC
CTAATTCTCAATAGAGATTTATCATTTCAAGACTTGGCAGAGAACCCATGT
AAAGTGGATTTACATACCCAAAACATTGATGGAGCATGGGGATCTGGGGT
GGGCTTTACATTAACGTGTATTGTAAGCCTGACAGAATGTA

Prospect Hill (GenBank X55129)

AGGAATGTGAAATGGCAAAAGAATTGGAGTCTCACAAGAAAAGTT
GTCCTAATGGTATGTGCCCTTACTGCATGAACCCTACAGAGTCTACTGAGT
CTGCCCTGCAAGCTCATTTCAAAGTGTGTAAACTTACAACAAGGTTCCAGG
AGAACCTTCGCAAGTCACTAAATCCATATGAGCCTAAACGAGGTTGCTAT
AGGACACTCTCTGTGTTTAGATATCGGAGTAGGTGCTTTGTGGGCCTTGTT
TGGTGCATCCTACTTGTATTAGAACTTGTCATATGGGCTGCAAGTGCGGAT-

ATGTGAGTATGATGGAAACACTCTTTCTGGTTACCAGCGGATGCTTGCAAC
AAGGGATTCTTTCCAGTCTTTCAACATTACAGAACCACATATTACCAGCAA
TTCACTTGAATGGGTAGATCCAGATAGTTCATTAAAGGATCATATTAATTT
GGTAGTTAATCGCGATGTATCATTTCAGGACTTATCTGAAAATCCCTGTCA
AGTTGGTGTGGCCGTGTCTTCCATTGATGGTGCATGGGGCTCAGGTGTGGG
TTTTAATCTGGTATGTAGTGTGAGTTTGACAGAATGTG

Tula virus (GenBank NC005228)

AAGGATGTGAGACTGCAAAGGAGCTAGAATCTCACAAAAAAAGCT
GTCCACATGGACAGTGTCCATACTGTCTCAACCCAACTGAAGCTACTGAGT
CTGCCCTACAGGCTCATTTTAAAGTCTGTAAGTTGACAACTAGGTTTCAAG
AGAATTTAAAGAAATCATTAAGTACATATGAGCCTAAACGTGGCCTCTATC
GAACACTCTCCATGTTTAGATACAAAAGCAAATGCTATGTGGGTTTGGTTT
GGTGTATTTTGTTAACTATGGAGTTGATAGTGTGGGCAGCTAGTGCTGAG--

ATGTCAGTATGATGGAAACACTGTATCTGGATATCAGAGAATGATTGCCA
CAAAAGATTCATTCCAGTCATTCAATATTACAGAACCCCATATTACAACAA
ATTCACTAGAATGGGTTGACCCAGATAGTTCTCTAAAGGACCATGTCAATC
TGATAGTAAACCGGGATCTATCTTTCCAAGATTTAGCTGAAAATCCATGTC
AGGTTGATTTAAGTGTATCATCAATTGATGGCGCATGGGGCTCAGGTGTGG
GGTTTAATTTAGTCTGCTCTGTCAGCCTTACAGAATGTG

Puumala virus (GenBank NC005223)

ATGAGTGTGAAACTGCTAAGGAGTTAGAATCACATAGAAAGAGCT
GTTCAATTGGTTCATGCCCTTATTGCCTTAATCCATCTGAGGCTACACCGTC
TGCTCTTCAAGCTCATTTTAAAGTTTGTAAACTAACATCACGGTTTCAGGA
AAATTTGAAGAAGTCACTAACAATGTATGAGCCAATGCAGGGTTGTTATC
GAACATTATCTCTATTTAGGTACCGCAGTAGATTTTTTGTAGGTTTAGTGTG
GTGTATGTTGCTTGTTTTAGAGCTAATTGTATGGGCTGCTAGTGCTGAG-----

ATGTCAGTTTGATGGGAATACAATTTCAGGTTATAAACGGATGGTTGCAAC
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TGCATTGGAGTGGATTGACCTAGATAGTTCACTTCGGGATCACATCAATGT
GATTGTAAGCCGTGATTTGTCCTTTCAGGATTTAAGTGAAACACCTTGTCA
AGTGGATTTGACAACATCAGCTACAGATGGGGCATGGGGTTCAGGAGTTG
GTTTTAACCTGGTATGTACTGTTAGTTTAACAGAATGCT

Hantaan virus (GenBank DQ371905)

ATGAGTGTGAGACTTATAAAGAACTAAAGGCACATGGGGTCTCATG
CCCACAATCCCAATGCCCTTATTGTTTCACCCACTGTGAGCCCACAGAAGC
TGCATTTCAGGCCCATTATAAAGTGTGTCAAGTTACTCATAGATTTAGGGA
TGATTTAAAGAAGACAGTTACTCCCCAGAACTTCACACCTGGTTGCTATCG
AACATTGAATTTATTCAGATATAAGAGTAGGTGTTATATTTTTACAATGTG
GGTTTTTCTTTTAGTCTTAGAATCAATCTTATGGGCAGCCAGTGCATCA------

TTGTGAATATGATGGGAATATGGTTTCAGGTTATAAAAAAGTAATGGCCA
CAATTGATTCTTTTCAATCCTTCAATACAAGCACTATGCATTTCACTGATGA
GAGGATAGAATGGAAAGACCCTGATGGGATGTTAAGGGACCATATTAACA
TTCTGGTTACAAAGGATATTGACTTTGATAATCTTGGTGAAAATCCCTGCA
AGATTGGATTACAAACATCCTCCATTGAAGGGGCATGGGGGTCTGGTGTA
GGCTTTACACTTACATGTTTGATATCACTGACAGAATGCT

Dobrava virus (GenBank NC005234)

ATGAGTGTGAAACAGGGAAGGAGCTTAAAGCCCATAATTTATCTTG
CCCTCAGTCACAGTGTCCTTATTGCTTTACACACTGTGAGCCTACAGAATC
TGCCTTTCAAGCACATTATAAAGTGTGCCAAGCAACACACAGATTTAGGG
ATGATTTAAAGAAAACAATAACACCTCAATCAACAAGCCCAGGTTGTTAC
CGGACATTAAATCTTTTTAGGTATAAAAGTAGATGTTACATCTTTACAGTG
TGGGTGACCTTACTAATCATTGAATCAATCATGTGGGCAGCTAGTGCATCA

GTGCGAGTATGATGGTAATATGGTCTCTGGGTATAAGAAAGTAATGGCAA
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Seoul Virus (GenBank NC005237)

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Sangassou virus (GenBank DQ268651) ----------

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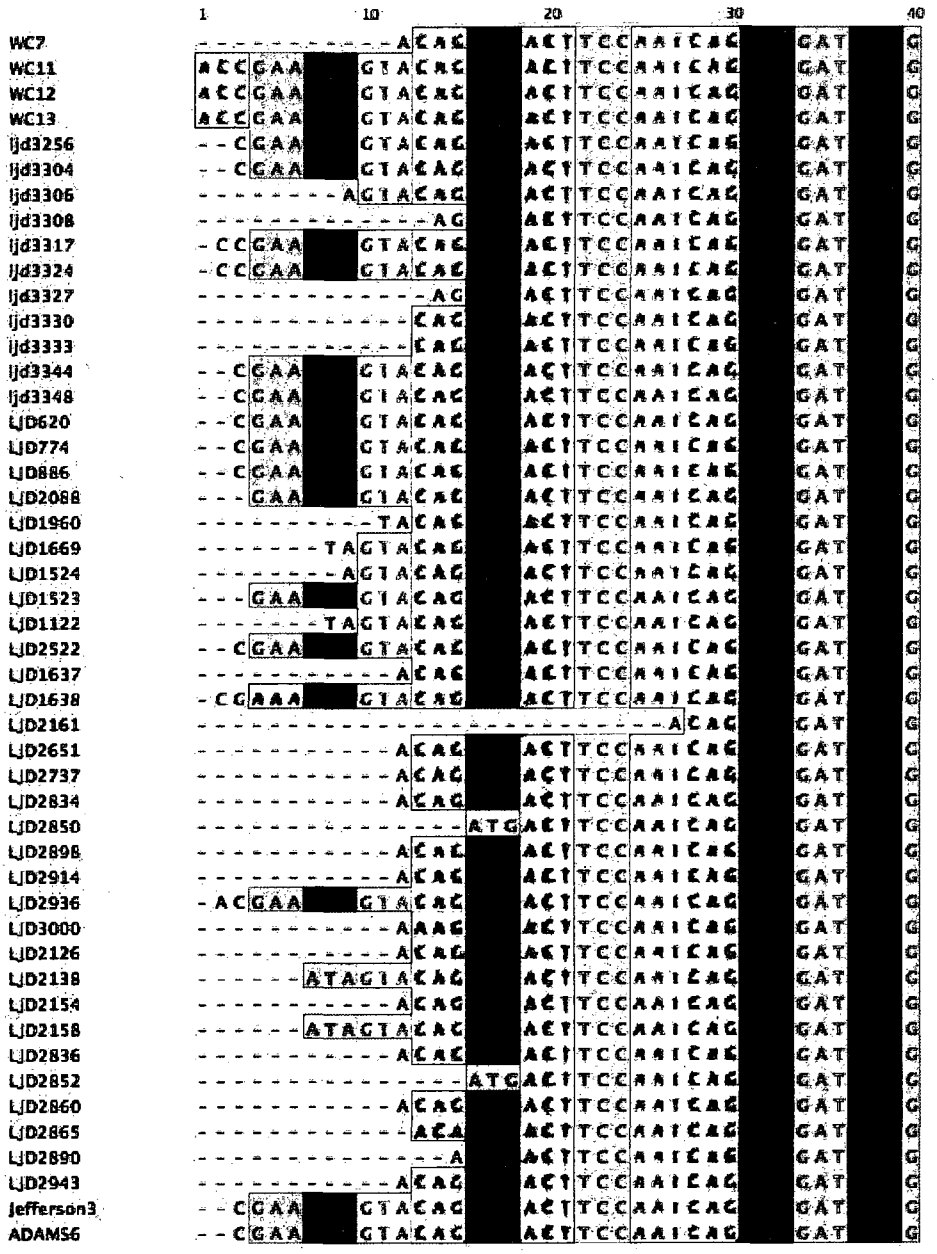
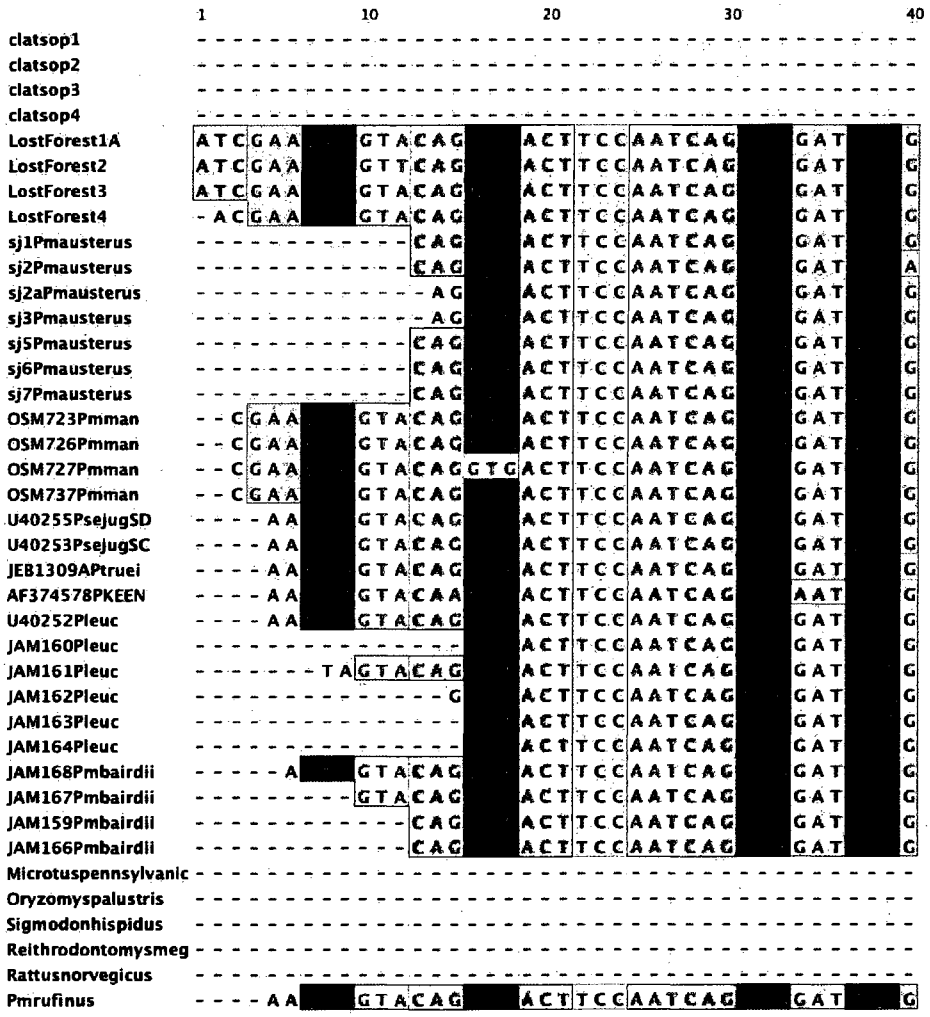
Appendix G: Rodent Multiple Sequence Alignment. Sequences of mitochondrial ND3, ND4, ND4L, and arginine tRNA genes aligned with one another by codon reading frame.

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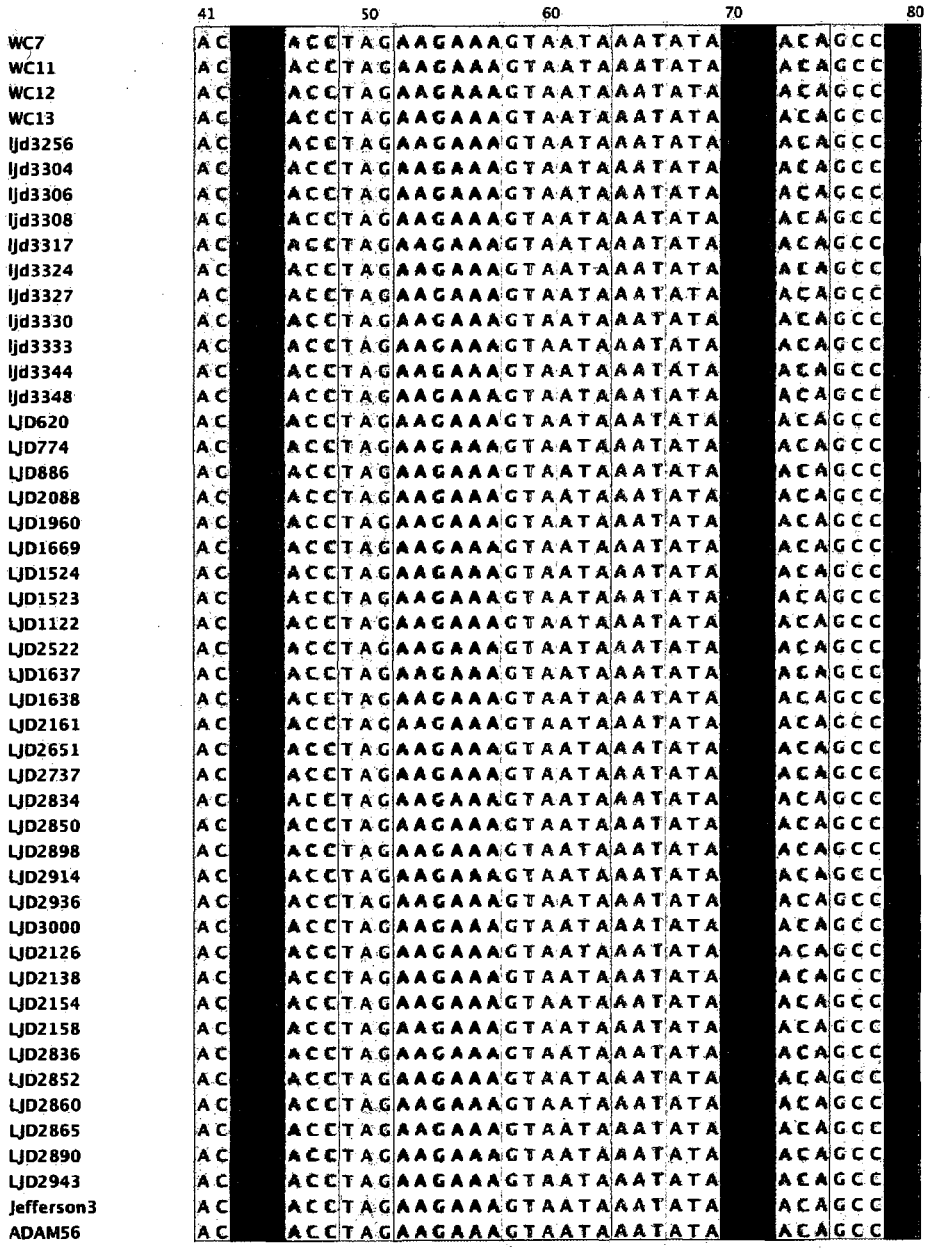
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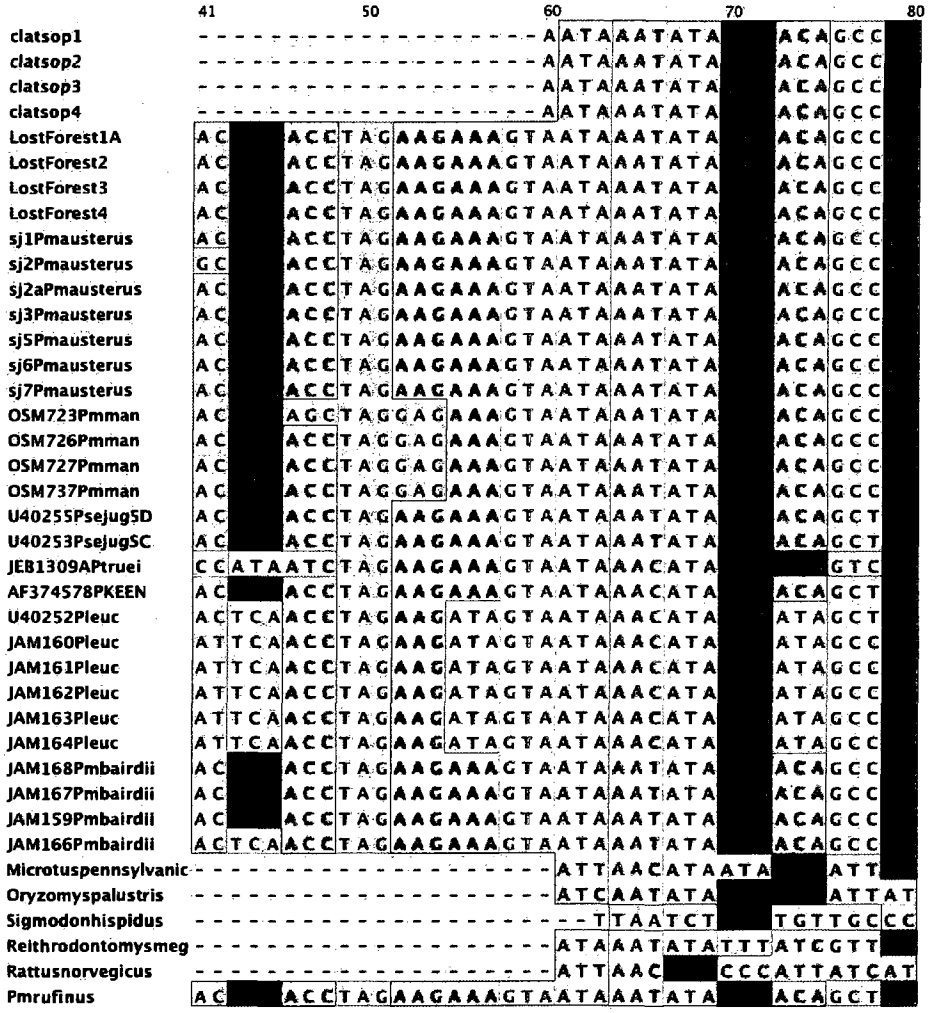
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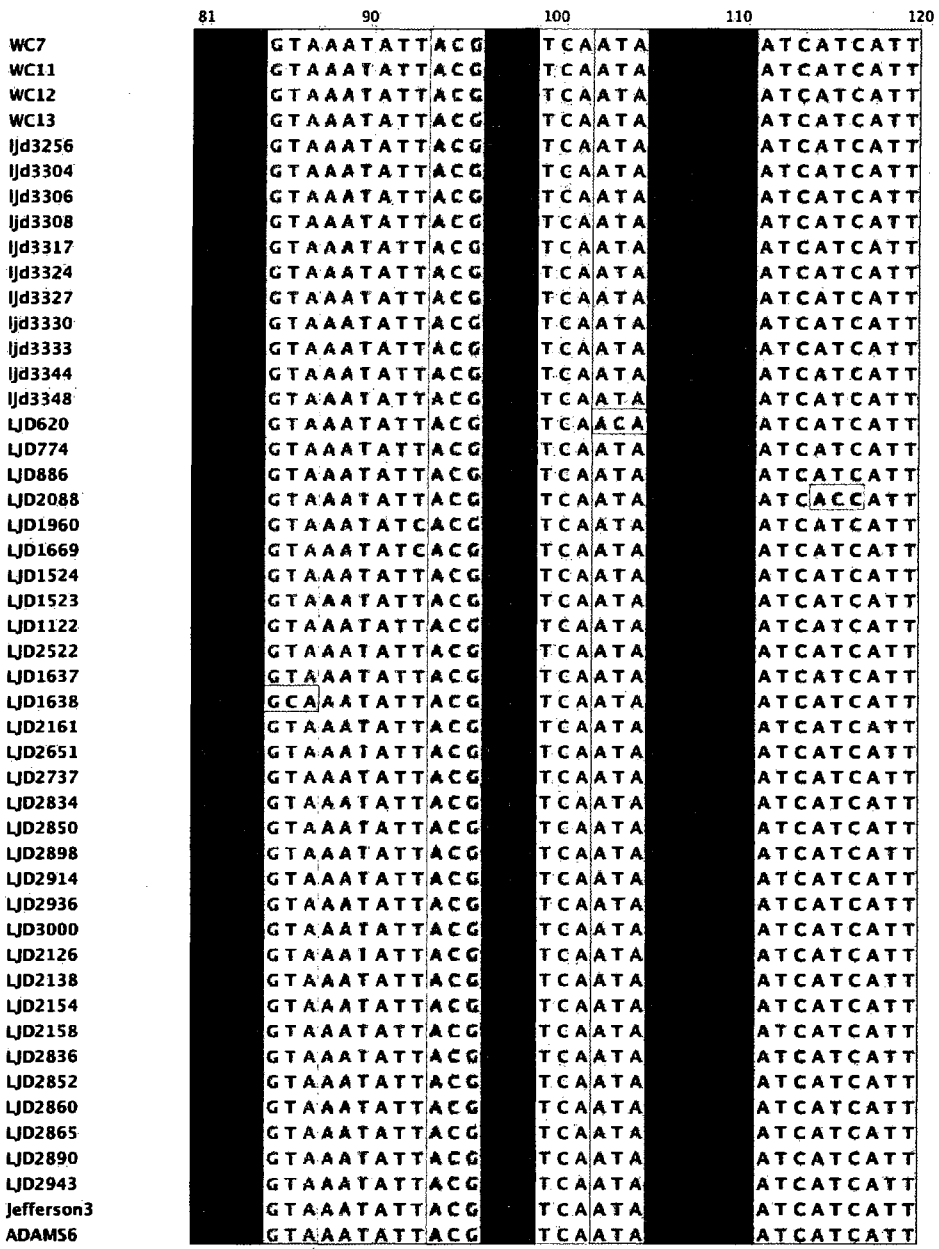
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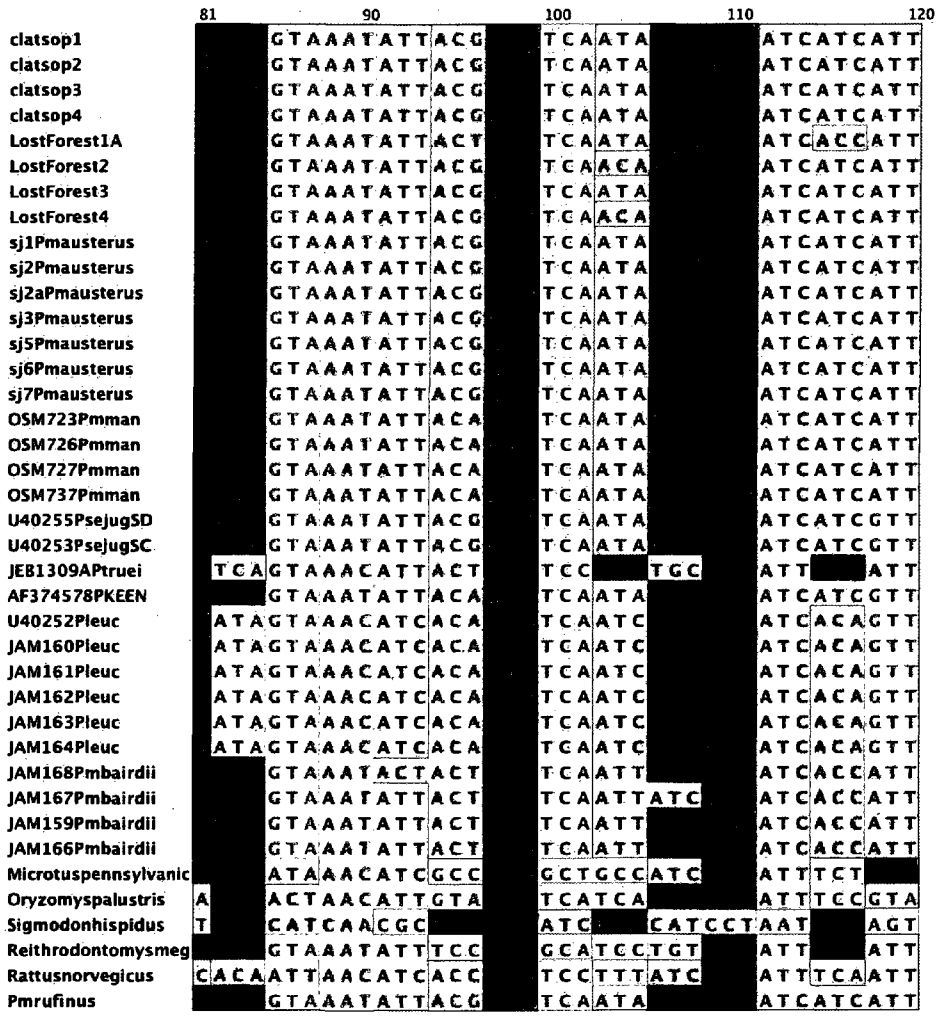
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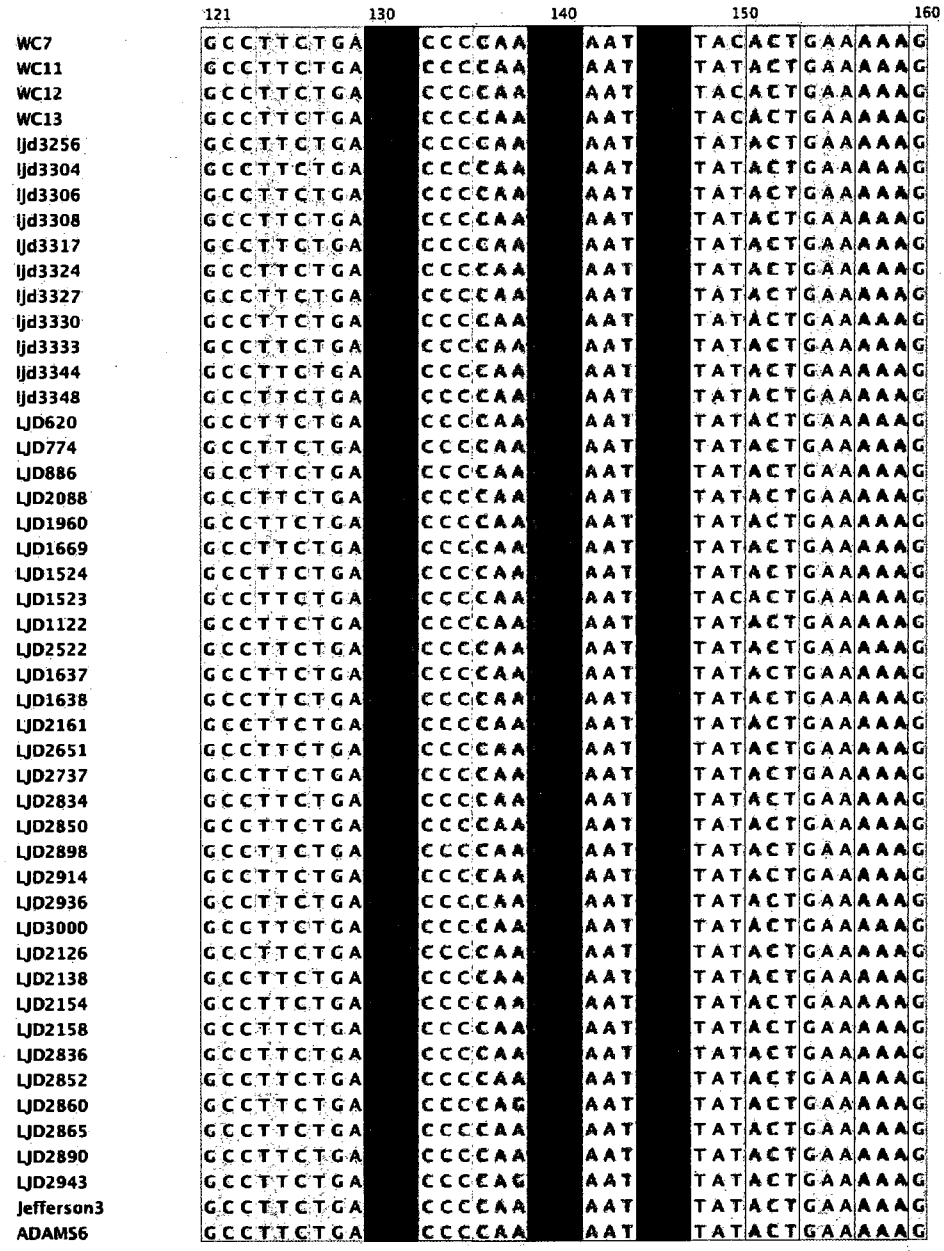
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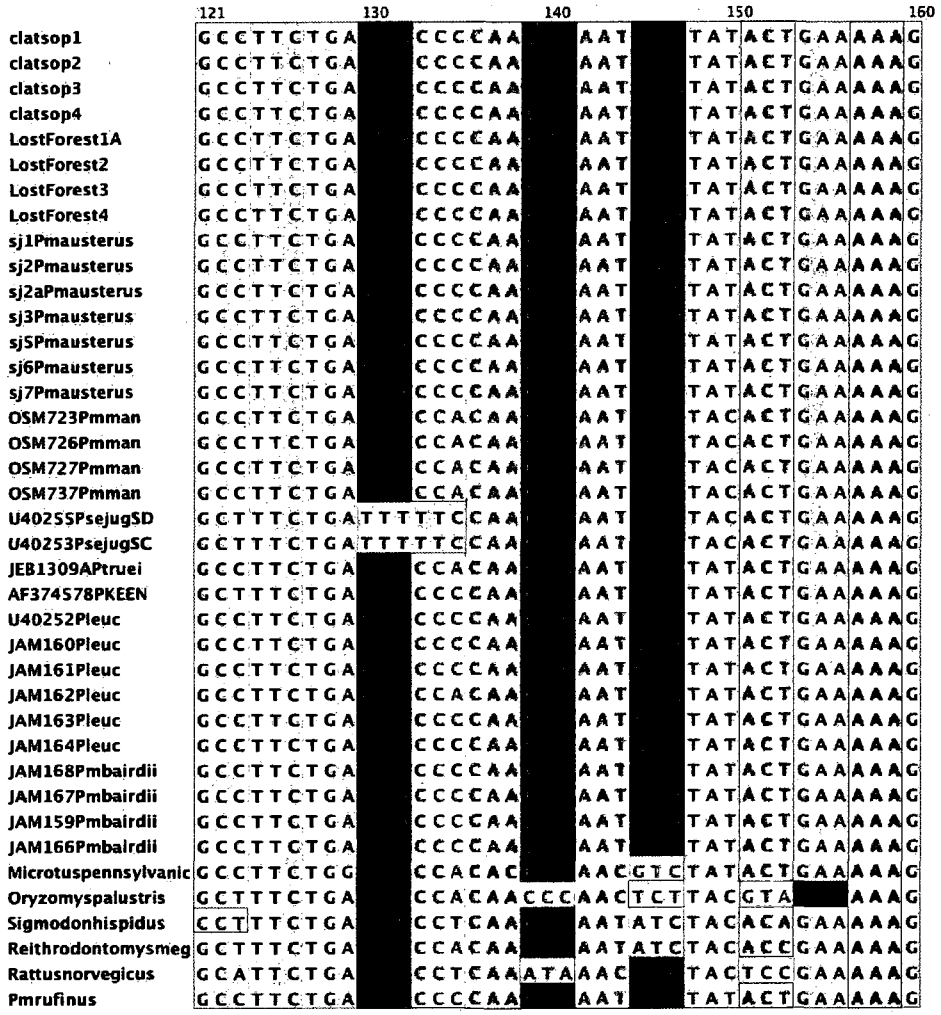
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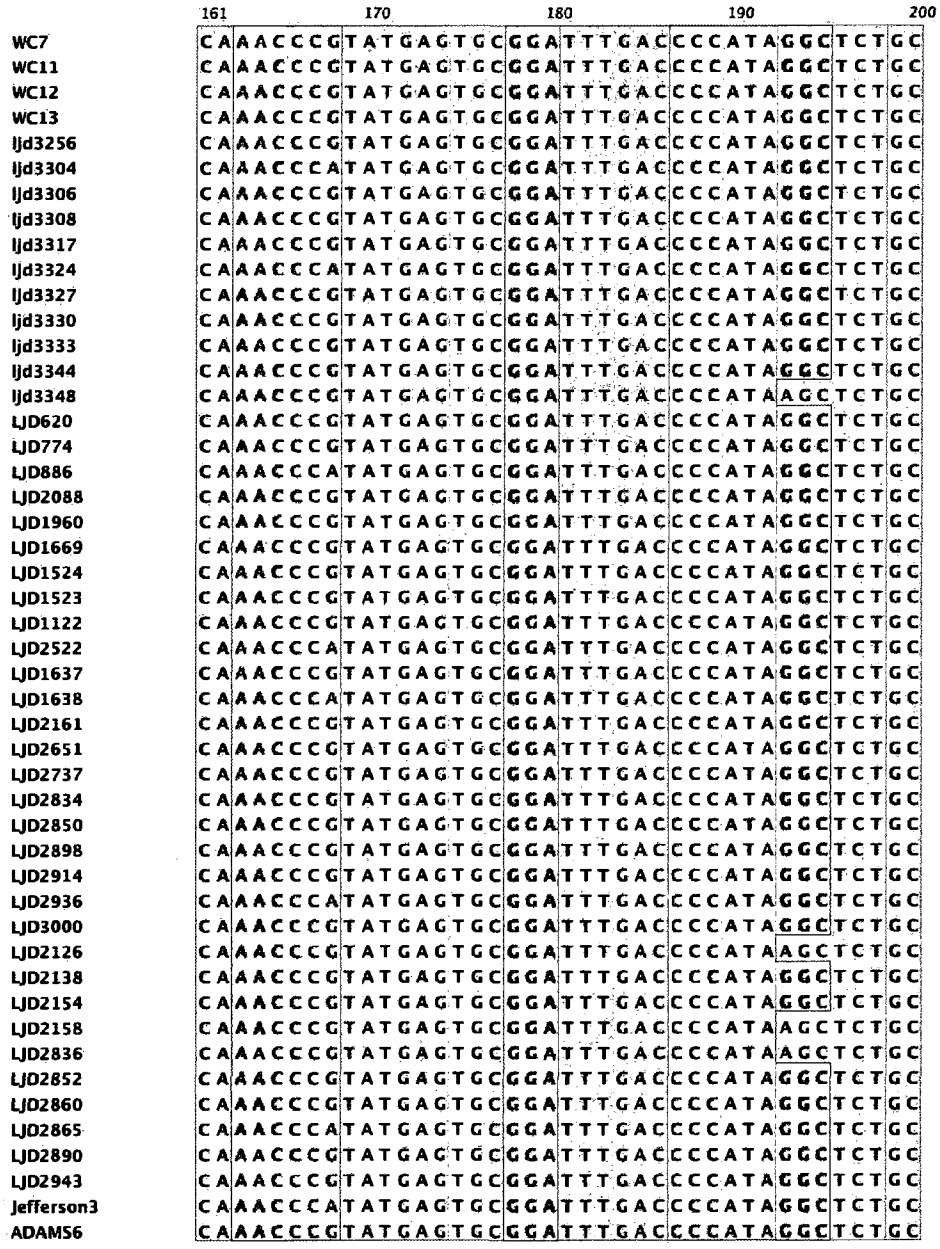
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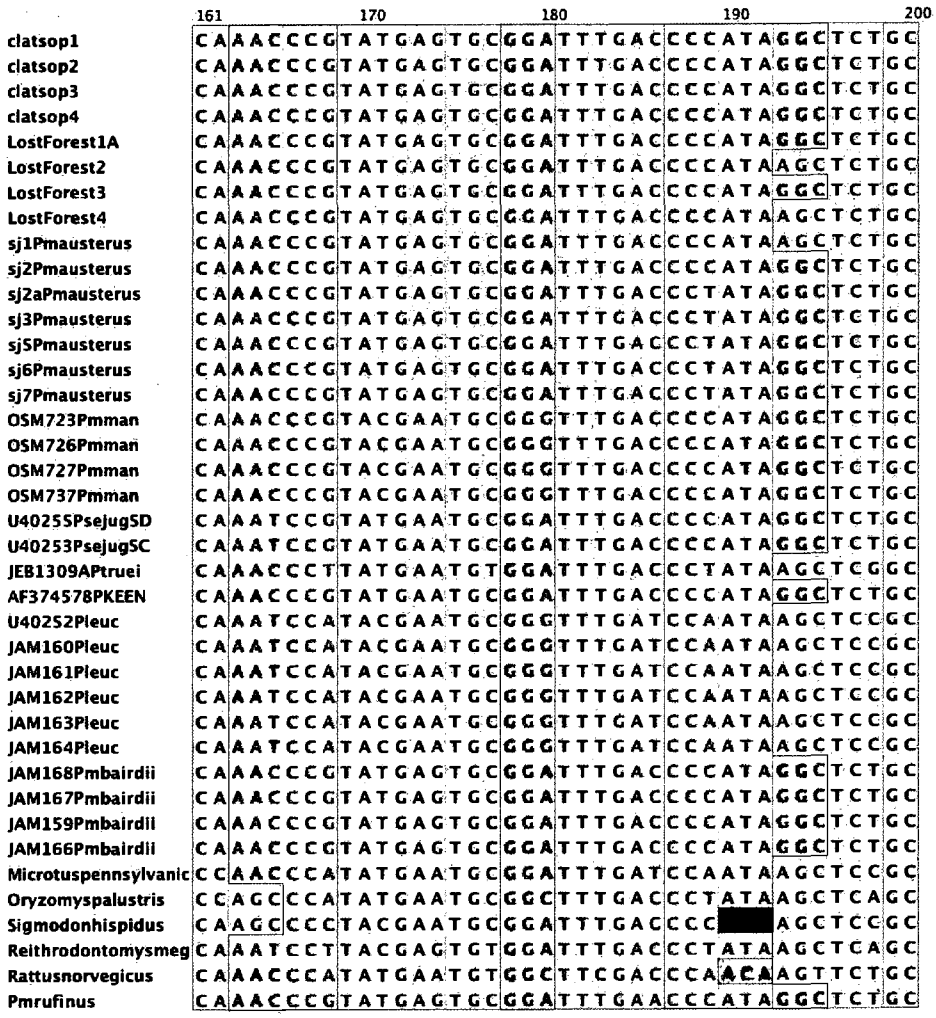
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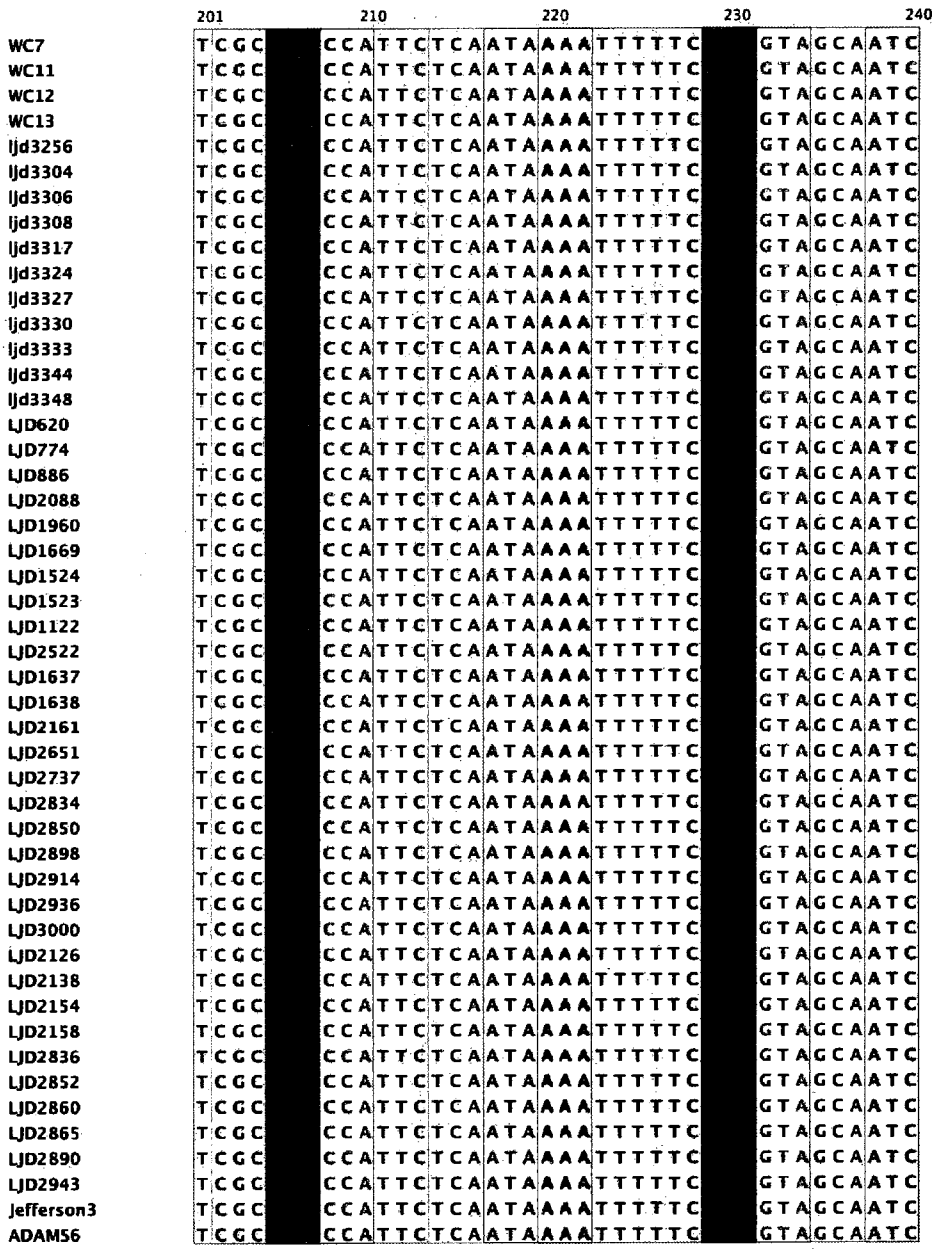
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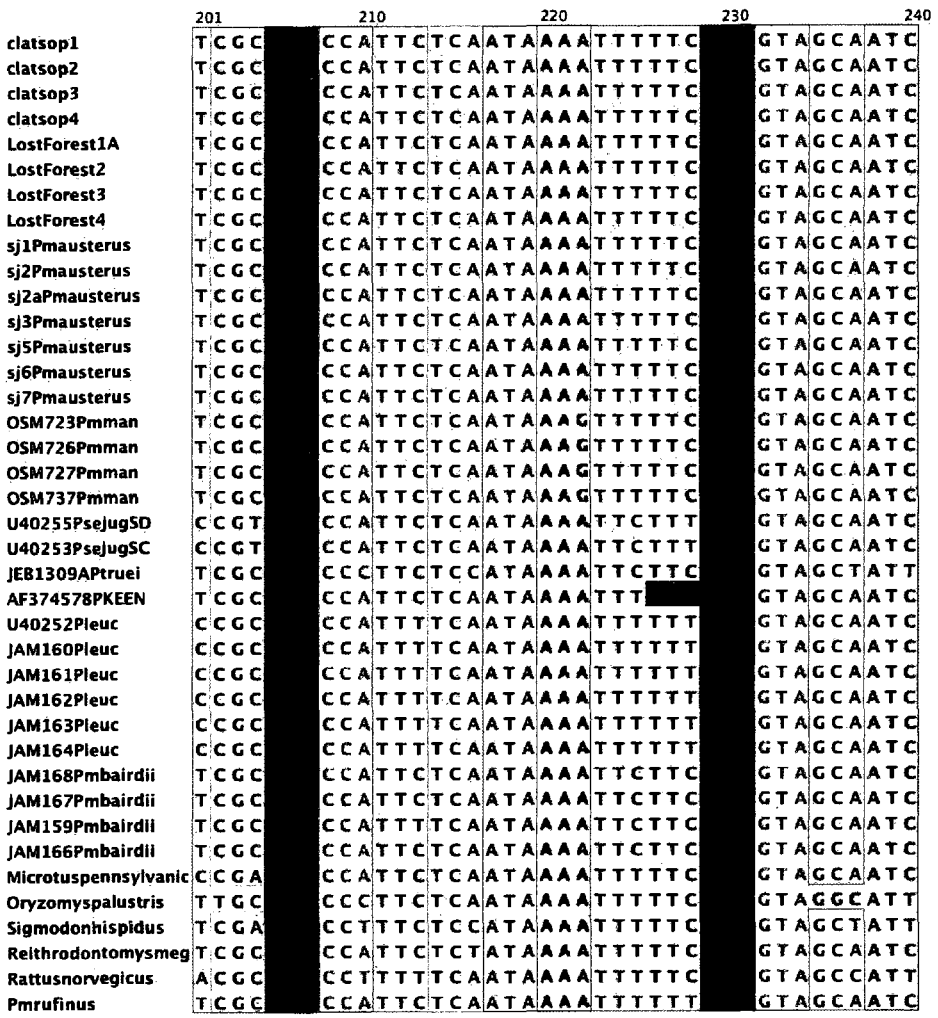
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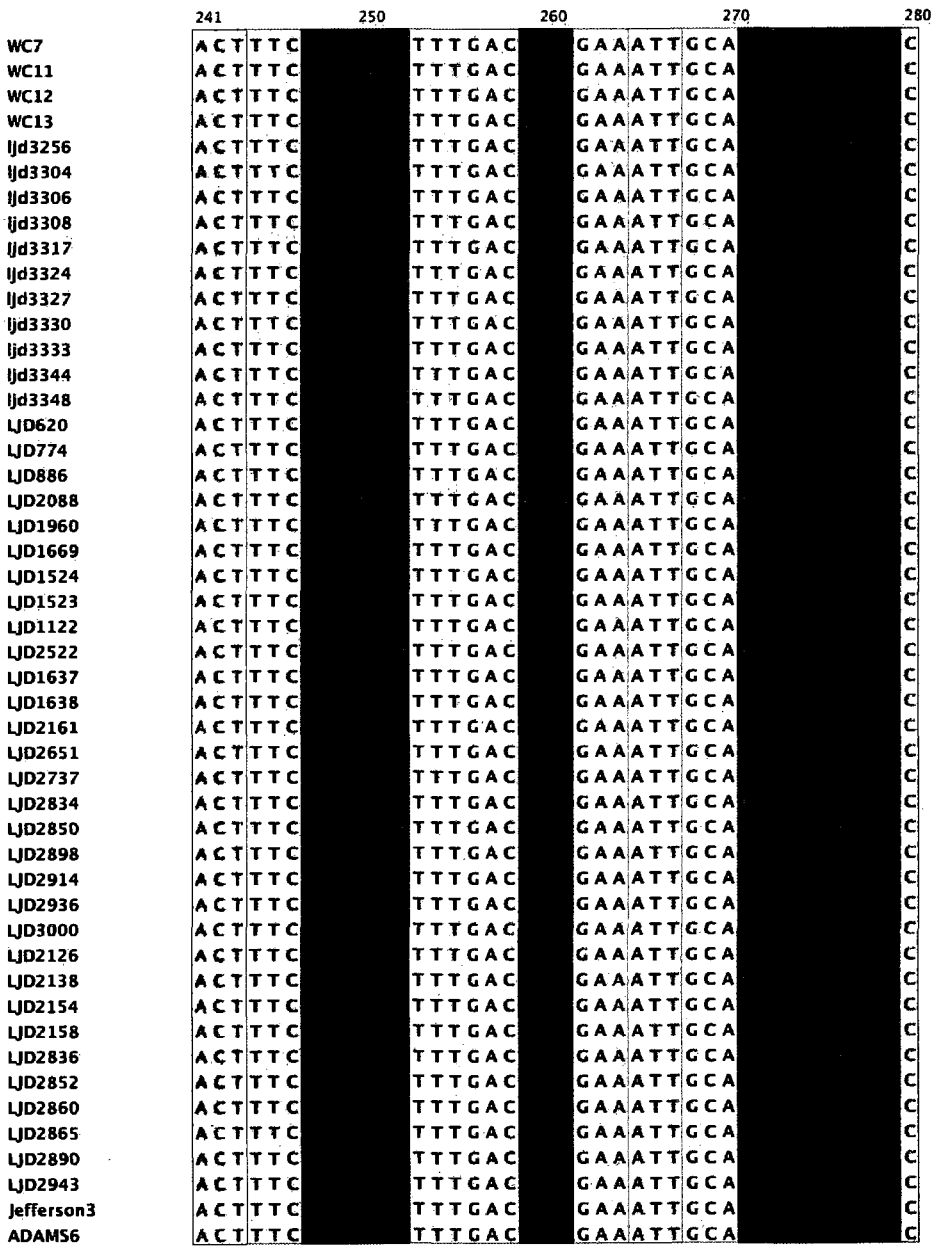
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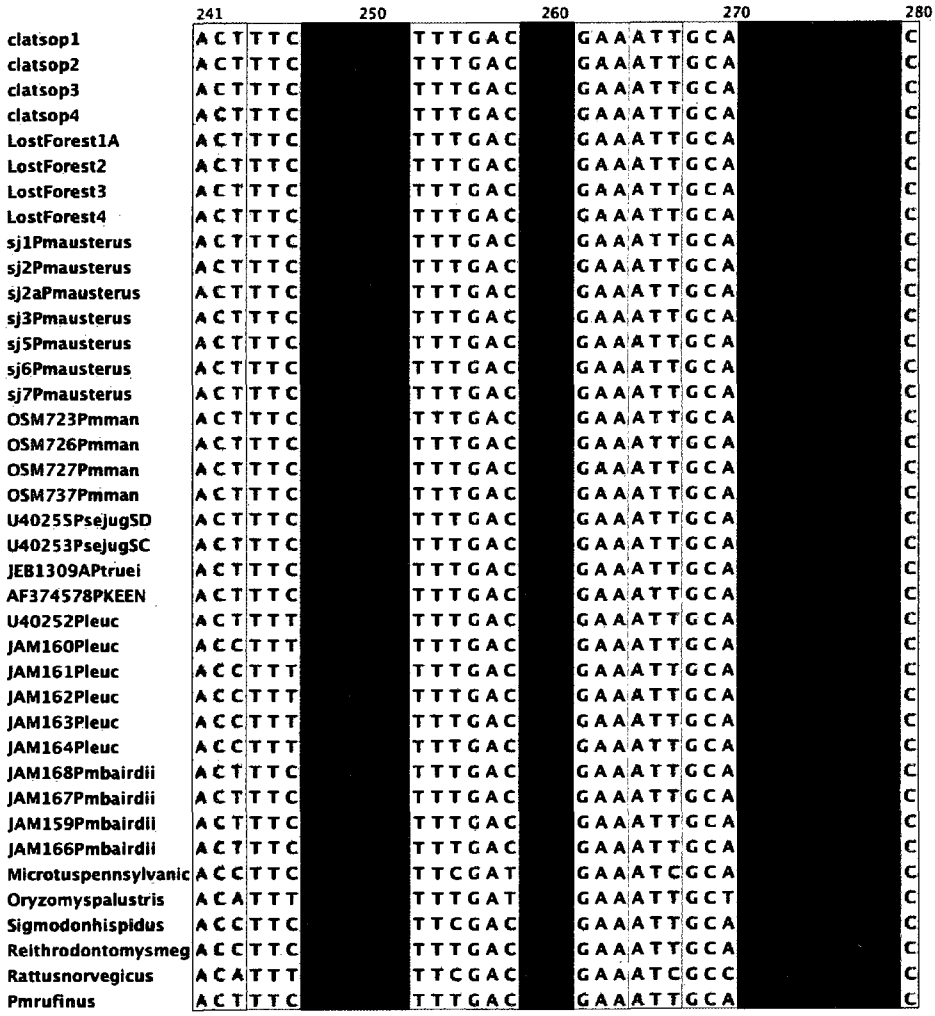
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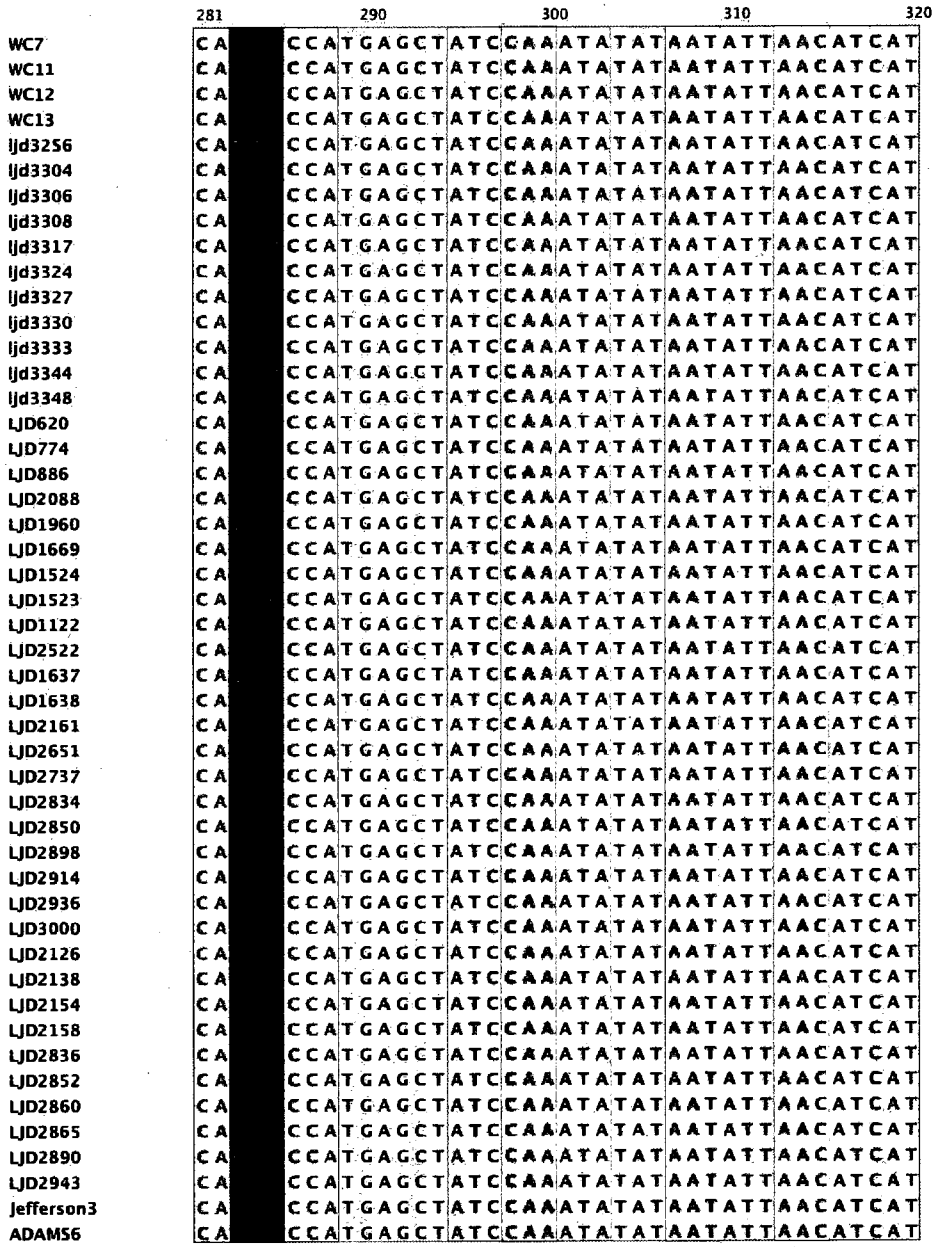
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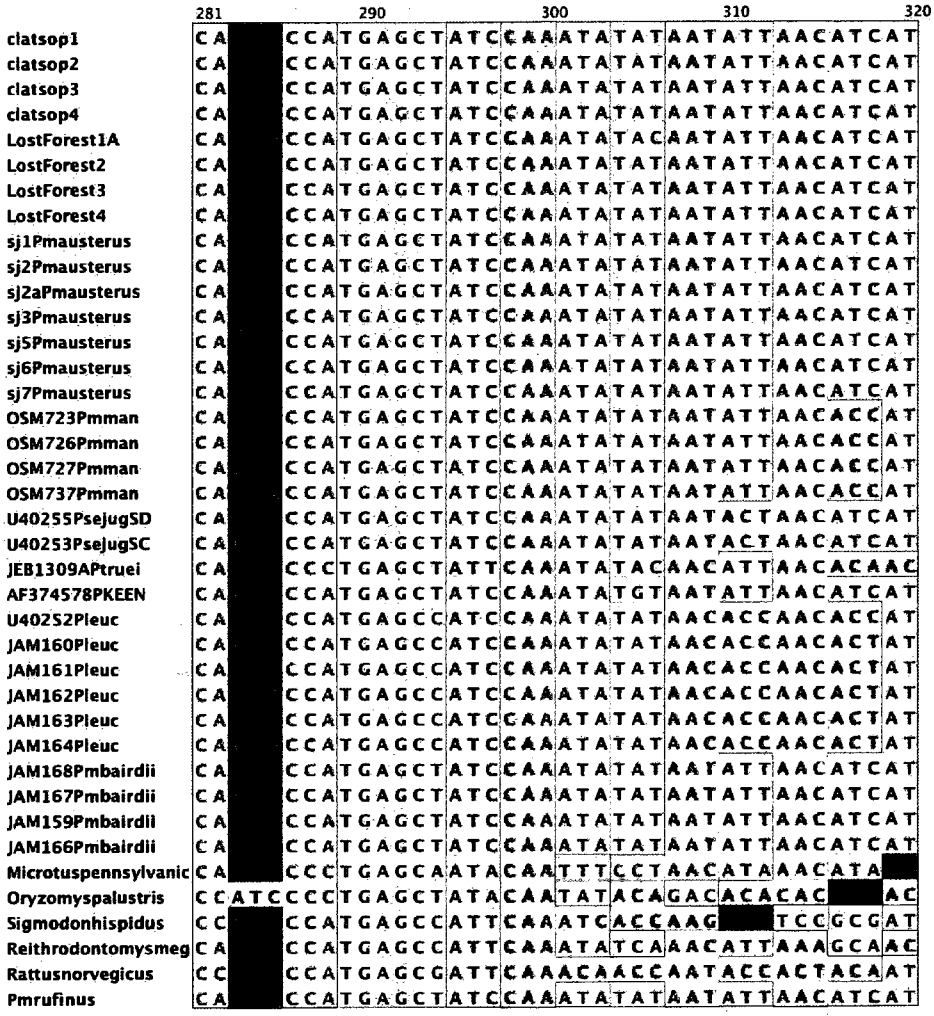
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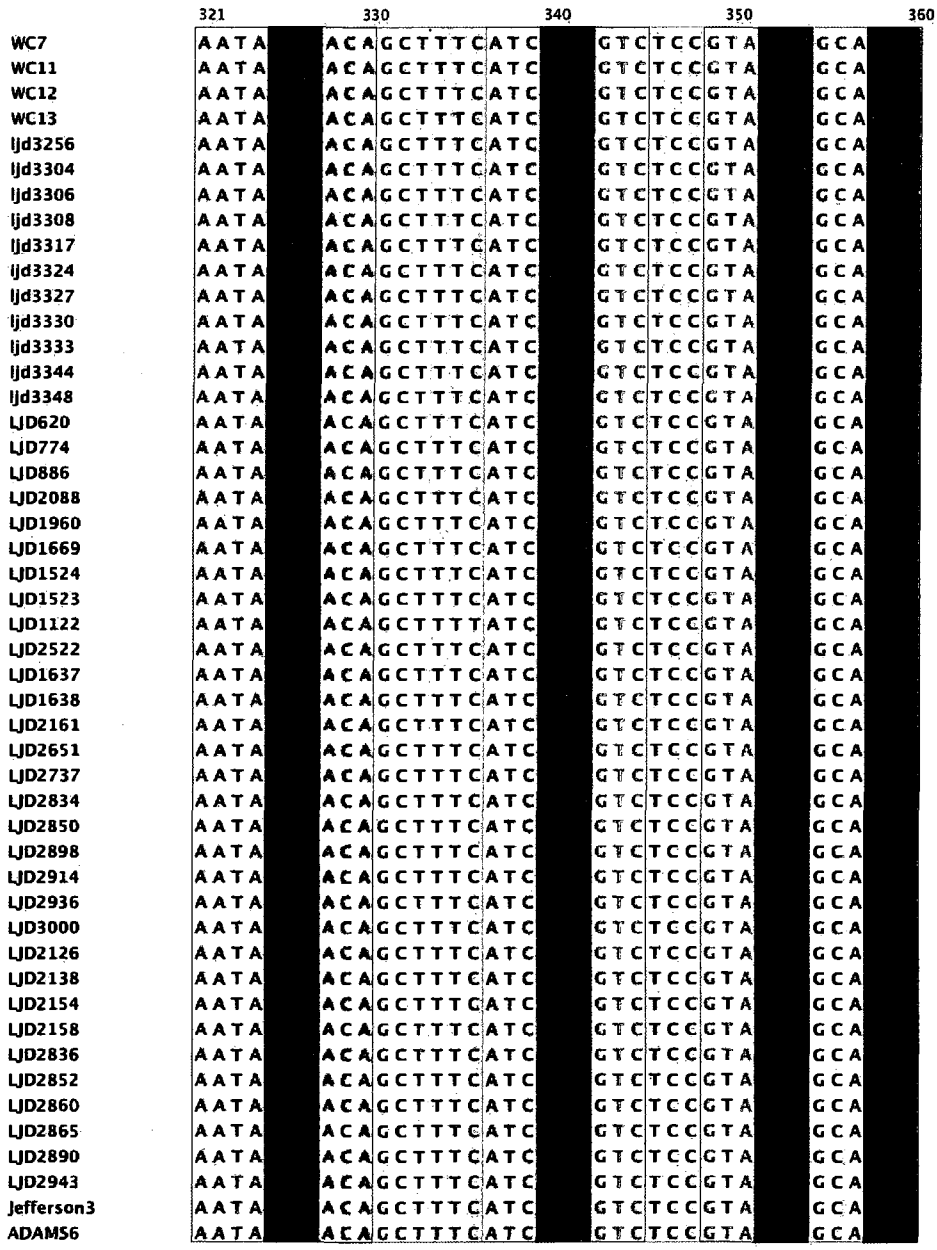
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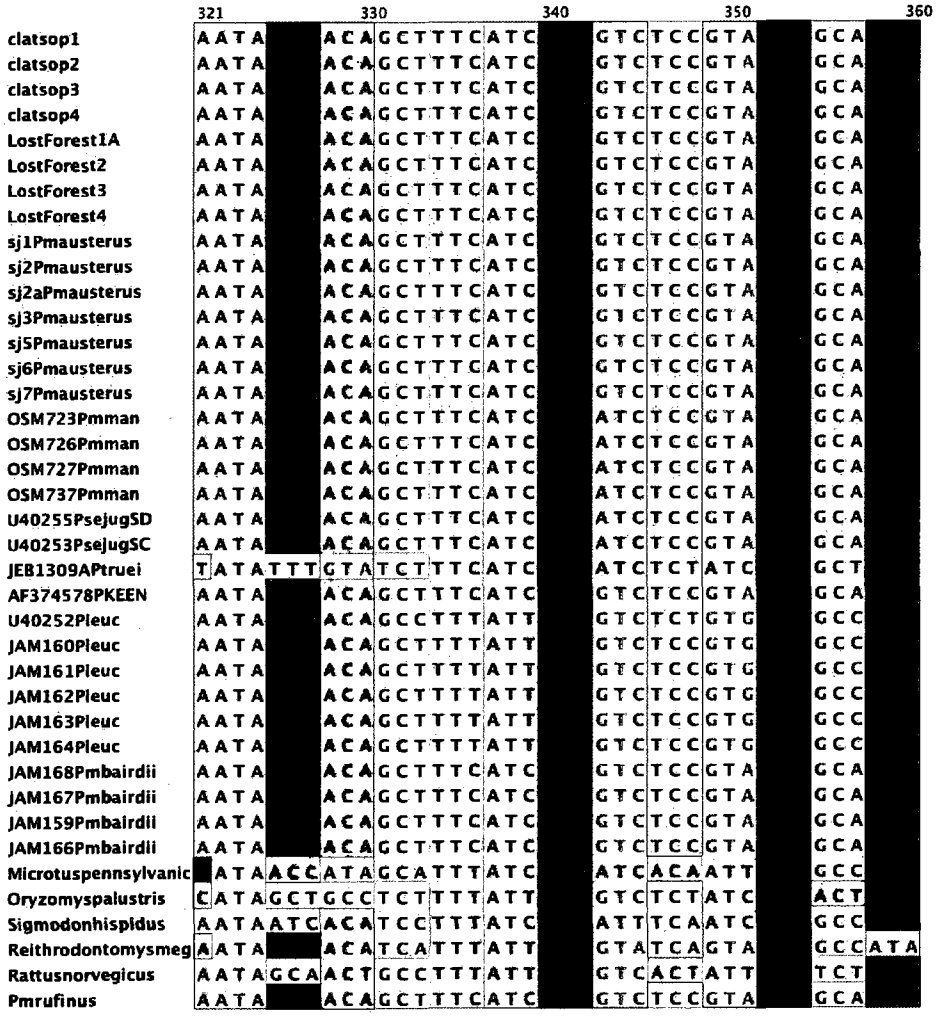
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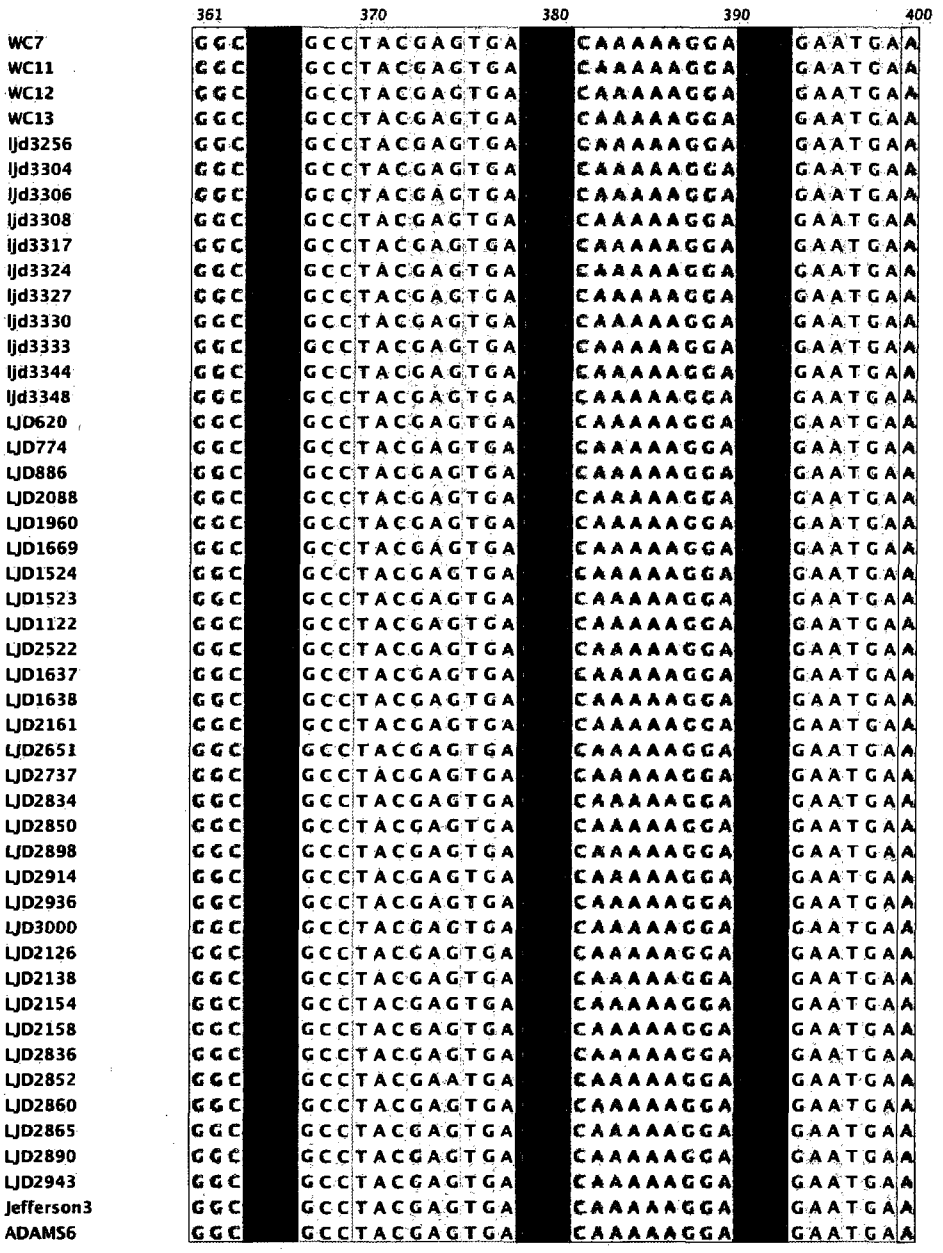
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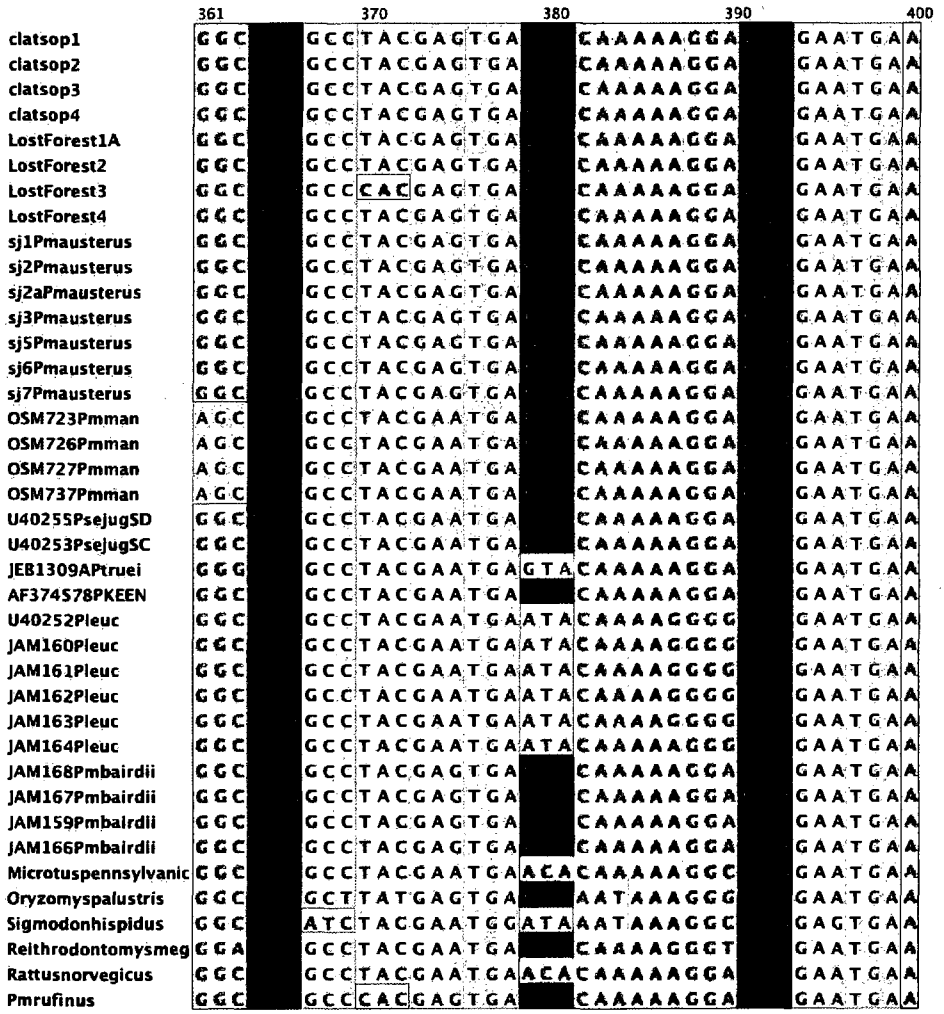
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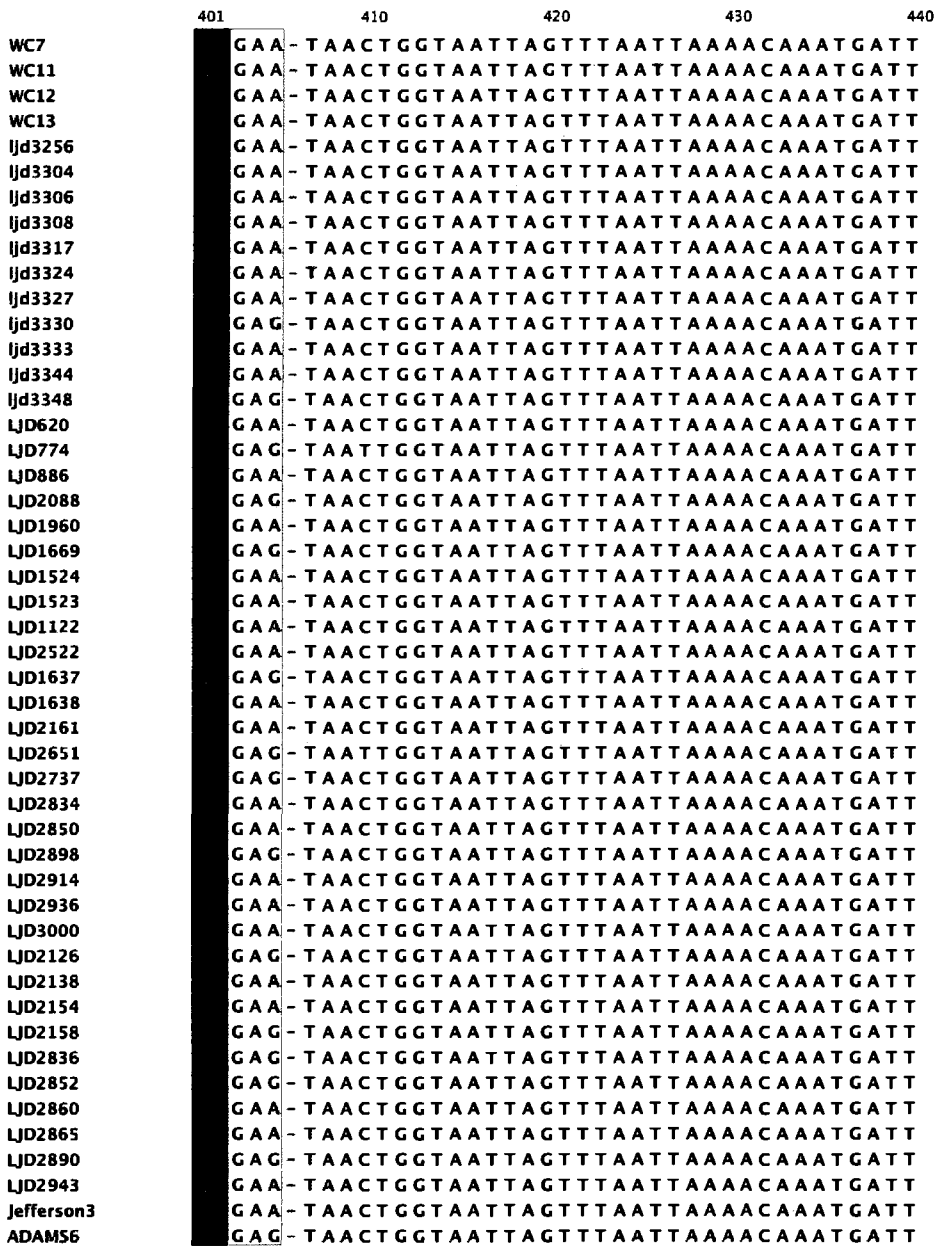
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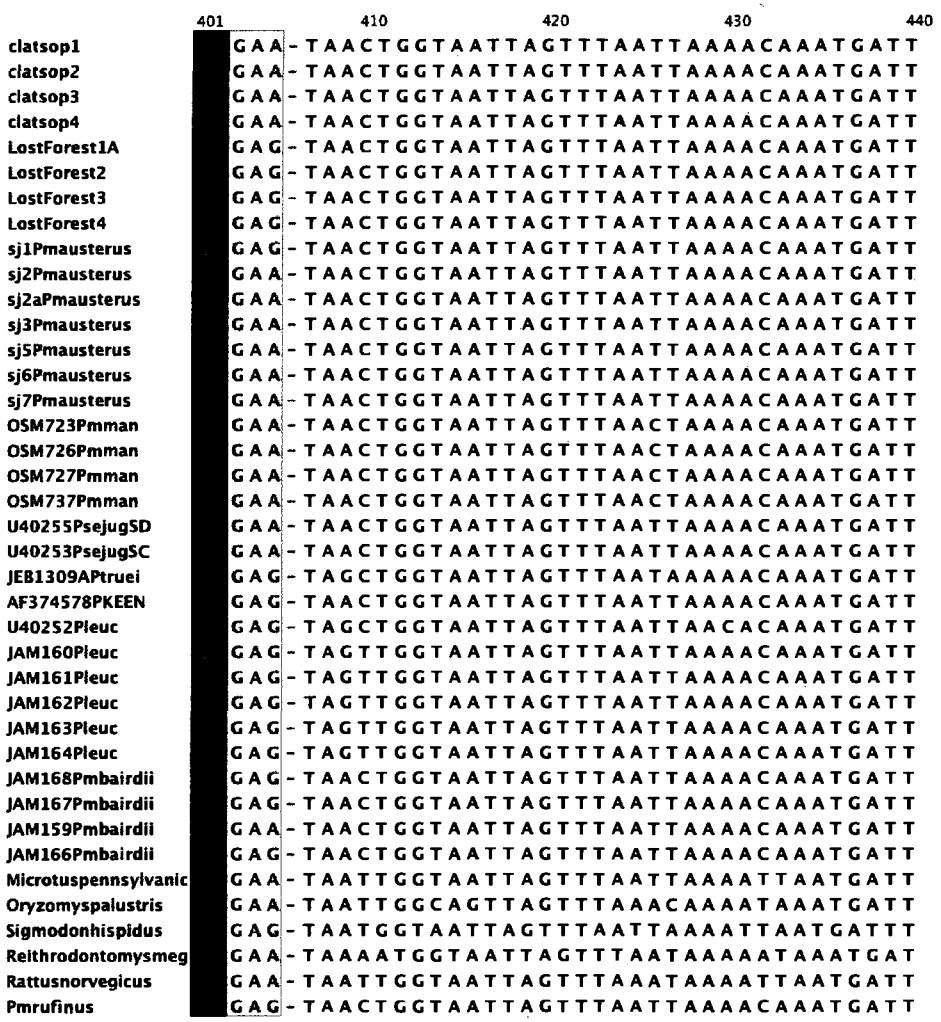
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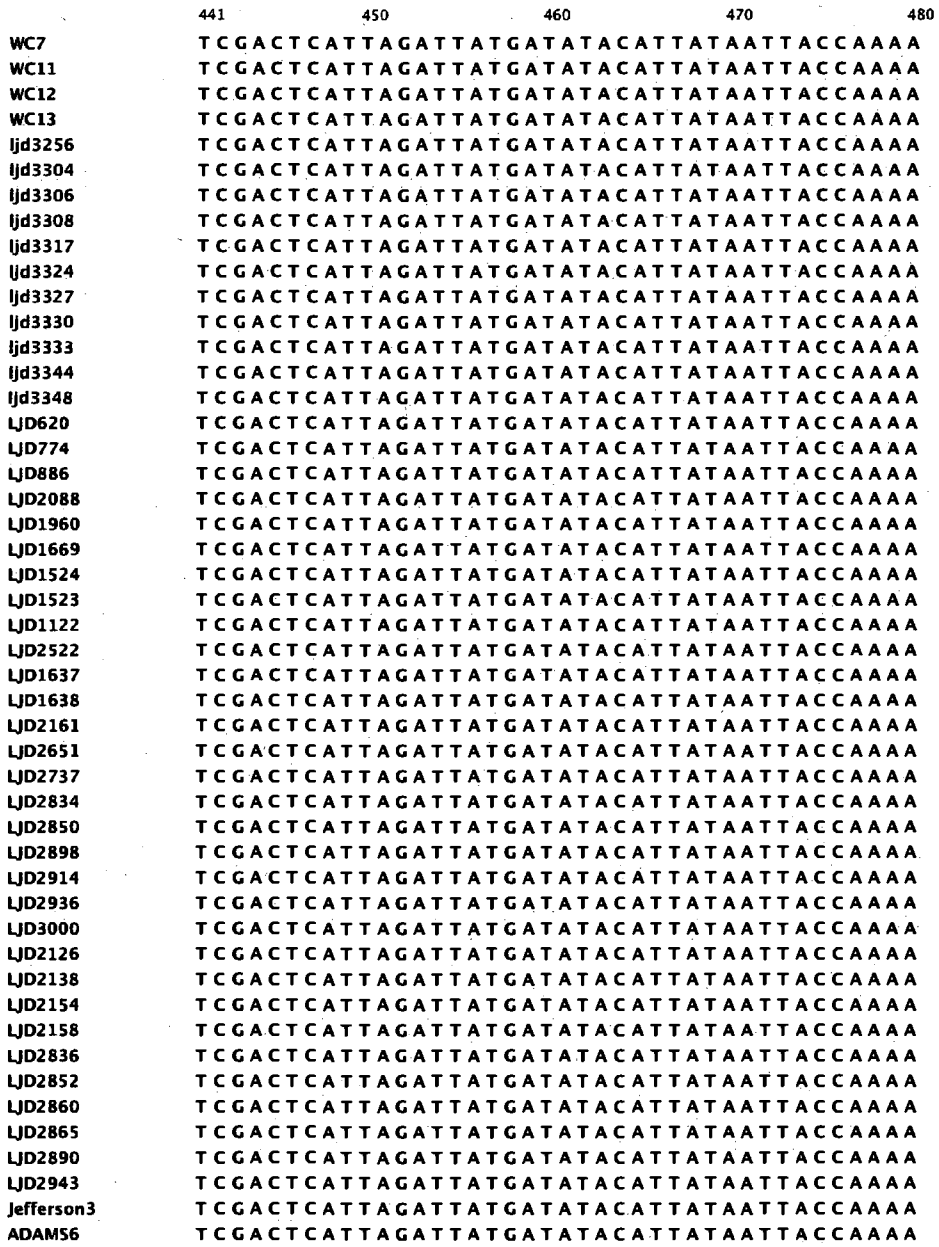
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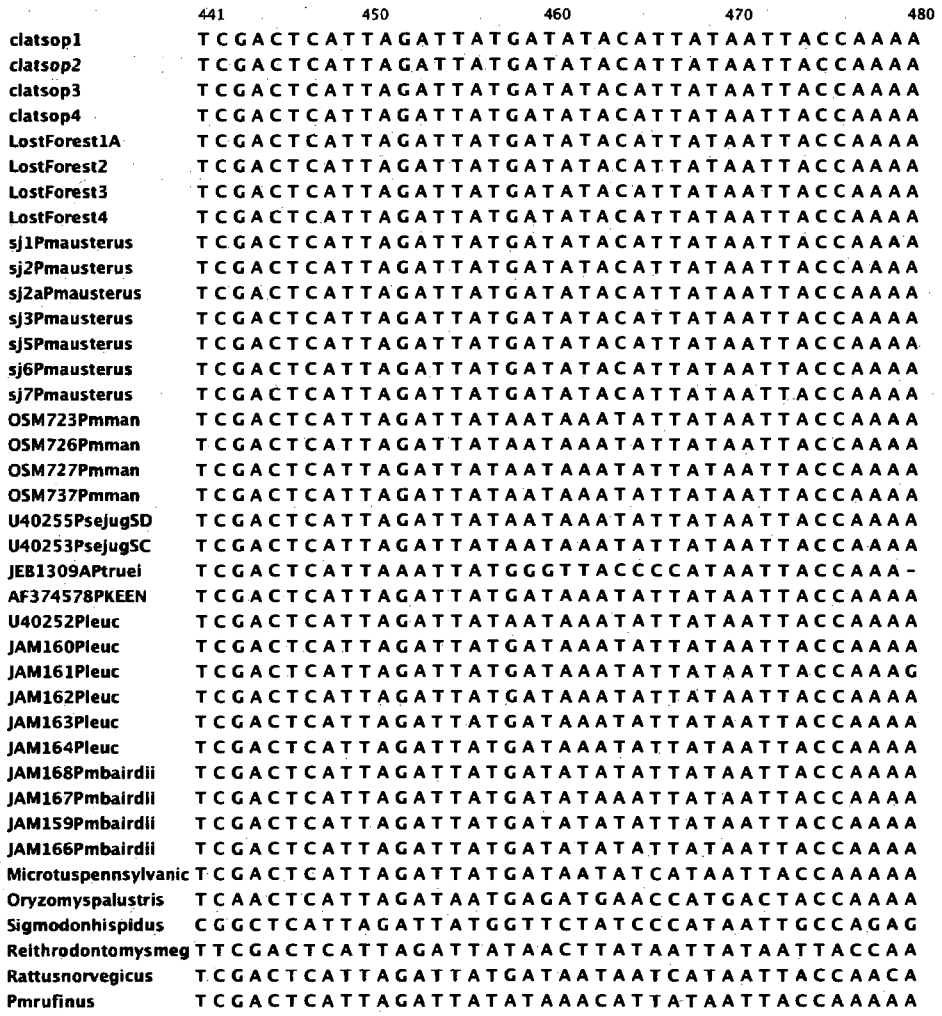
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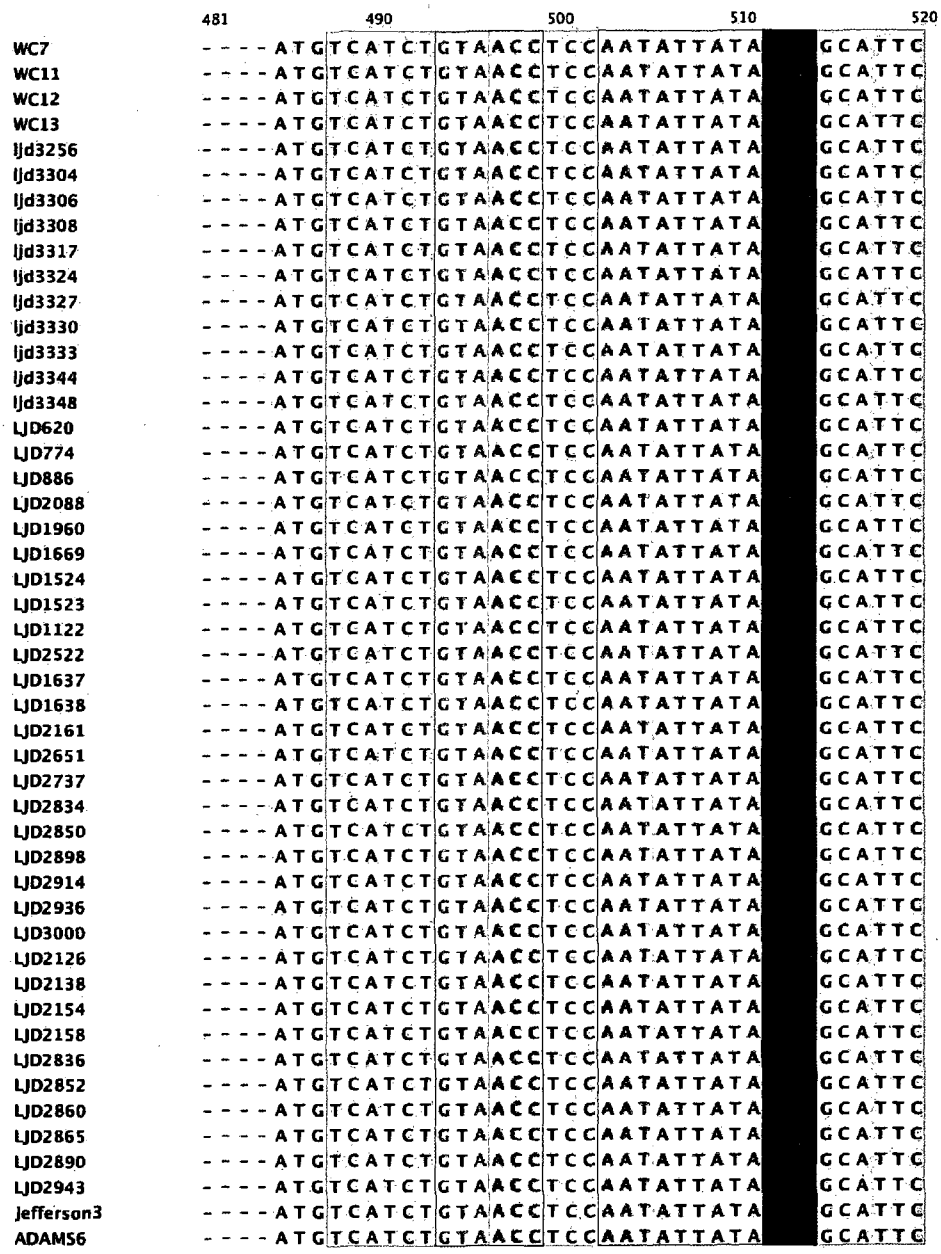
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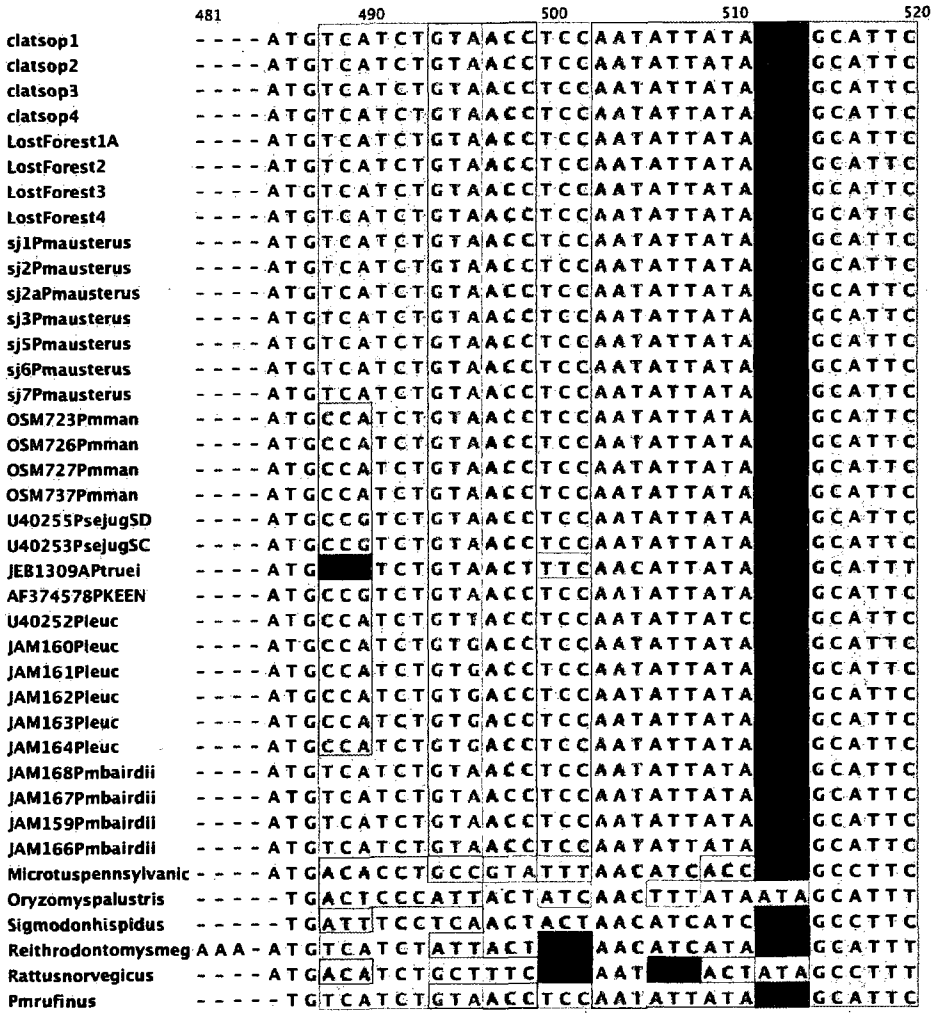
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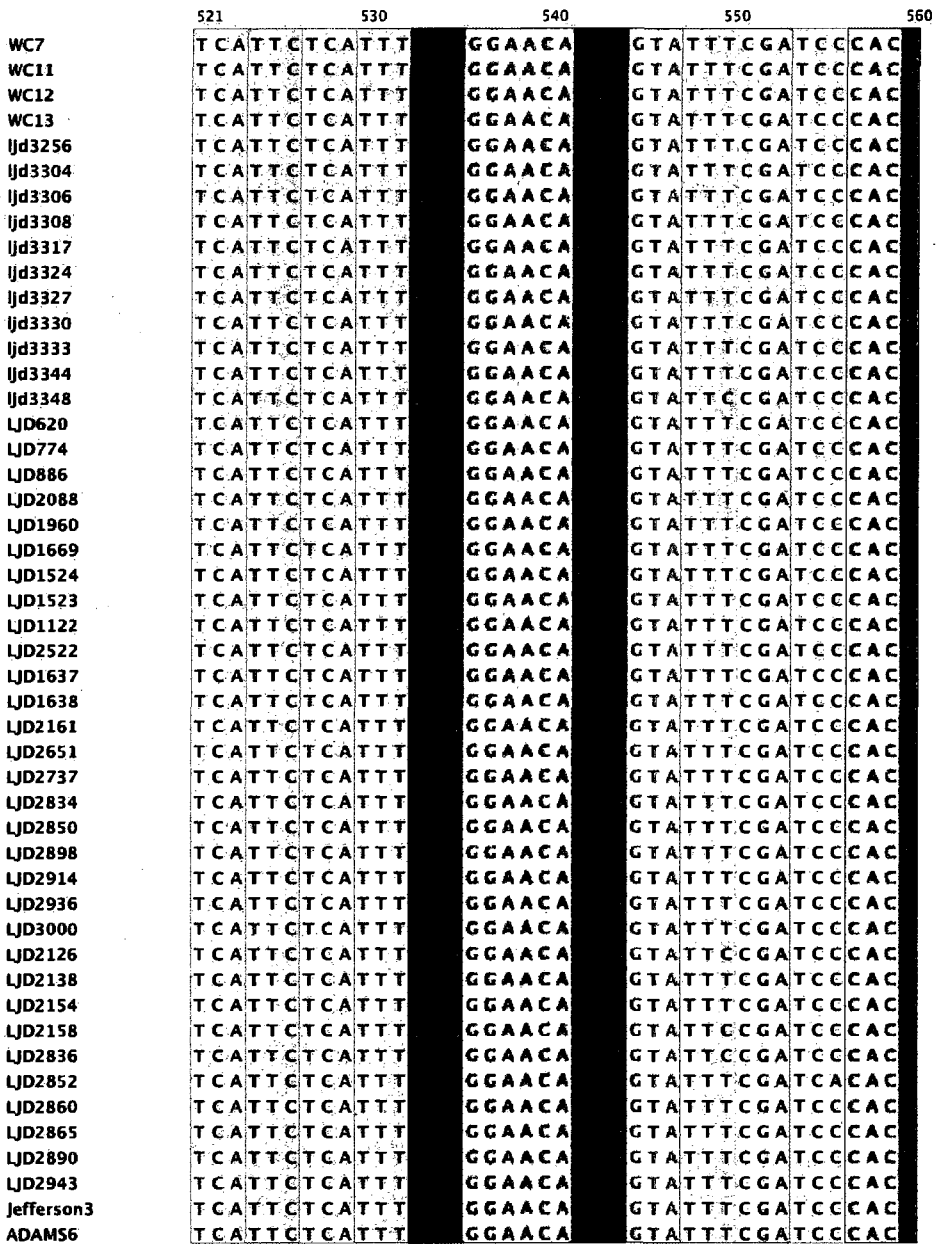
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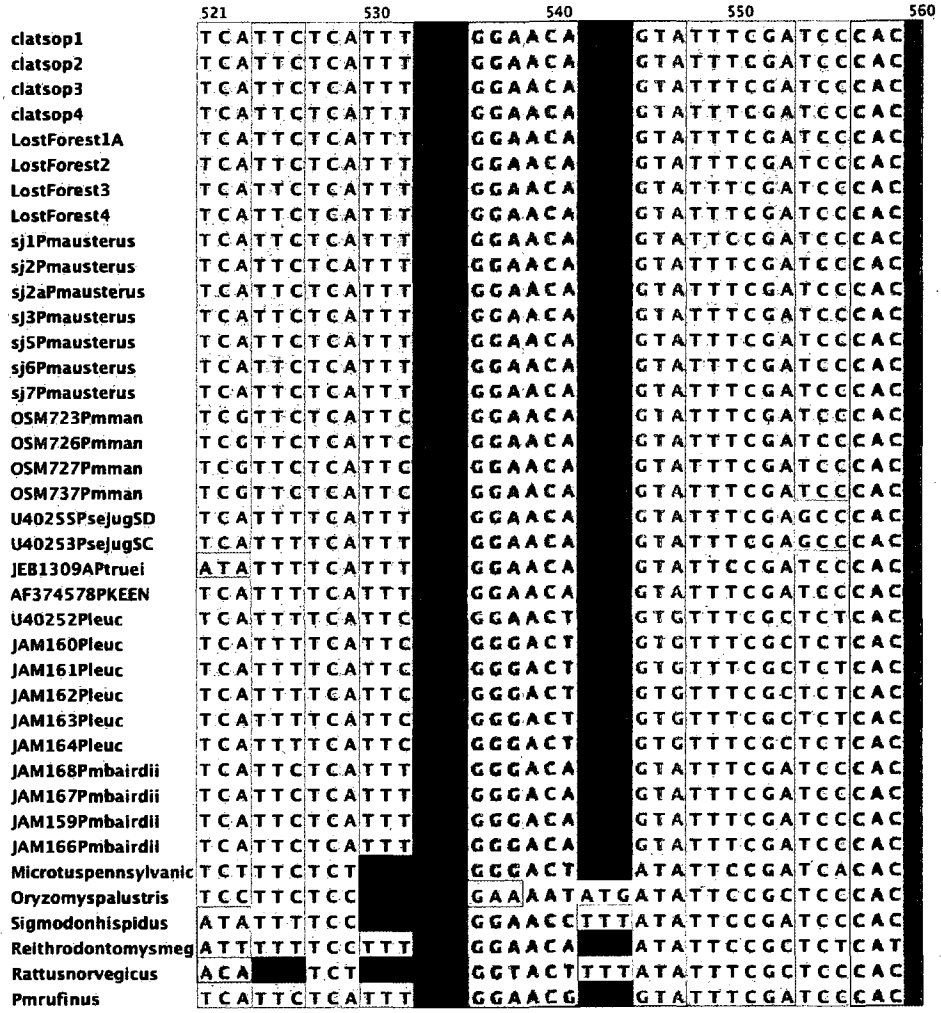
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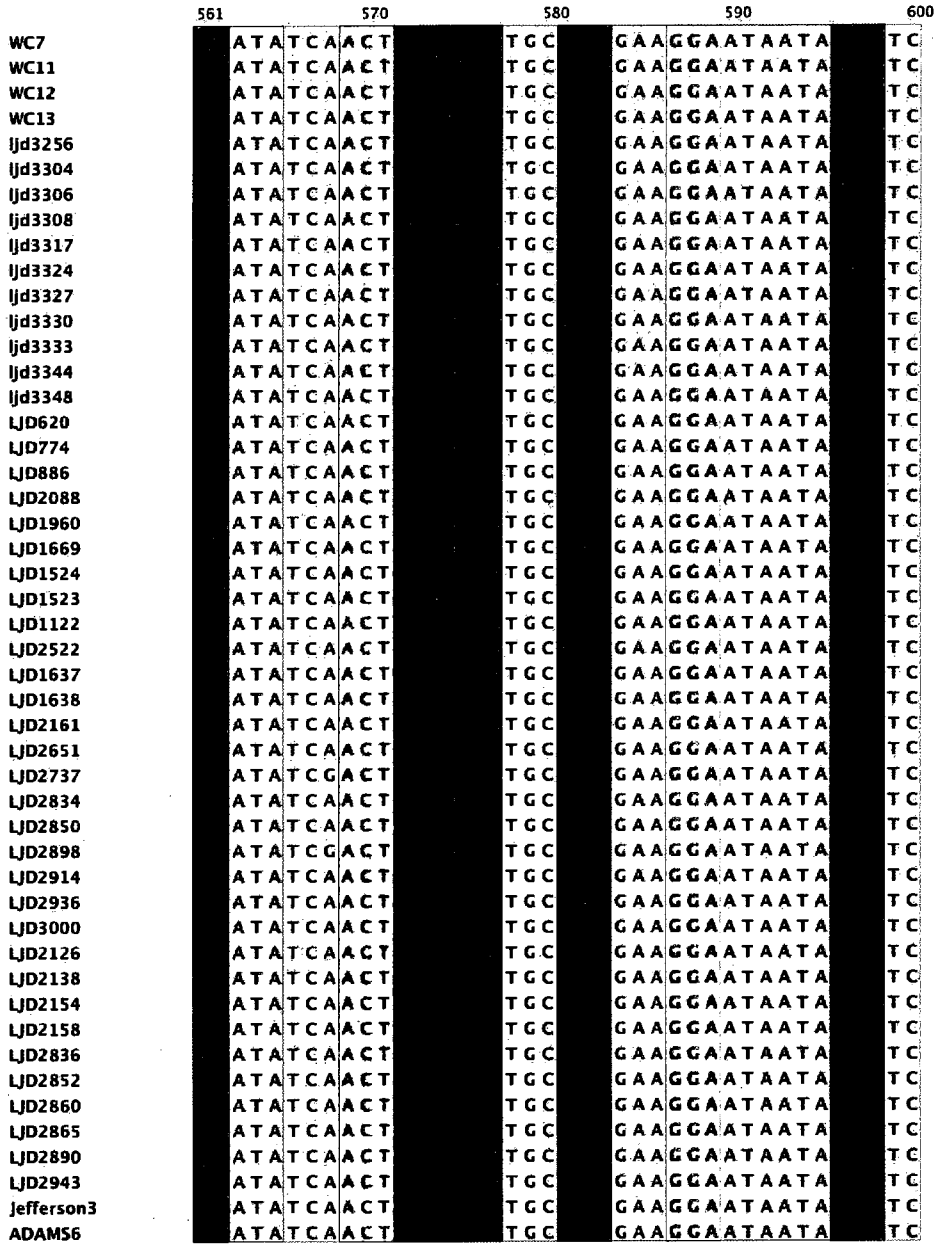
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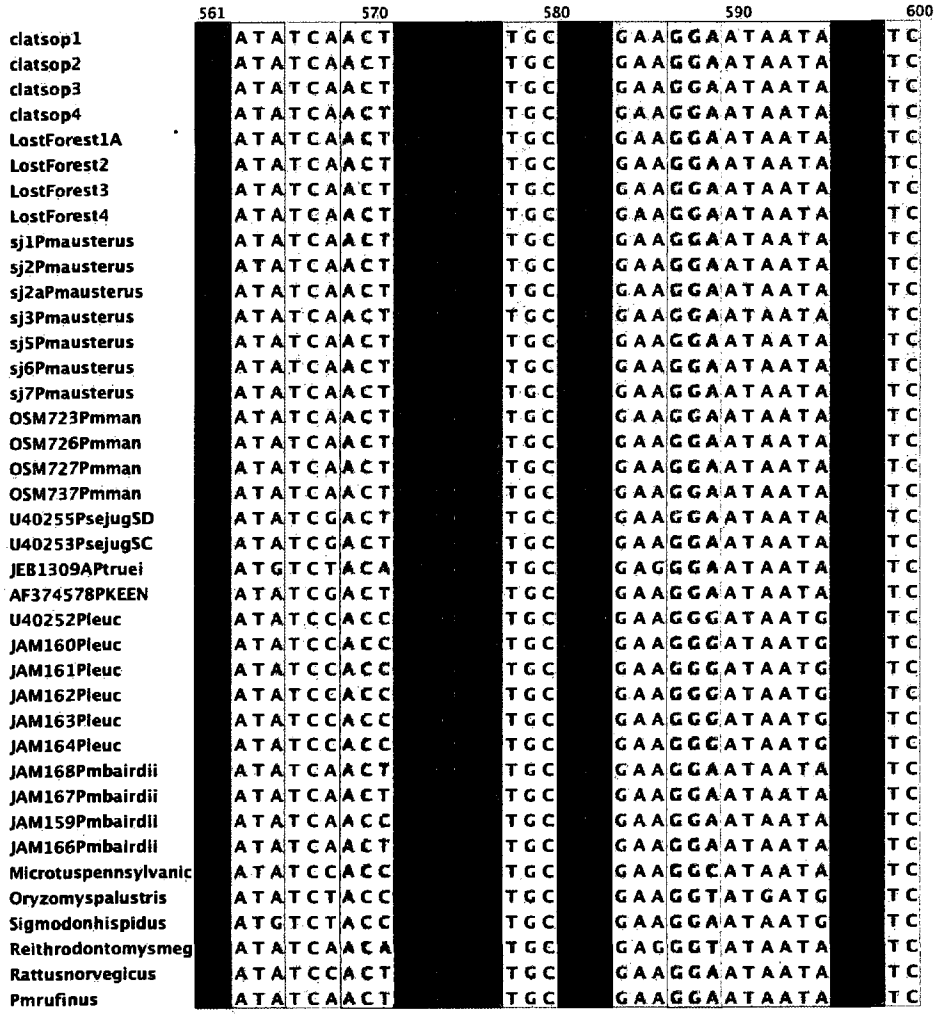
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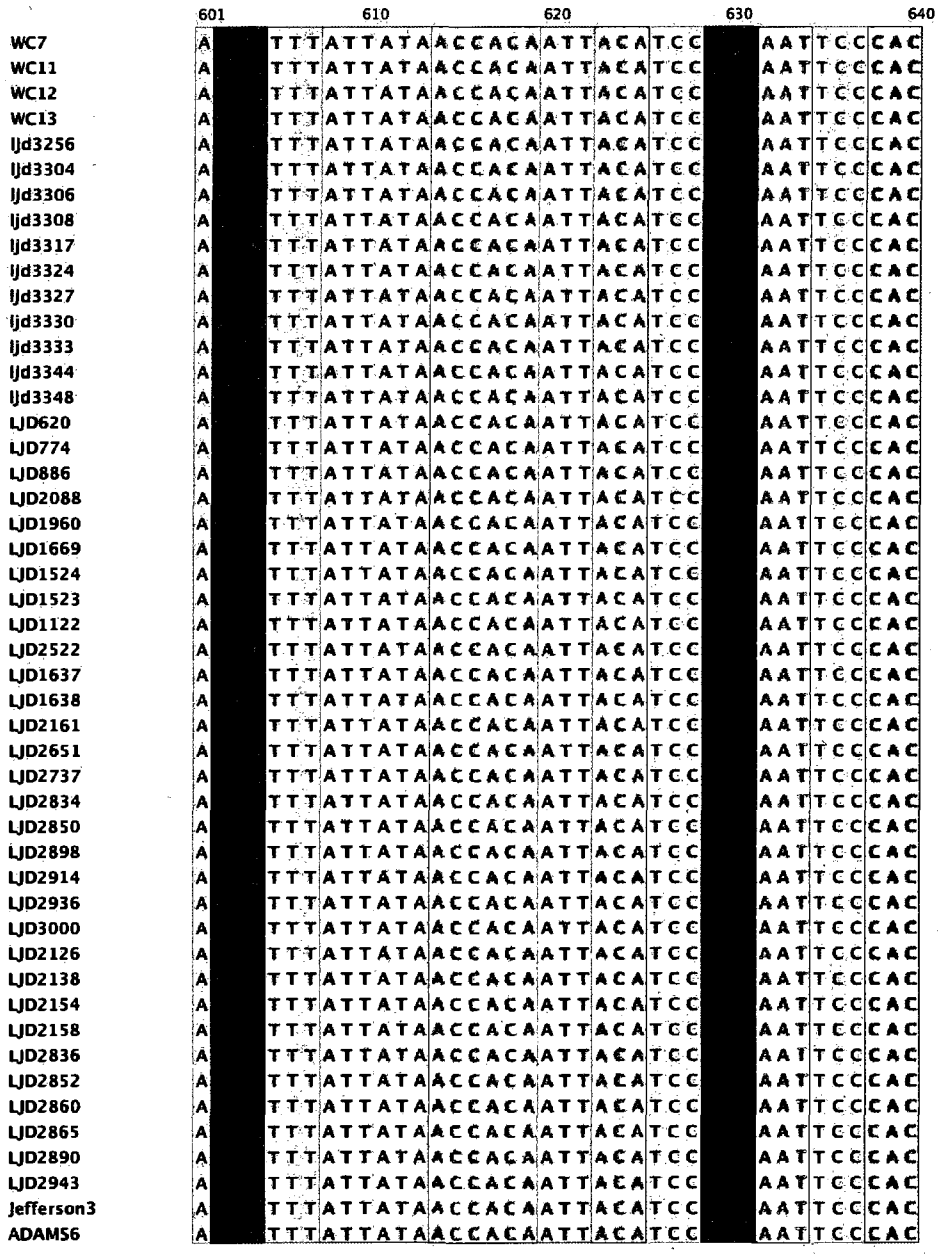
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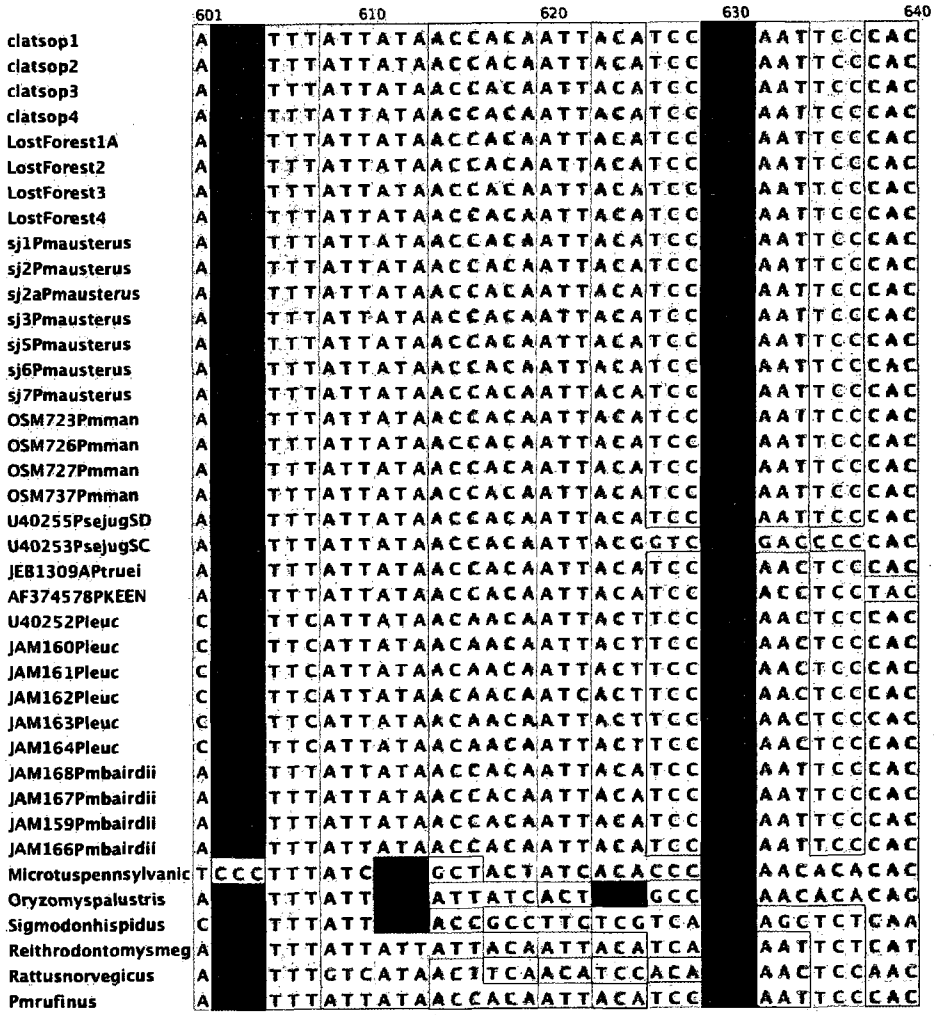
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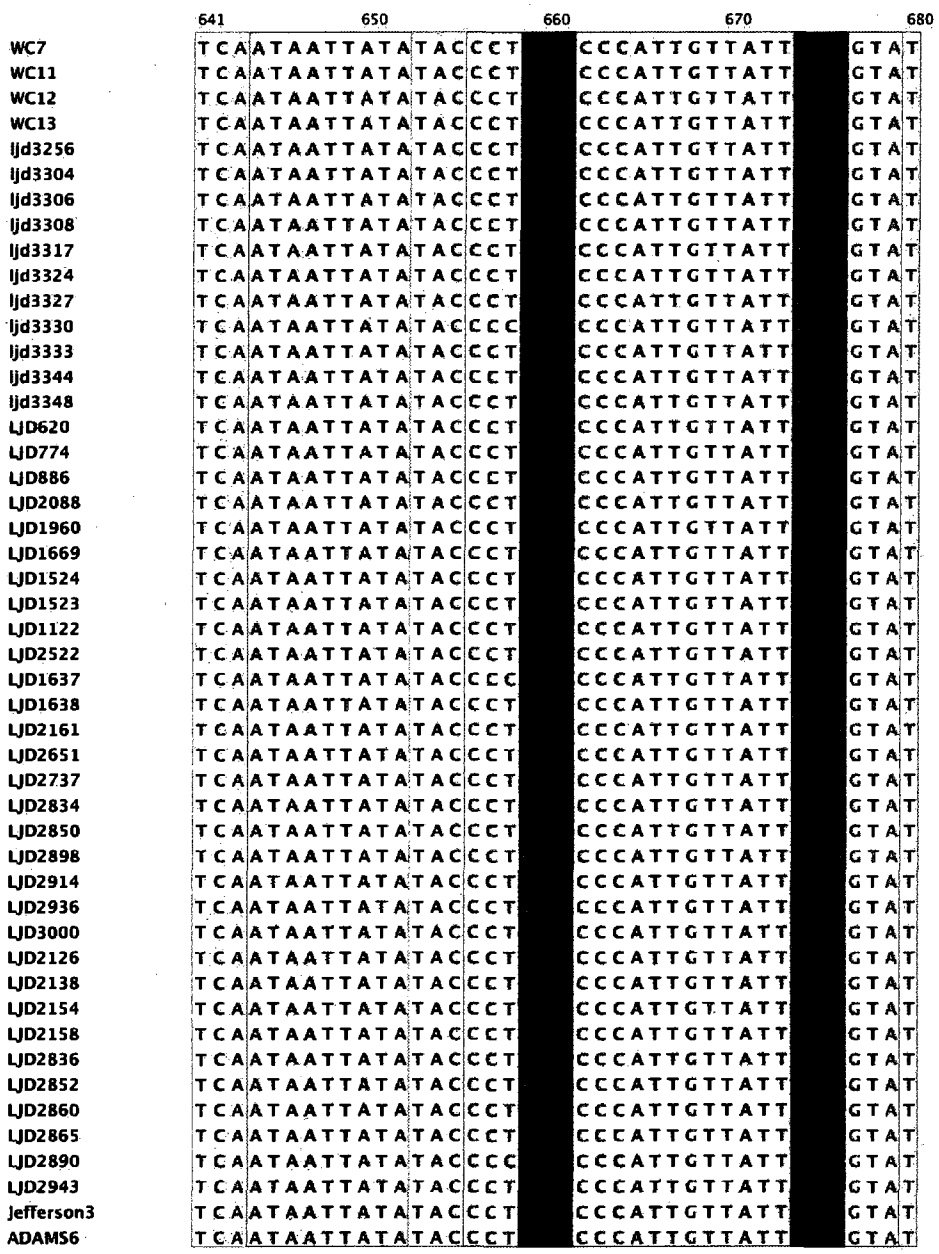
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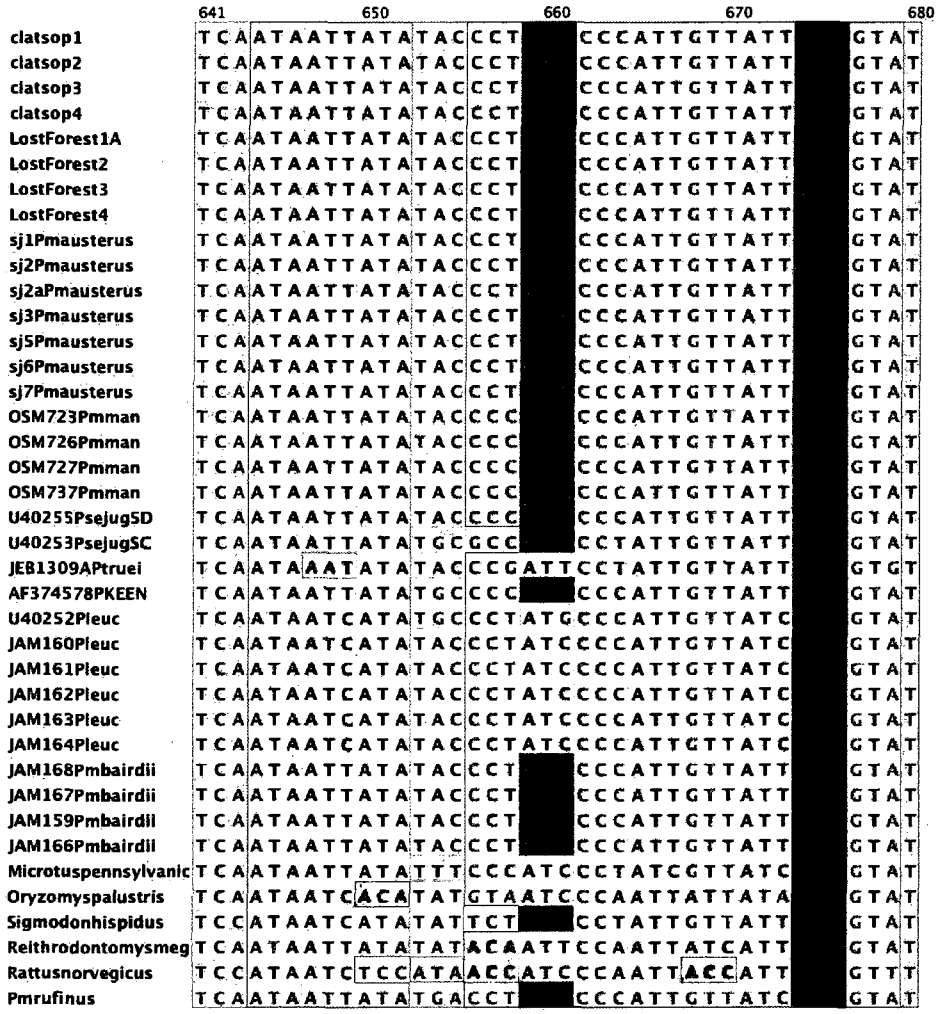
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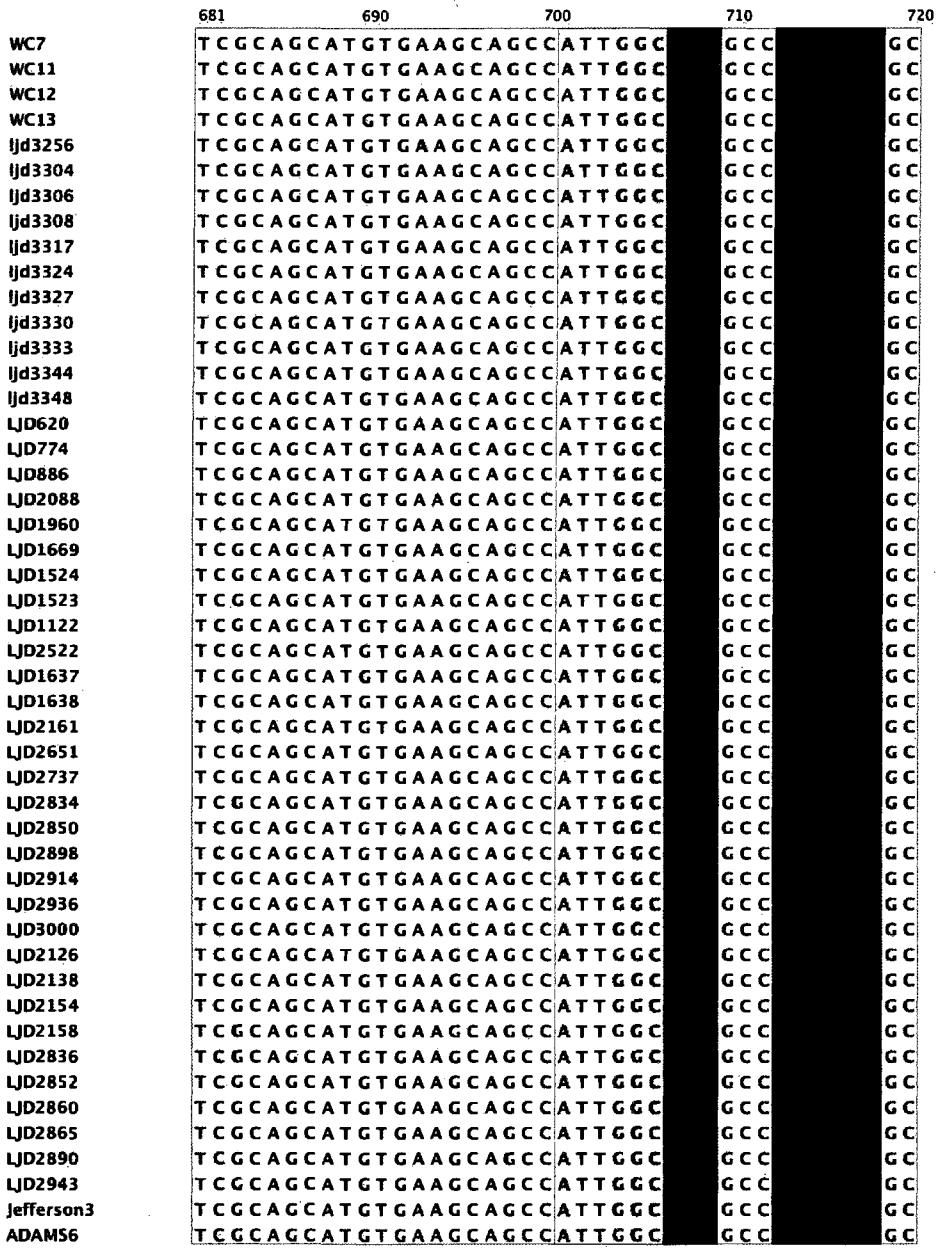
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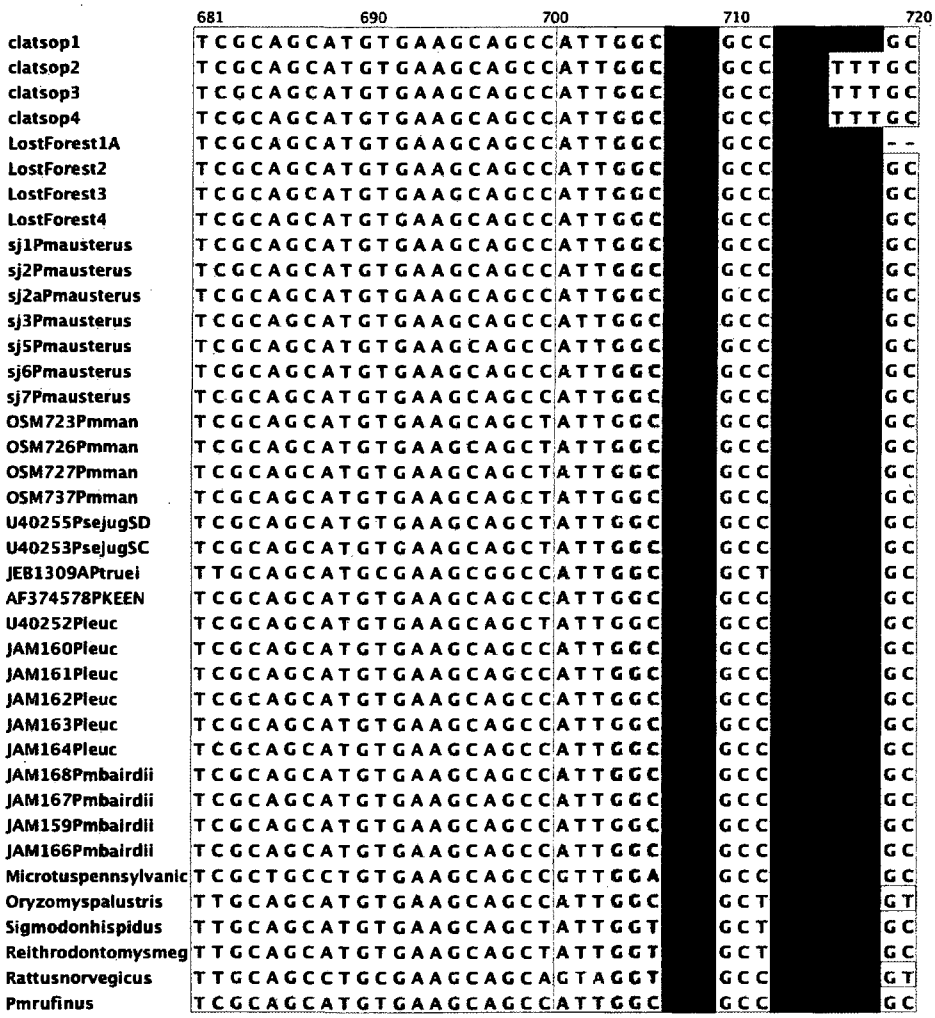
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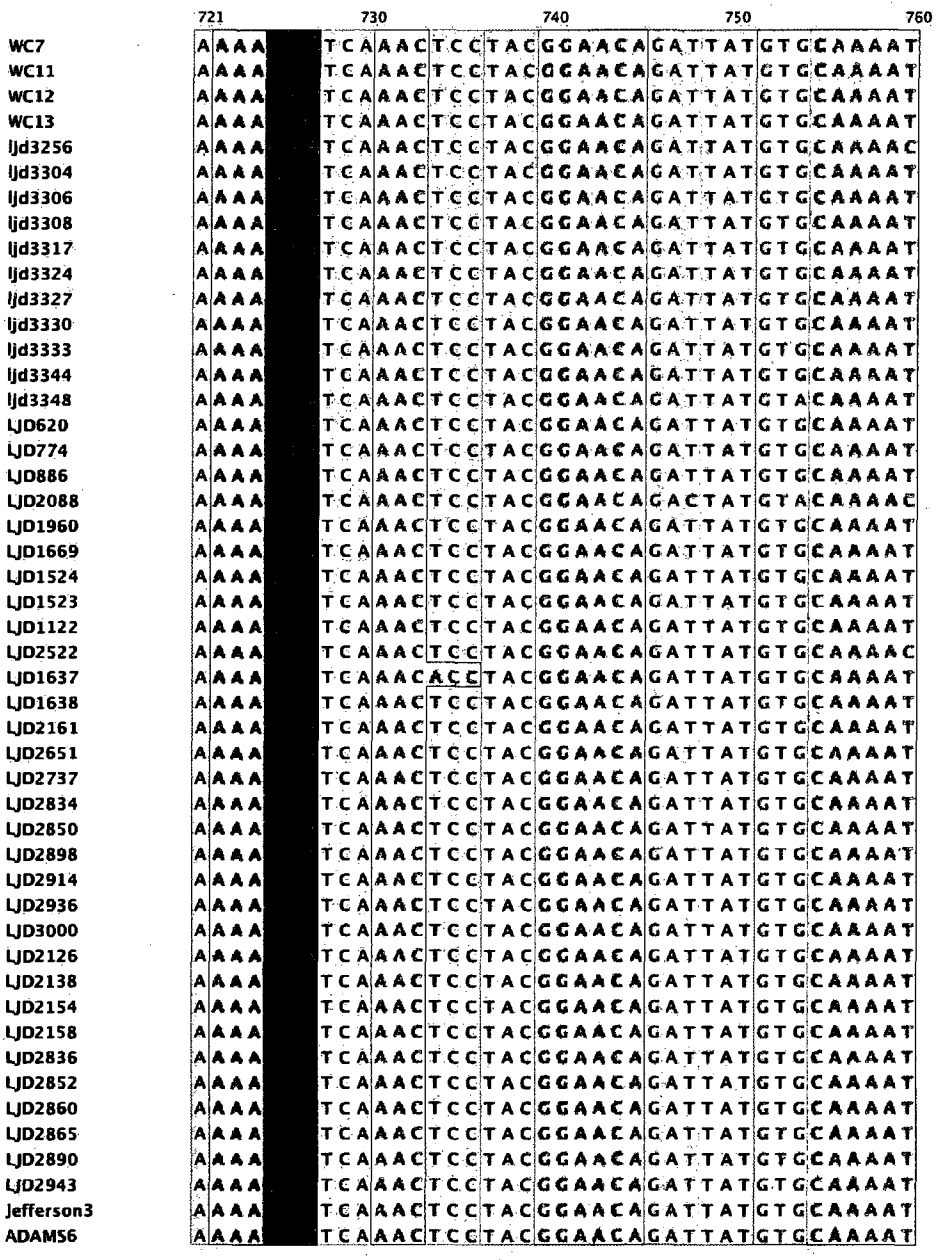
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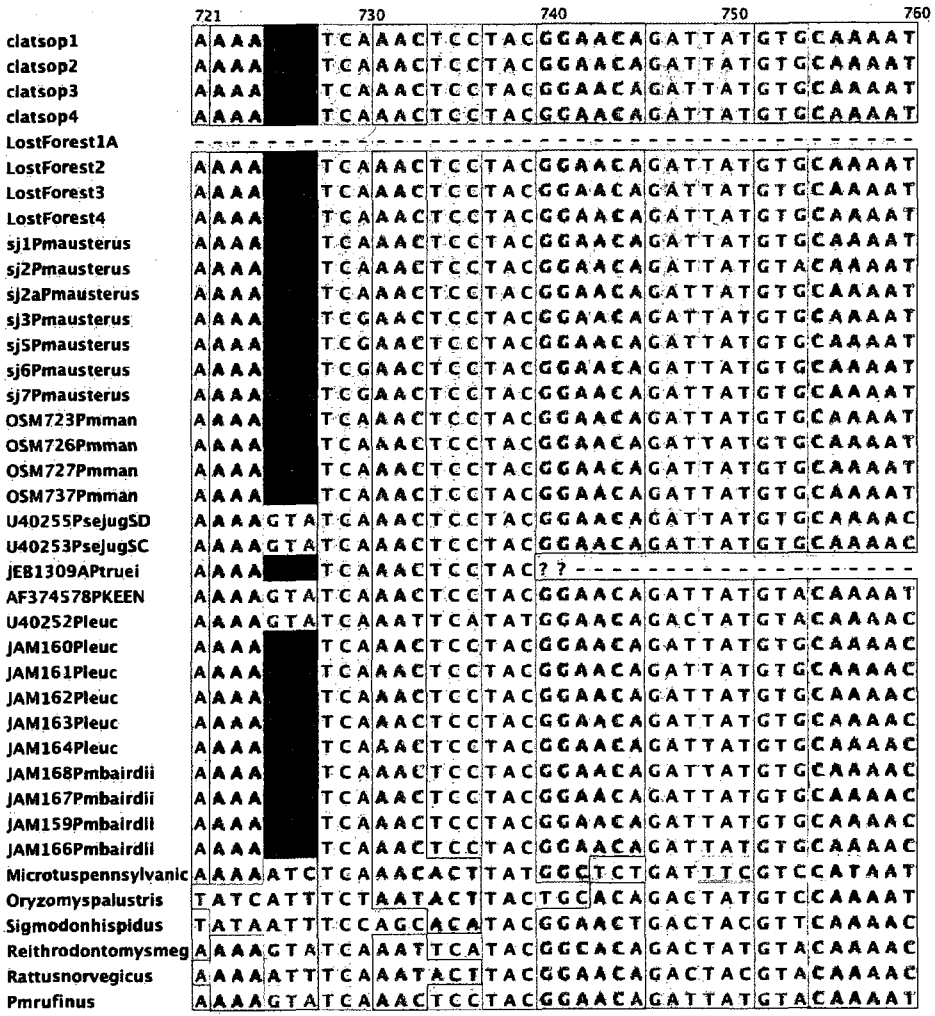
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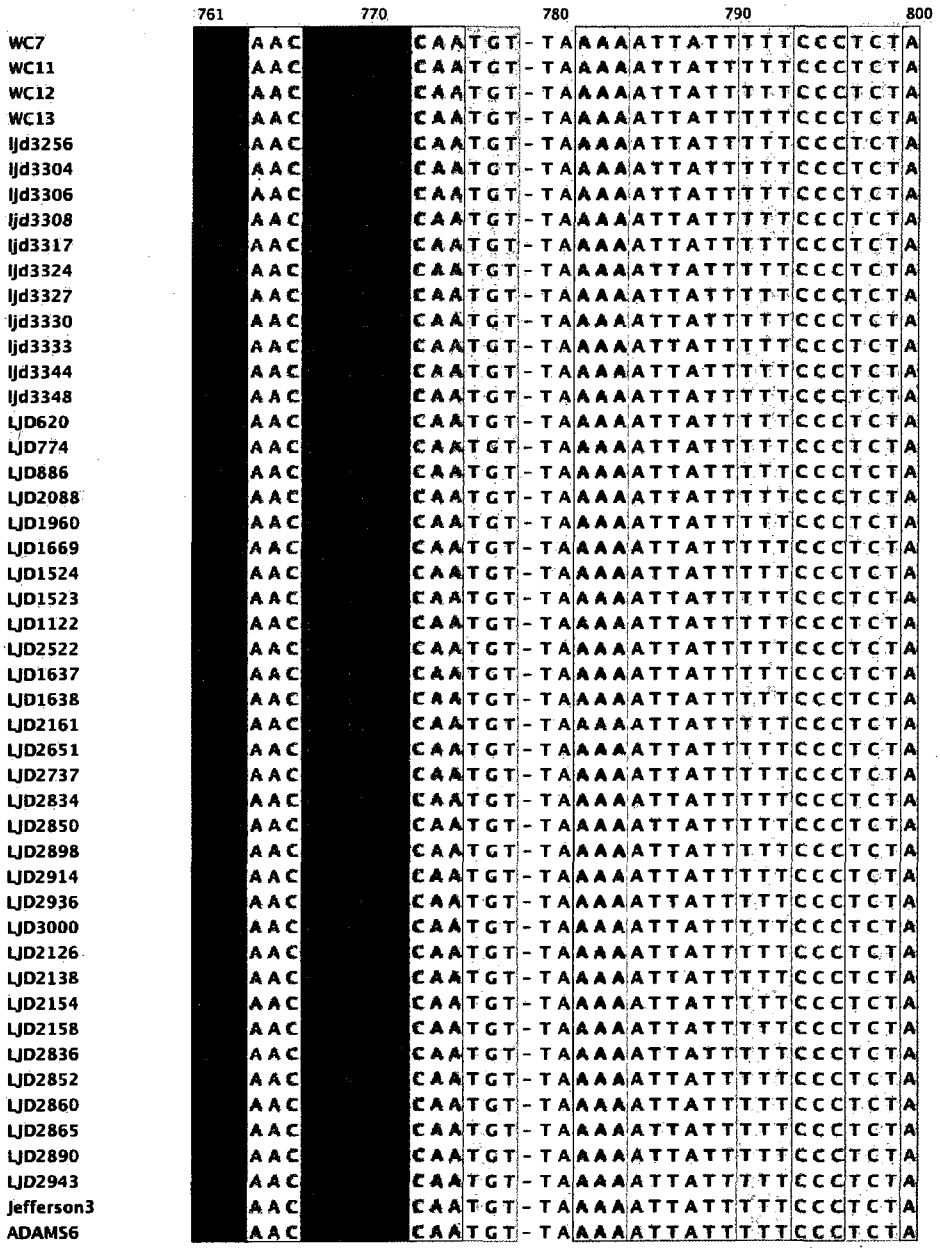
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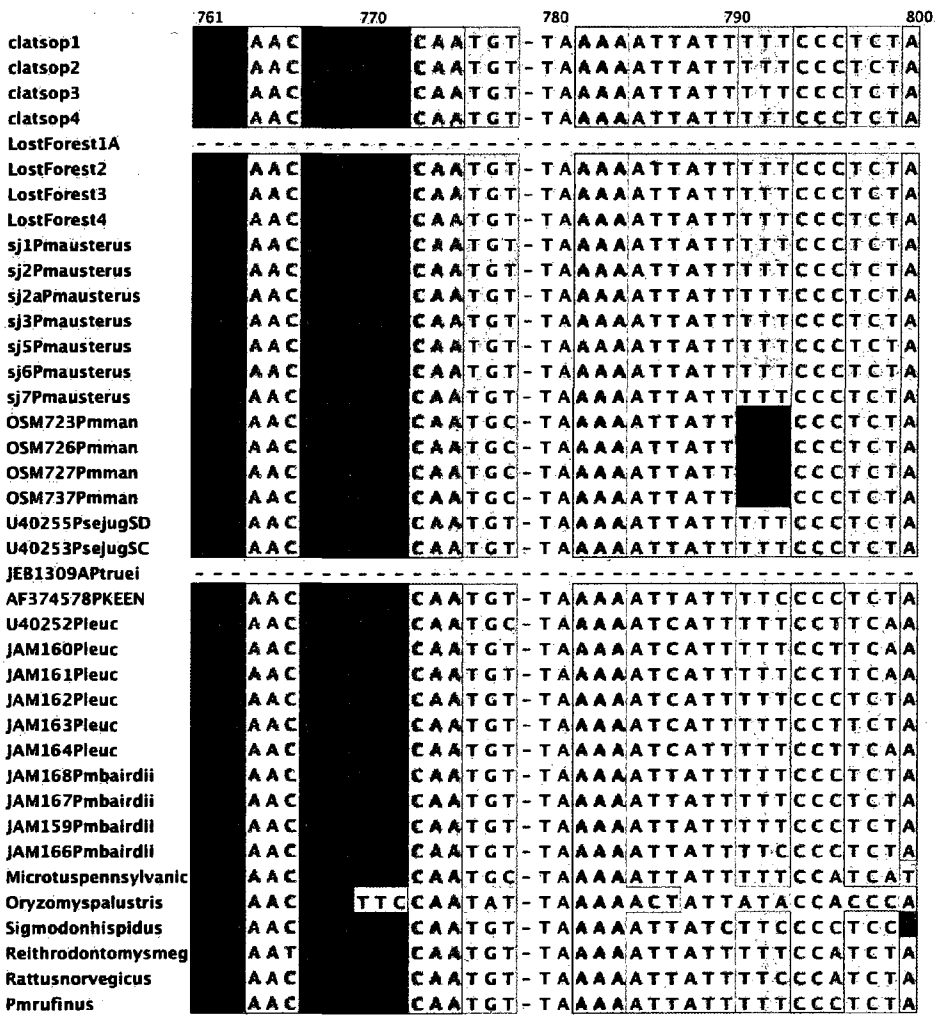
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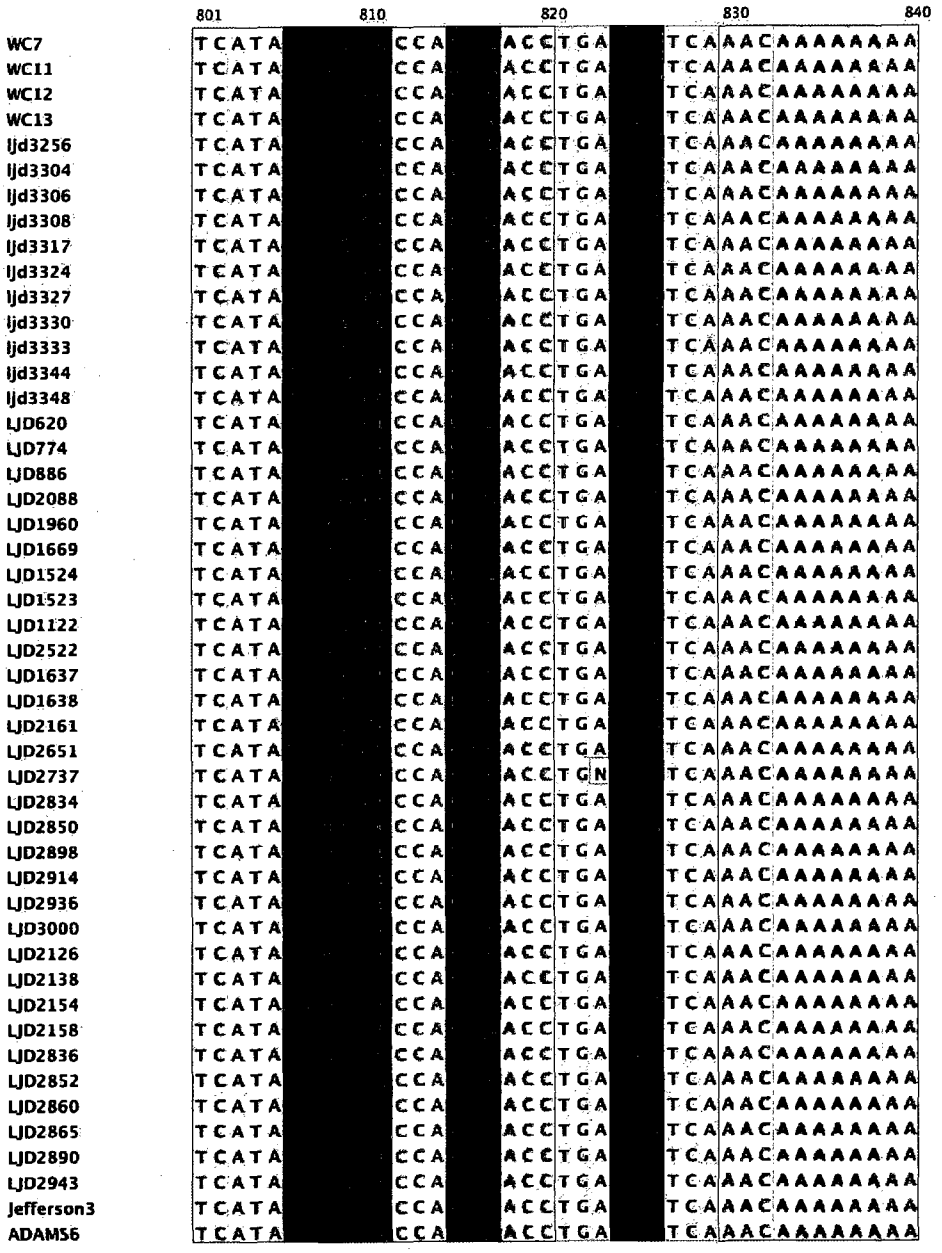
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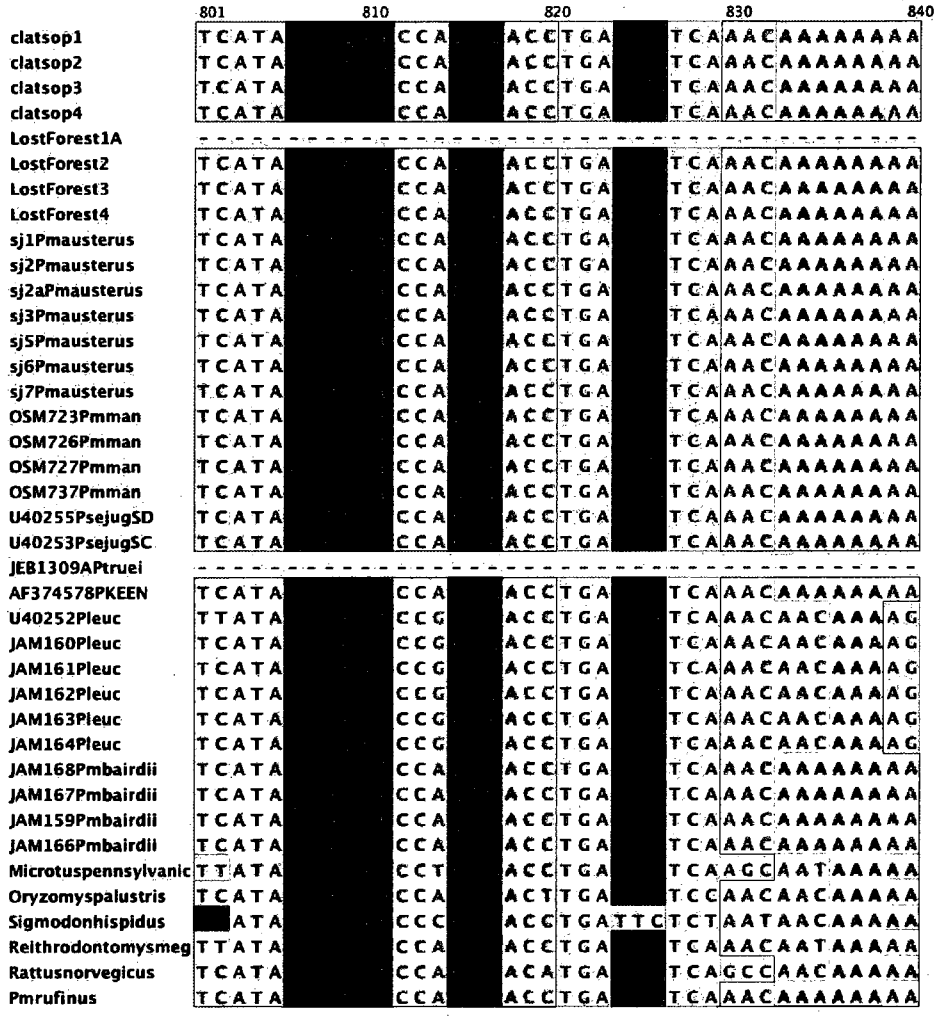
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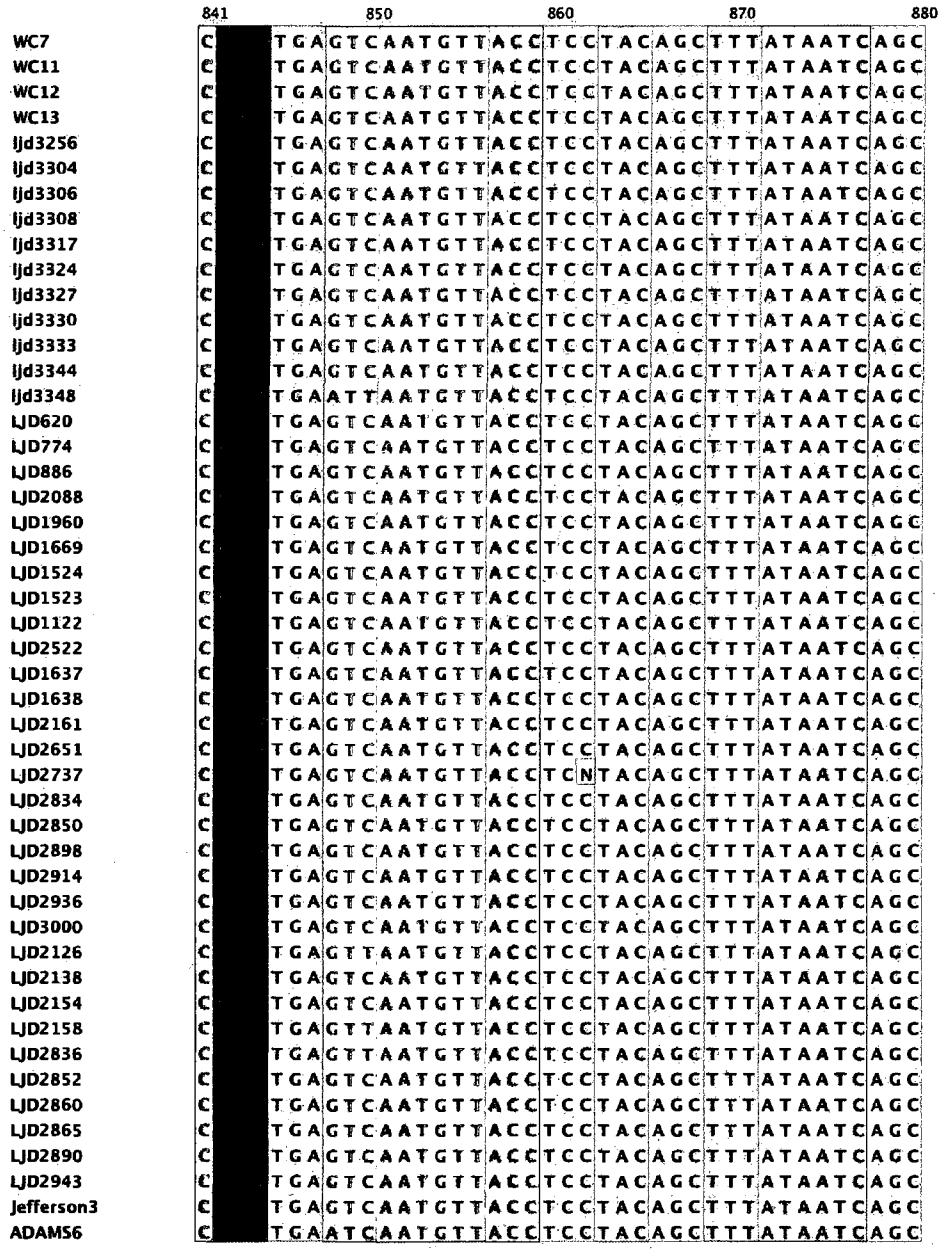
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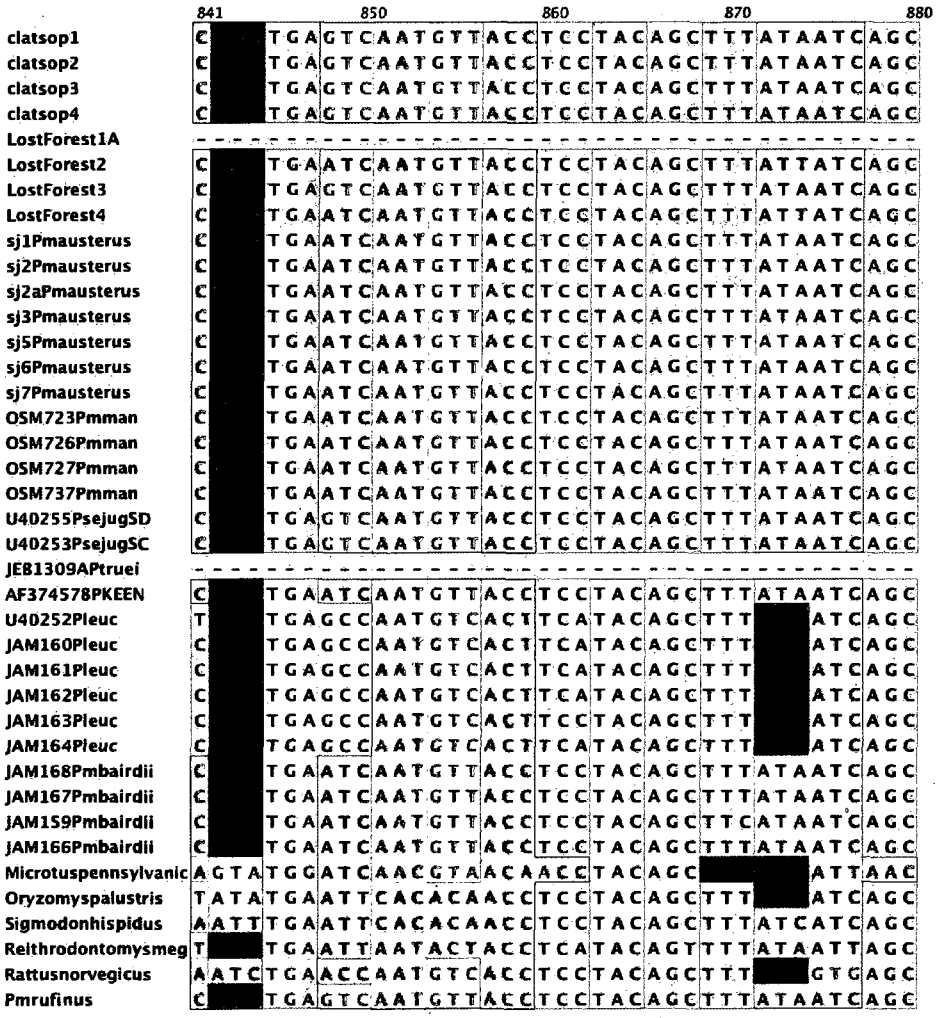
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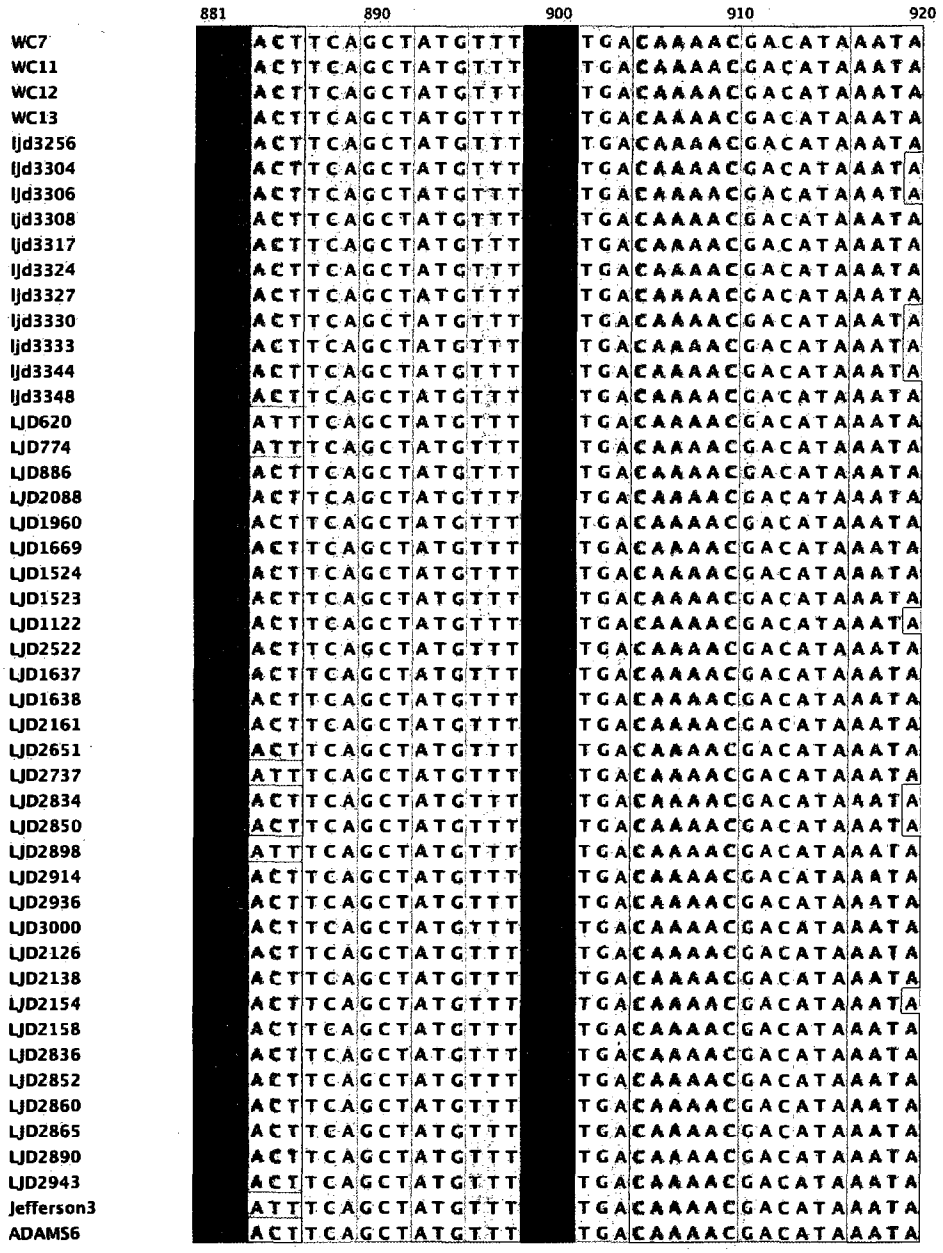
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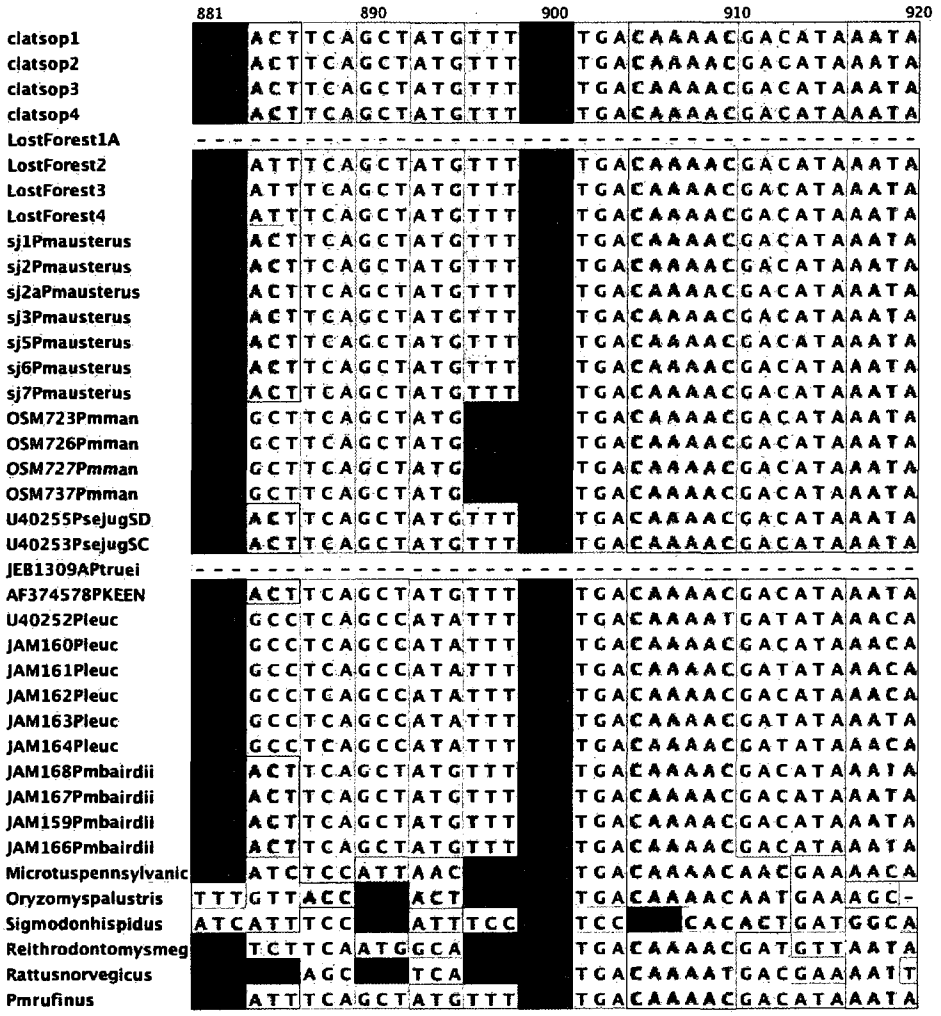
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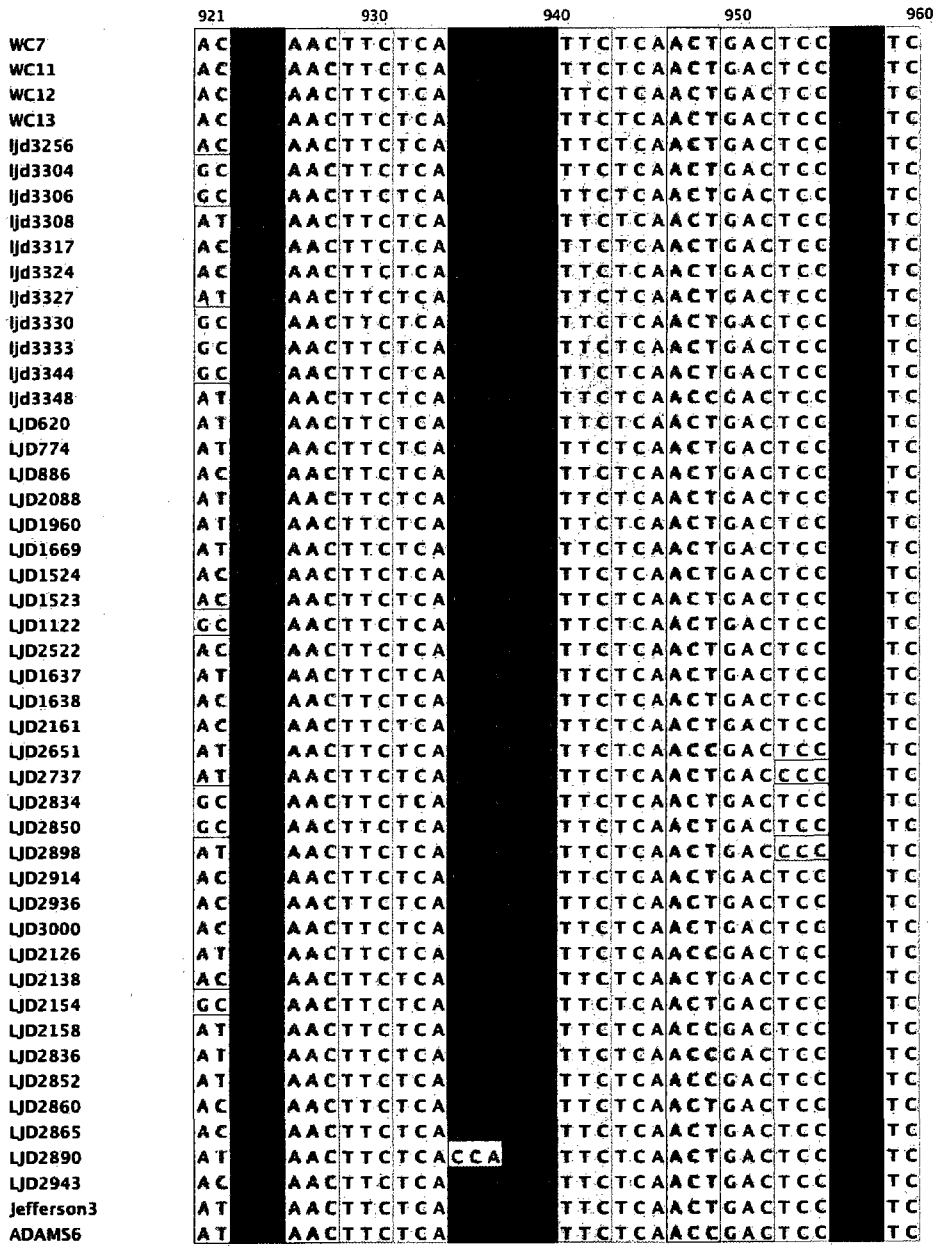
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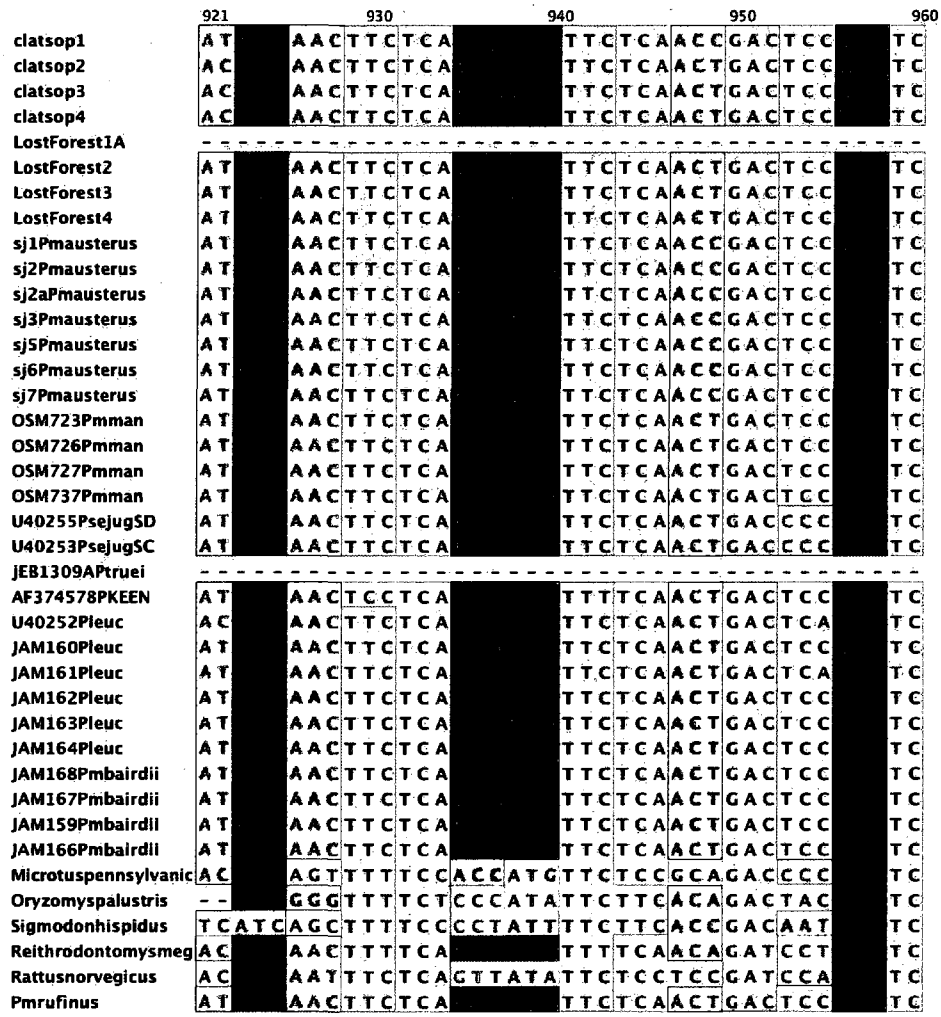
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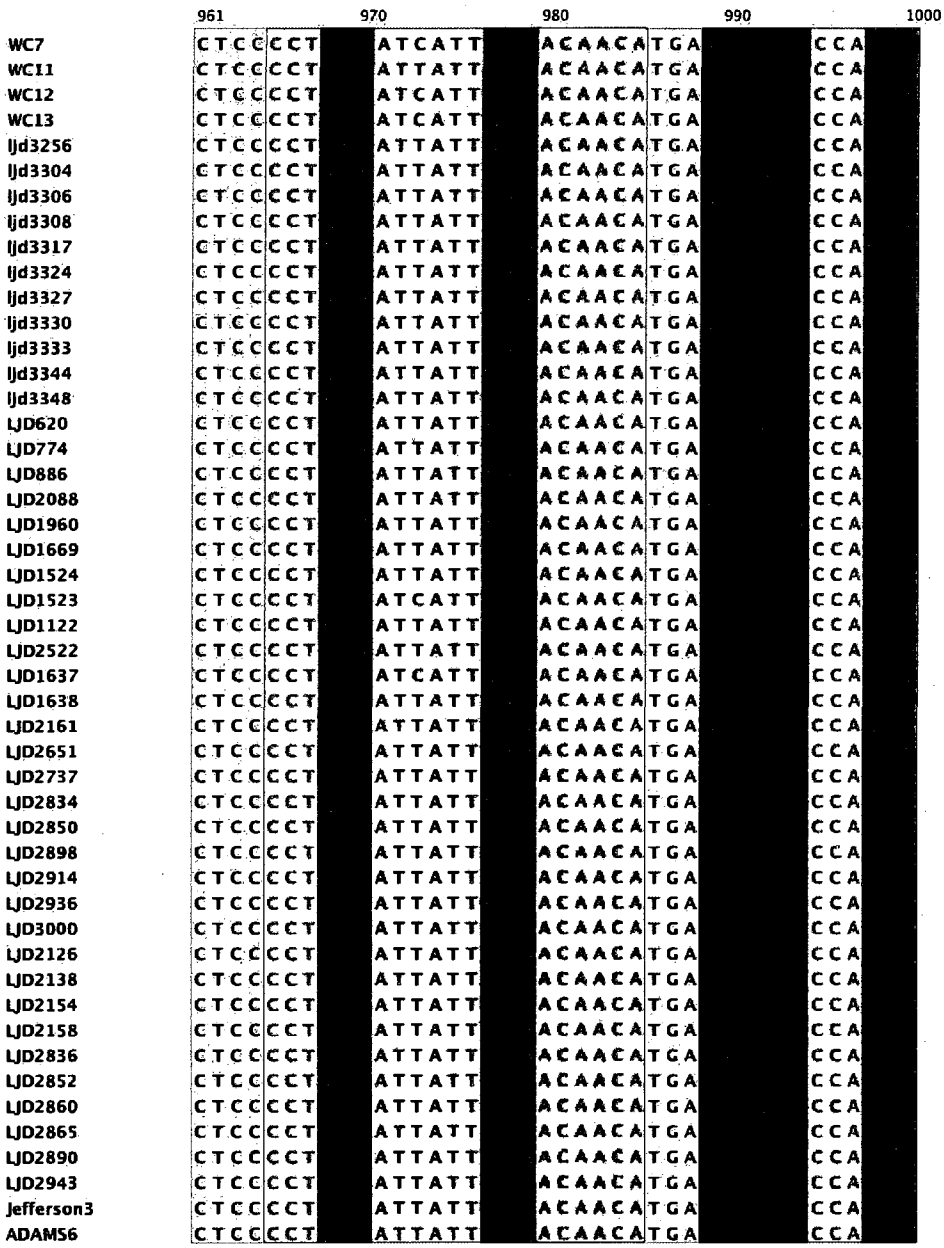
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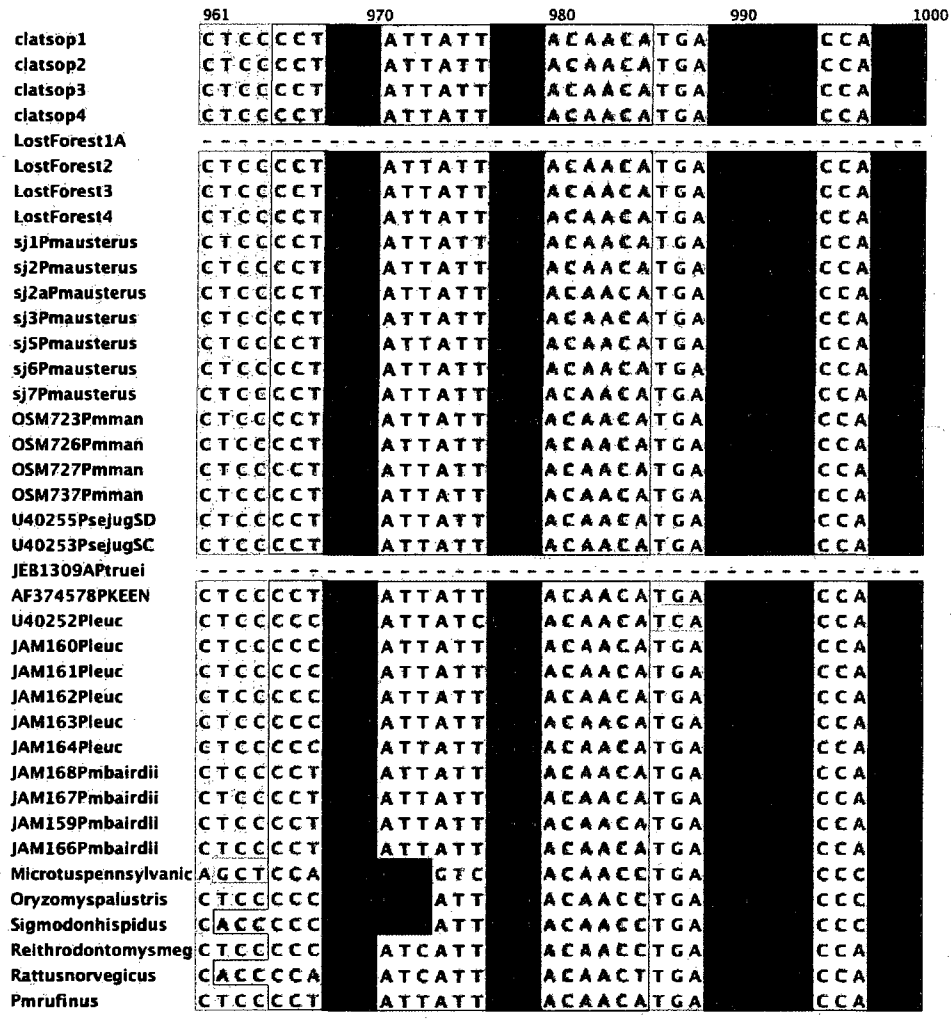
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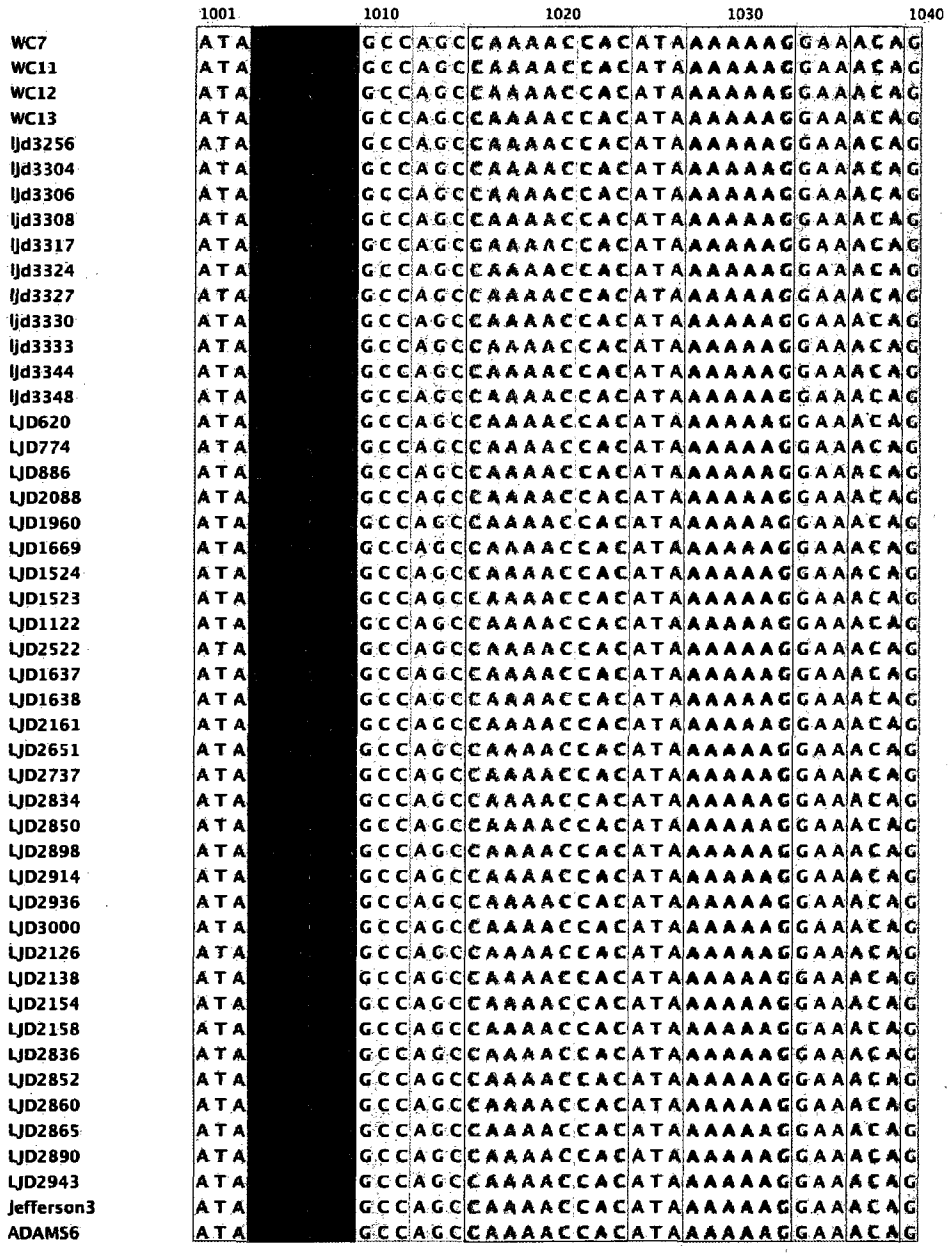
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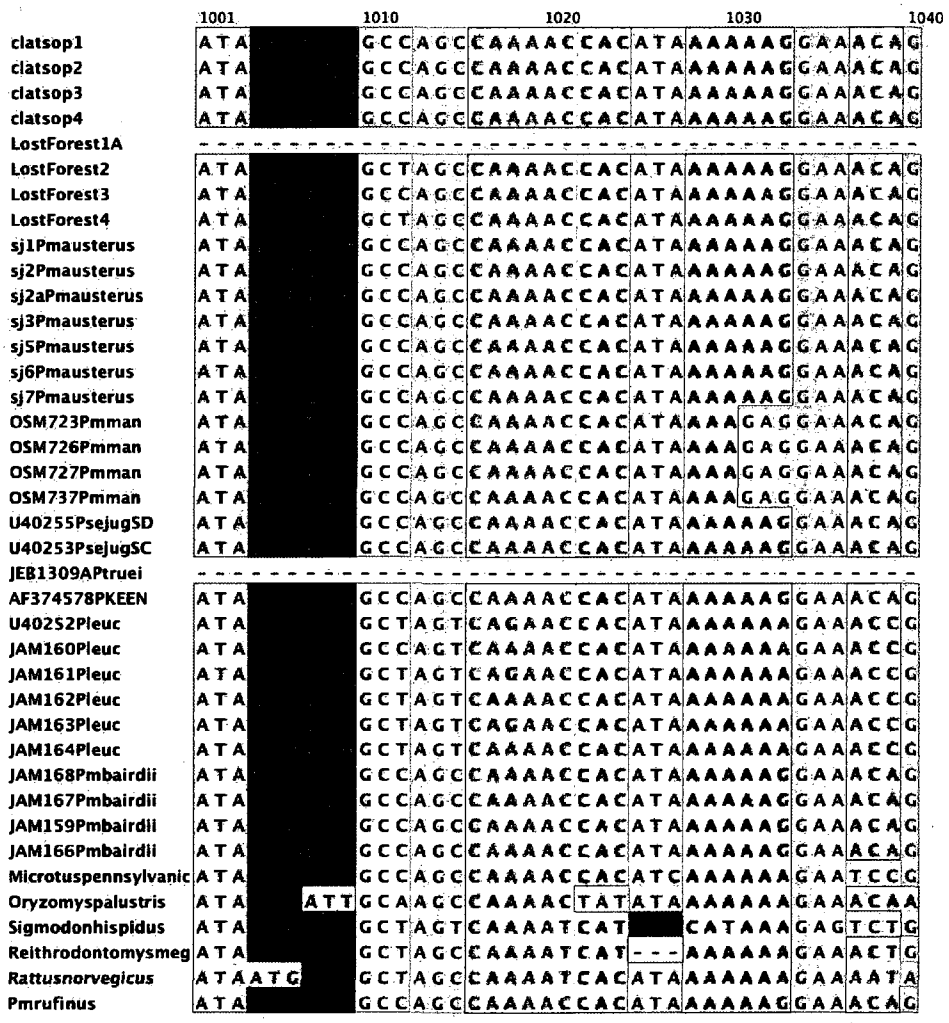
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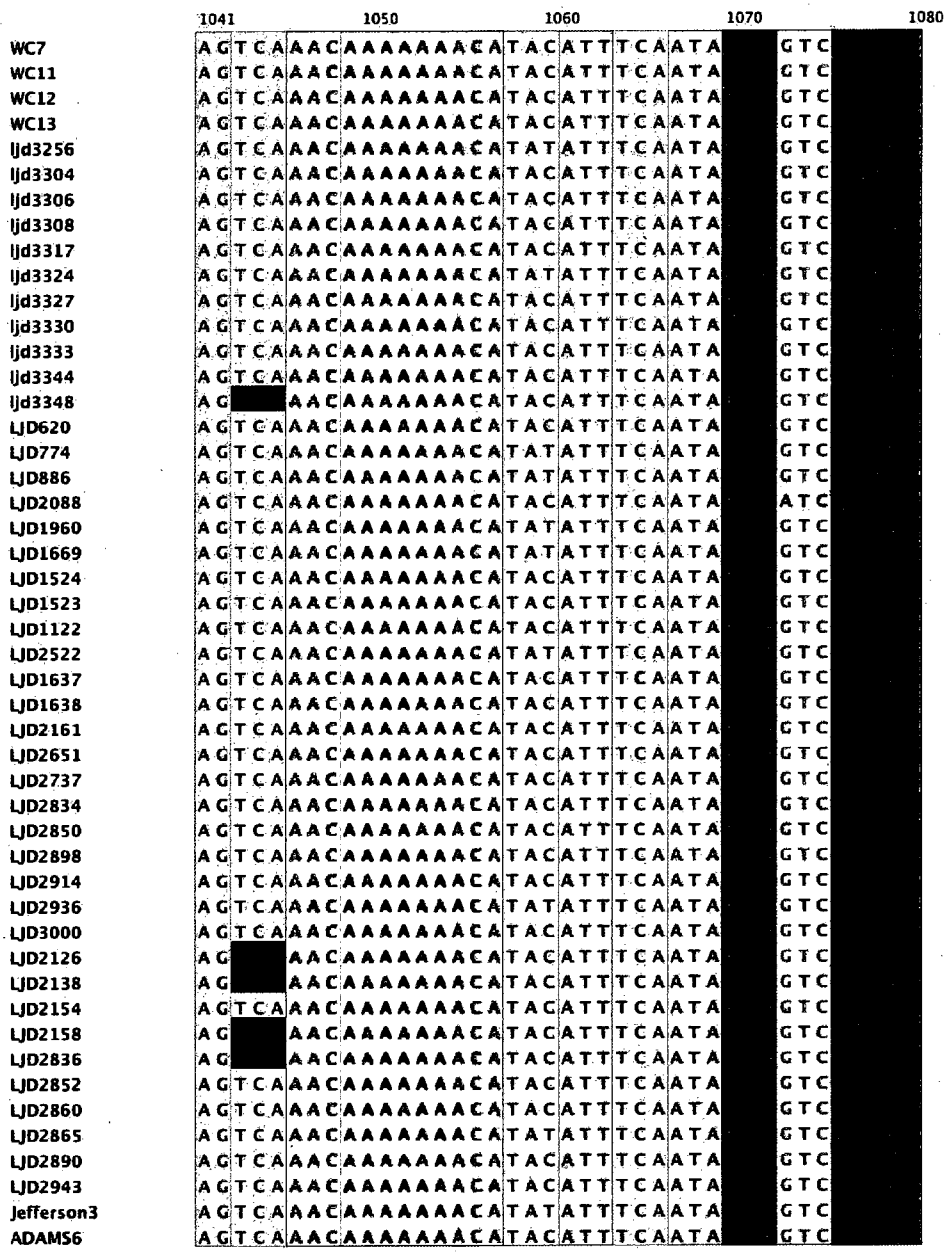
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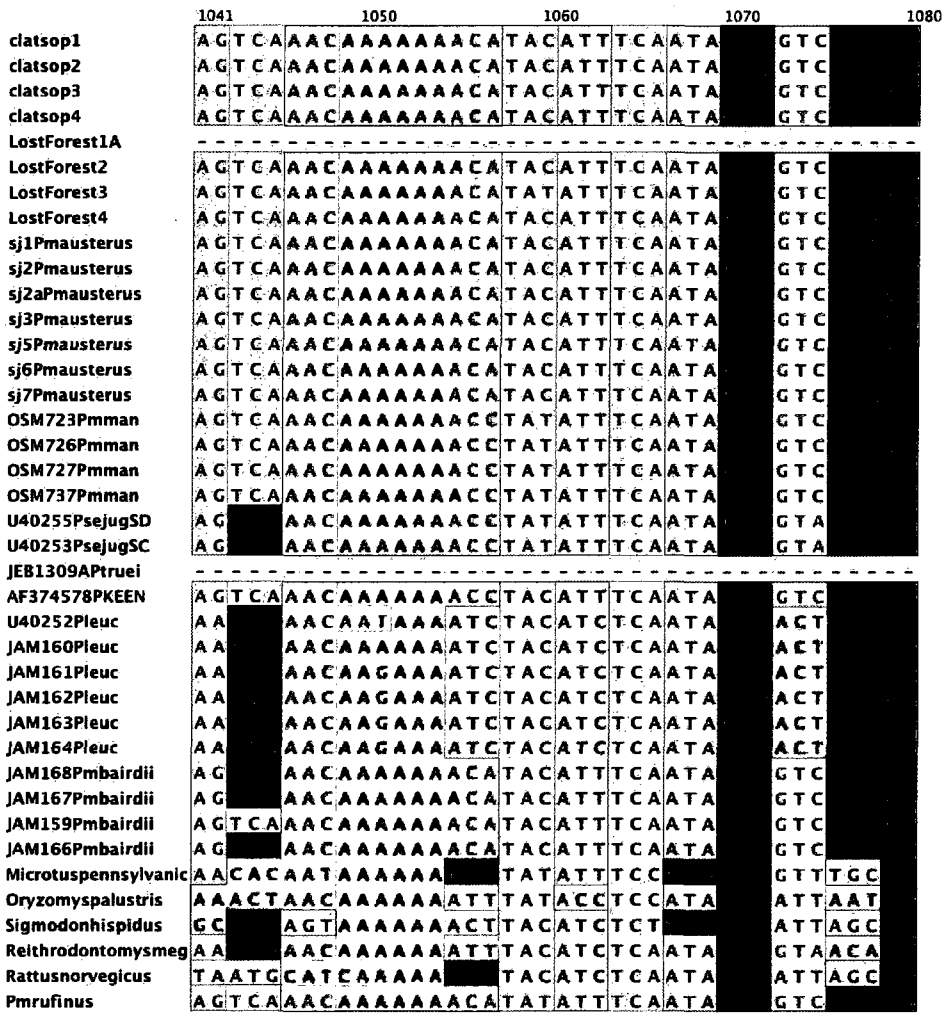
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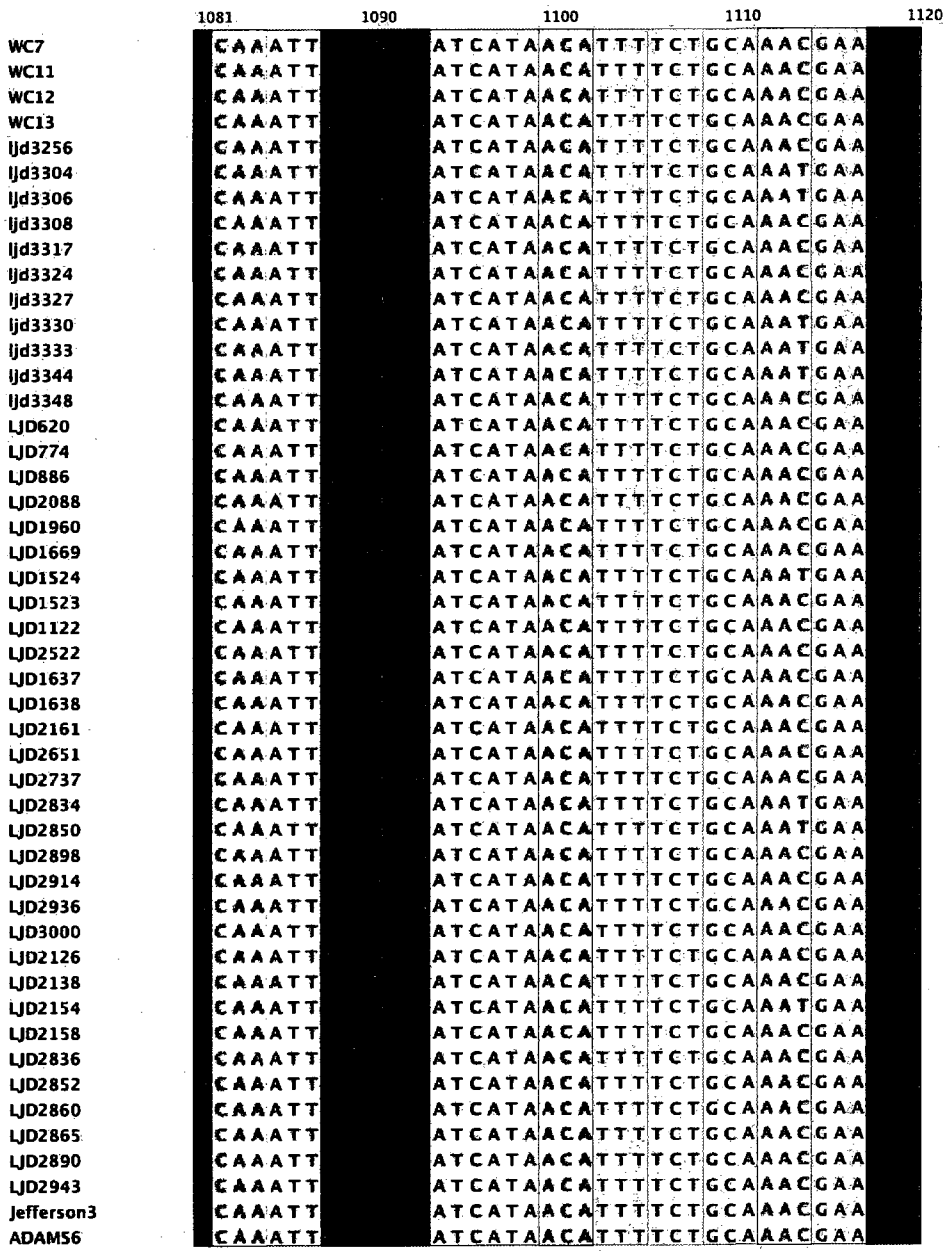
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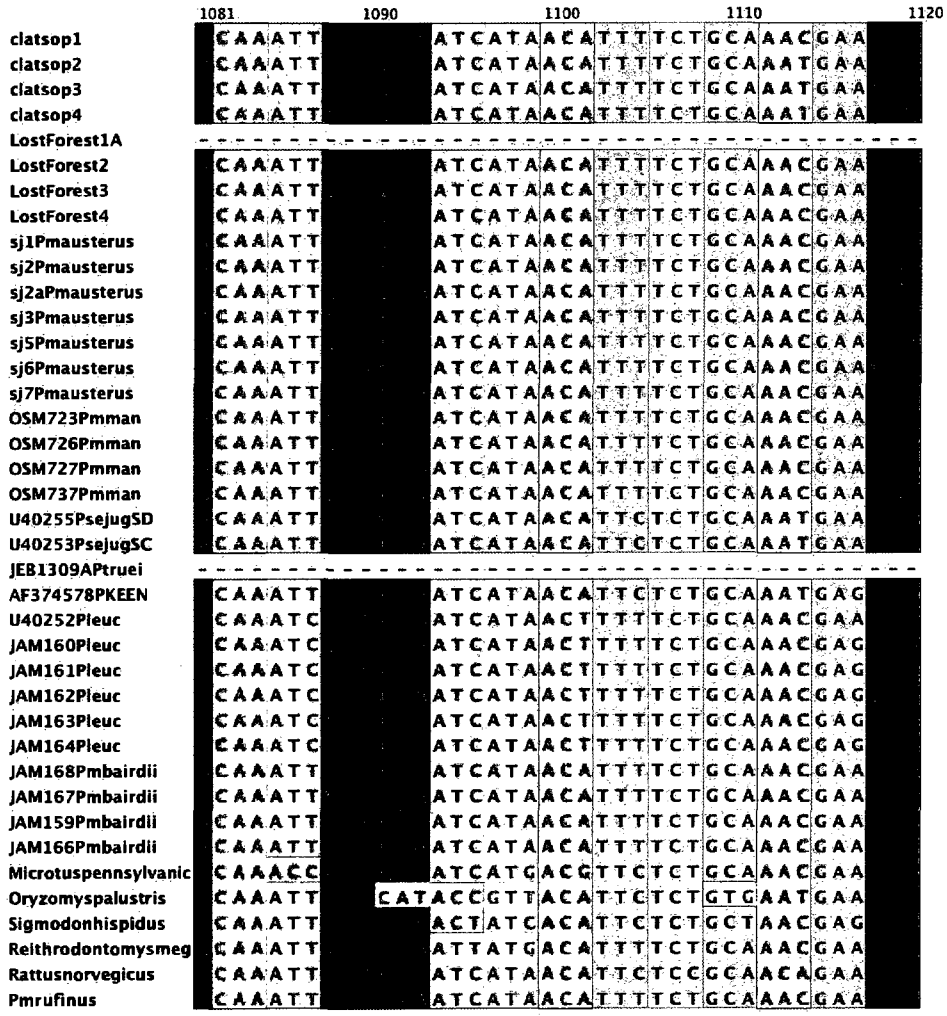
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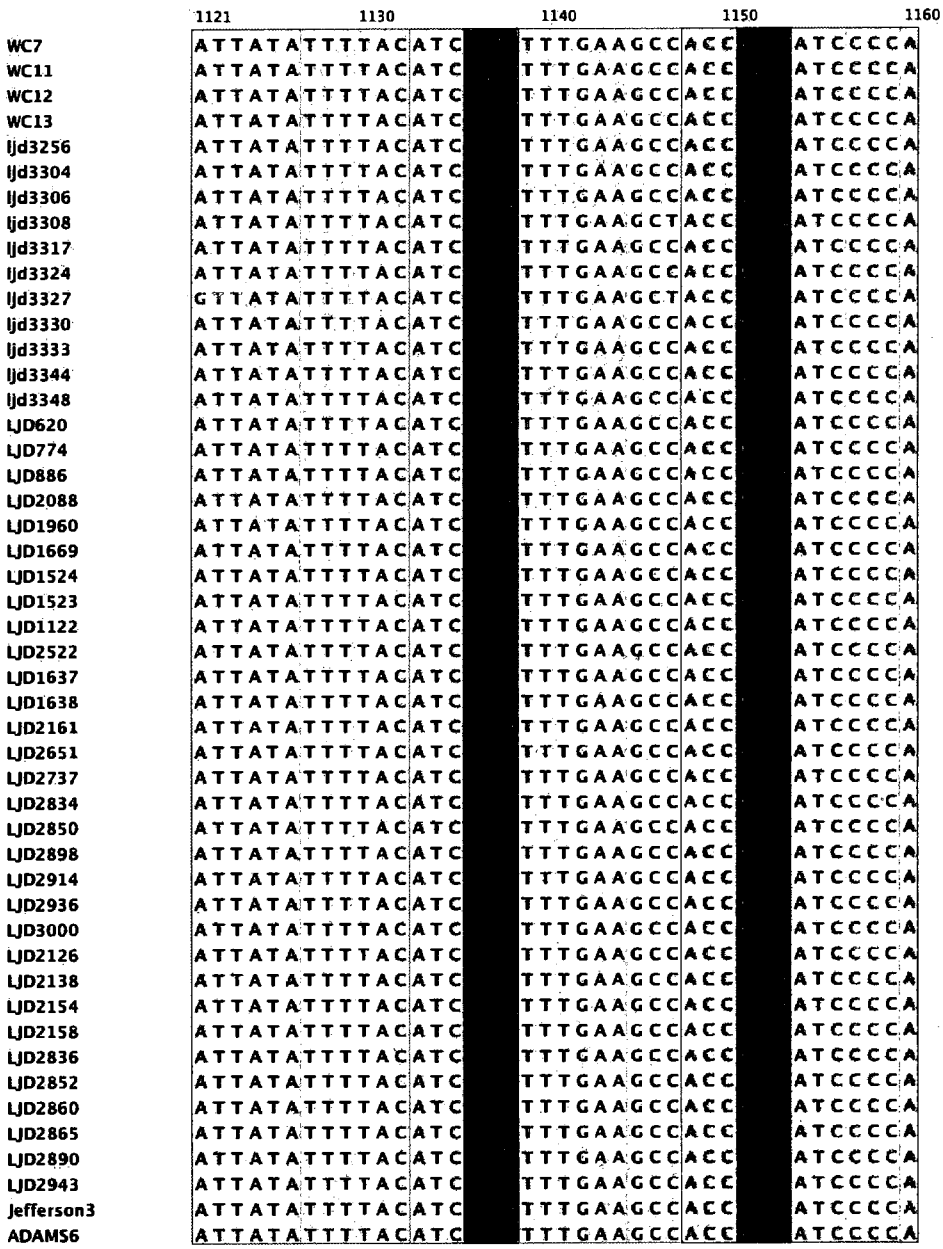
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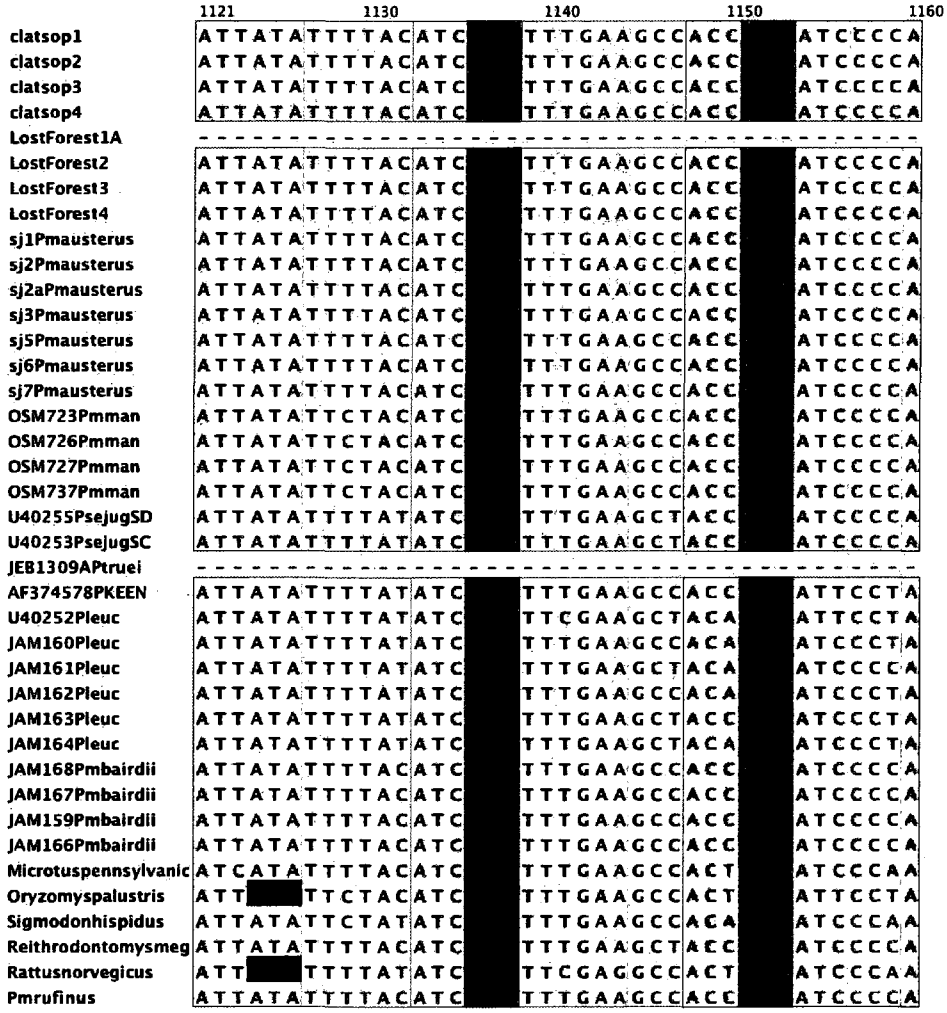
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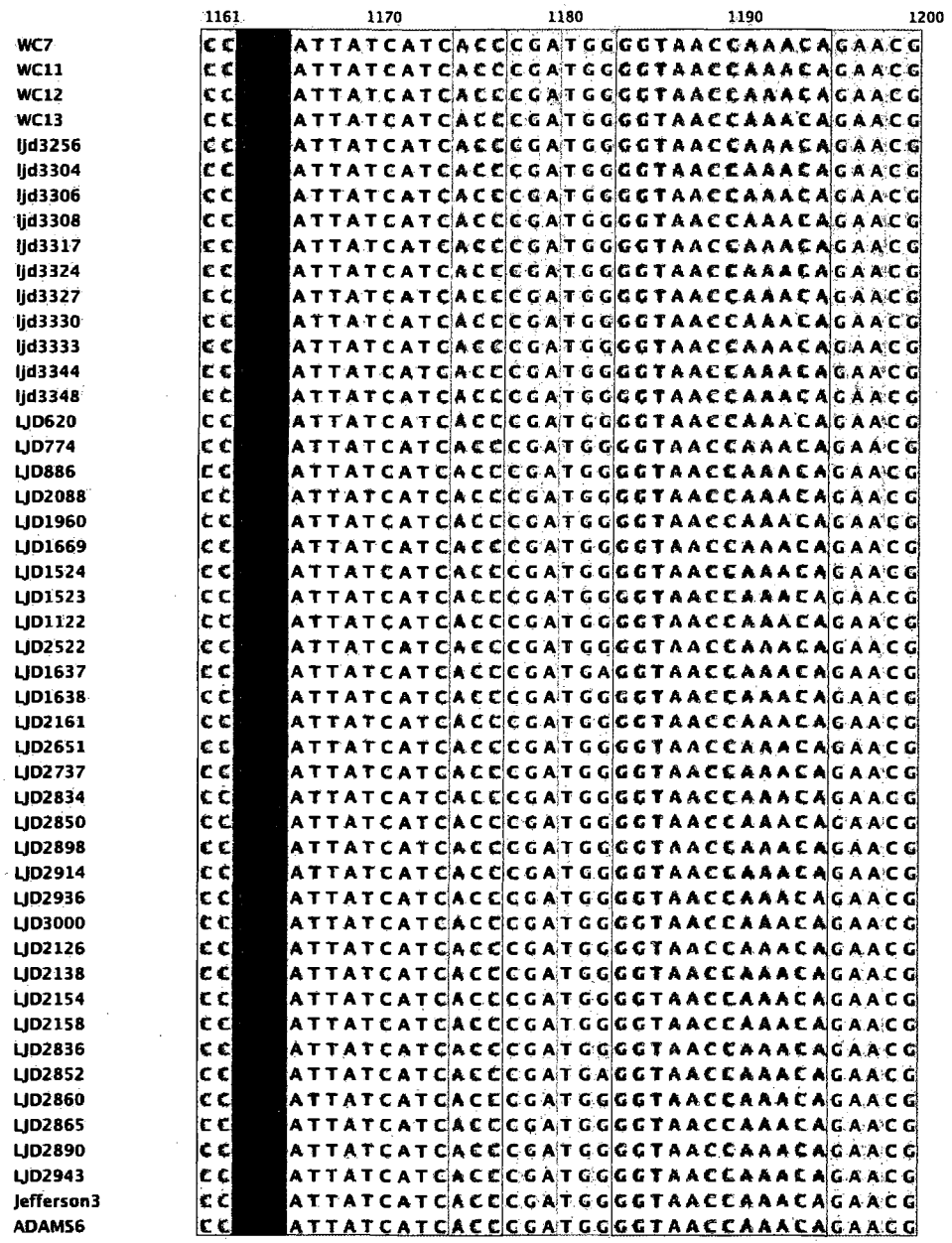
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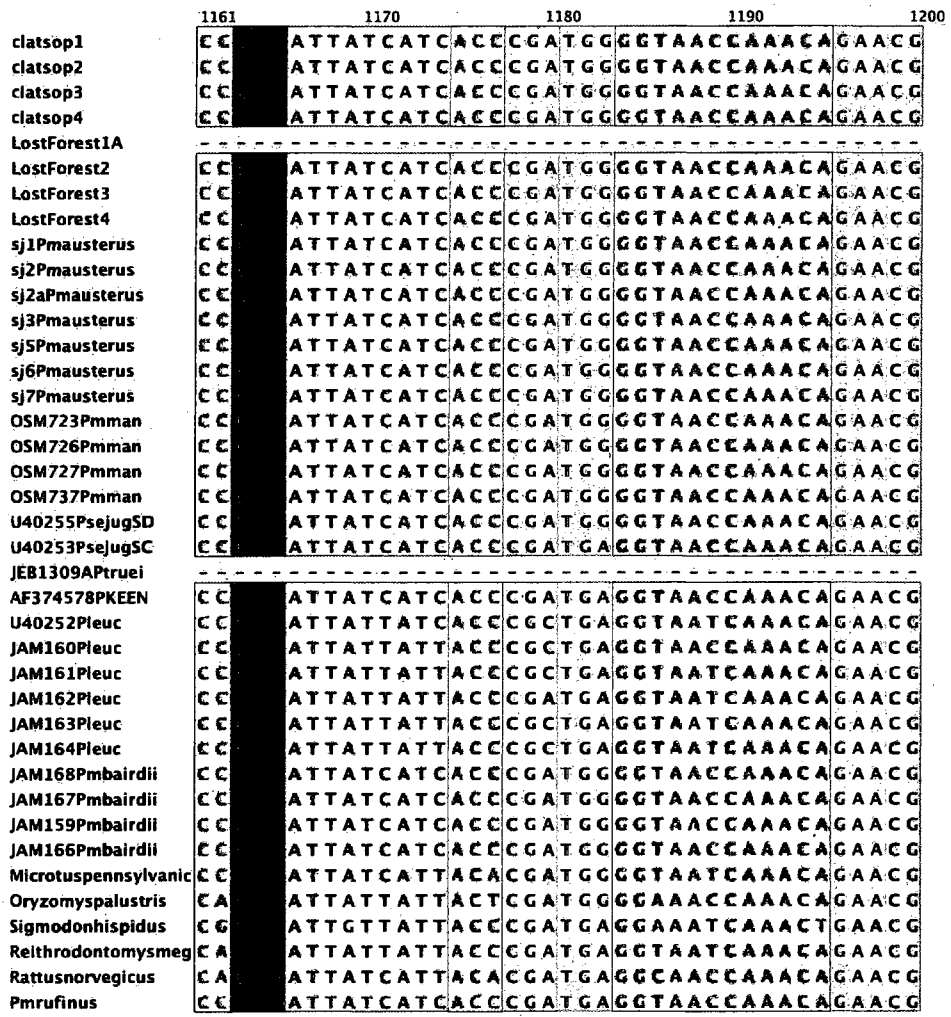
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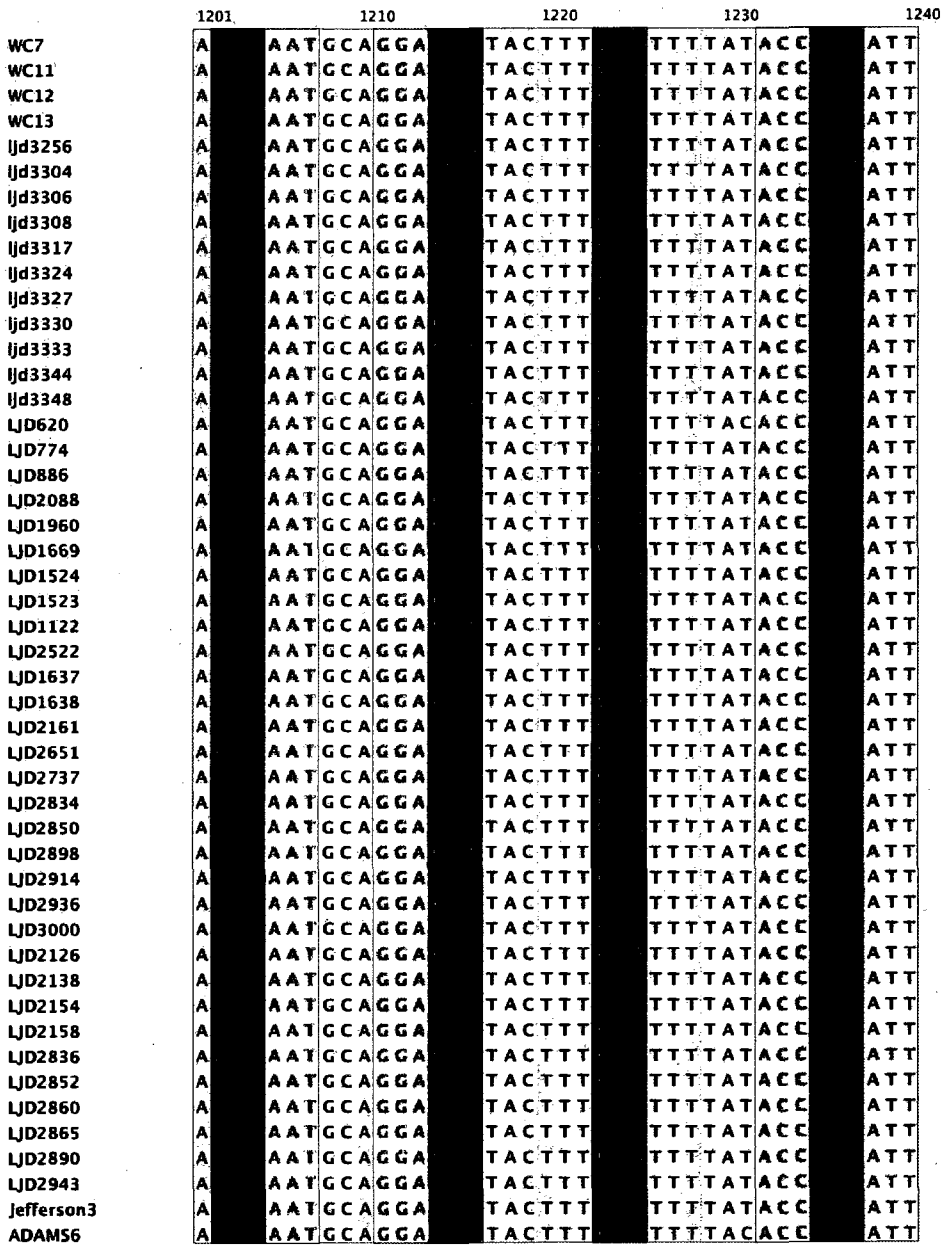
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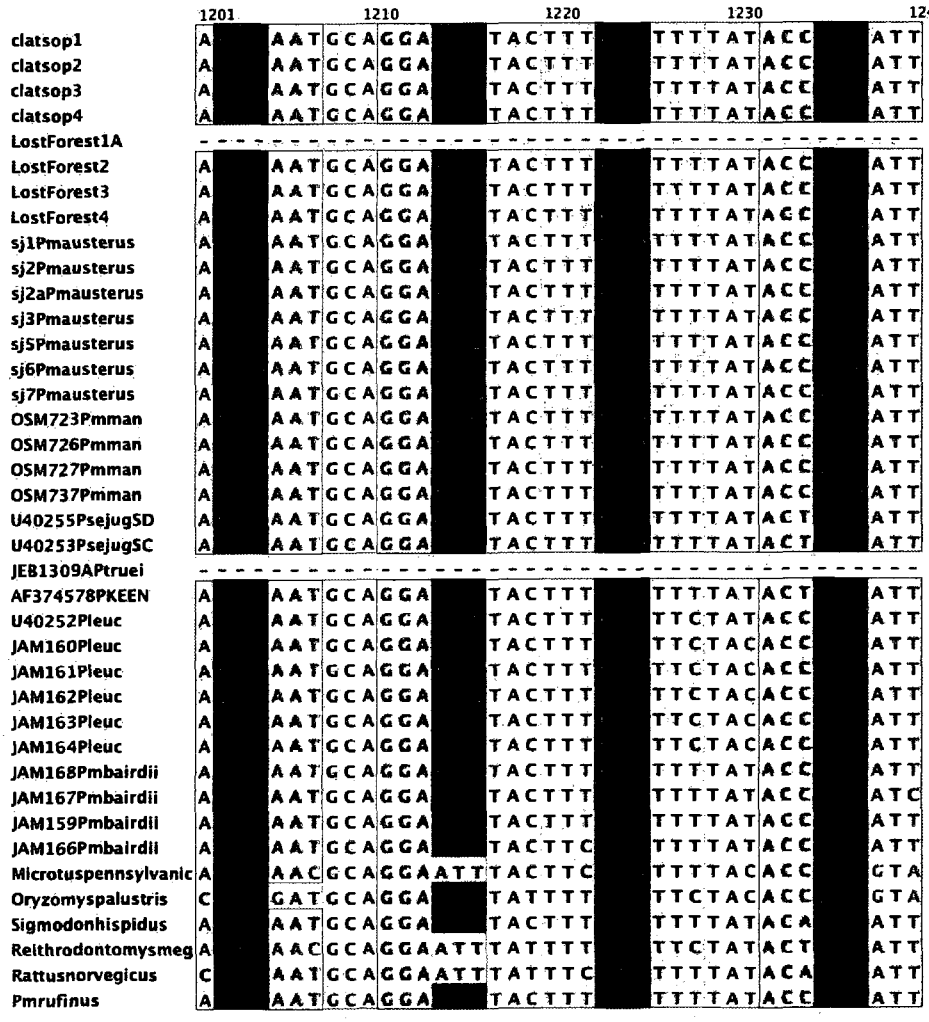
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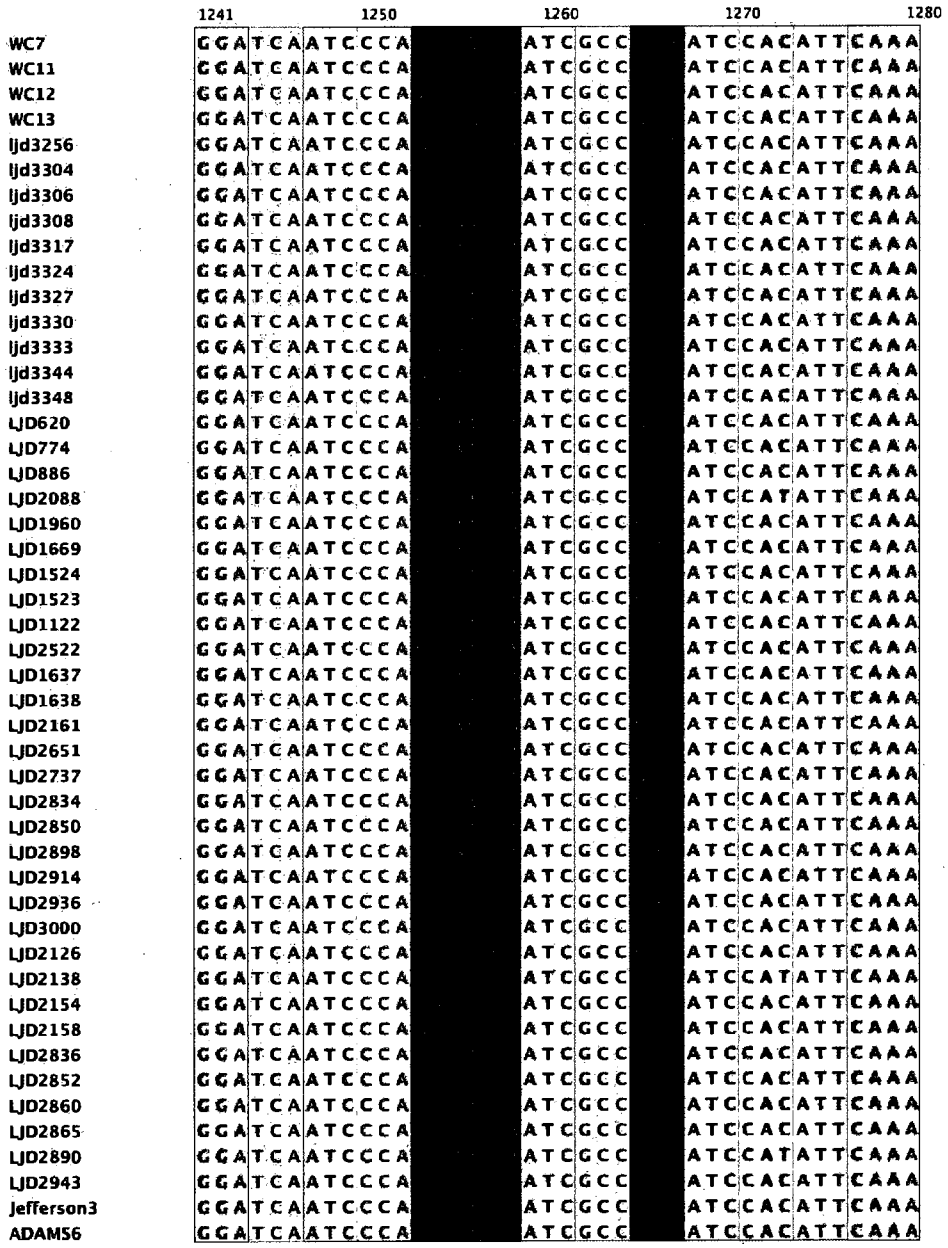
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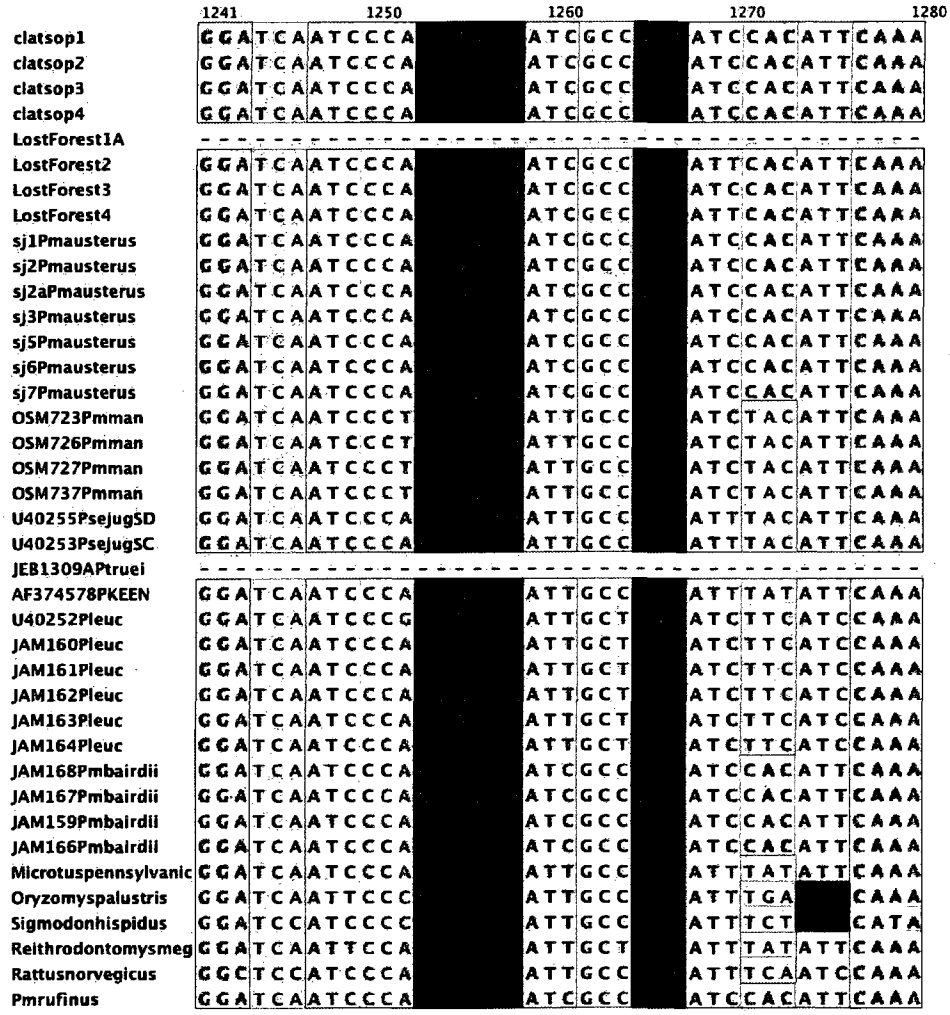
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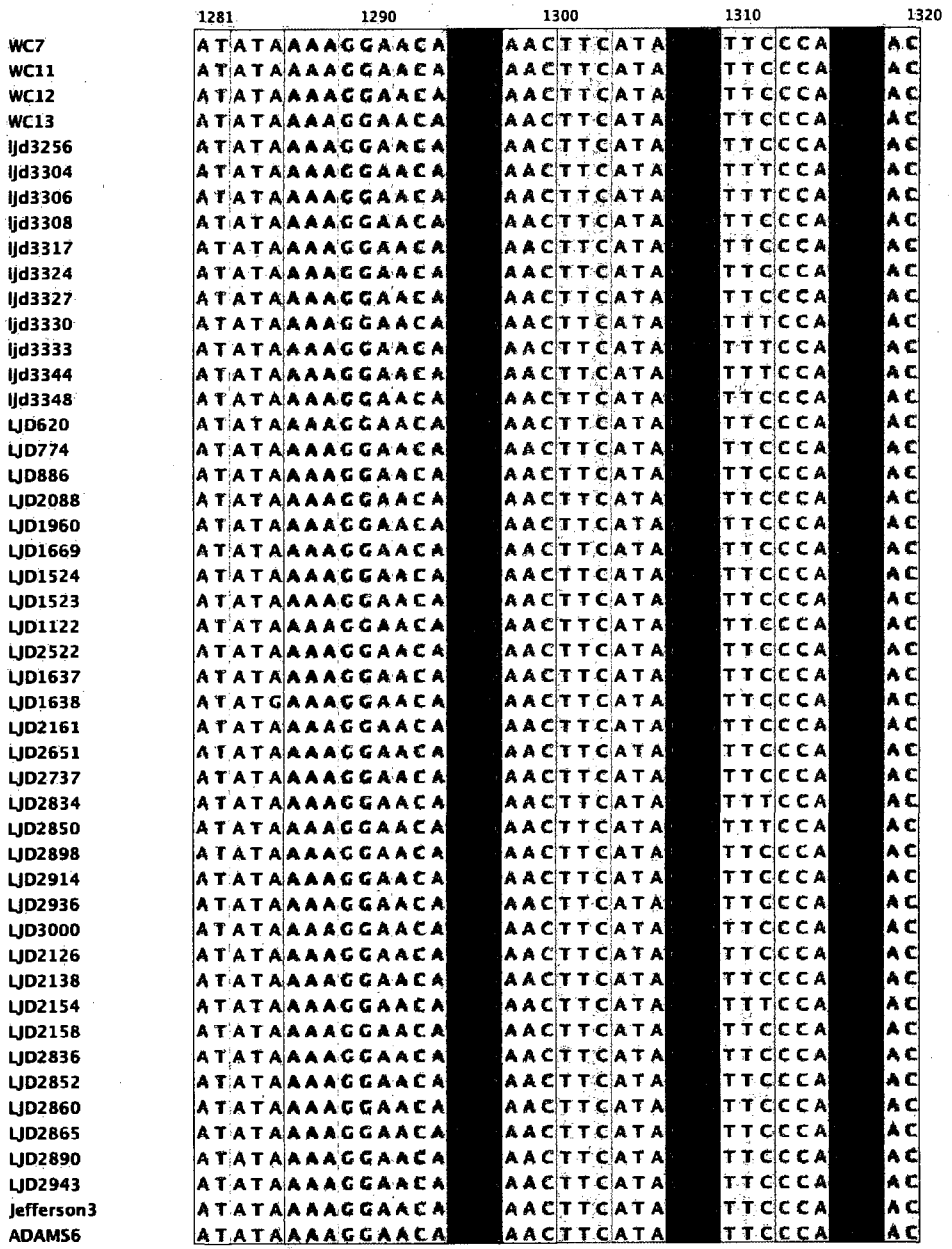
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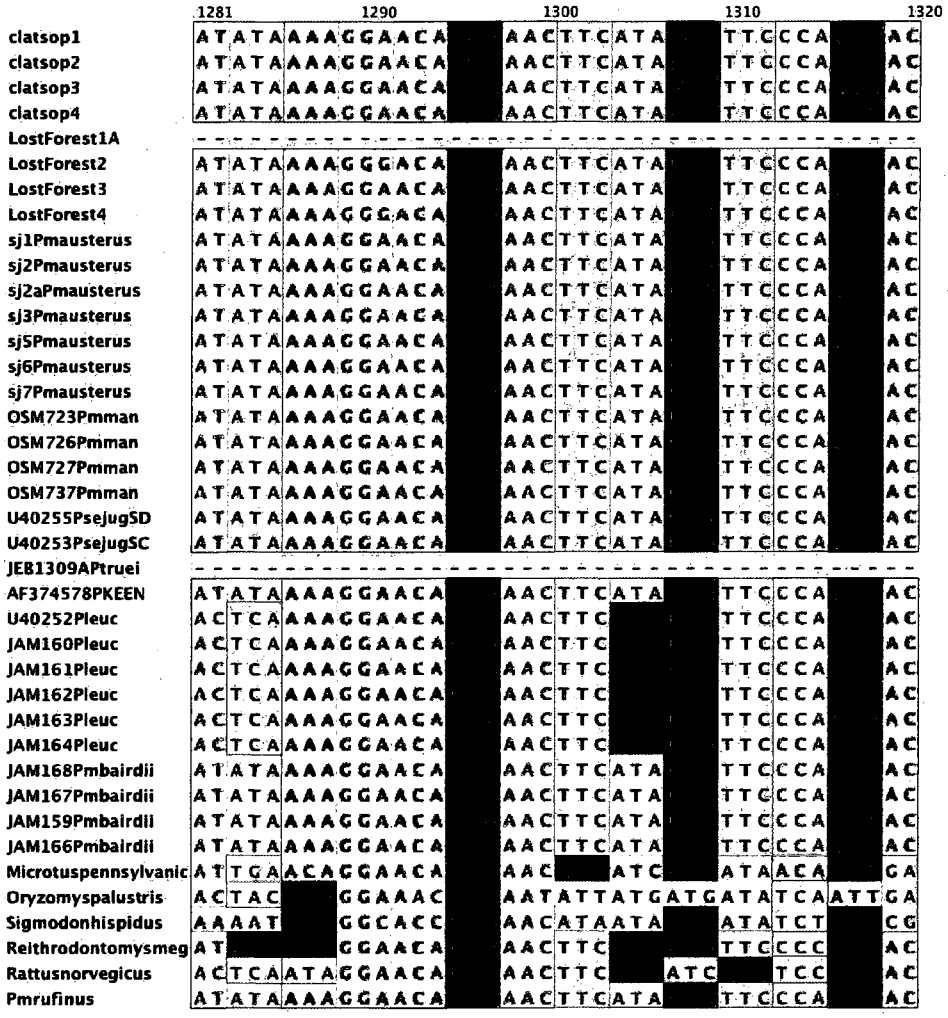
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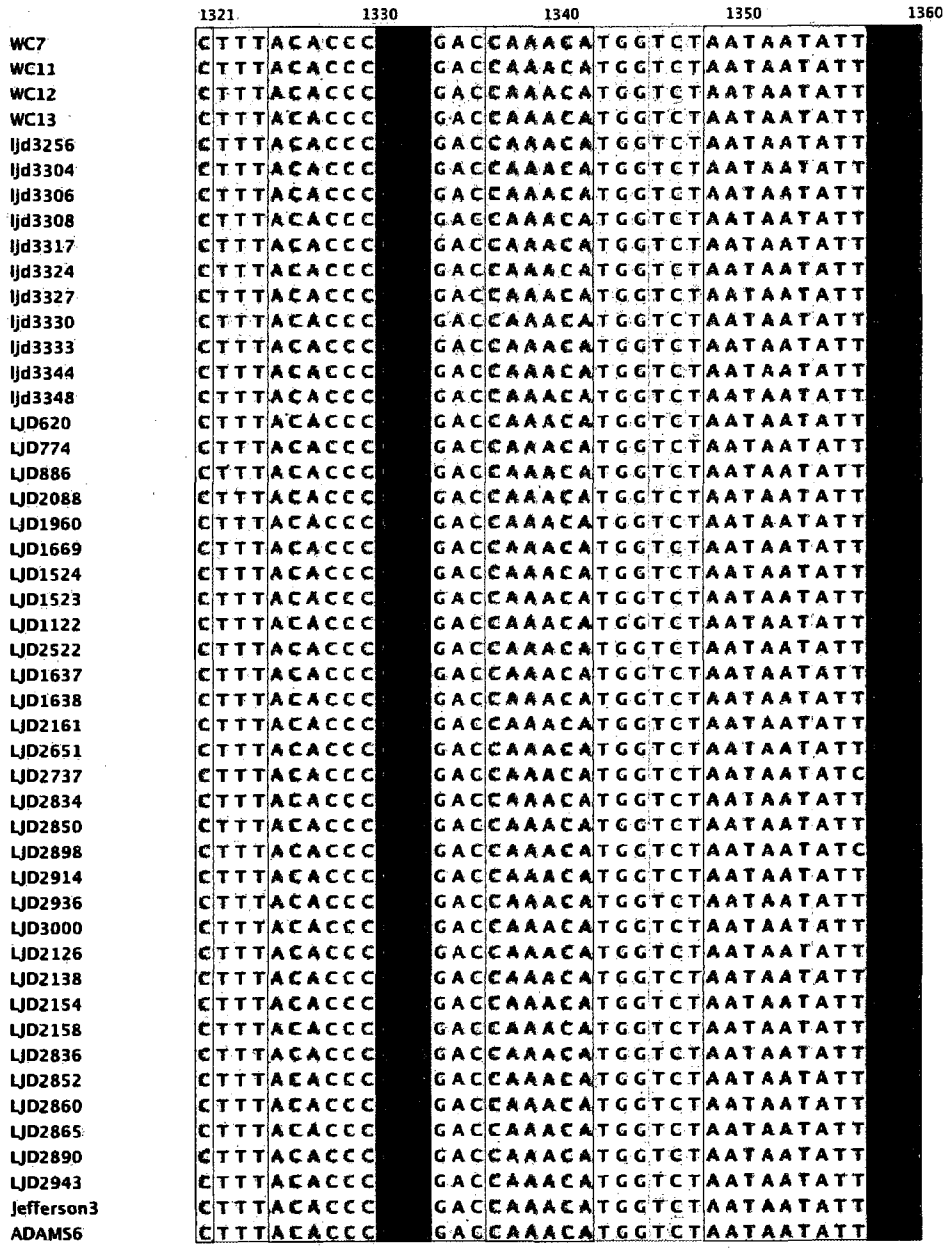
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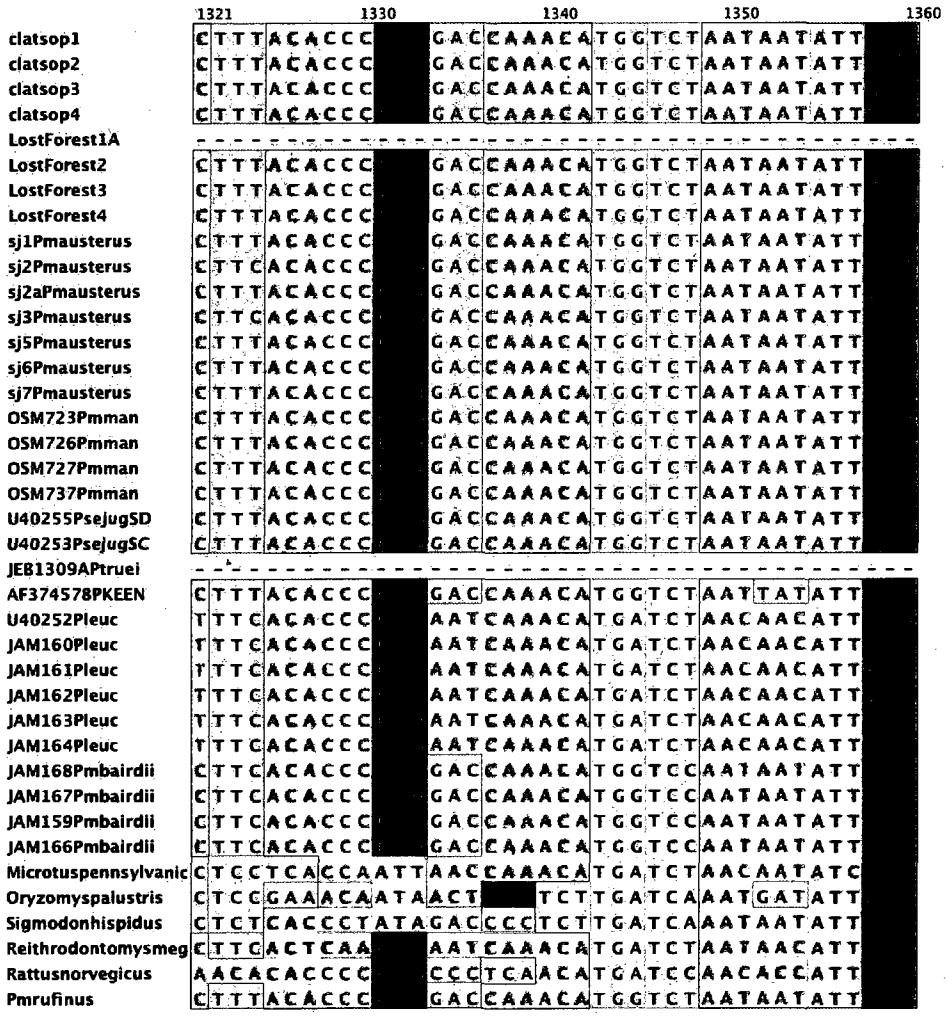
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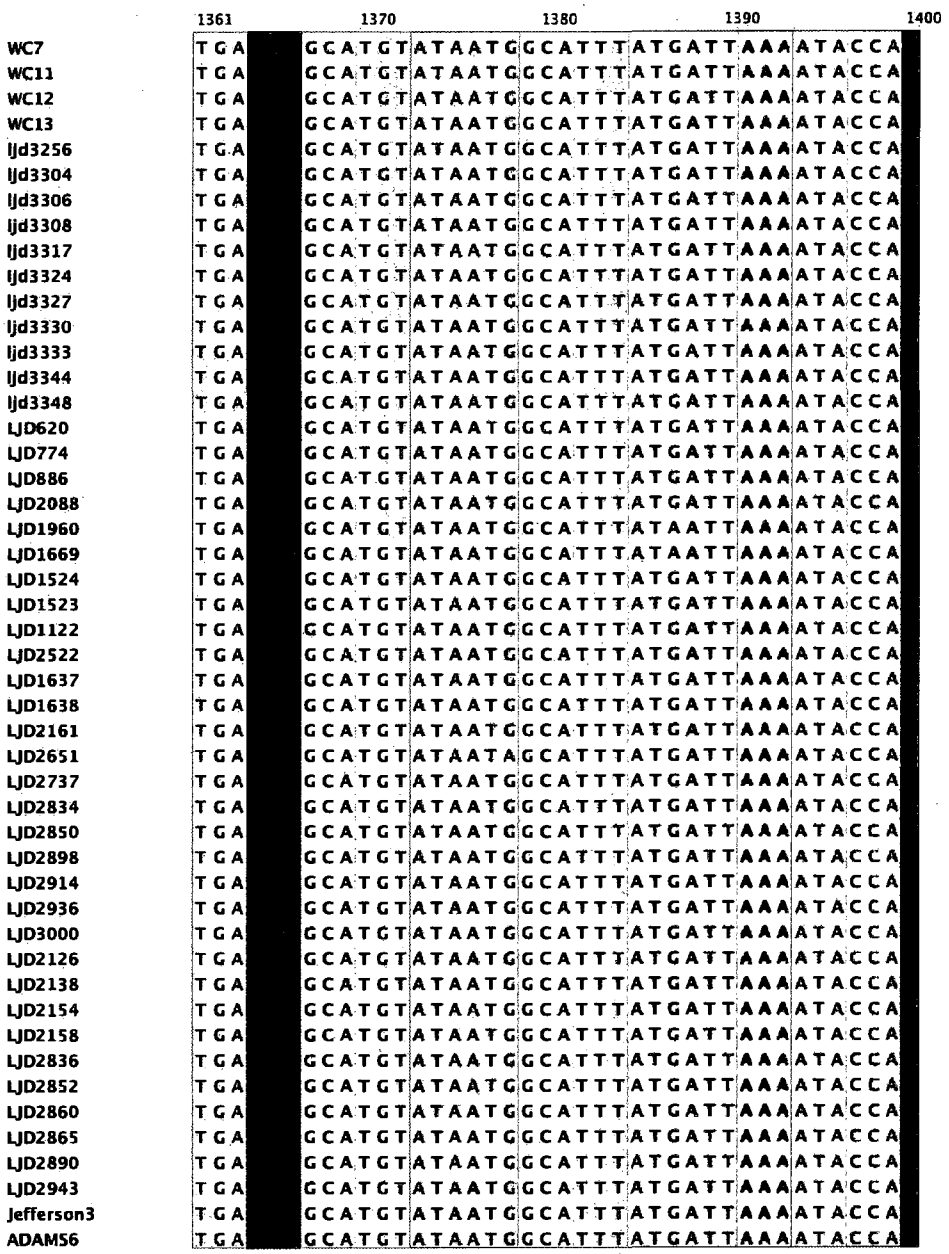
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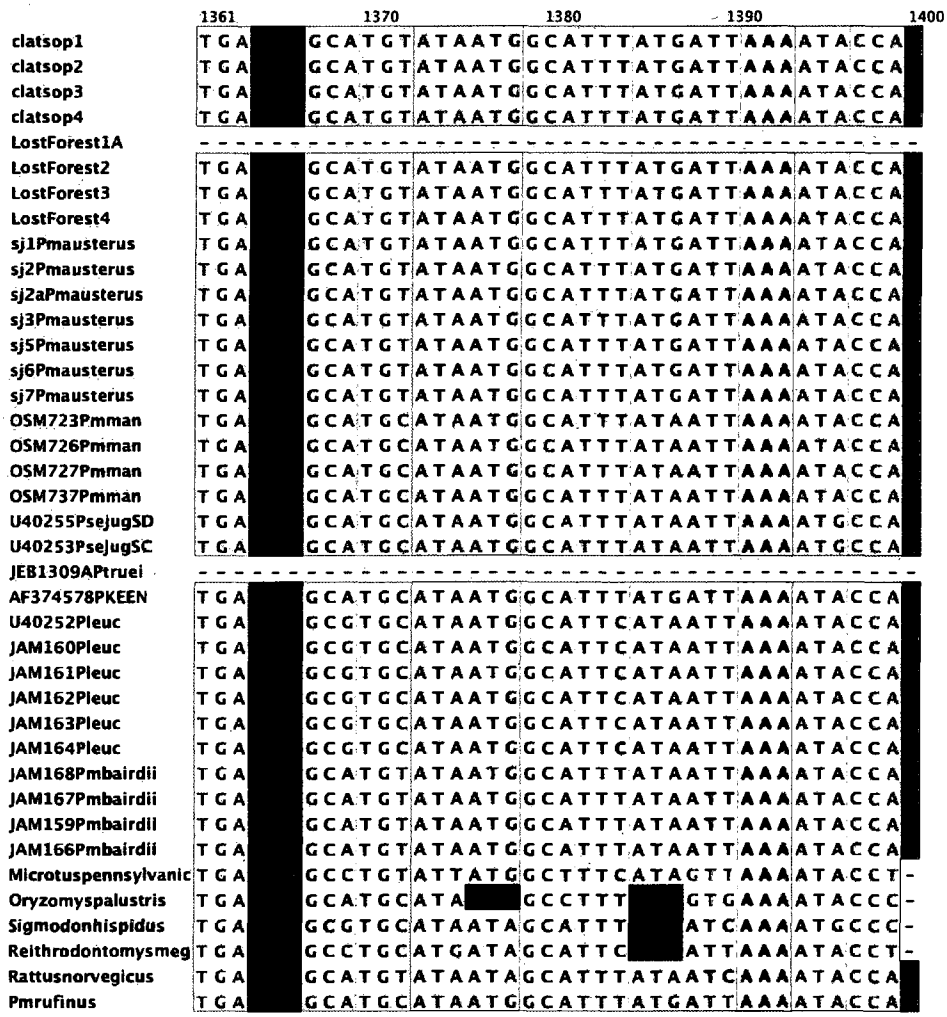
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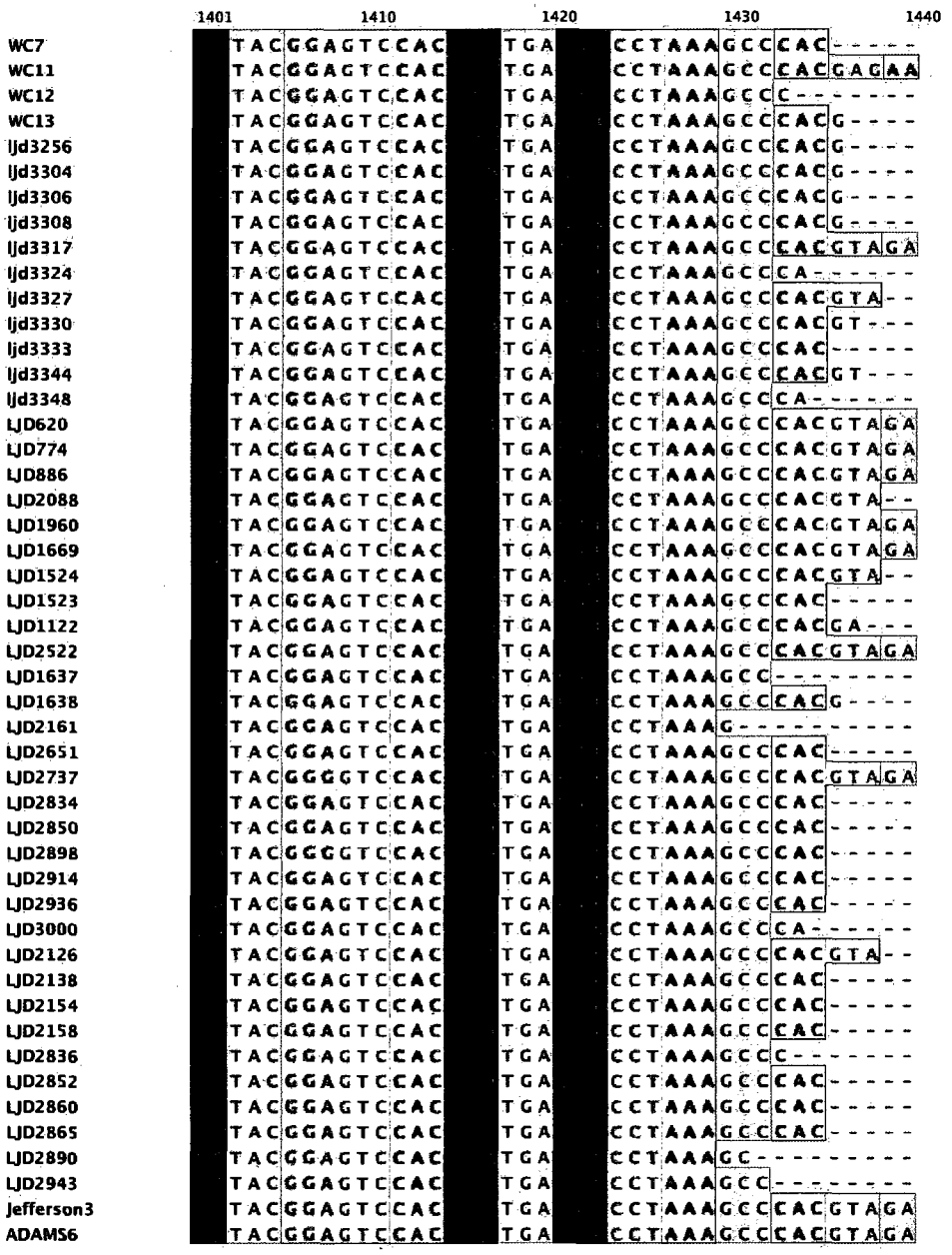
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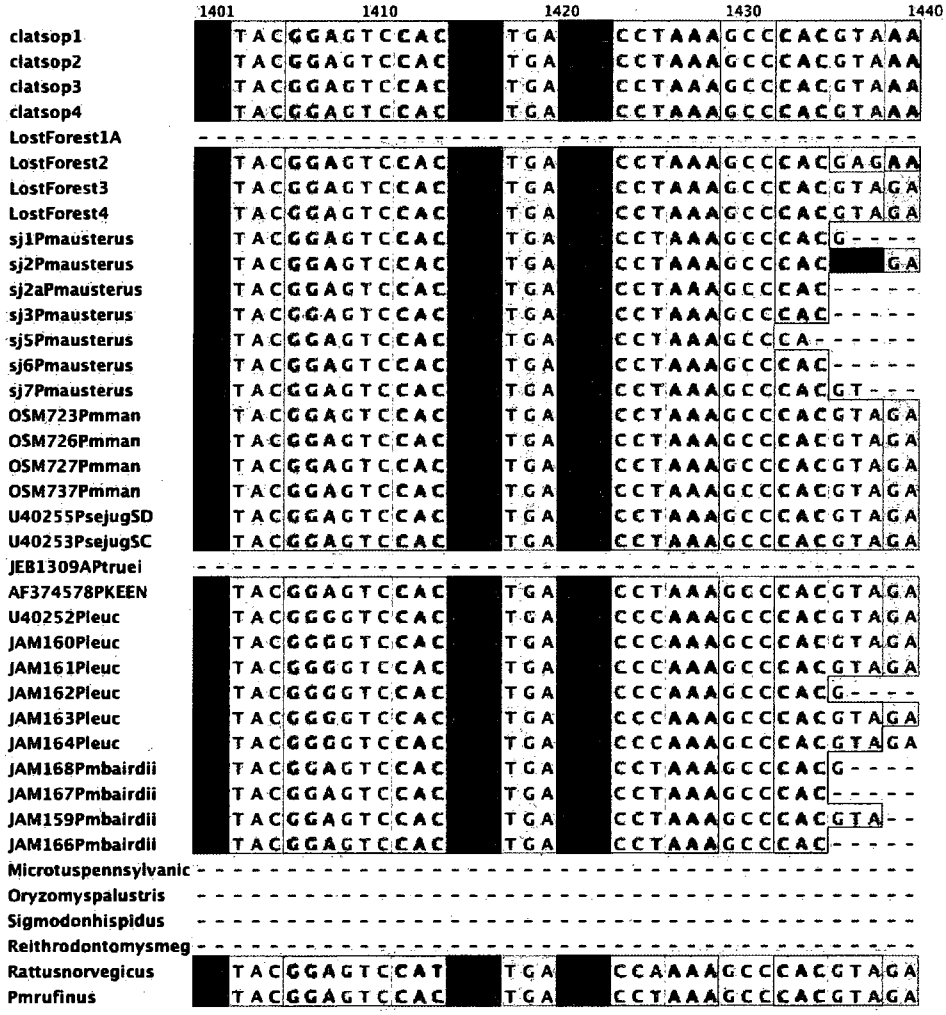
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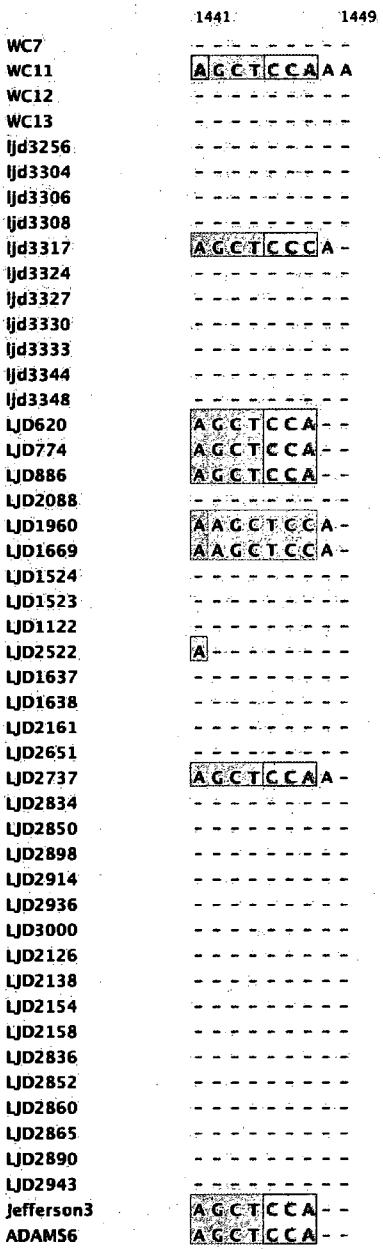
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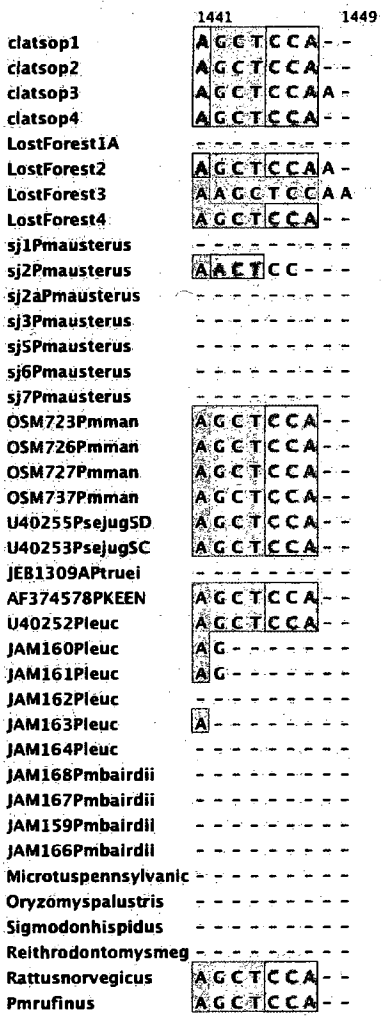
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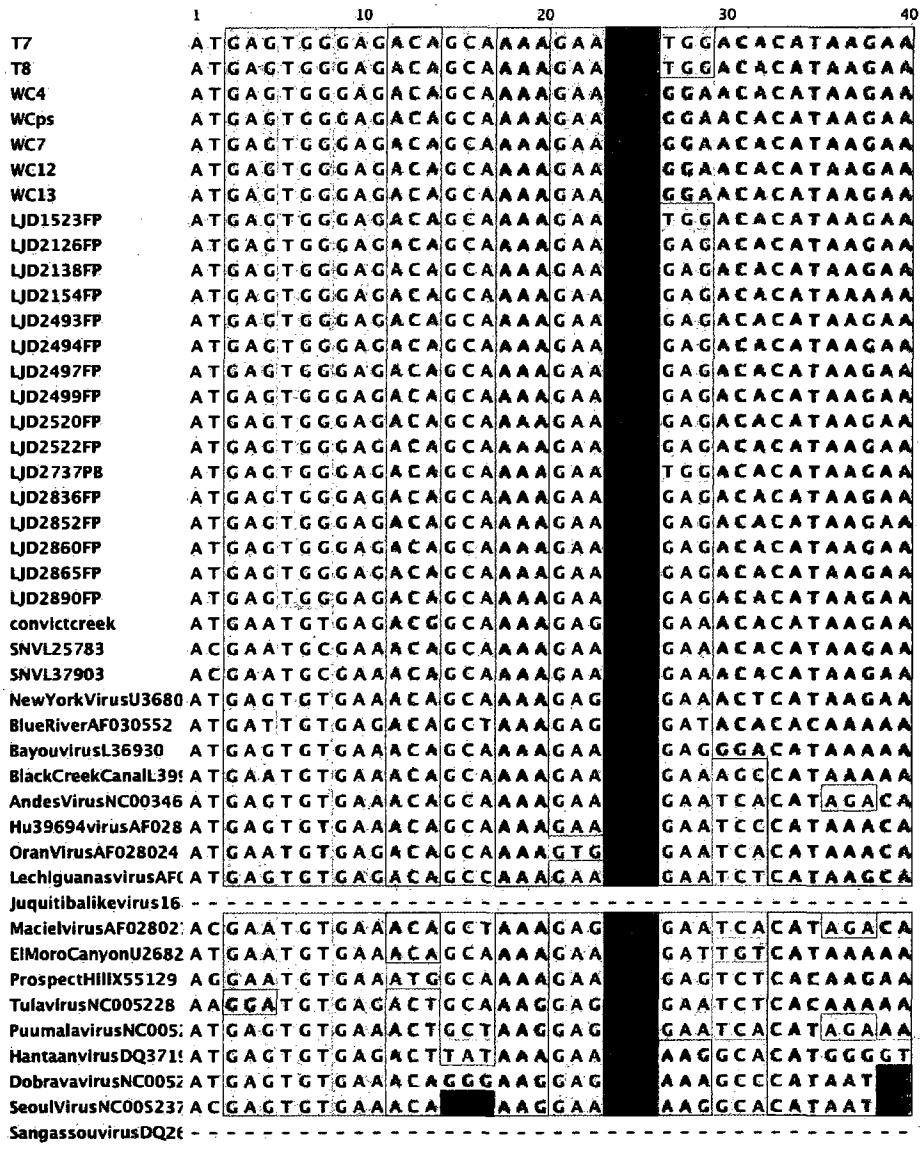
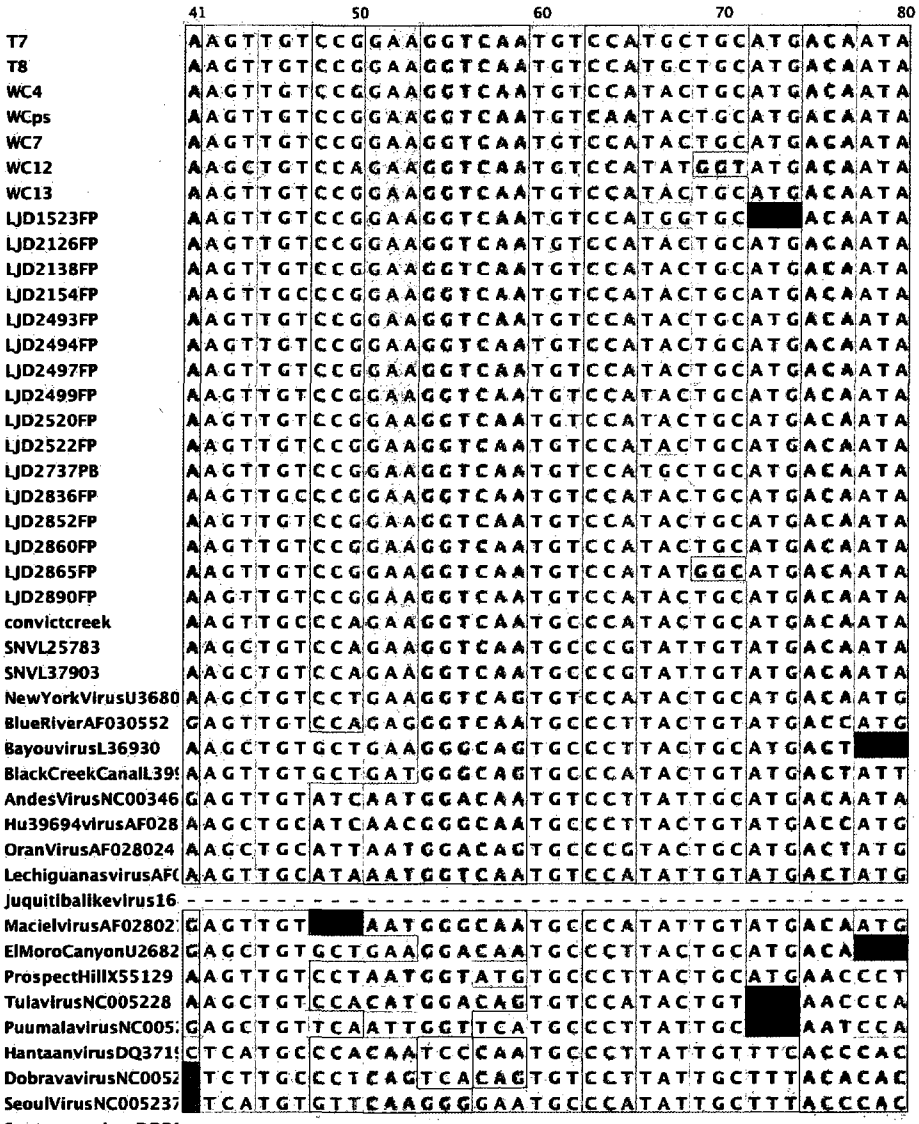
Appendix H: Hantavirus Multiple Sequence Alignment. Sequences of M segment G1/G2 glycoprotein precursor gene aligned with one another and adjusted to codon reading frame. T*=Troutdale, WC=Washington County, WCps=Washington County patient sample, LJD*=Portland area specimens collected for this research.

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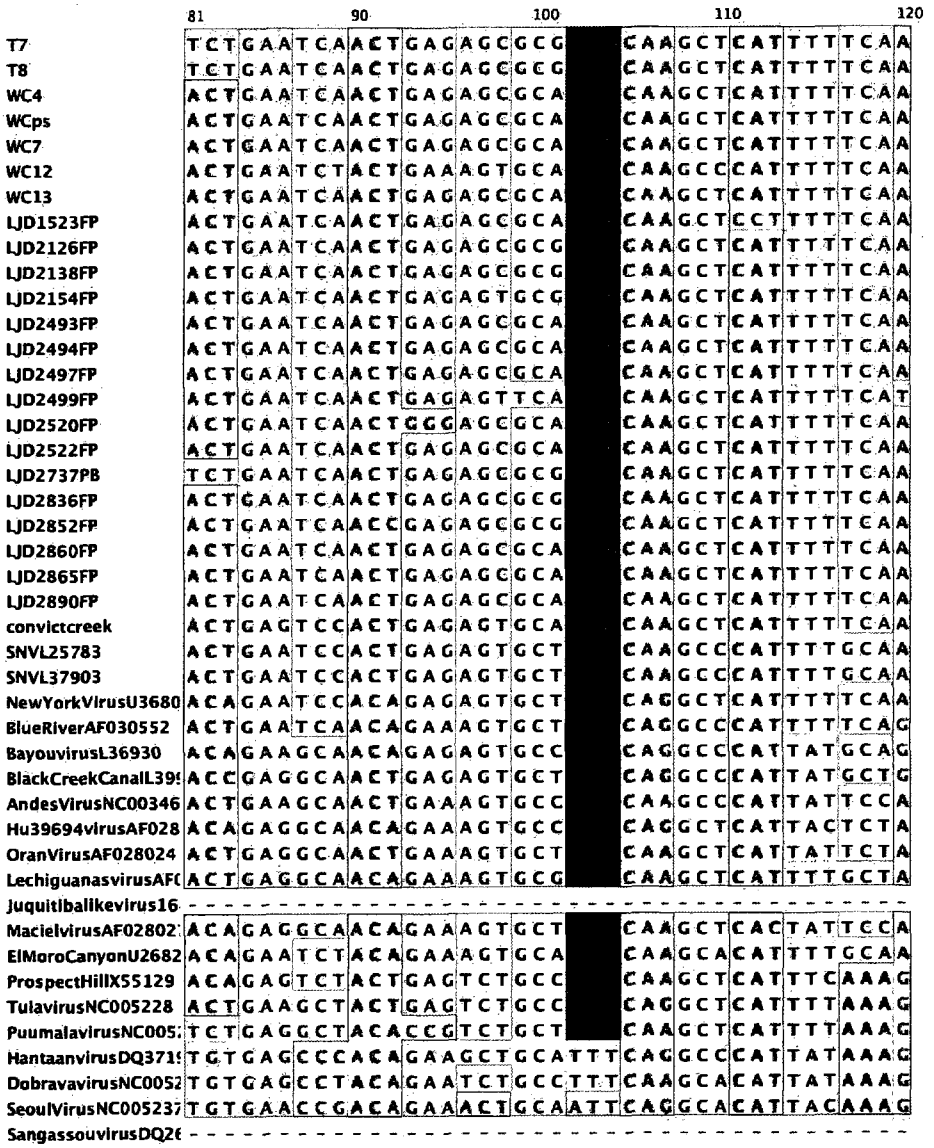
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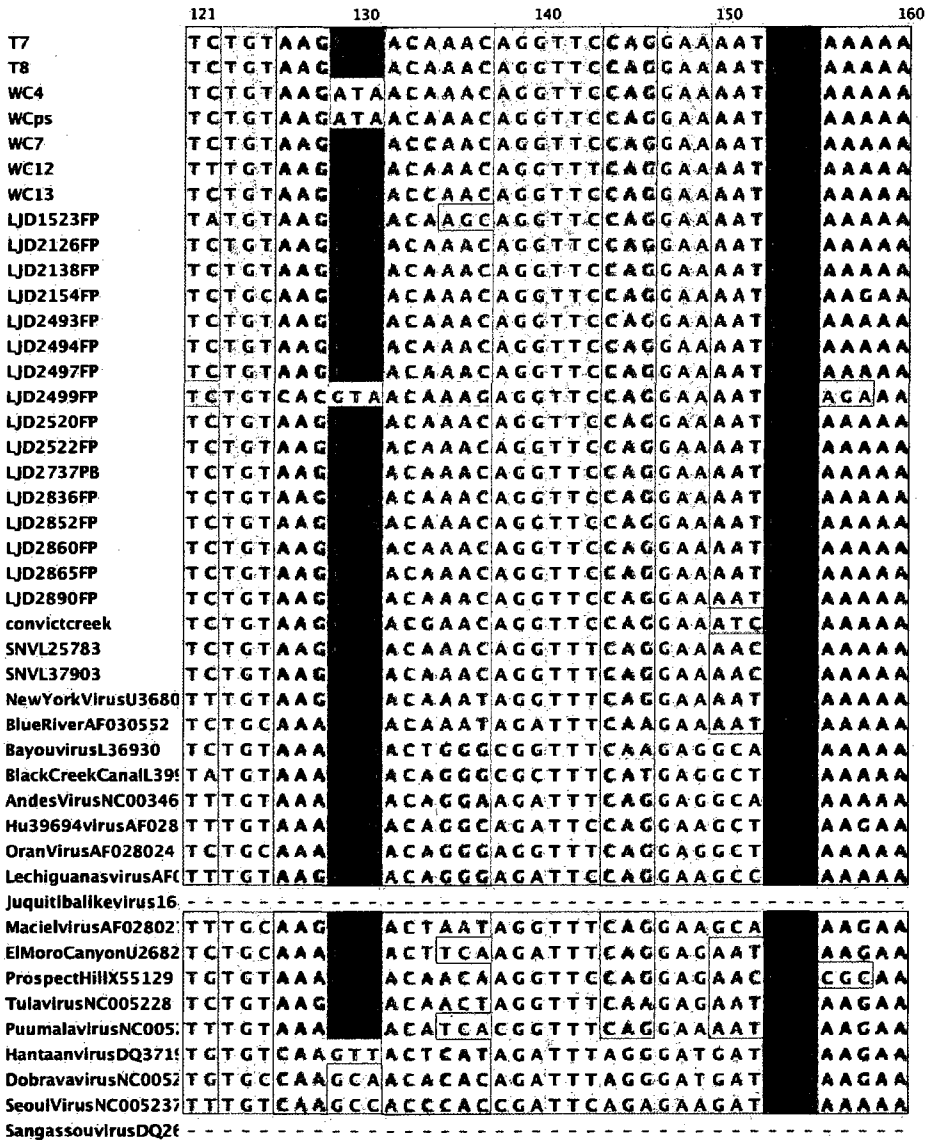
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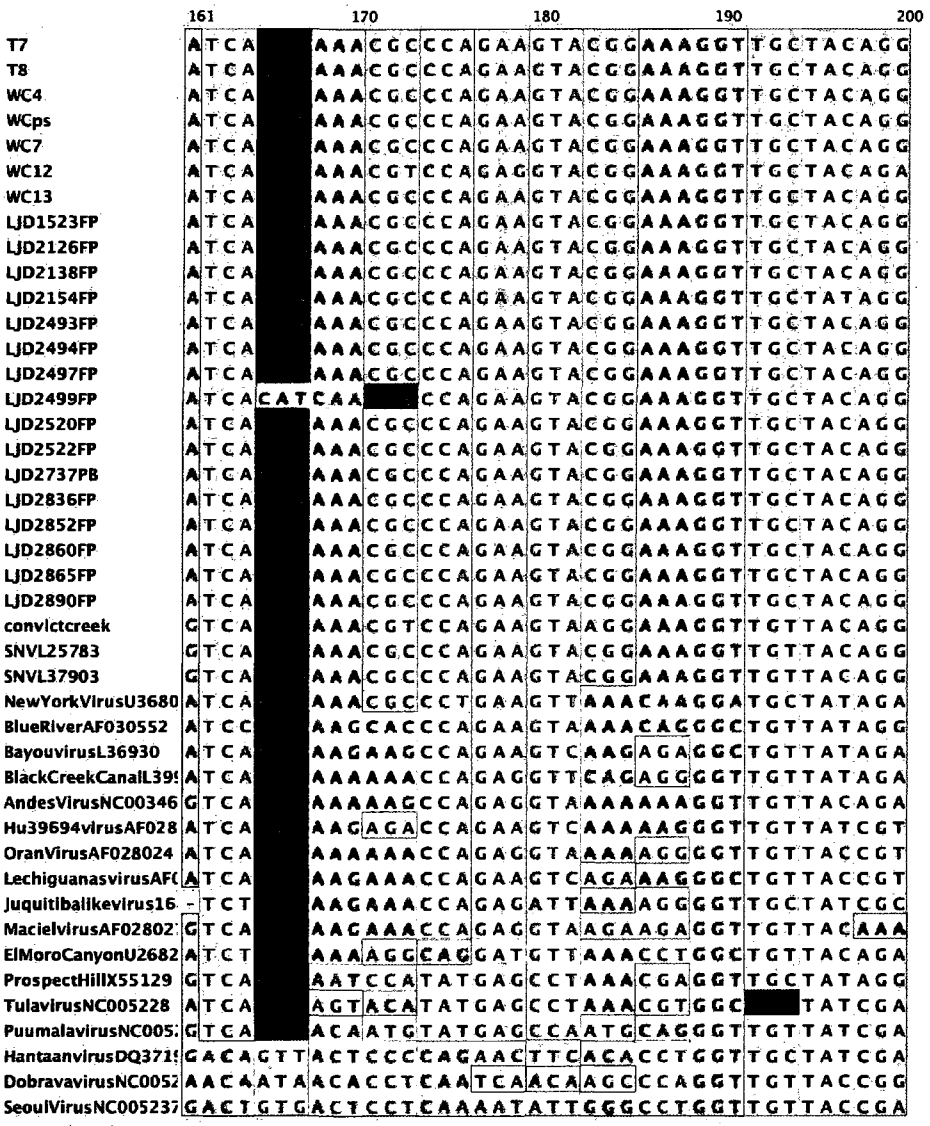
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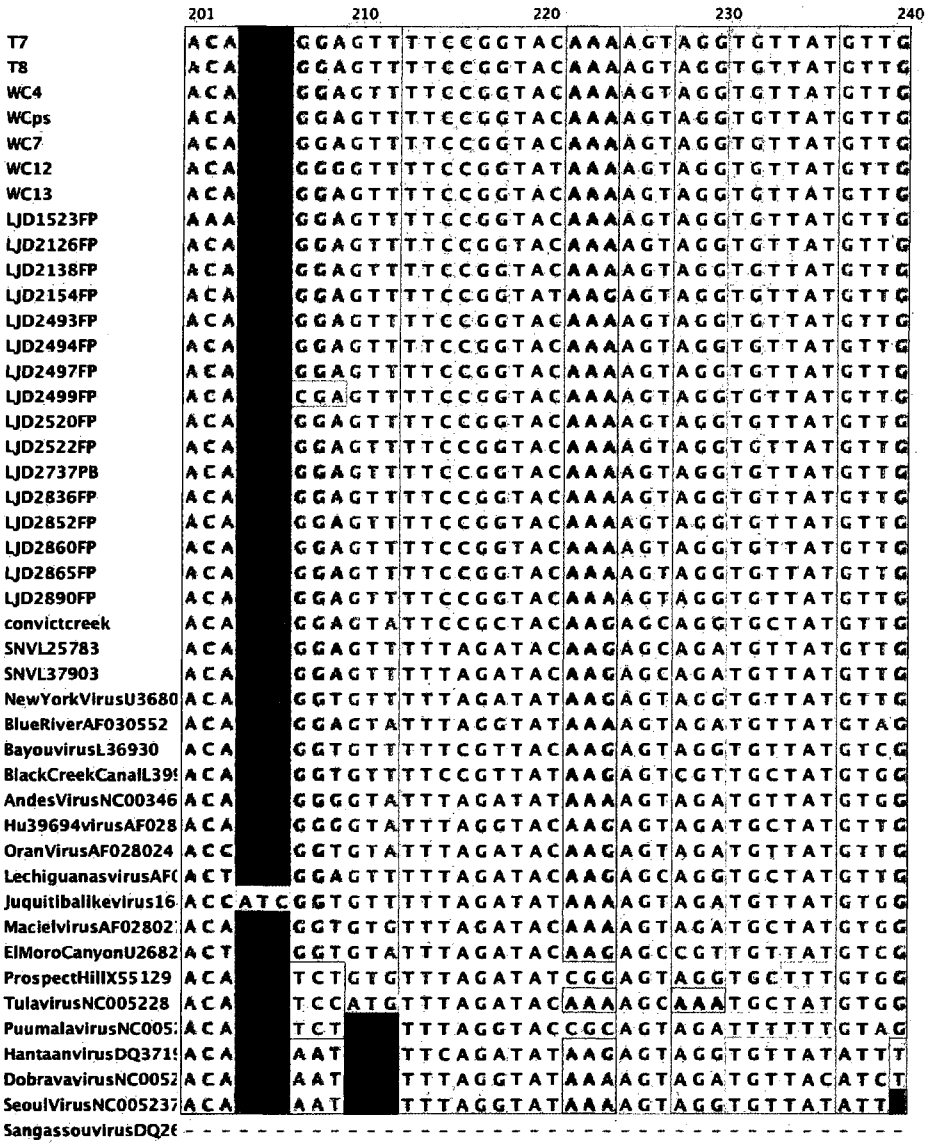
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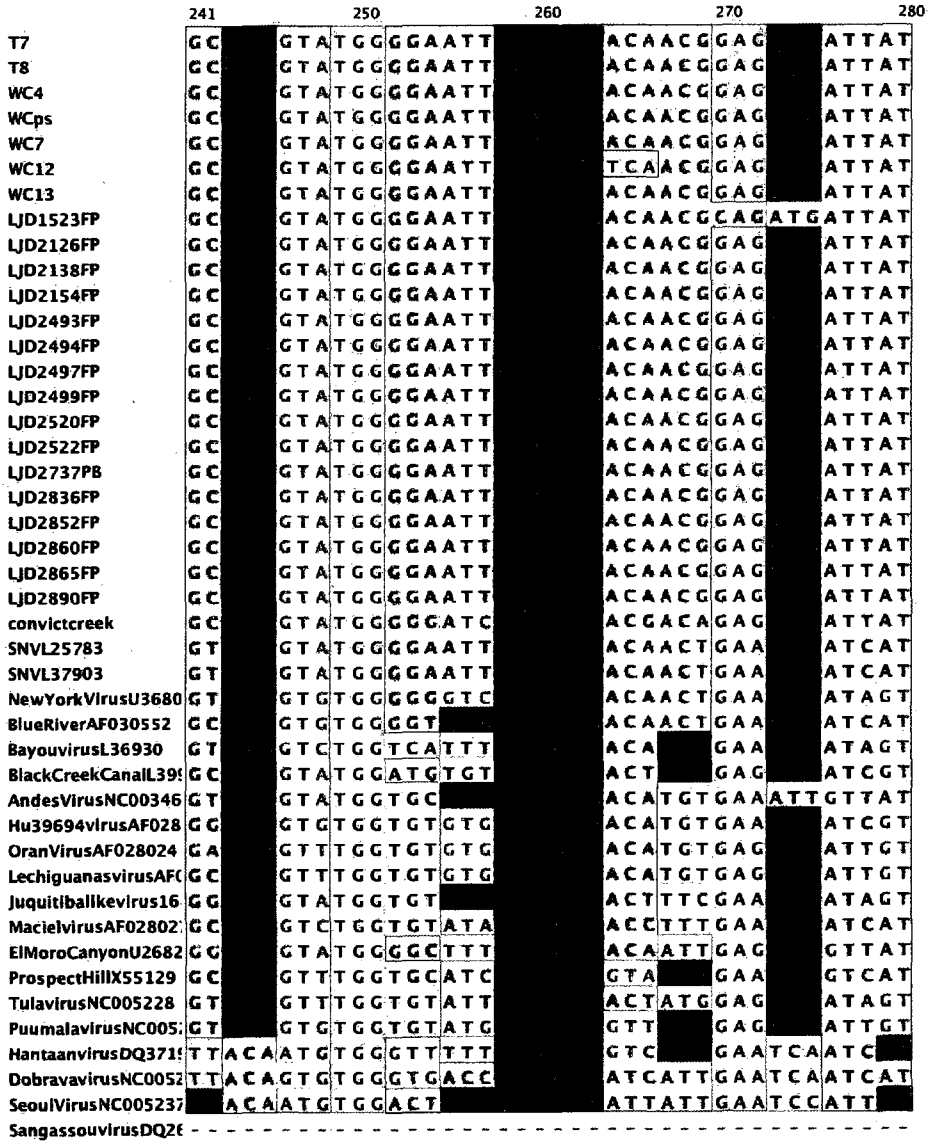
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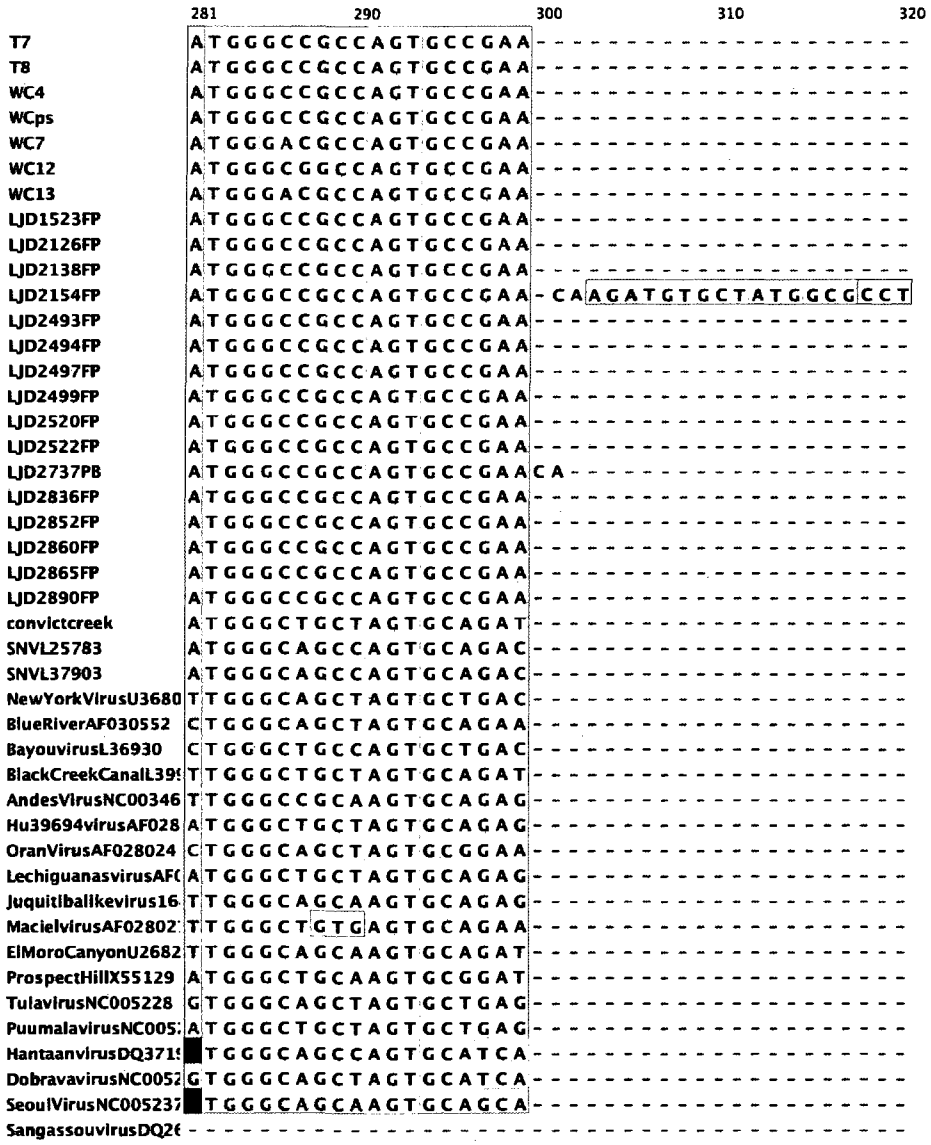
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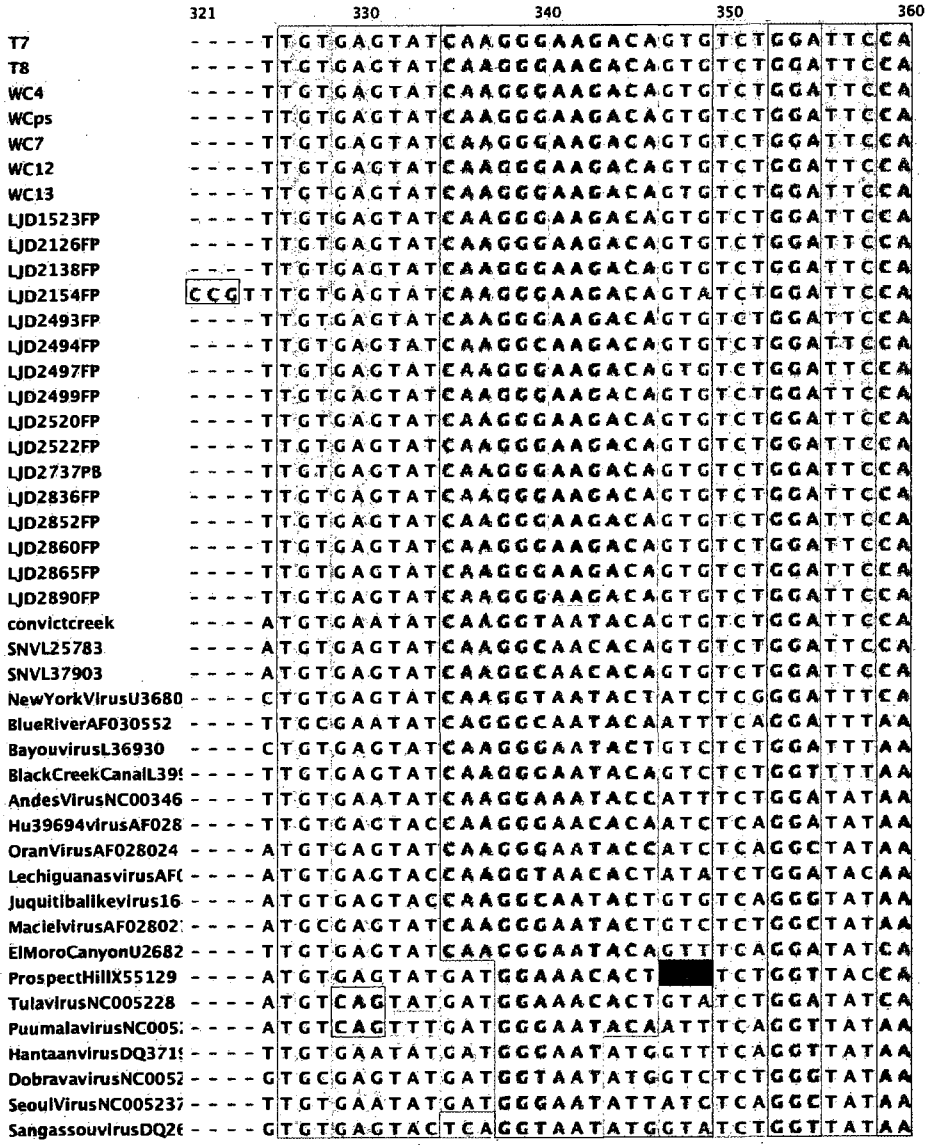
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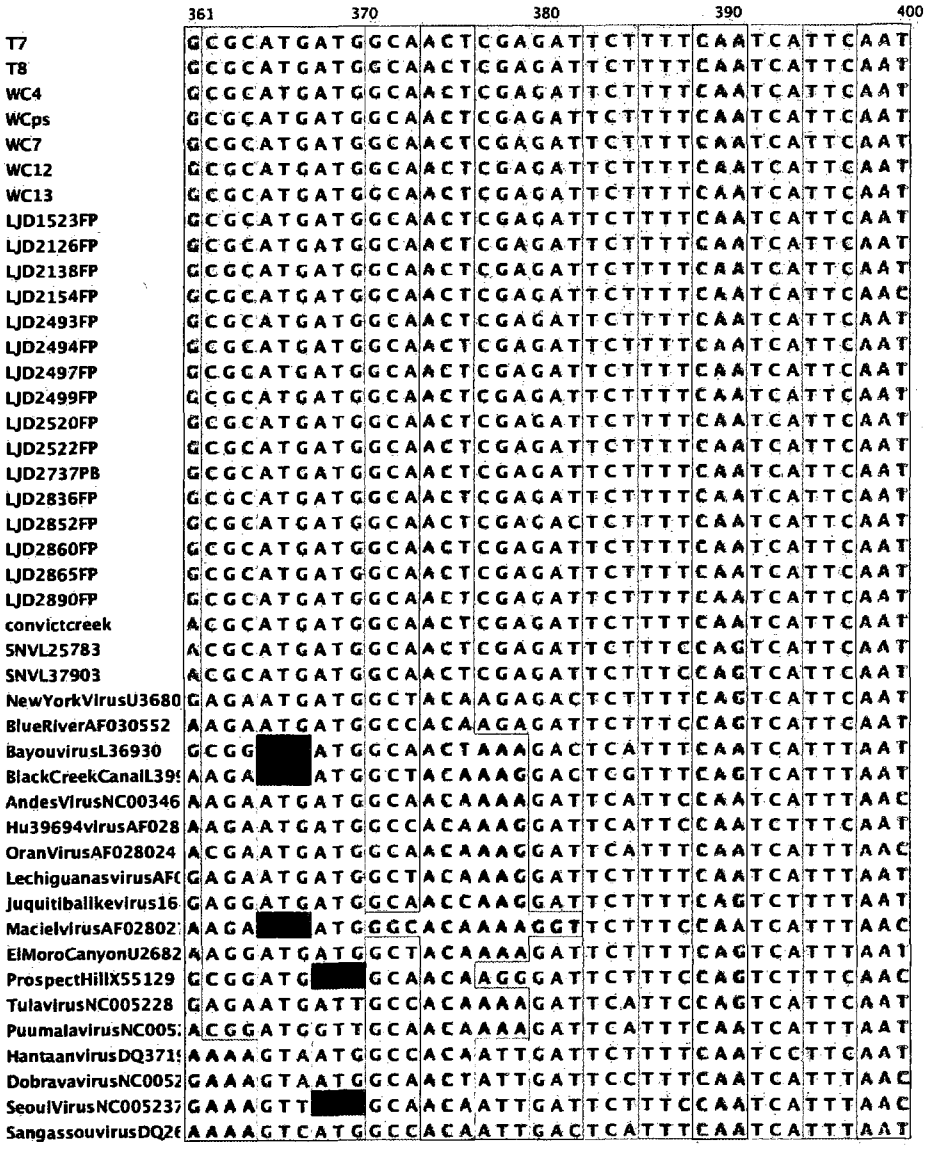
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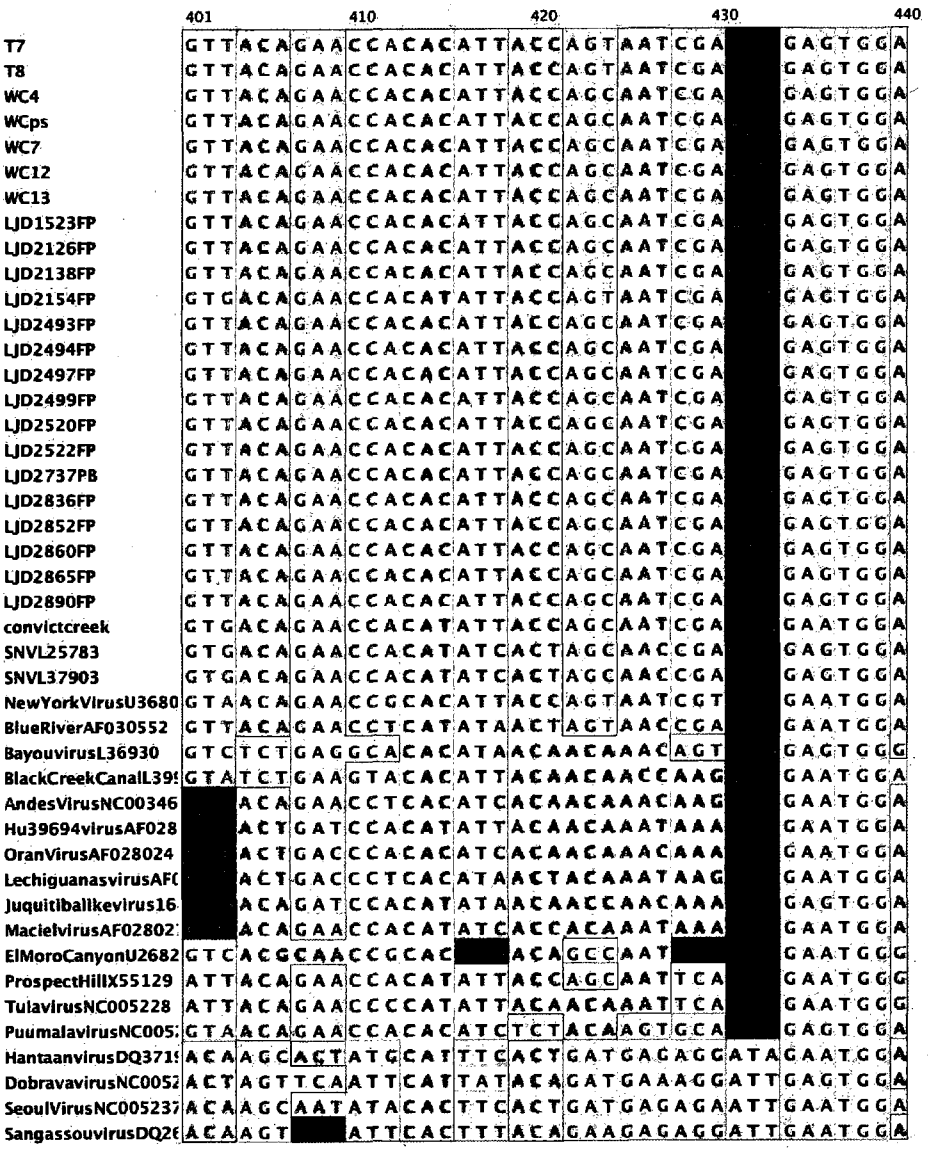
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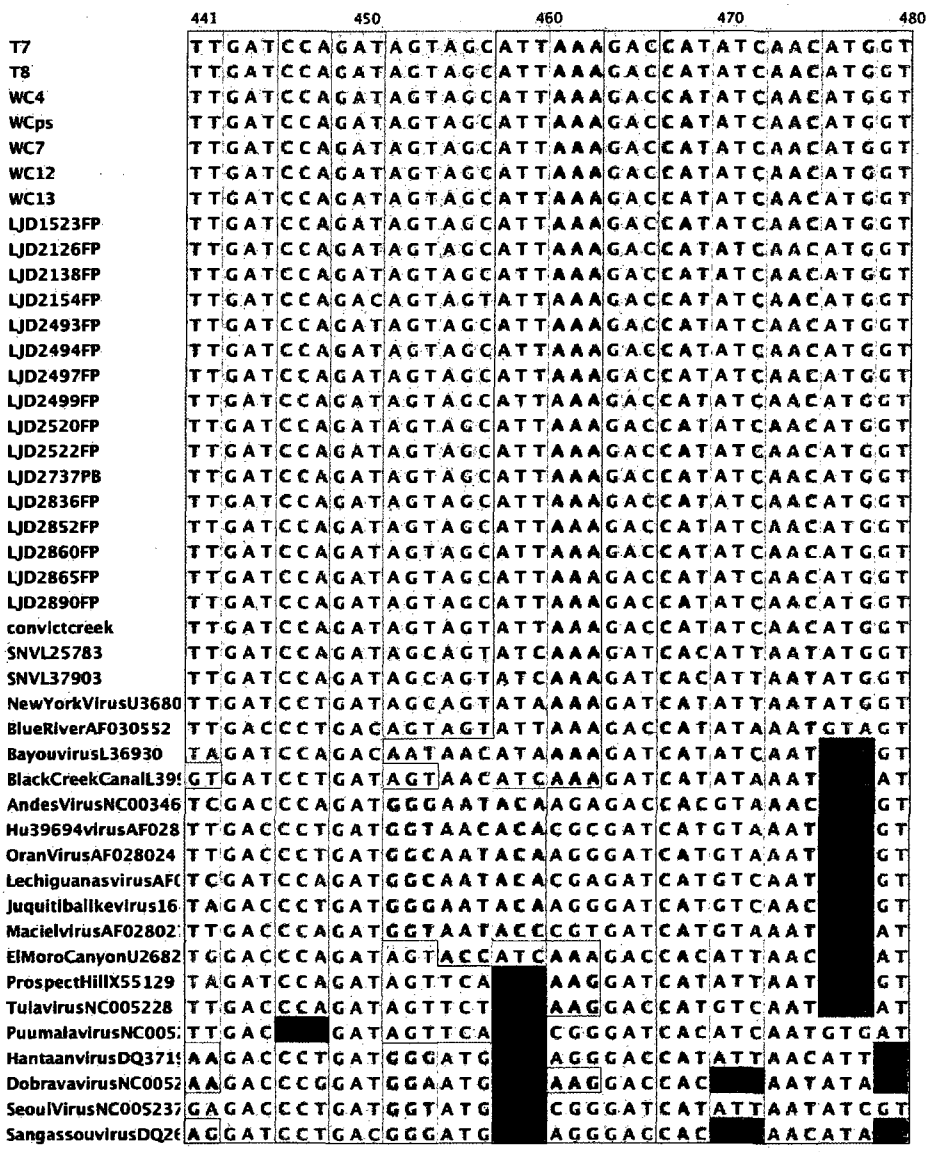
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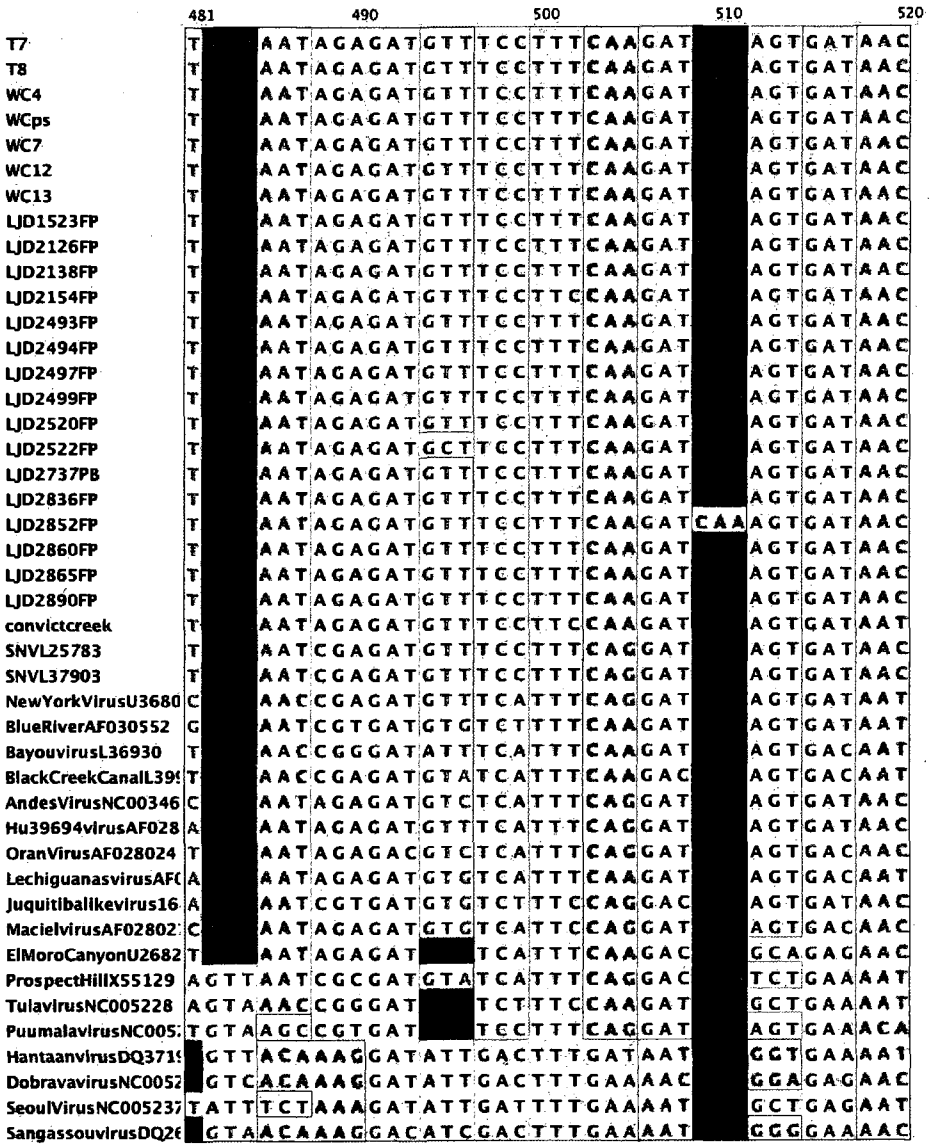
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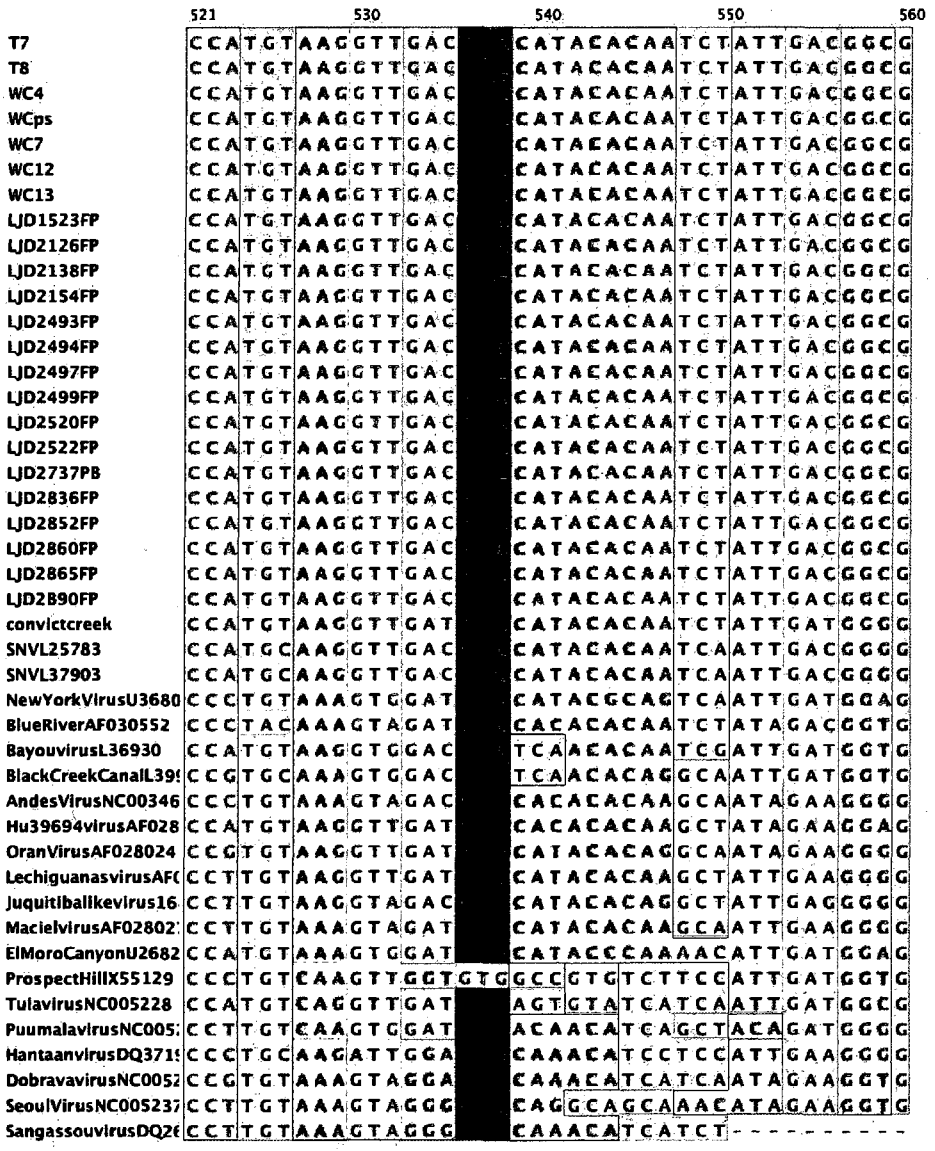
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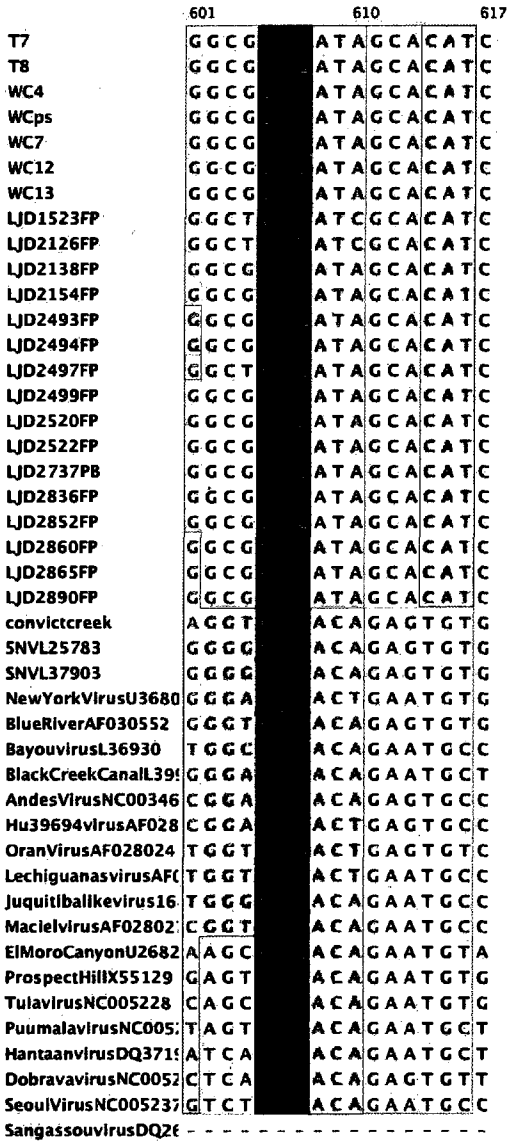
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