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Distribution and genetic structure of pocket gophers (Genus *Geomys*) in Kansas

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DISTRIBUTION AND GENETIC STRUCTURE OF POCKET GOPHERS

(GENUS GEOMYS) IN KANSAS

being

A Thesis Presented to the Graduate Faculty
of the Fort Hays State University in
Partial Fulfillment of the Requirements for
the Degree of Master of Science

by

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Approved_____

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This thesis for
the Master of Science Degree
by
Zachary J. Schwenke
has been approved

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ABSTRACT

The development of informed management practices and insightful research depends not only on an understanding of species natural history and ecology, but information regarding the distributions of these species and how they interact with adjacent taxa. The study of a species distribution can become complicated if the geographic variation within the species is not understood. Pocket gophers, including those in the genus *Geomys*, display morphological and chromosomal variation across their range, even within the same species. Genetic techniques, including Amplified Fragment Length Polymorphism (AFLP), have clarified population relationships and characterized zones of contact. Previous studies have suggested 2 species and up to 5 subspecies of *Geomys* in Kansas. Researchers have documented 1 contact zone in Osborne County between a population with small body size and lighter pelage in the west and a population that is larger and darker in the east. However, there has been little consensus over the taxonomic status of these 2 populations. Also, there has not been sufficient research that documents the presence and distribution of other distinct *Geomys* populations in Kansas. For my study, 143 pocket gophers were captured from throughout Kansas. Tissue samples of these specimens, including 1 additional sample from Lincoln County, Nebraska, were analyzed with AFLP by using 6 primer pair combinations. These data were then evaluated by using Principle Coordinate Analysis, the program STRUCTURE, and an unrooted phylogram generated by using distance values to determine the presence of genetically distinct taxa, their distributions in Kansas, and any level of genetic admixture among populations. Results were considered following the genetic species concept. Consensus among all 3 analyses suggested the presence of 4

genetically cohesive populations in Kansas with each having different degrees of genetic isolation. My research suggested that the northwestern taxonomic group, *Geomys halli*, was isolated genetically and was functioning as a species. Other taxa in Kansas were suggested to include, *G. bursarius majusculus* (eastern), *G. b. industrius* or *major* (south central), and *G. jugossicularis* (southwestern). The northwestern population was likely in secondary contact with the southwestern and eastern populations, suggested by a zone of sympatry, 1 hybrid, and little admixture. Determination of taxonomic rank was limited because the interactions among these taxa are unknown outside of Kansas.

Keywords: Admixture, AFLP, contact zone, *Geomys*, *G. bursarius*, *G. halli*, hybridization, introgression, Kansas

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PREFACE

My thesis is written in the style required by the Journal of Mammalogy, to which it will be submitted for publication.

INTRODUCTION

Researchers and natural resource managers need a clear understanding of species distributions. Knowledge of the geography of species or populations provides insight to its conservation status and factors that might impact its distribution. Misidentification of taxa in research, if not detected, has the potential to negatively impact biological and ecological studies, cause taxonomic confusion, and might lead to the extinction of unrecognized species (Bortolus 2008). Bortolus (2008) went on to suggest that if a species replaces another that has a similar phenotype, but is genetically and ecologically distinct, ecologists and land managers might not recognize changes in patterns and processes occurring in the landscape.

Geographic variation has been observed in many species (Hall 1981; Koch 1986; Lariviere and Pasitschniak-Arts 1996; Nevo and Bar-El 1976). Some species exhibit a gradual change in characteristics across their distributions (Storz et al. 2000), while other species change abruptly within their range (Phillips et al. 2007). Other populations might have characteristics unique to specific regions, such as lava flows (Hoekstra and Nachman 2003). If geographic variation within a species is not thoroughly understood, areas that exhibit clinal or abrupt change could be overlooked. Because species, subspecies, or the recognition of unique populations might be designated by observed patterns of variation, it is necessary to clarify where these populations occur and how they interact. Some taxonomic designations might not be warranted because the features change gradually across their distributions. Clines might occur where populations are not isolated genetically (Bradley and Baker 2001). Conversely, morphologically similar taxa

that have not been studied genetically could represent cryptic species (Baker and Bradley 2006). Investigation of geographic variation and contact zones clarify patterns of divergence (Taberlet et al. 1995).

Thorough documentation of current ranges, when compared to historical ranges, allows biogeographers to understand species history, phylogeographic changes, and factors that could impact species distributions (Avice 2000; Crisci et al. 2003). However, if sampling among species is done at too large of grain researchers will not be able to determine if species are allopatric, parapatric, paripatric, or sympatric. Inadequate knowledge of species distributions could result in inaccurate conclusions in historical biogeography.

Genetic studies have contributed to our understandings of species phylogenies. However, these studies are often conducted with few samples across large geographic areas. If proper grain and extent are not identified prior to these studies, predictions of how populations interact might be overlooked or misinterpreted (Archie et al. 1988; Roff and Bentzen 1989).

Reduction in gene flow between populations of a species can lead to divergence. Complete isolation of populations can result in selection against introgression of genetic material from sister populations if secondary contact occurs (Baker and Bradley 2006). Eventually, isolation could result in reproductive isolation and maintenance of unique genetic compositions.

The genetic species concept (Baker and Bradley 2006) focuses on genetic isolation rather than reproductive isolation. According to this concept, isolated genetic exchange does not compromise a population's evolutionary isolation. Species are

considered isolated if there is no gene flow. Characterization of a contact zone could be based on its geographic location, interaction of the taxa, potential mechanisms of isolation, direction of gene flow, and level of genetic isolation (Baker and Bradley 2006; Baker et al. 1989; Bradley et al. 1993). Historically, isolation was caused by abiotic barriers or extinction of adjoining populations. Human disturbance, such as roads, cultivation, and irrigation canals, have created barriers or corridors, caused local extinctions, introduced nonnative taxa, and have both created and removed suitable habitat for many species (e.g., Hoffman et al. 2007). Modern genetic techniques will likely be able to detect the impact of such factors on populations.

Amplified Fragment Length Polymorphism (AFLP) is a genetic fingerprinting technique that detects changes at restriction sites of DNA and insertion or deletion of DNA between restriction sites. AFLP has proven useful in delineating population and taxonomic boundaries. For example, this method has been used to characterize genetic continuity of eastern and western populations of hispid cotton rat (*Sigmodon hispidus*; Phillips et al. 2007), identified of hybridization in wild turkey (*Meleagris gallopavo mexicana* and *M. g. merriami*; Mock et al. 2001), and test relatedness of individuals at geographically separate nesting sites of willow flycatcher (*Empidonax traillii extimus*; Busch et al. 2000). The AFLP technique uses controlled conditions to ensure primer annealing and elongation of DNA fragments. Manipulating the number and diversity of primer sets produces ample data (Vos et al. 1995). The use of nuclear DNA allows detection of greater genetic diversity than allozyme, mitochondrial, or chromosomal techniques because of the inclusion of non-coding regions and, by comparison, the large number of base pairs involved (Davies et al. 1999). Moreover, nuclear DNA analyses are

useful in detecting genetic introgression, as opposed to similar analyses of maternally inherited genetic material such as mtDNA.

The pocket gopher, including the genus *Geomys*, is a fossorial rodent. *Geomys* is distributed throughout the Great Plains but also includes areas of the southwestern and southeastern United States, and Mexico (Fig. 1). *Geomys* currently is recognized to contain twelve species: *arenarius*, *attwateri*, *breviceps*, *bursarius*, *jugossicularis*, *knoxjonesi*, *lutescens*, *personatus*, *pinetis*, *streckeri*, *texensis*, and *tropicalis* (Chambers et al. 2009). In Kansas, *Geomys* occurs in soils described as loamy sand, sandy loam, sand, or clay loam (Hoffman et al. 2007). While they characterized soil types used by pocket gophers, Hoffman et al. (2007) described areas north of the Arkansas River that were uninhabited by pocket gophers, and areas only inhabited by *Cratogeomys castanops*. *Geomys* has gone through many taxonomic changes since the late 1800s (Mauk et al. 1999; Patton 2005). Various authors have hypothesized up to 2 species and 5 subspecies, in Kansas (Table 1).

The taxonomic status of *Geomys* in Kansas remains ambiguous. No consensus related to what taxa occur in Kansas, their geographic extent, or the level of genetic isolation has been made. Methods previously used to determine the relationships of *Geomys* that occur in Kansas, or have included Kansas specimens, include comparison of cranial (Burns et al. 1985; Genoways et al. 2008; Heaney and Timm 1983; Hendricksen 1973; Sudman et al. 1987; Villa-R and Hall 1947), external (Burns et al. 1985; Hendricksen 1973; Sudman et al. 1987), and bacular (Burns et al. 1985) morphology, pelage coloration (Genoways et al. 2008; Hendricksen 1973; Villa-R and Hall 1947), karyotypes (Burns 1985; Genoways et al. 2008; Hart 1978; Sudman et al. 1987), and

allozyme electrophoresis (Burns et al. 1985; Sudman et al. 1987). More recent research has involved genetic techniques including sequencing of mitochondrial 12S rRNA (Chambers et al. 2009; Genoways et al. 2008; Jolley et al. 2000), mitochondrial cytochrome-*b* (Chambers et al. 2009; Elrod et al. 2000; Genoways et al. 2008; Sudman et al. 2006), and interphotoreceptor retinoid-binding protein (*Rbp3*) gene (Chambers et al. 2009; Genoways et al. 2008).

Villa-R and Hall (1947) conducted an early study of *Geomys* in Kansas. They suggested that 5 subspecies of *G. bursarius* were present within Kansas: *lutescens*, *majusculus*, *major*, *jugossicularis*, and *industrius* (Fig. 2a). Villa-R and Hall (1947) described color and size differences among these taxa, with a general trend of individuals from eastern and southern Kansas being larger and darker than those in the western Kansas. Variation between eastern and western forms of *Geomys* in Osborne County has been reported (Burns et al. 1985; Genoways et al. 2008; Heaney and Timm 1983; Hendricksen 1973; Sudman et al. 1987). Additionally, Villa-R and Hall (1947) identified potential areas of morphological intergradation in Butler, Harper, Meade, McPherson, and Saline counties, and suggested further sampling in Comanche and Hodgeman counties.

Hendricksen (1973) conducted a survey of *Geomys* along a transect from the foothills of the Rocky Mountains east to the Missouri River. Her research showed an abrupt morphological and pelage color change in Osborne County between *G. b. lutescens* to the west and *G. b. majusculus* to the east. Hendricksen (1973) hypothesized this was an area of secondary contact. No implications for geographic distribution of

other taxa in Kansas were inferred from this study. Hart (1978) supported Villa-R and Hall (1947).

Heaney and Timm (1983) examined cranial morphology of *Geomys* north of Texas. They described no intergrades and recognized *G. b. bursarius*, *G. lutescens major*, and *G. l. lutescens* (Fig. 2b) as occurring in Kansas. Burns et al. (1985), using a variety of techniques, countered Heaney and Timm (1983) with specimens they considered to show intergradation. They suggested the taxa *lutescens* be placed as a subspecies under *G. bursarius*. Burns et al. (1985) maintained the usage of *major* as the subspecies in southern Kansas, but had no samples south of the Big Creek in Ellis County and used 3 samples east of Mitchell County

Sudman et al. (1987) referred to Villa-R and Hall (1947) and Hart (1978) for their use of taxonomy in Kansas (Fig. 2c). This research designated *Geomys* south of the Platt River, Nebraska, north of the Arkansas River, Kansas, and west of the contact zone in Osborne County as *G. b. halli*. Other taxa thought to occur in Kansas by Sudman et al. (1987) included *G. b. jugossicularis*, *G. b. industrius*, and *G. b. bursarius*. Kansas samples included in this study were limited to the range of *halli* and 4 samples from Finney County.

The majority of these studies have supported the elevation of the Nebraska Sandhills pocket gopher to a species, *G. lutescens* (Chambers et al. 2009; Elrod et al. 2000; Genoways et al. 2008; Jolley et al. 2000; Sudman et al. 2006). These studies were conducted throughout the range of *Geomys*. However, many used few or no samples from Kansas, or focused on *Geomys* within Nebraska (Genoways et al. 2008).

Two species, *G. bursarius* and *G. jugossicularis*, currently are hypothesized to occur in Kansas (Chambers et al. 2009; Genoways et al. 2008; Sudman et al. 2006). The purposes of my study were to 1) determine how many taxa of *Geomys* occur in Kansas by identifying the level of genetic continuity among sites and, 2) to study the level of genetic introgression among populations, if any introgression exists. Results of my study were considered in light of the genetic species concept (Baker and Bradley 2006).

METHODS

Capture site selection, sample collection, and sample preparation

For my study, sites were selected based on consideration of previous research while attempting to sample evenly among the distributions of all proposed taxa. Macabee gopher traps were set and anchored in tunnels of active burrows. Trapping occurred between July 2007 and April 2009. Efforts were made to excavate the tunnel system until a pair of traps could be set within the main tunnel junctions. Supplemental individuals were gathered throughout the trapping period (Kansas: Ellis County KK 1554; Meade County KK 1533; Morton County KK 1516 and 1517; Pratt County KK 1518. Nebraska: Lincoln County TK 54480).

Sample size of each site (n), site designation (bold number), and county of site follow, north to south, east to west (Fig. 3; Appendix III): **25** Lincoln County, (Nebraska, $n = 1$); **1** Rawlins County ($n = 4$); **2** Rooks County ($n = 2$); **3** Rooks County ($n = 2$); **4** Rooks County ($n = 7$); **5** Osborne County ($n = 7$); **6** Osborne County ($n = 11$); **8** Ellis County ($n = 16$); **13** Dickinson County ($n = 6$); **11** Russell County ($n = 6$); **12** Saline

County ($n = 3$); **9** Ellis County ($n = 1$); **10** Rush County ($n = 8$); **7** Ness County ($n = 6$); **16** Pawnee County ($n = 5$); **17** Greenwood County ($n = 9$); **14** Hamilton County ($n = 6$); **15** Kearny/Finney counties ($n = 8$); **22** Pratt County ($n = 1$); **19** Stanton County ($n = 1$); **18** Morton County ($n = 5$); **20** Meade County ($n = 7$); **21** Comanche County ($n = 8$); **23** Sumner County ($n = 7$); and **24** Cowley County ($n = 7$). All *Geomys* collected were prepared by using standard skin and skull voucher techniques. Voucher specimens, tissues (heart, kidney, liver, and spleen), and ancillary materials (embryos, external parasites, and internal parasites) were deposited in the Sternberg Museum of Natural History (MHP) at Fort Hays State University, Hays, Kansas. Spleen and a portion of liver were frozen in separate 2.0 mL cryovials. Heart, kidney, and a portion of liver were preserved in 150 mL centrifuge tubes with 95% ethanol.

DNA extraction and AFLP protocol

DNA was extracted from 15 to 20 mg of frozen spleen by using a DNeasy Blood and Tissue Kit (Qiagen Inc., Valencia, California). Tissue was placed in a 1.5 mL microcentrifuge tube with 180 μ L Buffer ATL, a tissue lysis buffer, and 20 μ L proteinase K. Samples were mixed by vortexing and then incubated at 56°C in a rotating hybridization oven for 6 to 8 h or overnight. Samples were then removed from the hybridization oven and vortexed for 15 s. Two hundred microliters (200 μ L) of Buffer AL, a lysis buffer, were added to the sample and mixed by vortexing. Two hundred microliters (200 μ L) of 95% ethanol were added and mixed by vortexing. This mixture was pipetted into DNeasy mini spin columns and placed in a 2 mL collection tube. These were centrifuged at 8,000 rpm for 1 min. Five hundred microliters (500 μ L) of Buffer

AW1, a buffer and reagent, were added to the DNeasy mini spin column and the spin column was placed in a new 2 mL collection tube. This was centrifuged at 8,000 rpm for 1 min. Five hundred microliters (500 μ L) of Buffer AW2, a buffer and reagent, were added to the DNeasy mini spin column and placed in a new 2 mL collection tube. This mixture was centrifuged at 14,000 rpm for 3 min. Two hundred microliters (200 μ L) of Buffer AE, an elution buffer, were pipetted into the DNeasy mini spin column and placed in a new 1.5 mL microcentrifuge tube. This mixture was left at room temperature for 1 min and then centrifuged at 8,000 rpm for 1 min. This resulted in the elution of DNA in Buffer AE. DNA concentrations were determined by using a NanoDrop ND-1000 UV-Vis Spectrophotometer (NanoDrop Technologies, Wilmington, Delaware). A concentration of 50ng/ μ L DNA was achieved by diluting DNA extraction product into new micro centrifuge tubes with sterile TE.

AFLP protocol followed methods modified from Vos et al. (1995), Phillips et al. (2007), and Kieschnick (2008) and was conducted at Tarleton State University, Stephenville, Texas. All digestion and polymerase chain reaction (PCR) reactions were achieved by using Techne Genius or TC-512 thermo-cyclers (Applied Biosystems, Foster City, California). For the restriction digest reaction, a master mix (11 parts diH₂O, 2 parts Buffer 3 [10X], 2 parts *AseI* Enzyme, at 10U/ μ L, and 1 part *EcoR1* Enzyme, at 20U/ μ L) was added with 4 μ L of 50ng/ μ L DNA into a 1.5 mL microcentrifuge tube for a total volume of 20 μ L. Samples were incubated at 37°C for 3 h.

Ligation adapters were prepared previously at a concentration of 50 μ M. The *AseI* and *EcoR1* adapters were added to a master mix (12 parts diH₂O, 4 parts 10X ligase buffer, 1.5 parts *AseI* adapter, 1.5 parts *EcoR1* adapter, and 1 part T4 DNA ligase).

Twenty microliters (20 μ L) of master mix were aliquoted into the restriction digest product. This mixture was incubated at 16°C for 10 h. At the end of the ligation reaction 160 μ L of 10mM Tris were added to each ligation product and mixed. All ligation products were amplified via PCR by using the following preselective primers: *EcoR1-C*: 5'-ACTGCGTACCAATTCC-3'; *AseI-T*: 5'GATCAGTCCTGAGRAATT-3'.

In a new microcentrifuge tube, 40 μ L of master mix (21 parts diH₂O, 10 parts Buffer [5X], 3 parts MgCl₂ [25 mM], 4 parts 10 mM dNTPs- A, T, C, G at 2.5 mM each, 0.75 parts preselective primer *EcoR1-C*, 0.75 parts preselective primer *AseI-T*, and 0.50 parts Taq DNA polymerase [5U/ μ L]) were added with 10 μ L diluted ligation product and mixed. The initial temperature of the preselective PCR amplification was 72°C. This was followed by 20 cycles of 94°C for 50 s, 56°C for 60 s, and 72°C for 120 s. At the end of the 20 cycles the reaction product was held at 4°C. Following the preselective amplification, 10 μ L of product was diluted into a new microcentrifuge tube with 180 μ L 10 mM Tris. This dilution was mixed and the remaining preselective PCR product was frozen for later use.

All possible *EcoR1/AseI* selective primer pairs were screened. Six selective primer pair combinations were chosen (Table 2) based on reaction clarity and number of polymorphisms. Pairs of selective primers include *EcoR1-CAC* with *AseI-TTT*, *AseI-TGA*, *AseI-TTC*, *AseI-TCT*, and *EcoR1-CAT* with *AseI-TAA*, *AseI-TTC*. Each selective primer pair was amplified by using the following procedure: in a new microcentrifuge, tube 20 μ L of selective master mix (9.65 parts diH₂O, 5 parts buffer [10X], 1.5 parts MgCl₂ [25 mM], 3 parts 10 mM dNTPs- A, T, C, G at 2.5 mM each, 0.3 parts selective *EcoR1* primer, 0.3 parts selective *AseI* primer, and 0.25 parts Taq

DNA polymerase [5U/ μ L]) were added with 5 μ L of diluted preselective product. The initial amplification conditions for the selective PCR amplification was one cycle of 94°C for 50 s, 65°C for 60 s, and 72°C for 120 s. Twelve remaining cycles lowered the annealing temperature 0.7°C per cycle, followed by 23 cycles of 94°C for 50 s, 56°C for 60 s, and 72°C for 120 s. At the end of the selective PCR amplification the product was held at 4°C. Samples were prepared for analysis by mixing 30 μ L sample loading solution for every 0.25 μ L 400 base pair size standard. In a 96-well sample loading tray 30 μ L of the above solution were aliquoted into each well. Then, 0.5 μ L of each selective PCR reaction product was added into each well. Wells were topped with mineral oil to avoid evaporation of the sample.

The *Eco*RI primers used in each selective reaction and size standard (GenomeLab, Beckman Coulter, Fullerton, California) were labeled fluorescently for detection by a Beckman-Coulter CEQ8000 Automated Genetic Analysis System (Beckman-Coulter, Inc., Fullerton, California). Software provided by Beckman-Coulter assigned fragment sizes in relation to size standards as the sample was drawn by capillary electrophoresis. Fragments that could be scored clearly as present or absent were included in the data set. Data sets were composed of 1s (present) and 0s (absent) at each fragment length for each individual. The resulting data matrix, which includes all used individuals and primer pairs, was used in all analyses (Appendix II).

Analyses

To visualize clusters of genetically similar individuals, a Principal Coordinate Analysis (PCO) was conducted by using the program GenAlEx, version 6, (Peakall and

Smouse 2006). The program STRUCTURE 2.2.3 (Pritchard et al. 2000) was used to estimate the number of genetic groups (K), to assign individuals to groups probabilistically, and to visualize genetic admixture of individuals (Q). STRUCTURE is a model-based clustering program that uses Markov chain Monte Carlo (MCMC), a Bayesian algorithm (Pritchard et al. 2000). The number of groups (K) was assigned before each test. Default parameters were used in conjunction with the admixture model. Choosing the admixture model allowed STRUCTURE to assume individuals could be of mixed ancestry and estimate the proportion of each individual's genotype that could be traced to each of the inferred groups (Kronforst et al. 2006). The burn-in value, and number of iterations for each test was set to 50,000. Because the program uses parameter values from the previous iteration and begins the Markov chain in a random configuration, 50,000 iterations were set as the burn-in value to reduce any effects that might be associated with the starting configuration (Pritchard et al. 2007). Twenty independent runs for K 1 to 6, totaling 120 runs, were executed. The best fit number of genetic groups (K) was selected based on values calculated from the posterior probabilities, $\Pr(K)$, calculated using the averaged estimated natural log probability of the data, $\ln P(K|X)$, (Pritchard et al. 2007), ΔK (Evanno et al. 2005), and observed trends of admixture (Q). The Nebraska sample, TK 54480, was excluded from this analysis because it was the only individual from this site and outside of the study extent. Program Paup 4.0b10 (Swofford 2000) with PAUPUp 1.0.3.1 Beta graphical interface (Calendini and Martin 2005) was used to create an unrooted tree by using the NeiLi restriction site distance setting. The tree was constructed by using neighbor joining.

RESULTS

Trapping and Samples

Trapping began 27 July 2007, ended 12 April 2009, and yielded 139 individuals. Four individuals were collected by other researchers and were brought to the Sternberg Museum of Natural History (Ellis County KK 1554; Meade County KK 1533; Morton County KK 1516 and 1517; Pratt County KK 1518). A tissue request was made to Texas Tech Museum for Nebraska samples considered to be *G. lutescens* (Lincoln County TK 54480). In all, 144 individuals were obtained from 25 sites within 21 Kansas counties (Fig. 3) and 1 Nebraska county (Appendix I) with an average of 5.76 specimens per site.

AFLP data were generated for 139 individuals from 25 sites (Appendix II). Individuals KK 1475, KK 1478, KK 1483, KK 1514, and KK 1540 from Rush, Ellis, Osborne, Sumner, and Rooks counties, respectively, did not produce usable AFLP results and were excluded. Six selective primers pairs were used which generated 467 DNA fragments between 70 and 393 base pairs. Three hundred of the 467 fragments (64%) were polymorphic, the remaining 167 fragments (36%) were monomorphic, being present in all individuals (Table 3).

Principle Coordinate Analysis

This analysis indicated geographic structure of the samples representing 4 clusters (Fig. 4). Axis 1 of the PCO explained 49.12% of the variation, axis 2 explained 19.20%, and axis 3 explained 11.88%. Cumulative variation explained by axis 1 and 2 of the PCO was 68.32%. Axis 1 essentially separated samples into 2 clusters, with the large cluster representing individuals from the southern and eastern portion of the state, and the

smaller cluster representing individuals from the northwestern portion of the state (Fig. 4). Axis 2 did not further separate the northwestern sample localities, but did separate the southern and eastern samples into loosely discernable groups.

The tightest cluster (NORTHWEST) were sites 1, 2, 3, 4, 5 (less KK 1490 and KK 1629); KK 1489 from site 6; sites 7, 8, 9, 10 (less KK 1474), and KK 1566 from site 15. The remaining sites created 3 clusters representing sites from the southwest, south central, and east. The top cluster (SOUTHWEST) included sites 14, 15 (less KK 1566), 18, and 19. The central cluster (SOUTH CENTRAL) included sites 16, KK 1499 from site 17, 21, 22, and 23. The lower cluster (EAST) included sites 6 (less KK 1489), 11, 12, 13, and 17 (less KK 1499). Characteristics of this PCO include site 20 intermediate to the top cluster (SOUTHWEST) and site 24 intermediate to the bottom cluster (EAST). An individual from Rush County, KK 1474, plotted between clusters composed of east northwest sites. Site 25, TK 54480, the single individual from Nebraska, plotted separately from all other clusters.

Program STRUCTURE

One hundred thirty-eight individuals were assigned to groups by using a Bayesian/MCMC simulation implemented in the program STRUCTURE from 20 independent runs of $K = 1$ to 6. The individual from site 25, TK 54480, was excluded from this analysis. Based on my results $K = 4$ was selected as the best-fit model for my data (Table 4). Formal methods for selecting K were not used because my data did not show a $P(K|X)$ nearest 1 within a single bell-curve. Pritchard et al. (2007) suggested that it is sensible to select K based on a model choice, when the true value of K is unknown,

by selecting the smallest value of K that captures the major structure in the data. This approach was selected because α was relatively constant throughout each MCMC and that the majority of individuals were assigned to one group or another with few individuals being strongly admixed. Also, $K = 4$ resulted in a low Markov chain standard error (Table 4). Number of genetic groups calculated by using ΔK was $K = 3$. However, my data likely contained hierarchical population structure. The program STRUCTURE and ΔK detected only the uppermost level of hierarchical structure and not all levels. It was probable that program STRUCTURE detected genetic groups at the species level but not the subspecies level. However, observed trends in Q supported 4 groups. With these factors considered, there was a strong indication of real population structure.

Graphical representations of individual group assignments and individual genetic composition are presented in (Figs. 5 and 6). The program STRUCTURE displayed the proportion of ancestry (Q) of each individual. When my data was sorted by site, individuals that were composed to different genetic composition could be identified by comparison to other individuals from that site. When my data was sorted by proportion of ancestry (Q), I detected where there were abrupt changes between genetic groups and where there were clinal transitions between genetic groups.

Sites and individuals assigned to the 4 groups, as determined by STRUCTURE, were as follows: group 1 (NORTHWEST) included sites 1, 2, 3, 4, 5 (less KK 1490), KK 1489 of site 6, 7, 8, 9, 10 (less KK 1474), KK 1566 of site 15, and KK 1514 of site 23; group 2 (EAST) included sites and individuals from KK 1490 of site 5, 6 (less KK 1489), KK 1474 of site 10, 11, 12, 13, 17 (less KK 1499), and site 24; group 3 (SOUTHWEST)

included sites and individuals from 14, 15 (less KK 1566), 18, and 19; group 4 (SOUTH CENTRAL) included sites and individuals from 16, KK 1499 of site 17, 20, 21, 22, 23. Twelve individuals showed levels of admixture. These individuals included KK 1474, site 10, with 40% admixture with group 1 (NORTHWEST), KK 1625, site 12, with <15% admixture with group 4 (SOUTH CENTRAL), KK 1559, site 14, with <10% admixture with group 1 (NORTHWEST), KK 1533, site 20, with 15% admixture with group 3 (SOUTHWEST), KK 1590, site 15, with <25% admixture with group 1 (NORTHWEST), KK 1499, site 17, with 15% admixture with group 2 (EAST), and all individuals of site 24, KK 1502 – 1508, with 10–50 % admixture with group 2 (EAST).

Phylogram

Results from PAUP supported 4 major clades (Fig. 7). The clade off the longest branch (NORTHWEST) is composed of sites 1, 2, 4, 5, 6, 7, 8, 9, and 10. A second clade (SOUTHWEST) was composed of sites 14, 15, 18, and 19. A third main branch was composed of 2 major clades. The terminal clade off of this branch (EAST) included the individuals KK 1490, KK 1629 of site 5, sites 6, 11, 12, 13, and 17. All individuals from site 24 separated this clade from the clade (SOUTH CENTRAL) containing site 16, individual KK 1499 of site 17, 21, 22, and 23. Adjacent to this clade were all the individuals of site 20. Two individuals, KK 1474 and TK 54480, were on 2 separate branches.

Analysis comparison

The PCO, STRUCTURE analysis, and the NeiLi unrooted tree supported 4 taxa in Kansas. The PCO and NeiLi unrooted tree both placed the Nebraska sample outside of all other clusters or clades. All analyses showed some individuals as being intermediate, admixed, or between groups but overall have strong consensus placing individuals within groups or clusters (Table 5). An individual plotted as an intermediate in all analyses is KK 1474 from site 10. STRUCTURE identified all individuals from site 24 as intermediates, except KK 1504.

DISCUSSION

The taxonomy of *Geomys* has been in flux for over a century. For example, the only species of *Geomys* to retain its original taxonomic status since its description is *G. personatus* (Mauk et al. 1999). The phylogeography of *Geomys* probably has been influenced by serial glaciations (Russell 1968), desertification, the deposition of soils by wind and water, and the dynamics of population refugia. Pocket gophers select certain soil types (Best 1973; Hoffman et al. 2007; Moulton et al. 1983). This influences distribution and dispersal in the landscape. Therefore, large areas of unsuitable soil might act as barriers to gene flow. Land use practices might influence distributions and gene flow of *Geomys* (Hoffman et al. 2007). Working hardened soils into agricultural fields and moving earth for raised roadways could allow for new habitat and dispersal corridors or alter existing habitat. Also, direct management of pocket gophers, such as bounty systems, trapping, poisoning, and other eradication efforts (Downhower and Hall 1966;

Scheffer 1910) might reduce gene flow, heterozygosity, effective population size, and cause local extinctions, (Hoffman et al. 2007).

From the 1940s through the 1980s researchers attempted to clarify the distribution and identity of Kansas taxa by using a variety of methods. There has been no consensus. Since 2000, genetic methods have been applied to the study of *Geomys* (Chambers et al. 2009; Elrod et al. 2000; Jolley et al. 2000; and Sudman et al. 2006). However, these studies lacked the appropriate resolution to describe species distributions and did not include all taxa of *Geomys*, which is needed to develop an accurate phylogeny.

Villa-R and Hall (1947), Hall (1981), and Elrod et al. (2000) suggested that there were 5 taxa within Kansas. Hart (1978) and Sudman et al. (1987) suggested 4 taxa. My analysis of nuclear genomic data also supported the existence of 4 taxa. These data presented herein provided useful information related to *Geomys* in Kansas including the number of taxa in Kansas; geographic extent of these taxa; provided a relative measure of genetic isolation among these taxa; and gave some insight into characteristics of the adjoining boundaries of these taxa (Fig. 8).

Population and taxonomic assessments

The taxon described as *halli* (Sudman et al. 1987) is supported in my study as a species. A single hybrid was documented from site 10, KK 1474, Rush County. Along its eastern boundary, in Osborne County, this taxon was sympatric with eastern Kansas taxon (*G. b. majusculus*). The area north of the Arkansas River is characterized by a hard pan soil type, and is also occupied by *Cratogeomys castanops* (Hoffman et al. 2007). This area might be an effective dispersal barrier. However, in Finney and Scott counties

there is an area of suitable soil connecting the range of *G. jugossicularis* to the range of *halli*. Site 15, Finney County, contained an individual of *halli*, KK 1566, which was sympatric with Kansas' southwestern taxon (*G. b. jugossicularis*). The eastern range limit of *Geomys halli* was Osborne and Smith counties and extended south to Rush County. The southern border of *halli* was suggested to be north of the Arkansas River, from northern Hamilton County east through southern Ness County and into Rush County (Fig. 8). Allopatric distributions with zones of sympatry, limited gene flow, and the 1 documented hybrid, supported Hendricksen's (1973) hypothesis that this taxon is experiencing secondary contact with the eastern taxon (*G. b. majusculus*). These data also suggested that *halli* is also in secondary contact with the southwestern taxon (*G. jugossicularis*).

Geomys in southwestern Kansas have long been considered to be *G. jugossicularis* (Villa-R and Hall 1947). This suggestions has been supported by other researchers. Recent research (Chambers et al. 2009; Genoways et al. 2008) has suggested *halli* is a subspecies of *G. jugossicularis*. My data suggested individuals within this region were *G. jugossicularis* with little admixture (<10%; Meade County, site 20) and a limited area of sympatry with *G. halli*. I suggested the range of *G. jugossicularis* in Kansas as to occur in the southwestern region, south of the range of *C. castanops*. Because of admixture in individuals from Meade County (site 20) my study suggested that the eastern edge of the range of *G. jugossicularis* was located in western Meade County. Considering geographic features, the range of *G. jugossicularis* likely remained north of the Red Hills region, possibly northeast into Ford County.

The taxon *G. b. majusculus* has been documented in Nebraska and south through eastern Kansas. This is consistent with my data. Genetic composition of site 11 (Russell County) was entirely eastern taxon. However, site 12 (Saline County) exhibited some admixing while 1 individual in site 17 (Greenwood County) was genetically similar with the south central taxon. Site 24 (Cowley County) was composed entirely of intergrades with the south central taxon. My research suggested a broad zone of introgression occurred from Barton County southeast to Greenwood and Cowley counties, including Butler County (Fig. 8). The main physiographic feature of this contact zone is the Arkansas River floodplain. This area of introgression potentially extends south of Cowley County into Oklahoma. The southern border of *G. b. majusculus* was shared with the south central taxon. The range of *Geomys b. majusculus* was east of the sympatric zone with *G. halli* eastward to the boundary of *Geomys*, an area from Johnson County southwest through Chautauqua County (Fig. 8). The area south and east of these counties contained no reported records of *Geomys*, which was likely the result of unsuitable soil types in the Ozark Mountain foothills.

The fourth taxon supported by my research occurred in south central Kansas. There are 2 potential epithets, *industrius* or *major*, because the extent of this taxon's range extended beyond Kansas. Genetic admixture occurred across a large area of contact with *G. b. majusculus*. Therefore, these data supported these individuals as a subspecies under *G. bursarius*. Its western extent was in Meade County and north to Pawnee County. Its northeastern boundary was shared with *G. b. majusculus*. In Kansas, this taxon's southeastern edge was Sumner County (site 23). Its range was likely the Red Hills region, and the area north to the Arkansas River. The Red Hills region in Kansas is

east of Meade County and the southwestern area of Sumner County. If the south central taxon inhabits the Red Hills region it likely followed that pattern into Oklahoma.

Geomys lutescens is supported by my research. Although only a single sample was included from *G. lutescens*, 2 analyses suggested little genetic similarity with Kansas taxa. The range of this taxon is described in Genoways et al. (2008) and Sudman et al. (1987).

Conclusions

The purpose of my study was to determine if there were any genetically distinct taxa of *Geomys* in Kansas and, if there were, to describe where they occurred and provide an indication of the level of genetic isolation of these taxa. My data suggested the presence of 4 taxa. There are potentially 3 species of *Geomys* in Kansas: *Geomys halli*, *Geomys jugossicularis*, and *Geomys bursarius*; *G. bursarius* in Kansas consists of *G. b. majusculus* and *G. b. industrius/major*. However, without knowing how these taxa extend and interact into Colorado, New Mexico, Oklahoma, and eastern Nebraska only a limited inference of taxonomic rank is possible. In Kansas there are 4 areas of contact and genetic exchange, as well as 2 areas that might function as abiotic barriers. Current understanding of *Geomys* would benefit from further characterization of these contact zones, investigation into the possible abiotic barrier north of the Arkansas River, and thorough sampling of *Geomys* in Colorado, New Mexico, and Oklahoma.

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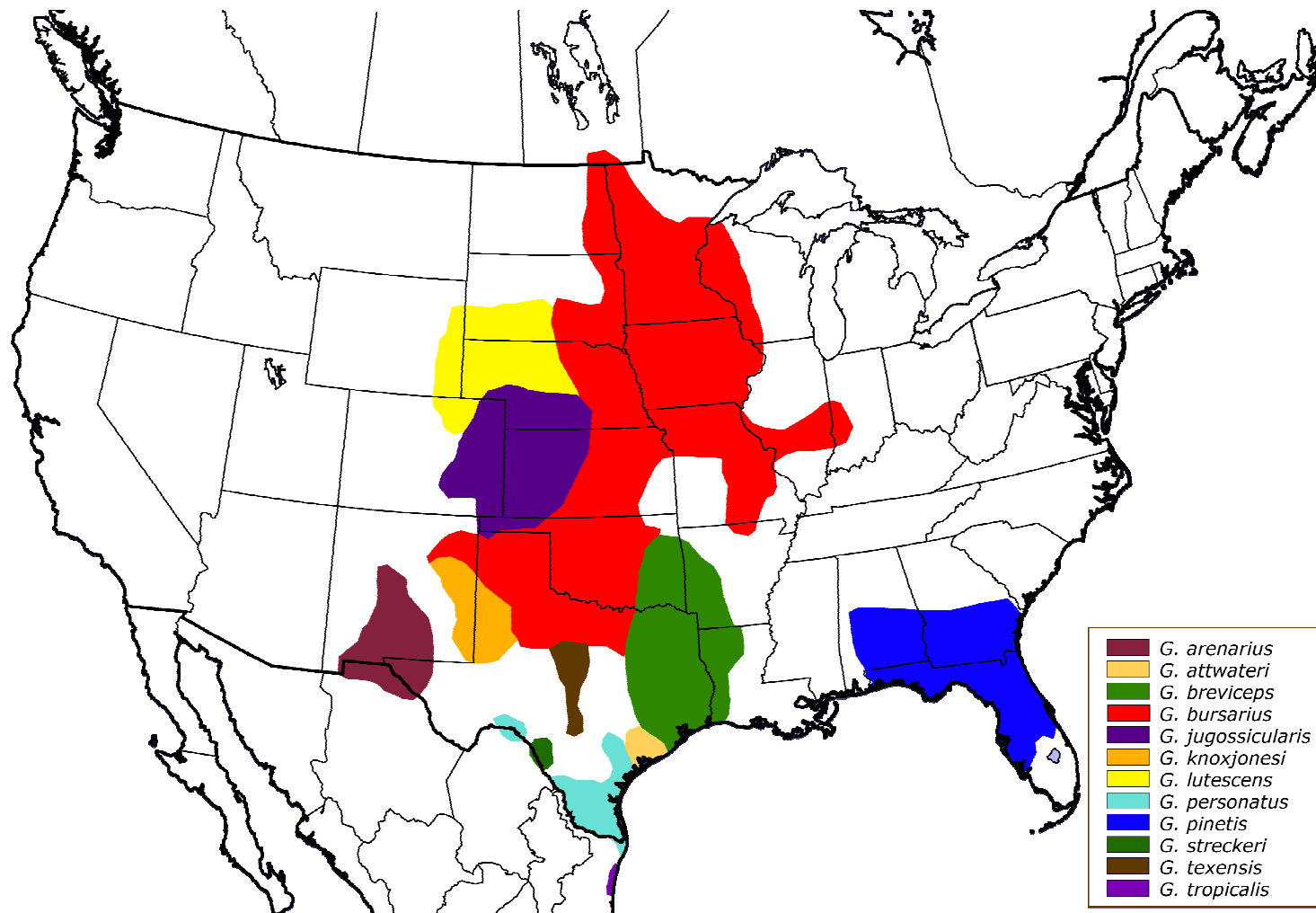


Figure 1.— Range of the species of pocket gopher (genus *Geomys*). Each color represents 1 of 12 currently recognized species of *Geomys*. Modified from Chambers et al. (2009).

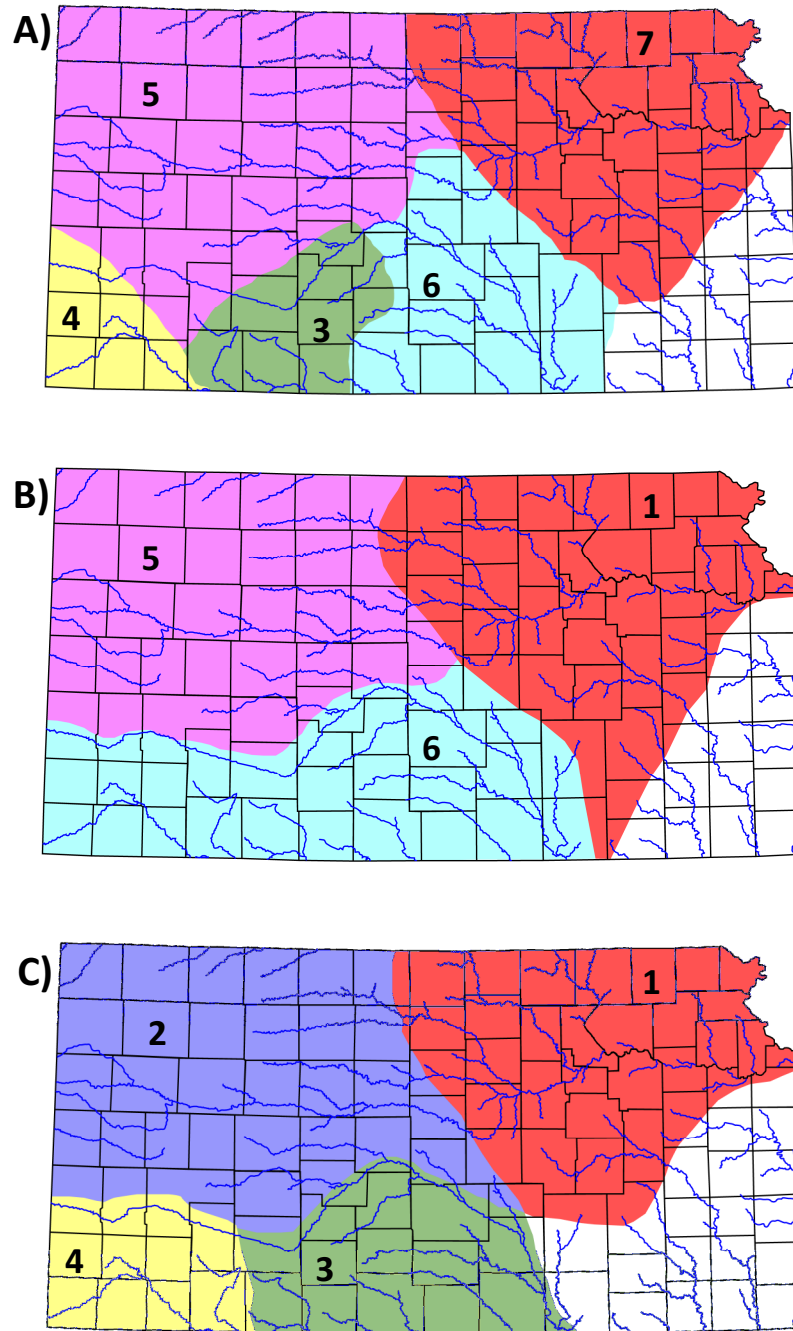


Figure 2.— Hypothesized distributions of taxa within *Geomys* in Kansas modified from Burns et al. (1985), Sudman et al. (1987), and Villa-R and Hall (1947). A) Villa-R and Hall (1947); B) Heaney and Timm (1983) from Burns et al. (1985); C) Sudman et al. (1987). Numbers represent taxa: 1) *bursarius*; 2) *halli*; 3) *industrius*; 4) *jugossicularis*; 5) *lutescens*; 6) *major*; 7) *majusculus*.

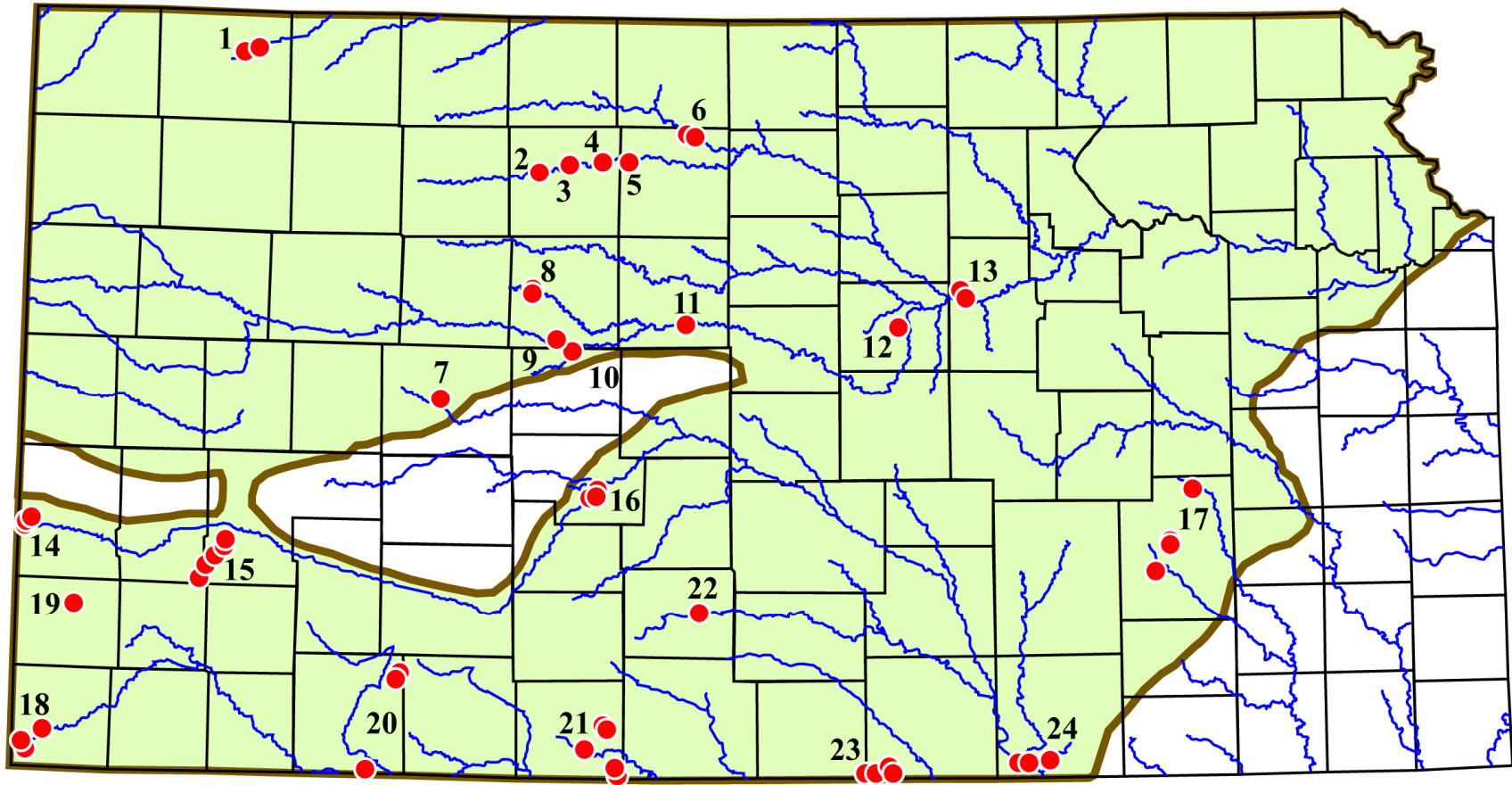


Figure 3.— Locations of Kansas samples, labeled by site, included in my study with range of *Geomys*. Range modified from Hall (1981) and Hoffman et al. (2007)

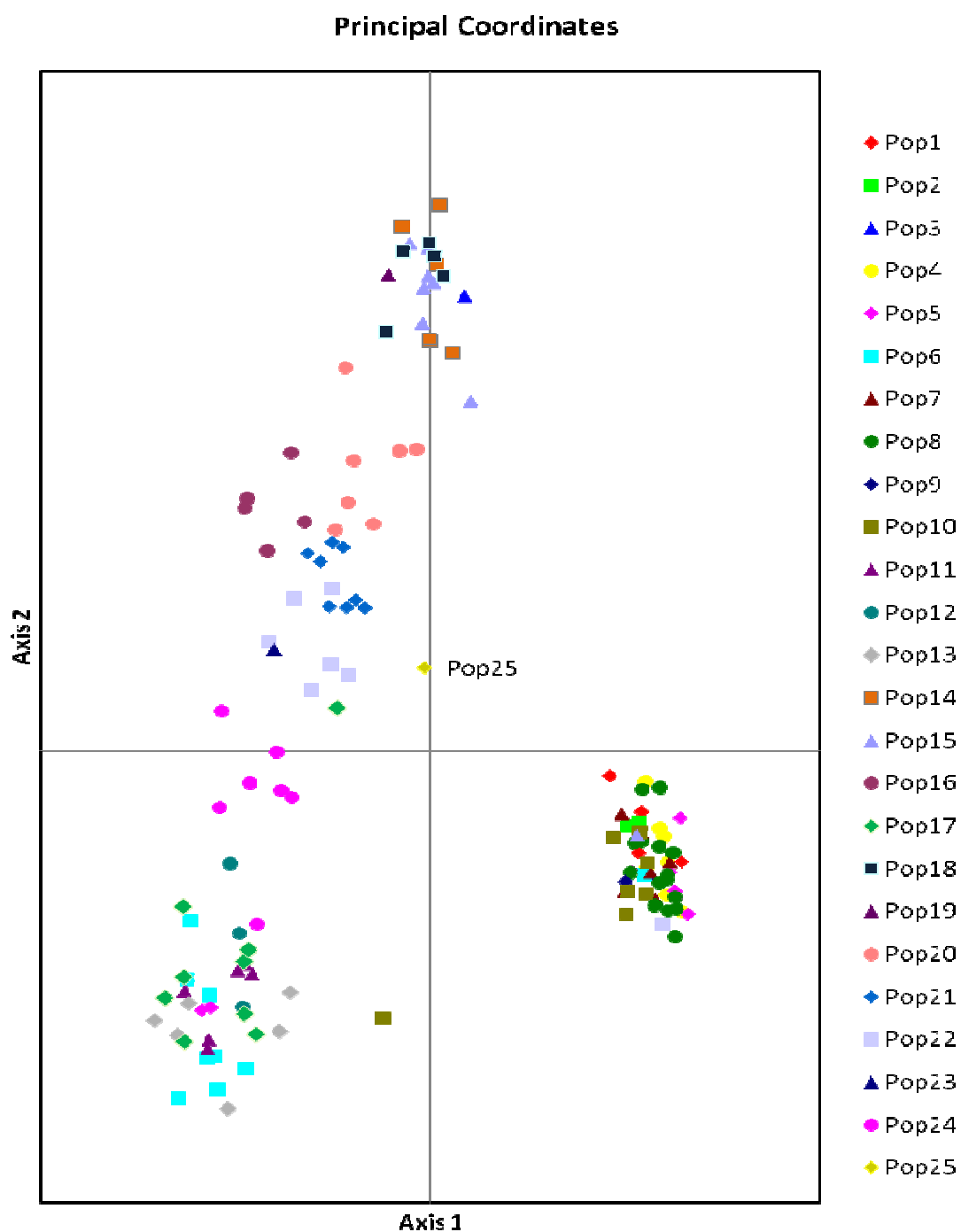


Figure 4.— Principle coordinate analysis (Axis 1 versus Axis 2) showing clustering of genetically similar individuals. Each symbol represents an individual. Site numbers refer to those in text. Axis 1 explained 49.12% and Axis 2 explained 19.20% of the variations in the data.

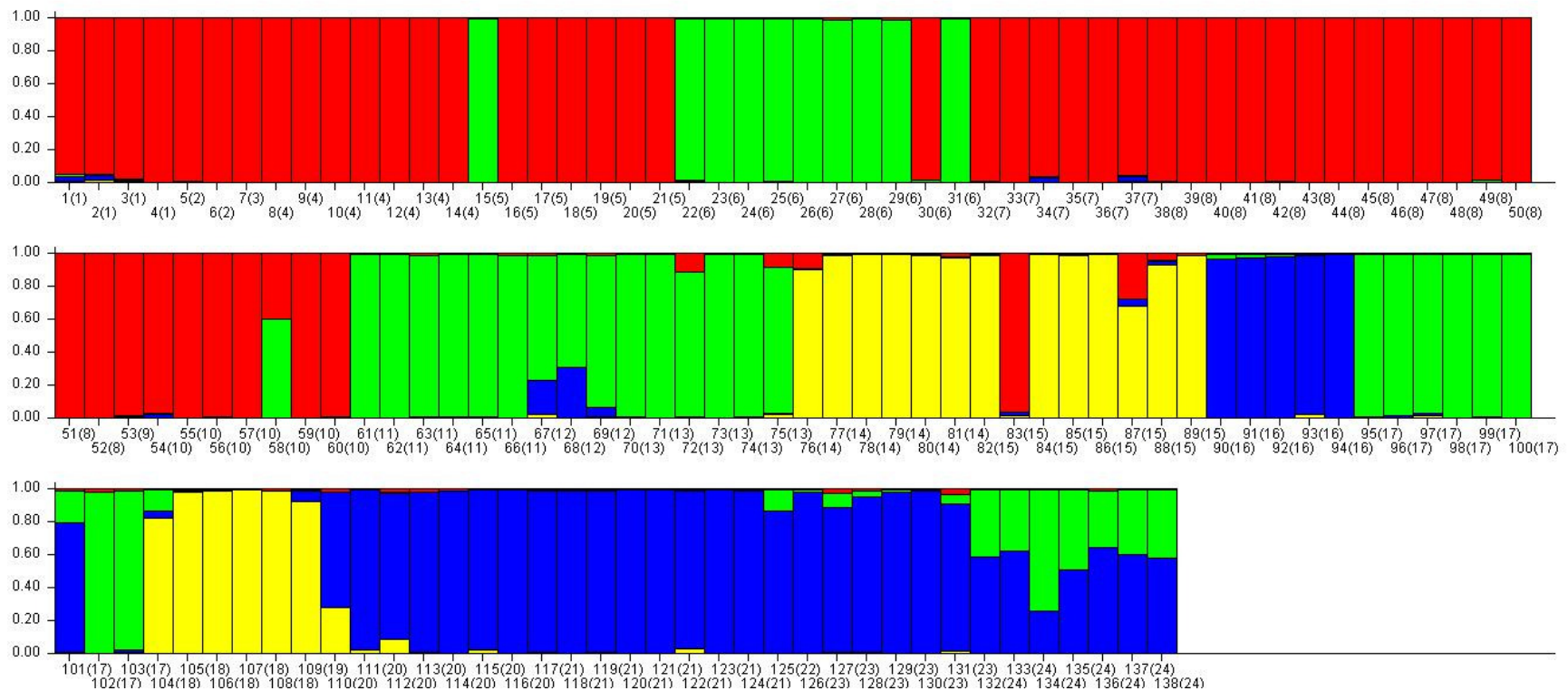


Figure 5.— Graphical results from program STRUCTURE showing individual genetic composition and population assignment. Each vertical bar symbolizes an individual’s genotypic composition by a color representing 1 of the 4 populations defined by STRUCTURE: Red = northwestern population, (*halli*); Green = eastern population (*majusculus*); Yellow = southwestern population (*jugossicularis*); Blue = south central population (*industrius* or *major*). The y-axis displayed the proportion of similarity (Q) of each individual. Under each vertical bar is an individual number and its site designation in parenthesis.

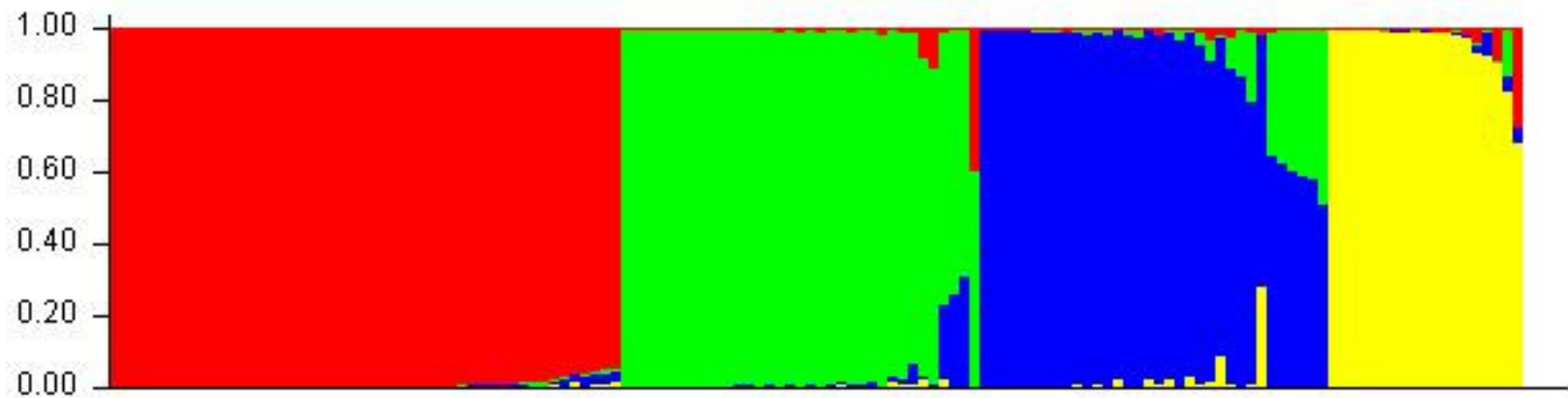


Figure 6.— Compressed graphical results from program STRUSTRUCTURE showing individual genetic composition and population assignment sorted by similarity (Q). Each vertical bar symbolizes an individual's genotypic composition by a color representing 1 of the 4 populations defined by STRUSTRUCTURE: Red = northwestern population, (*halli*); Green = eastern population (*majusculus*); Yellow = southwestern population (*jugossicularis*); Blue = south central population (*industrius* or *major*). The y-axis displayed the proportion of similarity (Q) of each individual.

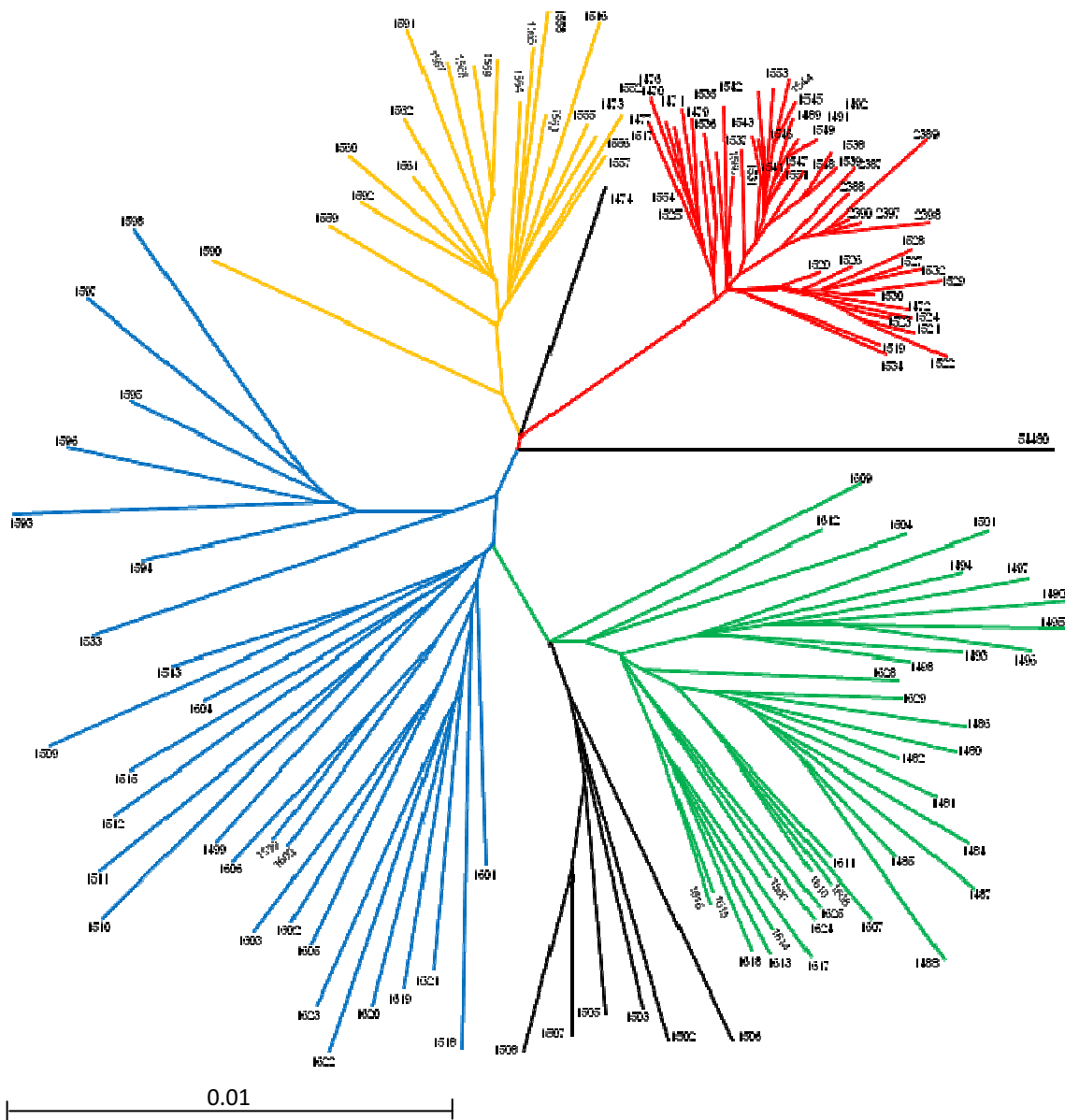


Figure 7.— Unrooted phylogram of Kansas *Geomys* based on NeiLi distance neighbor joining developed in program PAUP displaying individual KK numbers. Colors group clades by population: Red = northwestern population, (*halli*); Green = eastern population (*majusculus*); Yellow = southwestern population (*jugossicularis*); Blue = south central population (*industrius* or *major*); Black = Nebraska sample (TK 54480), hybrid (KK1474), or intergrades (Site 24). The documented hybrid (KK 1474) and the Nebraska, *G. luteceus* (TK 54480) were on separate terminal braches.

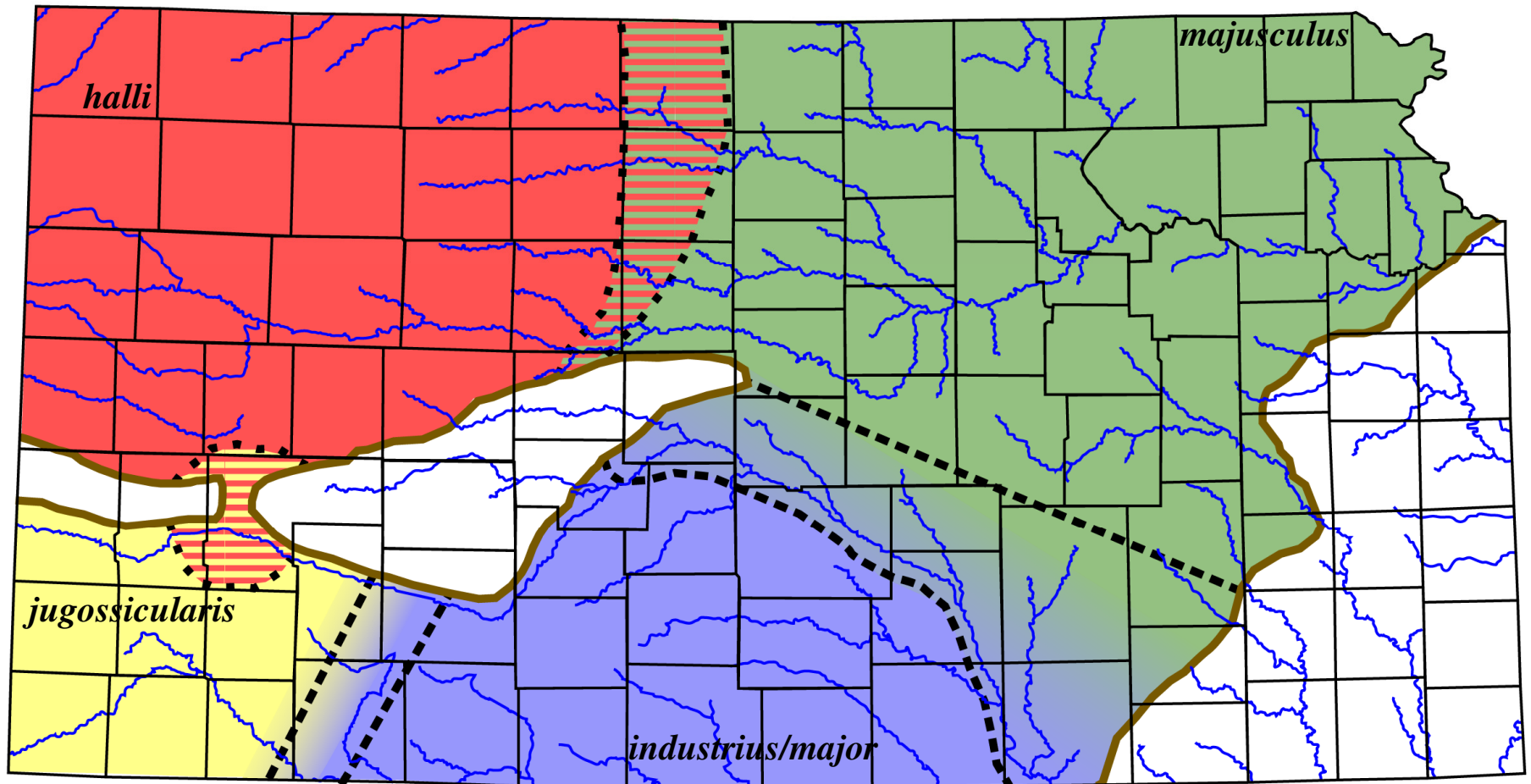


Figure 8.— Suggested distribution and taxa of Kansas supported by results from my study. Areas with gradated color and dashed boundaries are zones of intergradations. Areas with hatched colors are zones of sympatry.

Table 1.— Taxonomic history of *Geomys* in Kansas. Number of species and subspecies considered within Kansas; name of species, taxa considered as subspecies, and principle methods mentioned in literature. Symbols: x's mark taxa included within Kansas; o's mark taxa not mentioned or included. Baird (1857) and Merriam (1890, 1895) cited from Villa and Hall (1947). Authorities 2000 to present are broad scale research not focusing on Kansas taxa.

Authority	Number of Species	Number of Subspecies	Species	Taxa Referred to as Subspecies						Method	
				<i>bursarius</i>	<i>majusculus</i>	<i>major</i>	<i>jugossicularis</i>	<i>industrius</i>	<i>lutescens</i>		<i>halli</i>
Baird 1857	2		<i>bursarius</i> , <i>breviceps</i>								
Merriam 1890	1	2	<i>bursarius</i>	x					x		
Merriam 1895	2		<i>bursarius</i> , <i>lutescens</i>	x					x		
Villa-R and Hall 1947	1	5	<i>bursarius</i>		x	x	x	x	x		Cranial
Russell 1968	1		<i>bursarius</i>								Fossil cranial
Hendricksen 1972	1	2	<i>bursarius</i>		x				x		Cranial, external, pelage and soil color
Hart 1978	1	4	<i>bursarius</i>			x	x	x	x		Karyotypic
Hall 1981	1	5	<i>bursarius</i>		x	x	x	x	x		
Heaney and Timm 1983	2	3	<i>bursarius</i> , <i>lutescens</i>	x		x				x	Cranial
Burns et al. 1985	1	3	<i>bursarius</i>	x		x				x	Cranial, external, bacular, karyotypic, electrophoretic
Sudman et al. 1987	1	4	<i>bursarius</i>	x			x	x		x	Cranial, external, karyotypic, electrophoretic
Jolley et al. 2000	2		<i>bursarius</i> , <i>lutescens</i>		x	x	o	o		x	Mitochondrial 12S rRNA
Elrod et al. 2000	1	5	<i>bursarius</i>		x	x	x	x		x	mtDNA cytochrome- <i>b</i>
Sudman et al. 2006	2		<i>bursarius</i> , <i>lutescens</i>		x	x	x	x		x	mtDNA cytochrome- <i>b</i>
Genoways et al. 2008	2		<i>bursarius</i> , <i>jugossicularis</i>		x	o	x	o		x	Karyotypic, mtDNA cytochrome- <i>b</i> , <i>Rpb3</i> gene, cranial, pelage color
Chambers et al. 2009	2		<i>bursarius</i> , <i>jugossicularis</i>				x	o		x	Mitochondrial 12S rRNA, <i>Rpb3</i> gene, mtDNA cytochrome- <i>b</i>

Table 2.— Selective primers used during AFLP selective polymerase chain reactions. Asterisks indicate primers that were labeled fluorescently for detection by capillary electrophoresis.

Primers	Sequence
<i>EcoR1</i> -CAT*	5'-ACTGCGTACCAATTCCAT-3'
<i>EcoR1</i> -CAC*	5'-ACTGCGTACCAATTCCAC-3'
<i>AseI</i> -TAA	5'GATCAGTCCTGAGRAATTAA-3'
<i>AseI</i> -TCT	5'GATCAGTCCTGAGRAATTCT-3'
<i>AseI</i> -TGA	5'GATCAGTCCTGAGRAATTGA-3'
<i>AseI</i> -TTC	5'GATCAGTCCTGAGRAATTTC-3'
<i>AseI</i> -TTT	5'GATCAGTCCTGAGRAATTTT-3'

Table 3.— Six selective primers used with number of loci scored, number and proportion of polymorphic and monomorphic loci, including range of fragment lengths for each selective primer pair.

Primer Pair	Number of loci scored	Number of polymorphic loci	Number of monomorphic loci	Range of fragment lengths
<i>EcoR1</i> -CAC/ <i>Ase1</i> -TCT	60	44 (73%)	16 (27%)	82-364
<i>EcoR1</i> -CAC/ <i>Ase1</i> -TGA	50	32 (64%)	18 (36%)	86-393
<i>EcoR1</i> -CAC/ <i>Ase1</i> -TTC	67	48 (72%)	19 (28%)	74-313
<i>EcoR1</i> -CAC/ <i>Ase1</i> -TTT	90	59 (66%)	31 (34%)	70-388
<i>EcoR1</i> -CAT/ <i>Ase1</i> -TAA	99	59 (61%)	40 (40%)	72-359
<i>EcoR1</i> -CAT/ <i>Ase1</i> -TTC	101	58 (57%)	43 (43%)	70-374
Total	467	300 (64%)	167 (36%)	70-393

Table 4.— Root Inference of populations based on the $P(K|X)$ as calculated from the Estimated ln Probability of Data ($\ln P(K|X)$) by using program STRUCTURE. Mean $\ln P(K|X)$, Markov chain standard error, mean α were derived from 20 independent runs of 100,000 iterations.

K value	Mean $\ln P(K X)$	$P(K X)$	MCSE	Mean α
1	-102982.1	0	0.088	-
2	-101024.48	2.5299E-214	0.134	0.07
3	-100649.25	2.30898E-51	0.199	0.04
4	-100542.975	3.2966E-05	0.187	0.03
5	-100562.195	1.48227E-13	0.186	0.03
6	-100532.655	0.999967034	0.180	0.03

Table 5.— Selected individuals showing percent admixture and consensus of individual assignment to populations (NW, E, SW, SC, or I (Intermediate)) among analyses (PCO, STRUCTURE, unrooted phylogram).

Individual	Capture Site	Population assignment			~% admixed	Admixed with
		PCO	STRUCTURE	Phylogram		
KK 1490	5	E	E	E	0	
KK 1629	5	E	E	E	0	
KK 1489	6	NW	NW	NW	0	
KK 1474	10	I	E	I	40	NW
KK 1625	12	E	E	E	15	SC
KK 1566	15	NW	NW	NW	0	
KK 1499	17	SC	SC	SC	15	E
KK 1533	20	I	SC	I	15	SW
KK 1593	20	I	SC	I	0	
KK 1594	20	I	SC	I	10	SW
KK 1595	20	I	SC	I	0	
KK 1596	20	I	SC	I	0	
KK 1597	20	I	SC	I	0	
KK 1598	20	I	SC	I	0	
KK 1502	24	I	I	I	50	E/SC
KK 1503	24	I	I	I	50	E/SC
KK 1504	24	I	E	I	10	SC
KK 1505	24	I	E	I	30	SC
KK 1506	24	I	I	I	50	E/SC
KK 1507	24	I	E	I	50	E/SC
KK 1508	24	I	E	I	40	SC

APPENDIX I

Specimens examined

Appendix 1.—All Kansas specimens of the plains pocket gopher (*Geomys*) collected during the course of my study listed with their unique tissue number. Specimens were housed in the Sternberg Museum of Natural History, Fort Hays State University (MHP). Localities were arranged alphabetically by county and reference locations, then by latitude (north to south) with respect to reference location and by longitude (west to east) at each particular latitude.

Comanche: 7.5 mi N, 8.3 mi W Aetna, (37.19344 N, 99.11512 W, KK1602); 2.4 mi S, 5.9 mi W Aetna, (37.04895 N, 99.06978 W, KK1599); 2.4 mi S, 5.9 mi W Aetna, (37.04888 N, 99.06985 W, KK1606); 3.9 mi S, 5.3 mi W Aetna, (37.02713 N, 99.05918 W, KK1600); 5.1 mi S, 4.8 mi W Aetna, (37.00843 N, 99.05106 W, KK1601); 4.3 mi S, 11.5 mi E Coldwater, (37.207 N, 99.12452 W, KK1603); 4.65 mi S, 11.25 mi E Coldwater, (37.20218 N, 99.12319 W, KK1604); 9.3 mi S, 6.75 mi E Coldwater, (37.13573 N, 99.20389 W, KK1605). **Cowley:** 0.45 mi N, 2.8 mi E Arkansas City, (37.06875 N, 96.8649 W, KK1505); 1.85 mi E Arkansas City, (37.06083 N, 97.00442 W, KK1507); 0.1 mi S, 1.85 mi E Arkansas City, (37.06027 N, 97.00455 W, KK1508); 0.15 mi S, 1.85 mi E Arkansas City, (37.05974 N, 97.00478 W, KK1506); 1.3 mi S, 3.9 mi E Arkansas City, (37.05668 N, 96.96838 W, KK1504); 1.3 mi S, 3.9 mi E Arkansas City, (37.05647 N, 96.96713 W, KK1503); 1.3 mi S, 3.9 mi E Arkansas City, (37.05642 N, 96.96719 W, KK1502). **Dickinson:** 1 1/3 mi N, 4.47 mi W Abilene, (38.93674 N, 97.3157 W, KK1612); 1/2 mi N, 4.53 mi W Abilene, (38.92505 N, 97.29821 W, KK1609); 0.1 mi N, 4.51 mi W Abilene, (38.91954 N, 97.29771 W, KK1610); 4.45 mi W Abilene, (38.91785 N, 97.2964 W, KK1611); 4.48 mi W Abilene, (38.91812 N, 97.297 W, KK1607); 4.47 mi W Abilene, (38.91839 N, 97.29665 W, KK1608). **Ellis:** 0.5 mi S, 4.1 mi E Ellis, (38.93194 N, 99.48382 W, KK1526); 0.5 mi S, 4.1 mi E Ellis, (38.93189 N, 99.4819 W, KK1523); 0.5 mi S, 4.1 mi E Ellis, (38.93153 N, 99.48149 W, KK1532); 0.5 mi S, 4.1 mi E Ellis, (38.93143 N, 99.48394 W, KK1521); 0.5 mi S, 4.1 mi E Ellis, (38.93122 N, 99.4815 W, KK1531); 0.5 mi S, 4.1 mi E Ellis, (38.9311 N, 99.4815 W, KK1530); 0.5 mi S, 4.1 mi E Ellis, (38.93087 N, 99.48158 W, KK1522); 0.5 mi S, 4.1 mi E Ellis, (38.93081 N, 99.4815 W, KK1529); 0.5 mi S, 4.1 mi E Ellis, (38.93066 N, 99.48195 W, KK1528); 0.5 mi S, 4.1 mi E Ellis, (38.9305 N, 99.48198 W, KK1527); 0.5 mi S, 4.1 mi E Ellis, (38.92988 N, 99.48373 W, KK1520); 0.5 mi S, 4.1 mi E Ellis, (38.92746 N, 99.4837 W, KK1524); 1 mi S, 4 mi E Ellis, (38.92334 N, 99.48981 W, KK1479); 1 mi S, 4 mi E Ellis, (38.9228 N, 99.48833 W, KK1478); 1 mi S, 4 mi E Ellis, (38.92262 N, 99.48714 W, KK1525); 1 mi S, 4 mi E Ellis, (38.92197 N, 99.48556 W, KK1519); 1.3 mi N, 2.3 mi W Schoenchen, (38.732 N, 99.3745 W, KK1554). **Finney:** 1.4 mi S, 0.2 mi W Holcomb, (37.96622 N, 100.99328 W, KK1592); 4.45 mi S, 0.2 mi E Holcomb, (37.92188 N, 100.98607 W, KK1591); 4.8 mi S, 0.2 mi W Holcomb, (37.91684 N, 100.99431 W, KK1568); 4.8 mi S, 0.2 mi W Holcomb, (37.91665 N, 100.99411 W, KK1569); 4.8 mi S Holcomb, (37.91687 N, 100.99269 W, KK1590); 8.15 mi S, 1.32 mi W Holcomb, (37.8678 N, 101.01115 W, KK1567); 11 mi S, 4.5 mi W Holcomb, (37.8295 N, 101.07941 W, KK1566). **Greenwood:** Eureka Lake, 5.5 mi N, 1 mi W Eureka, (37.90506 N, 96.30112 W, KK1501); Eureka Lake, 5.5 mi N, 1.3 mi W Eureka, (37.90433 N, 96.31272 W, KK1499); Eureka Lake, 4.75 mi N Eureka, (37.8929 N, 96.29004 W, KK1494); Eureka Lake, 4.75 mi N Eureka, (37.89239 N, 96.28929 W, KK1495); Eureka Lake, 4.75 mi N Eureka, (37.89225 N, 96.28921 W, KK1496); Eureka Lake, 4.75 mi N Eureka, (37.89173 N, 96.28919 W, KK1497); 0.9 mi S, 3.6 mi W Eureka, (37.8103 N, 96.35497 W, KK1498); Madison City Lake, 1.8 mi S, 0.6 mi W Madison, (38.1099 N, 96.15067 W, KK1500); Madison City Lake, 1.8 mi S, 0.6 mi W Madison, (38.10894 N, 96.14758 W, KK1493). **Hamilton:** 1 mi S, 0.5 mi E Coolidge, (38.02712 N, 101.999 W, KK1559); 1.3 mi S, 0.3 mi W Coolidge, (38.02304 N, 102.01496 W, KK1560); 1.3 mi S, 0.5 mi W Coolidge, (38.02272 N, 102.01606 W, KK1561); 1.33 mi S, 0.5 mi W Coolidge, (38.02267 N, 102.01649 W, KK1562); 2.4 mi S, 0.5 mi W Coolidge, (38.00697 N, 102.01821 W, KK1563); 2.9 mi S, 0.5 mi W Coolidge, (37.99968 N, 102.01817 W, KK1564). **Kearney:** 12.6 mi N, 12.48 mi E Ulysses, (37.76407 N, 101.12605 W, KK1565). **Meade:** 0.8 mi N, 3.8 mi E Fowler, (37.39738 N, 100.12593 W, KK1598); 0.45 mi N, 3.8 mi E Fowler, (37.39275 N, 100.12585 W, KK1595); 2.5 mi E Fowler, (37.38714 N, 100.14999 W, KK1593); 3.02 mi E Fowler, (37.38711 N, 100.14048 W, KK1597); 3.17 mi E Fowler, (37.38715 N, 100.1377 W, KK1594); 3.25 mi E Fowler, (37.38714 N, 100.13612 W, KK1596); 18 mi S, 1.6 mi E Meade, (37.01528 N, 100.30686 W, KK1533). **Morton:** 8.25 mi N, 0.25 mi W Elkart, (37.12729 N,

101.90255 W, KK1517); 4 mi N, 6 mi W Elkhart, (37.06654 N, 102.00587 W, KK1516); 3.3 mi N, 5.8 mi W Elkhart, (37.05611 N, 101.99475 W, KK1557); 3.1 mi N, 5.7 mi W Elkhart, (37.0528 N, 101.99328 W, KK1556); 3.1 mi N, 5.7 mi W Elkhart, (37.05278 N, 101.99321 W, KK1555). **Ness:** 5.75 mi N, 4.6 mi W Ness City, (38.53631 N, 99.99252, KK 2388), 5.75 mi N, 4.6 mi W Ness City, (38.53642 N, 99.99292, KK 2389), 5.75 mi N, 4.6 mi W Ness City, (38.53596 N, 99.99246, KK 2390), 5.75 mi N, 4.6 mi W Ness City, (38.53567 N, 99.99227, KK 2397), 5.75 mi N, 4.6 mi W Ness City, (38.53644 N, 99.99353, KK 2398), 2.1 mi N, 4 mi W Ness City, (38.4831 N, 99.98531 W, KK 2387). **Osborne:** 1.1 mi S, 3.3 mi W Alton, (39.45414 N, 99.00751 W, KK1491); 1.1 mi S, 3.3 mi W Alton, (39.45374 N, 99.00745 W, KK1492); 1.3 mi S, 3.3 mi W Alton, (39.4521 N, 99.01141 W, KK1490); 1.15 mi S, 3.15 mi W Alton, (39.45393 N, 99.00846 W, KK1551); 1.15 mi S, 3.15 mi W Alton, (39.45391 N, 99.00815 W, KK1552); 1.15 mi S, 3.15 mi W Alton, (39.45382 N, 99.00487 W, KK1553); 1.15 mi S, 3.15 mi W Alton, (39.45298 N, 99.00864 W, KK1549); 1.5 mi S, 1.75 mi E Portis, (39.5426 N, 98.66364 W, KK1487); 1.5 mi S, 1.75 mi E Portis, (39.54156 N, 98.6641 W, KK1486); 1.5 mi S, 1.75 mi E Portis, (39.54153 N, 98.66418 W, KK1480); 1.5 mi S, 1.75 mi E Portis, (39.54152 N, 98.66405 W, KK1481); 1.5 mi S, 1.75 mi E Portis, (39.54151 N, 98.66306 W, KK1488); 1.5 mi S, 1.75 mi E Portis, (39.54104 N, 98.66226 W, KK1482); 1.5 mi S, 1.75 mi E Portis, (39.54095 N, 98.66385 W, KK1484); 1.5 mi S, 1.75 mi E Portis, (39.54058 N, 98.66426 W, KK1485); 1.5 mi S, 1.75 mi E Portis, (39.5404 N, 98.66337 W, KK1483); 1.7 mi S, 0.4 mi E Portis (39.53904 N, 98.68491 W, KK 1629); 1.7 mi S, 0.75 mi E Portis, (39.53838 N, 98.67904 W, KK1489). **Pawnee:** 4.24 mi S, 0.2 mi E Larned, (38.11928 N, 99.09515 W, KK1623); 4.45 mi S Larned, (38.11627 N, 99.09907 W, KK1619); 6.45 mi S, 1.53 mi W Larned, (38.08726 N, 99.12698 W, KK1622); 6.45 mi S, 0.95 mi W Larned, (38.08723 N, 99.11588 W, KK1620); 6.45 mi S, 0.95 mi W Larned, (38.08715 N, 99.11543 W, KK1621). **Pratt:** 1 mi N, 3 mi E, (37.65844 N, 98.68277 W, KK1518). **Rawlins:** 2 mi N, 3 mi E Atwood, (39.83411 N, 100.99242 W, KK1534); 1.4 mi N, 2.2 mi E Atwood, (39.82685 N, 101 W, KK1535); 0.2 mi N, 1.5 mi E Ludell, (39.85737 N, 100.92816 W, KK1536); 0.2 mi N, 1.9 mi E Ludell, (39.85754 N, 100.92391 W, KK1537). **Rooks:** 1.25 mi S, 0.5 mi W Stockton, (39.41998 N, 99.2739 W, KK1540); 1.25 mi S, 0.5 mi W Stockton, (39.41918 N, 99.27422 W, KK1541); 2.8 mi S, 8.3 mi W Stockton, (39.3989 N, 99.42441 W, KK1539); 2.8 mi S, 8.3 mi W Stockton, (39.39872 N, 99.42453 W, KK1538); 1 mi S, 2.45 mi W Woodston, (39.44309 N, 99.13974 W, KK1546); 1 mi S, 2.45 mi W Woodston, (39.4418 N, 99.14188 W, KK1547); 1 mi S, 2.45 mi W Woodston, (39.44175 N, 99.14225 W, KK1548); 1 mi S, 2.45 mi W Woodston, (39.4417 N, 99.1424 W, KK1542); 1 mi S, 2.45 mi W Woodston, (39.44141 N, 99.14205 W, KK1545); 1.3 mi S, 2.5 mi W Woodston, (39.43669 N, 99.14161 W, KK1544); 1.3 mi S, 2.5 mi W Woodston, (39.43661 N, 99.14167 W, KK1543). **Rush:** 1.4 mi S, 2.25 mi E Scheoche, (38.6956 N, 99.28992 W, KK1475); 1.4 mi S, 2.25 mi E Scheoche, (38.69489 N, 99.29053 W, KK1474); 1.4 mi S, 2.25 mi E Scheoche, (38.69444 N, 99.29005 W, KK1477); 1.4 mi S, 2.25 mi E Scheoche, (38.69389 N, 99.29057 W, KK1470); 1.4 mi S, 2.25 mi E Scheoche, (38.69384 N, 99.28963 W, KK1473); 1.4 mi S, 2.25 mi E Scheoche, (38.69372 N, 99.29028 W, KK1471); 1.4 mi S, 2.25 mi E Scheoche, (38.69348 N, 99.28773 W, KK1472); 1.4 mi S, 2.25 mi E Scheoche, (38.69281 N, 99.28897 W, KK1476). **Russell:** 6.15 mi S, 1.57 mi W Bunker Hill, (38.79937 N, 98.73323 W, KK1617); 6.15 mi S, 1.57 mi W Bunker Hill, (38.79838 N, 98.73393 W, KK1618); 6.15 mi S, 1.57 mi W Bunker Hill, (38.79757 N, 98.7325 W, KK1614); 6.15 mi S, 1.57 mi W Bunker Hill, (38.79738 N, 98.73357 W, KK1616); 6.15 mi S, 1.57 mi W Bunker Hill, (38.79663 N, 98.73264 W, KK1615); 6.15 mi S, 1.57 mi W Bunker Hill, (38.78749 N, 98.73299 E, KK1613). **Saline:** 1.8 mi E Bavaria, (38.79752 N, 97.71619 W, KK1624); 1.8 mi E Bavaria, (38.79739 N, 97.71624 W, KK1625), 1.8 mi R Bavaria (38.79473 N, 97.7192 W, KK 1628). **Stanton:** 3.51 mi N, 0.6 mi W Johnson City, (37.62128 N, 101.76172 W, KK1558). **Sumner:** 8.75 mi W Caldwell, (37.03395 N, 97.76544 W, KK1515); 0.55 mi W Caldwell, (37.03171 N, 97.61665 W, KK1513); 0.5 mi S, 5.4 mi W Caldwell, (37.02426 N, 97.70044 W, KK1514); 1.0 mi S Caldwell, (37.01787 N, 97.607 W, KK1512); 1.2 mi S Caldwell, (37.01754 N, 97.60702 W, KK1511); 1.35 mi S Caldwell, (37.01273 N, 97.607 W, KK1510); 1.35 mi S Caldwell, (37.01273 N, 97.60671 W, KK1509).

APPENDIX II

*AFLP Data, Tissue Number, Capture Site and County, Assigned Population by Fragment
Length of Selective Primer*

KK#	Site	Primer Pair, Length		EcoRI-CAC/AseI-TCT														
		Pop.	County	82	91	95	104	105	108	117	119	122	124	127	128	129	133	136
1534	1	NW	Rawlins	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1535	1	NW	Rawlins	1	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1536	1	NW	Rawlins	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1537	1	NW	Rawlins	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1538	2	NW	Rooks	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1539	2	NW	Rooks	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1541	3	NW	Rooks	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1542	4	NW	Rooks	0	1	1	1	1	0	1	1	1	0	1	0	1	1	1
1543	4	NW	Rooks	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1544	4	NW	Rooks	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1545	4	NW	Rooks	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1546	4	NW	Rooks	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1547	4	NW	Rooks	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1548	4	NW	Rooks	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1490	5	E	Osborne	1	1	1	1	1	0	1	1	0	0	1	1	1	1	1
1491	5	NW	Osborne	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1492	5	NW	Osborne	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1549	5	NW	Osborne	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1551	5	NW	Osborne	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1552	5	NW	Osborne	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1553	5	NW	Osborne	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1629	5	NW	Osborne	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1480	6	E	Osborne	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1481	6	E	Osborne	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1482	6	E	Osborne	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1484	6	E	Osborne	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1485	6	E	Osborne	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1486	6	E	Osborne	0	1	1	1	1	0	1	1	0	0	1	1	1	1	1
1487	6	E	Osborne	0	1	1	1	1	0	1	1	0	0	1	1	1	1	1
1488	6	NW	Osborne	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1489	6	E	Osborne	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
2387	7	NW	Ness	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
2388	7	NW	Ness	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
2389	7	NW	Ness	0	0	1	1	1	0	1	1	0	0	1	0	1	1	1
2390	7	NW	Ness	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
2397	7	NW	Ness	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
2398	7	NW	Ness	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1479	8	NW	Ellis	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1519	8	NW	Ellis	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1520	8	NW	Ellis	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1521	8	NW	Ellis	0	0	1	1	1	0	1	1	0	0	1	0	1	1	1
1522	8	NW	Ellis	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1523	8	NW	Ellis	0	0	1	1	1	0	1	1	0	0	1	0	1	1	1
1524	8	NW	Ellis	0	0	1	1	1	0	1	1	0	0	1	0	1	1	1
1525	8	NW	Ellis	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1526	8	NW	Ellis	0	0	1	1	1	0	1	1	0	0	1	0	1	1	1
1527	8	NW	Ellis	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1528	8	NW	Ellis	0	0	1	1	1	0	1	1	0	0	1	0	1	1	1
1529	8	NW	Ellis	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1530	8	NW	Ellis	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1531	8	NW	Ellis	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1532	8	NW	Ellis	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1554	9	NW	Ellis	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1470	10	NW	Rush	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1471	10	NW	Rush	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1472	10	NW	Rush	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1473	10	NW	Rush	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1474	10	Hyb	Rush	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1476	10	NW	Rush	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1477	10	NW	Rush	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1613	11	E	Russell	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1614	11	E	Russell	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1615	11	E	Russell	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1616	11	E	Russell	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1617	11	E	Russell	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1618	11	E	Russell	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1624	12	E	Saline	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1625	12	E	Saline	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1628	12	E	Saline	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1607	13	E	Dickinson	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1608	13	E	Dickinson	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1

KK#	Site	Primer Pair, Length		EcoRI-CAC/AseI-TCT														
		Pop.	County	82	91	95	104	105	108	117	119	122	124	127	128	129	133	136
1609	13	E	Dickinson	0	1	1	1	1	0	1	1	1	0	1	1	1	1	1
1610	13	E	Dickinson	0	1	1	1	1	0	1	1	0	0	1	1	1	1	1
1611	13	E	Dickinson	0	1	1	1	1	0	1	1	0	1	1	0	1	1	1
1612	13	E	Dickinson	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1559	14	SW	Hamilton	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1560	14	SW	Hamilton	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1561	14	SW	Hamilton	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1562	14	SW	Hamilton	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1563	14	SW	Hamilton	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1564	14	SW	Hamilton	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1565	15	SW	Kearney	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1566	15	NW	Finney	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1567	15	SW	Finney	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1568	15	SW	Finney	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1569	15	SW	Finney	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1590	15	SW	Finney	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1591	15	SW	Finney	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1592	15	SW	Finney	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1619	16	SC	Pawnee	0	1	1	1	1	0	1	1	0	1	1	0	1	1	1
1620	16	SC	Pawnee	0	1	1	1	1	0	1	1	0	1	1	0	1	1	1
1621	16	SC	Pawnee	0	1	1	1	1	0	1	1	0	1	1	0	1	1	1
1622	16	SC	Pawnee	0	1	1	1	1	0	1	1	0	1	1	0	1	1	1
1623	16	SC	Pawnee	0	1	1	1	1	0	1	1	0	1	1	0	1	1	1
1493	17	E	Greenwood	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1494	17	E	Greenwood	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1495	17	E	Greenwood	1	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1496	17	E	Greenwood	1	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1497	17	E	Greenwood	1	1	1	1	1	0	1	1	0	1	1	1	0	1	1
1498	17	E	Greenwood	1	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1499	17	SC	Greenwood	0	1	1	1	1	0	1	1	0	1	1	0	1	1	1
1500	17	E	Greenwood	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1501	17	E	Greenwood	1	1	1	1	1	0	1	1	0	0	1	1	1	1	1
1516	18	SW	Morton	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1517	18	SW	Morton	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1555	18	SW	Morton	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1556	18	SW	Morton	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1557	18	SW	Morton	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1558	19	SW	Stanton	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1533	20	SC	Meade	1	1	1	1	1	0	1	1	0	1	1	0	1	1	1
1593	20	SC	Meade	0	1	0	1	1	0	1	1	0	1	1	0	1	1	1
1594	20	SC	Meade	0	1	1	1	1	0	1	1	0	1	1	0	1	1	1
1595	20	SC	Meade	0	1	1	1	1	0	1	1	0	1	1	0	1	1	1
1596	20	SC	Meade	0	1	1	1	1	0	1	1	0	1	1	0	1	1	1
1597	20	SC	Meade	0	1	1	1	1	0	1	1	0	1	1	0	1	1	1
1598	20	SC	Meade	0	1	1	1	1	0	1	1	0	1	1	0	1	1	1
1599	21	SC	Comanche	0	1	1	1	1	0	1	1	0	1	1	0	1	1	1
1600	21	SC	Comanche	0	1	1	1	1	0	1	1	0	1	1	0	1	1	1
1601	21	SC	Comanche	0	1	1	1	1	0	1	1	0	1	1	0	1	1	1
1602	21	SC	Comanche	1	1	1	1	1	0	1	1	0	1	1	0	1	1	1
1603	21	SC	Comanche	0	1	1	1	1	0	1	1	0	1	1	0	1	1	1
1604	21	SC	Comanche	0	1	1	1	1	0	1	1	0	1	1	0	1	1	1
1605	21	SC	Comanche	0	1	1	1	1	0	1	1	0	1	1	0	1	1	1
1606	21	SC	Comanche	0	1	1	1	1	0	1	1	1	1	1	0	1	1	1
1509	22	SC	Sumner	0	1	1	1	1	0	1	1	0	1	1	0	1	1	1
1510	22	SC	Sumner	0	1	1	1	1	0	1	1	0	1	1	0	1	1	1
1511	22	SC	Sumner	0	1	1	1	1	0	1	1	0	1	1	0	1	1	1
1512	22	SC	Sumner	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1513	22	SC	Sumner	0	1	1	1	1	0	1	1	0	1	1	0	1	1	1
1515	22	SC	Sumner	0	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1518	23	SC	Pratt	1	1	1	1	1	0	1	1	0	0	1	0	1	1	1
1502	24	Inter.	Cowley	1	1	1	1	1	1	1	1	0	0	1	0	1	0	1
1503	24	Inter.	Cowley	0	1	1	1	1	0	1	1	0	1	1	0	1	1	1
1504	24	Inter.	Cowley	0	1	1	1	1	0	1	1	0	1	1	0	1	1	1
1505	24	Inter.	Cowley	0	1	1	1	1	0	1	1	0	1	1	0	1	1	1
1506	24	Inter.	Cowley	1	1	1	1	1	0	1	1	0	1	1	0	1	1	1
1507	24	Inter.	Cowley	0	1	1	1	1	0	1	1	0	1	1	0	1	1	1
1508	24	Inter.	Cowley	0	1	1	1	1	0	1	1	0	1	1	0	1	1	1
54480	25	-	Lincoln, NE	0	1	1	1	1	0	1	1	1	1	1	0	1	1	1

<i>EcoRI-CAC/AseI-TCT</i>																			
KK#	139	151	152	153	154	159	160	162	163	164	183	186	189	193	195	202	203	205	206
1534	0	0	1	0	0	1	0	0	0	1	0	1	1	0	1	1	0	0	0
1535	0	0	1	0	0	1	0	0	1	1	0	1	1	0	1	1	0	0	0
1536	0	0	1	0	0	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1537	0	0	1	0	0	1	0	0	0	1	0	1	1	0	1	0	0	0	0
1538	0	0	1	0	0	1	0	0	1	1	0	1	1	0	1	1	0	0	0
1539	0	0	1	0	0	1	0	0	0	1	0	1	1	0	1	1	0	0	0
1541	0	0	1	0	0	1	0	0	0	1	0	1	1	0	1	0	0	0	0
1542	0	0	1	0	0	1	0	0	0	1	0	1	1	0	1	1	0	0	0
1543	0	0	1	0	0	1	0	0	0	1	0	1	1	0	1	0	0	0	0
1544	0	0	1	0	0	1	0	0	0	1	0	1	1	0	1	1	0	0	0
1545	0	0	1	0	0	1	0	0	0	1	0	1	1	0	1	1	0	0	0
1546	0	0	1	0	0	1	0	0	0	1	0	1	1	0	1	0	0	0	0
1547	0	0	1	0	0	1	0	0	0	1	0	1	1	0	1	0	0	0	0
1548	0	0	1	0	0	1	0	0	0	1	0	1	1	0	1	1	0	0	0
1490	0	0	1	1	1	1	0	0	1	0	0	1	1	0	1	0	0	0	0
1491	0	0	1	0	0	1	0	0	0	1	0	1	1	0	1	0	0	0	0
1492	0	0	1	0	0	1	0	0	0	1	0	1	1	0	1	0	0	0	0
1549	0	0	1	0	0	1	0	0	0	1	0	1	1	0	1	0	0	0	0
1551	0	0	1	0	0	1	0	0	0	1	0	1	1	0	1	0	0	0	0
1552	0	0	1	0	0	1	0	0	1	1	0	1	1	0	1	1	0	0	0
1553	0	0	1	0	0	1	0	0	0	1	0	1	1	0	1	0	0	0	0
1629	0	1	1	0	1	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1480	0	0	1	0	1	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1481	0	0	1	0	0	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1482	0	0	1	0	1	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1484	0	0	1	0	0	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1485	0	0	1	0	1	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1486	0	0	1	0	1	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1487	0	0	1	0	1	1	0	0	1	1	0	1	1	0	1	1	0	0	0
1488	0	0	1	0	0	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1489	0	0	1	0	0	1	0	0	0	1	0	1	1	0	1	0	0	0	0
2387	0	0	1	0	0	1	0	0	0	1	0	1	1	0	1	1	0	0	0
2388	0	0	1	0	0	1	0	0	0	1	0	1	1	0	1	1	0	0	0
2389	0	0	1	0	0	1	0	0	1	1	0	1	1	0	1	1	0	0	0
2390	0	0	1	0	0	1	0	0	0	1	0	1	1	0	1	1	0	0	0
2397	0	0	1	0	0	1	0	0	0	1	0	1	1	0	1	1	0	0	0
2398	0	0	1	0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	0
1479	0	0	1	0	0	1	1	0	1	0	0	1	1	0	1	1	0	0	0
1519	0	0	1	0	0	1	0	0	0	1	0	1	1	0	1	1	0	0	0
1520	0	0	1	0	0	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1521	0	0	1	0	0	1	0	0	1	0	0	1	1	0	1	0	0	0	0
1522	0	0	1	0	0	1	0	0	1	0	0	1	1	0	1	0	0	0	0
1523	0	0	1	0	0	1	0	0	1	0	0	1	1	0	1	0	0	0	0
1524	0	0	1	0	0	1	0	0	1	1	0	1	1	0	1	1	0	0	0
1525	0	0	1	0	0	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1526	0	0	1	0	0	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1527	0	0	1	0	0	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1528	0	0	1	0	0	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1529	0	0	1	0	0	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1530	0	0	1	0	0	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1531	0	0	1	0	0	1	0	0	0	1	0	1	1	0	1	1	0	0	0
1532	0	0	1	0	0	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1554	0	0	1	0	0	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1470	0	0	1	0	0	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1471	0	0	1	0	0	1	0	0	0	1	0	1	1	0	1	1	0	0	0
1472	0	0	1	0	0	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1473	0	0	1	0	0	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1474	0	0	1	0	1	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1476	0	0	1	0	0	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1477	0	0	1	0	0	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1613	0	0	1	1	1	1	0	0	0	0	0	1	1	0	1	1	0	0	0
1614	0	0	1	1	1	1	0	0	0	1	0	1	1	0	1	1	0	0	0
1615	0	0	1	1	1	1	0	0	1	1	0	1	1	0	1	1	0	0	0
1616	0	0	1	0	1	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1617	0	0	1	0	1	1	0	0	0	0	0	1	1	0	1	1	0	0	0
1618	0	0	1	0	0	1	0	0	0	1	0	1	1	0	1	1	0	0	0
1624	0	0	0	1	0	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1625	0	1	0	0	1	1	0	0	0	0	1	1	1	0	1	1	0	0	0
1628	0	1	1	0	0	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1607	0	0	1	0	1	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1608	0	0	1	0	0	1	0	0	1	0	0	1	1	0	1	1	0	0	0

<i>EcoRI-CAC/AseI-TCT</i>																			
KK#	139	151	152	153	154	159	160	162	163	164	183	186	189	193	195	202	203	205	206
1609	0	0	1	1	1	1	0	0	0	1	0	1	1	0	1	1	0	0	0
1610	0	0	1	0	1	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1611	0	0	1	0	0	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1612	0	0	1	0	0	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1559	0	1	1	0	0	1	0	0	1	0	0	1	1	0	1	1	1	1	0
1560	0	1	0	0	0	1	0	0	1	0	0	1	1	0	1	1	1	1	0
1561	0	1	1	0	0	1	0	0	1	0	0	1	1	0	1	1	0	1	0
1562	0	1	1	0	0	1	0	0	1	0	0	1	1	0	1	1	1	1	0
1563	0	1	1	0	0	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1564	0	1	0	0	1	1	0	0	1	0	0	1	1	0	1	1	1	1	0
1565	0	1	1	0	0	1	0	0	1	0	0	1	1	0	1	1	1	1	0
1566	0	1	0	0	0	1	0	0	0	0	0	1	1	0	1	1	0	0	0
1567	0	0	1	0	0	1	0	0	1	0	0	1	1	0	1	1	1	1	0
1568	0	0	1	0	0	1	1	0	1	0	0	1	1	0	1	1	1	1	0
1569	0	0	1	0	0	1	1	0	1	0	0	1	1	0	1	1	1	1	0
1590	0	0	1	0	0	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1591	0	1	1	0	0	1	0	0	1	0	0	1	1	0	1	1	0	0	0
1592	0	0	1	0	0	1	0	0	1	0	0	1	1	0	1	1	1	1	0
1619	0	1	1	0	1	1	0	0	1	1	0	1	1	0	1	1	0	0	0
1620	0	1	1	0	1	1	0	1	1	0	0	1	1	0	1	1	0	0	0
1621	0	1	0	0	1	1	0	0	0	1	0	1	1	0	1	1	0	0	0
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1623	0	0	1	0	1	1	0	0	0	1	0	1	1	0	1	1	0	0	0
1493	0	0	1	1	0	1	0	0	1	0	0	1	1	0	1	1	0	0	0
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1498	0	0	1	1	1	1	0	0	1	0	0	1	1	0	1	0	0	0	0
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1501	0	1	0	1	0	1	0	0	0	0	0	1	1	0	1	1	0	0	0
1516	0	1	0	0	0	1	0	0	1	0	0	1	1	0	1	1	1	1	0
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1511	0	0	1	0	1	1	0	0	0	0	0	1	1	0	1	1	0	0	0
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1508	0	0	0	1	1	1	0	0	0	1	0	1	1	0	1	1	0	0	0
54480	0	0	1	0	0	1	0	0	1	1	0	1	1	0	1	1	0	0	1

<i>EcoRI-CAC/AseI-TCT</i>																			
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1527	0	1	1	0	1	0	1	0	0	0	0	1	1	0	0	1	1	1	0
1528	0	1	1	0	1	0	1	0	0	0	0	1	1	0	0	1	1	1	1
1529	0	1	1	0	1	0	1	0	0	0	1	1	1	0	1	1	1	1	1
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1625	1	1	1	0	1	0	0	0	1	0	0	1	1	0	0	1	1	1	1
1628	1	1	1	0	1	0	0	0	1	0	0	1	1	0	0	1	1	1	1
1607	1	1	1	0	1	0	0	0	1	0	0	1	1	0	0	1	1	1	1
1608	1	1	1	0	1	0	0	0	1	0	0	1	1	0	0	1	1	1	1

<i>EcoRI-CAC/AseI-TCT</i>																			
KK#	237	249	252	263	271	272	273	275	286	288	289	291	292	294	301	302	307	315	317
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1612	1	1	1	0	1	0	0	0	1	0	0	1	1	0	0	1	1	1	1
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1621	1	1	1	0	1	0	0	0	1	0	0	1	1	0	0	1	1	1	0
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54480	0	1	1	0	1	0	1	0	0	0	0	1	1	1	0	0	1	1	1

KK#	CAC/TCT			EcoRI-CAC/AseI-TGA															
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<i>EcoRI-</i> CAC/AseI-TGA																			
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1471	0	1	0	0	1	0	1	1	0	0	1	1	0	0	1	0	0	1	1
1472	0	1	0	0	1	0	1	1	0	0	1	1	0	0	1	0	1	1	1
1473	0	1	0	0	1	0	1	1	0	0	1	1	0	0	1	0	1	1	1
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1607	0	1	1	0	0	0	1	1	0	0	1	1	1	0	0	0	1	1	1
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KK#	<i>EcoRI</i> - CAC/AseI-TGA																			
	153	155	156	157	160	165	167	173	174	190	206	208	224	229	232	242	243	245	247	
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1610	0	1	0	0	0	0	1	1	0	0	1	1	1	0	0	1	1	1	1	
1611	0	1	0	0	0	0	1	1	0	0	1	1	1	0	1	0	1	1	1	
1612	0	1	0	0	0	0	1	1	0	0	1	1	0	0	0	0	1	1	1	
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1511	0	1	0	0	0	0	1	1	0	0	1	1	1	1	1	1	0	1	1	
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1507	0	1	1	0	0	0	1	1	0	0	1	1	0	0	1	0	0	1	1	
1508	0	1	1	0	0	0	1	1	0	0	1	1	1	0	1	0	1	1	1	
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KK#	EcoRI-CAC/AseI-TTC																		
	272	275	293	294	295	303	309	312	313	315	317	332	343	345	347	366	367	389	393
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1541	0	1	0	1	0	1	0	0	1	1	0	1	0	1	0	1	1	0	1
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1490	0	1	0	1	0	0	0	0	1	1	0	0	0	1	0	1	1	0	1
1491	0	1	0	1	0	1	0	0	1	1	0	1	0	1	0	1	1	0	1
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1607	0	1	0	1	1	0	0	0	1	1	0	0	0	1	1	1	1	0	1
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KK#	EcoRI-CAC/AseI-TTC																			
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KK#	EcoRI-CAC/AseI-TTC																			
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1611	1	0	0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	0	0	0
1612	1	0	0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	0	0	0
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1499	0	1	0	0	1	1	1	0	1	0	1	1	0	1	1	0	0	0	0	0
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1501	1	1	0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	0	0	0
1516	0	1	0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	0	0	0
1517	1	1	0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	0	0	0
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1533	1	0	0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	0	0	0
1593	1	1	1	0	1	0	1	0	1	0	1	1	0	1	1	0	0	0	0	0
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1602	1	1	0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	0	0	0
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1511	1	0	0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	0	0	0
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1518	1	1	0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	0	0	0
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1508	1	0	0	0	1	0	1	0	1	0	1	1	0	1	1	0	1	1	1	1
54480	1	0	0	0	1	0	1	0	1	0	1	1	0	1	1	0	0	0	0	0

KK#	EcoRI-CAC/AseI-TTC																		
	149	152	154	158	159	162	163	166	168	169	171	173	174	179	182	183	184	185	186
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1536	1	0	0	1	0	1	1	1	0	1	1	1	0	0	1	1	0	0	0
1537	1	0	0	1	0	1	1	1	0	1	1	1	0	0	1	1	0	0	0
1538	1	0	0	1	0	1	1	1	0	1	1	1	0	0	1	0	0	0	0
1539	1	0	0	1	0	1	1	1	0	1	1	1	0	0	1	1	0	0	0
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1491	1	0	0	1	0	1	1	1	0	1	1	1	0	0	0	1	0	0	0
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1549	1	0	0	1	0	1	1	1	0	1	1	1	0	0	1	1	0	0	0
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1479	1	0	0	1	0	1	1	1	0	1	1	1	0	0	0	1	0	0	0
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1607	1	1	1	0	0	1	1	1	0	1	1	0	0	0	1	0	1	0	0
1608	1	0	1	1	0	1	1	1	0	1	1	1	0	1	0	1	1	0	0

<i>EcoRI-CAC/AseI-TTC</i>																			
KK#	149	152	154	158	159	162	163	166	168	169	171	173	174	179	182	183	184	185	186
1609	1	0	1	1	0	1	1	1	0	1	1	1	0	1	1	1	1	0	0
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1611	1	0	1	0	0	1	1	1	0	1	1	1	0	1	1	0	1	0	0
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<i>EcoRI-CAC/AseI-TTC</i>																			
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KK#	<i>EcoRI</i> -CAC/ <i>AseI</i> -TTC										<i>EcoRI</i> -CAC/ <i>AseI</i> -TTT									
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KK#	EcoRI-CAC/AseI-TTC									EcoRI-CAC/AseI-TTT										
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1508	0	1	1	1	1	1	1	1	1	0	0	1	1	0	1	1	0	1	1	
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<i>EcoRI-CAC/AseI-TTT</i>																			
KK#	93	94	99	101	105	109	112	114	120	128	133	138	142	146	152	154	162	166	171
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2387	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	0
2388	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	0
2389	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	1
2390	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	1
2397	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	0
2398	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	0
1479	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	1
1519	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	0
1520	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	1
1521	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	1	1	1
1522	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	1	1	1
1523	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	1	1	1
1524	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	1	1	1
1525	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	1
1526	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	1
1527	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	1	1	1
1528	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	1	1	1
1529	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	1	1	1
1530	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	1	1	1
1531	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	0
1532	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	1	1	1
1554	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	1
1470	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	1
1471	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	1
1472	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	1	1	1
1473	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	1
1474	1	0	0	1	1	0	1	0	1	1	0	1	1	1	1	1	0	1	1
1476	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	1
1477	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	1	1	1
1613	0	0	0	1	1	0	1	0	1	1	0	0	1	1	1	1	0	1	0
1614	1	0	0	1	1	1	0	0	1	1	0	1	1	1	1	1	0	1	0
1615	1	0	0	1	1	1	1	0	1	1	0	0	1	1	1	1	0	1	1
1616	1	0	0	1	1	1	0	0	1	1	0	0	1	1	1	1	0	1	1
1617	1	0	0	1	1	0	1	0	1	1	0	0	1	1	1	1	0	1	0
1618	1	0	0	1	1	0	1	0	1	1	0	1	1	1	1	1	0	1	0
1624	1	0	0	1	1	1	1	0	1	1	0	0	1	1	1	1	0	1	0
1625	1	0	0	1	1	1	1	0	1	1	0	1	1	1	1	1	0	1	0
1628	1	0	0	1	1	1	1	0	1	1	0	1	1	1	1	1	0	1	0
1607	1	0	0	1	1	1	1	0	1	1	0	0	1	1	1	1	0	1	0
1608	1	0	0	1	1	1	1	0	1	1	0	0	1	1	1	1	0	1	0

<i>EcoRI-CAC/AseI-TTT</i>																			
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1610	1	0	0	1	1	1	0	0	1	1	0	0	1	1	1	1	0	1	0
1611	1	0	0	1	1	1	1	0	1	1	0	0	1	1	1	1	0	1	0
1612	1	0	0	1	1	0	1	0	1	1	0	0	1	1	1	1	0	1	0
1559	1	0	0	1	1	0	1	0	1	1	0	0	1	1	1	1	0	1	0
1560	1	0	0	1	1	0	1	0	1	1	0	0	1	1	1	1	0	1	0
1561	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	0
1562	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	0
1563	1	0	0	1	1	0	1	0	1	1	0	0	1	1	1	1	0	1	0
1564	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	0
1565	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	0
1566	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	0	0	1	0
1567	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	0
1568	1	0	0	1	1	0	1	0	1	1	0	0	1	1	1	1	0	1	0
1569	1	0	0	1	1	0	1	0	1	1	0	0	1	1	1	1	0	1	0
1590	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	0
1591	1	0	0	1	1	0	1	0	1	1	0	0	1	1	1	1	0	1	0
1592	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	0
1619	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	0
1620	1	0	0	1	1	1	0	0	1	1	1	0	1	1	1	1	0	1	0
1621	1	0	0	1	1	0	0	0	1	1	0	1	1	1	1	1	0	1	0
1622	1	1	0	1	1	1	0	0	1	1	0	0	1	1	1	1	0	1	0
1623	1	0	1	1	1	1	0	0	1	1	0	0	1	1	1	1	0	1	0
1493	1	0	0	1	1	1	1	0	1	1	0	0	1	1	1	1	0	1	1
1494	1	0	0	1	1	1	0	0	1	1	0	0	1	1	1	1	0	1	1
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1496	1	0	0	1	1	1	1	0	1	1	0	1	1	1	1	1	0	1	1
1497	1	0	0	1	1	1	1	0	1	1	0	1	1	1	1	1	0	1	1
1498	1	0	0	1	1	1	1	0	1	1	0	0	1	1	1	1	0	1	1
1499	1	0	0	1	1	1	1	1	1	1	0	0	1	1	1	1	0	1	0
1500	1	0	0	1	1	1	1	0	1	1	0	0	1	1	1	1	0	1	0
1501	1	0	0	1	1	1	0	0	1	1	0	1	1	1	1	1	0	1	1
1516	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	0
1517	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	0
1555	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	0
1556	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	0
1557	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	0
1558	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	0
1533	1	0	0	1	1	1	0	0	1	1	0	0	1	1	1	1	0	1	1
1593	1	1	0	1	1	0	0	0	1	1	1	0	1	1	1	1	0	1	1
1594	1	1	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	1
1595	1	0	0	1	1	0	0	0	1	1	0	0	1	1	0	1	0	1	0
1596	1	0	0	1	1	0	0	0	1	1	1	0	1	1	1	1	0	1	0
1597	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	0
1598	1	1	0	1	1	1	0	0	1	1	0	0	1	1	1	1	0	1	1
1599	1	1	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	0
1600	1	0	0	1	1	0	0	0	1	1	1	0	1	1	1	1	0	1	0
1601	1	1	0	1	1	1	0	0	1	1	0	0	1	1	1	1	0	1	0
1602	1	0	0	1	1	1	0	0	1	1	1	0	1	1	1	1	0	1	0
1603	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	1
1604	1	0	0	1	1	1	0	1	1	1	1	0	1	1	1	1	0	1	0
1605	1	0	0	1	1	1	0	1	1	1	1	0	1	1	1	1	0	1	1
1606	1	1	0	1	1	0	0	1	1	1	0	0	1	1	1	1	0	1	1
1509	1	0	0	1	1	1	0	0	1	1	0	0	1	1	1	1	0	1	0
1510	1	0	0	1	1	1	0	0	1	1	0	0	1	1	1	1	0	1	0
1511	1	0	0	1	1	0	0	1	1	1	1	0	1	1	1	1	0	1	0
1512	1	0	0	1	1	1	0	1	1	1	0	0	1	1	1	1	0	1	0
1513	1	0	0	1	1	1	0	1	1	1	0	0	1	1	1	1	0	1	0
1515	1	0	0	1	1	1	1	0	1	1	0	0	1	1	1	1	0	1	0
1518	1	0	1	1	1	1	0	1	1	1	0	0	1	1	1	1	0	1	1
1502	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	0
1503	1	0	0	1	1	1	1	1	1	1	0	0	1	1	1	1	0	1	0
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1505	1	0	0	1	1	1	0	0	1	1	0	0	1	1	1	1	0	1	0
1506	1	0	0	1	1	1	0	0	1	1	0	0	1	1	1	1	0	1	0
1507	1	0	0	1	1	1	0	0	1	1	0	0	1	1	1	1	0	1	0
1508	1	0	0	1	1	1	0	0	1	1	0	0	1	1	1	1	0	1	0
54480	1	0	0	1	1	0	0	0	1	1	0	0	1	1	1	1	0	1	1

KK#	EcoRI-CAC/AseI-TTT																		
	173	174	175	178	179	182	184	189	194	198	202	204	208	214	215	219	221	222	225
1534	1	0	0	1	0	1	1	0	1	1	0	1	1	1	0	0	1	1	0
1535	1	0	0	1	0	1	1	0	1	1	0	1	1	1	0	0	0	1	0
1536	1	0	0	1	0	1	1	0	1	1	0	1	1	1	0	0	1	1	0
1537	1	1	0	1	0	1	1	0	1	1	1	1	1	1	0	0	0	1	0
1538	1	0	0	1	0	1	1	0	1	1	0	1	1	1	0	0	0	1	0
1539	1	0	0	1	0	1	1	0	1	1	0	1	1	1	0	0	0	1	0
1541	1	0	0	1	0	1	1	0	1	1	1	1	1	1	0	0	0	1	0
1542	1	1	0	1	0	1	1	0	1	1	1	1	1	1	0	0	0	1	0
1543	1	1	0	1	0	1	1	0	1	1	1	1	1	1	0	0	0	1	0
1544	1	1	0	1	0	1	1	0	1	1	1	1	1	1	0	0	0	1	0
1545	1	1	0	1	0	1	1	0	1	1	1	1	1	1	0	0	0	1	0
1546	1	1	0	1	0	1	1	0	1	1	1	1	1	1	0	0	0	1	0
1547	1	0	0	1	0	1	1	0	1	1	1	1	1	1	0	0	0	1	0
1548	0	1	0	1	0	1	1	0	1	1	0	1	1	1	0	0	0	1	0
1490	1	0	0	1	0	1	1	0	1	1	0	1	1	1	0	0	1	0	0
1491	1	0	0	1	0	1	1	0	1	1	1	1	1	1	0	0	0	1	0
1492	1	0	0	1	0	1	1	0	1	1	1	1	1	1	0	0	0	1	0
1549	1	0	0	1	0	1	1	0	1	1	1	1	1	1	0	0	0	1	0
1551	1	0	0	1	0	1	1	0	1	1	1	1	1	1	0	0	0	1	0
1552	1	1	0	1	0	1	1	0	1	1	1	1	1	1	0	0	0	1	1
1553	1	0	0	1	0	1	1	0	1	1	1	1	1	1	0	0	0	1	0
1629	1	0	0	1	0	1	1	0	1	1	0	1	1	1	0	0	1	0	0
1480	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	0	1	0	0
1481	0	1	0	1	0	1	1	0	1	1	0	1	1	1	0	0	1	0	0
1482	0	1	0	1	0	1	1	0	1	1	0	1	1	1	0	0	1	0	0
1484	1	0	0	1	0	1	1	0	1	1	0	1	1	1	0	0	1	0	0
1485	1	0	0	1	0	1	1	0	1	1	0	1	1	1	0	0	1	0	0
1486	1	0	0	1	0	1	1	0	1	1	0	1	1	1	0	0	1	0	0
1487	1	0	0	1	0	1	1	0	1	1	0	1	1	1	0	0	1	0	0
1488	0	1	0	1	0	1	1	0	1	1	0	1	1	1	0	0	1	0	0
1489	1	0	0	1	0	1	1	0	1	1	1	1	1	1	0	0	0	1	0
2387	1	0	0	1	0	1	1	0	1	1	0	1	1	1	0	0	0	1	0
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2389	1	1	0	1	0	1	1	0	1	1	1	1	1	1	0	0	0	1	0
2390	1	1	0	1	0	1	1	0	1	1	1	1	1	1	0	0	0	1	0
2397	1	1	0	1	0	1	1	0	1	1	1	1	1	1	0	0	0	1	0
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1479	1	0	0	1	0	1	1	0	1	1	0	1	1	1	0	0	0	1	0
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1520	1	0	0	1	0	1	1	0	1	1	1	1	1	1	0	0	0	1	0
1521	1	0	0	1	0	1	1	0	1	1	1	1	1	1	0	0	0	1	0
1522	1	0	0	1	0	1	1	0	1	1	1	1	1	1	0	0	0	1	0
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1524	1	0	0	1	0	1	1	0	1	1	0	1	1	1	0	0	0	1	0
1525	1	0	0	1	0	1	1	0	1	1	1	1	1	1	0	0	0	1	0
1526	1	0	0	1	0	1	1	0	1	1	1	1	1	1	0	0	0	1	0
1527	1	0	0	1	0	1	1	0	1	1	0	1	1	1	0	0	0	1	0
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1529	1	0	0	1	0	1	1	0	1	1	1	1	1	1	0	0	0	1	0
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1531	1	0	0	1	0	1	1	0	1	1	0	1	1	1	0	0	0	1	0
1532	1	0	0	1	0	1	1	0	1	1	1	0	1	1	1	0	0	1	0
1554	1	0	0	1	0	1	1	0	1	1	0	1	1	1	0	0	0	1	0
1470	1	1	0	1	0	1	1	0	1	1	0	1	1	1	0	0	0	1	0
1471	1	1	0	1	0	1	1	0	1	1	0	1	1	1	0	0	0	1	0
1472	1	0	0	1	0	1	1	0	1	1	0	1	1	1	0	0	0	1	0
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1474	1	0	1	1	0	1	1	0	1	1	0	1	1	1	0	0	1	1	1
1476	1	0	1	1	0	1	1	0	1	1	0	1	1	1	0	0	0	1	1
1477	1	0	1	1	0	1	1	0	1	1	1	1	1	1	0	0	0	1	1
1613	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	0	0	1	0
1614	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	0	0	1	0
1615	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	0	0	1	0
1616	1	0	0	1	0	0	1	0	1	1	0	1	1	1	1	0	0	1	0
1617	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	0	0	1	0
1618	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	0	0	1	0
1624	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	0	1	0	0
1625	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	0	1	0	0
1628	1	0	0	1	0	1	1	0	1	1	0	1	1	1	0	0	1	0	0
1607	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	0	1	0	0
1608	1	0	0	1	0	1	1	0	1	1	0	1	1	1	0	0	1	0	0

<i>EcoRI-CAC/AseI-TTT</i>																			
KK#	173	174	175	178	179	182	184	189	194	198	202	204	208	214	215	219	221	222	225
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1610	1	0	0	1	0	1	1	0	1	1	0	1	1	1	0	0	1	0	0
1611	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	0	1	0	0
1612	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	0	0	1	0
1559	1	0	0	1	0	1	1	0	1	1	0	1	1	1	1	0	0	1	0
1560	1	0	0	1	0	1	1	0	1	1	0	1	1	1	0	0	0	1	0
1561	1	0	0	1	0	1	1	0	1	1	0	1	1	1	0	0	0	1	0
1562	1	0	0	1	0	1	1	0	1	1	0	1	1	1	0	0	0	1	0
1563	1	0	0	1	0	1	1	0	1	1	0	1	1	1	0	0	0	1	0
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<i>EcoRI-CAC/AseI-TTT</i>																				
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1502	1	0	1	1	1	1	0	0	0	0	1	0	0	1	1	0	0	1	1	
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1505	1	0	0	1	1	0	0	0	1	1	1	0	0	1	1	0	0	1	1	
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1508	1	0	1	0	0	0	0	0	0	0	1	1	0	1	1	0	0	1	1	
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KK#	EcoRI-CAC/AseI-TTT																		
	277	285	296	304	325	326	328	330	332	339	342	348	350	354	355	359	363	364	365
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1607	0	0	1	1	1	0	1	1	1	1	1	1	0	1	1	1	0	0	1
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KK#	EcoRI-CAC/AseI-TTT																		
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1590	0	0	1	1	1	0	0	1	1	1	1	1	0	1	1	1	1	0	0
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KK#	<i>EcoRI-CAC/AseI-TTT</i>				<i>EcoRI-CAT/AseI-TAA</i>															
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1520	0	1	1	1	1	1	1	1	0	1	1	1	1	0	1	1	1	1	1	1
1521	0	1	1	1	1	1	1	1	0	1	1	1	1	0	1	1	1	1	1	1
1522	0	1	1	1	1	1	1	1	0	1	1	1	1	0	1	1	0	1	1	1
1523	0	1	1	1	1	1	1	1	0	1	1	1	1	0	1	1	1	1	1	1
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1527	0	1	1	1	1	1	1	1	0	1	1	1	1	0	1	1	1	1	1	1
1528	0	1	1	1	1	1	1	1	0	1	1	1	1	0	1	1	1	1	1	1
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1628	0	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1
1607	0	1	1	1	1	1	1	1	1	0	1	1	1	0	1	1	1	1	1	1
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KK#	<i>EcoRI</i> -CAC/ <i>AseI</i> -TTT					<i>EcoRI</i> -CAT/ <i>AseI</i> -TAA													
	367	369	374	377	388	72	77	80	81	82	88	92	93	96	97	98	102	103	106
1609	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
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1612	0	1	1	1	1	1	1	0	1	1	1	1	0	1	1	1	1	1	1
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1621	0	1	1	1	1	1	1	0	1	0	1	1	0	1	1	1	1	1	1
1622	0	1	1	1	1	1	1	0	1	0	1	1	0	1	1	1	1	1	1
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1493	0	1	1	1	1	1	1	0	1	0	1	1	0	1	1	1	1	1	1
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1497	0	1	1	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1
1498	0	1	1	1	1	1	1	0	1	0	1	1	0	1	1	1	1	1	1
1499	0	1	1	1	1	1	1	1	0	0	1	1	0	1	1	1	1	1	1
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1501	0	1	1	1	1	1	1	0	1	1	1	1	0	1	1	1	1	1	1
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1533	0	1	1	1	1	1	1	0	1	1	1	1	0	1	1	1	1	1	1
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1599	0	1	1	1	1	1	1	0	1	0	1	1	0	0	1	0	1	1	1
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1601	0	1	1	1	1	1	1	0	1	0	1	1	0	1	1	1	1	1	1
1602	0	1	1	1	1	1	1	0	1	0	1	1	0	1	1	1	1	1	1
1603	0	1	1	1	1	1	1	1	1	0	1	1	0	1	1	0	1	1	1
1604	0	1	1	1	1	1	1	1	1	0	1	1	0	1	1	1	1	1	1
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1606	0	1	1	1	1	1	1	0	1	0	1	1	0	1	1	0	1	1	1
1509	0	1	1	1	1	1	1	1	1	0	1	1	0	1	1	1	1	1	1
1510	0	1	1	1	1	1	1	0	1	0	1	1	0	1	1	0	1	1	1
1511	0	1	1	1	1	1	1	0	1	0	1	1	0	1	1	0	1	1	1
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1515	0	1	1	1	1	1	1	0	1	0	1	1	0	1	1	1	1	1	1
1518	0	1	1	1	1	1	1	0	1	1	1	1	0	1	1	1	1	1	1
1502	0	1	1	1	1	1	1	1	1	0	1	1	0	1	1	1	1	1	1
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1506	0	1	1	1	1	1	1	0	1	1	1	1	0	1	1	1	1	1	1
1507	0	1	1	1	1	1	1	0	1	0	1	1	0	1	1	1	1	1	1
1508	0	1	1	1	1	1	1	1	1	0	1	1	0	1	1	1	1	1	1
54480	0	1	1	1	1	1	1	0	1	0	1	0	0	1	1	1	1	1	1

<i>EcoRI</i> -CAT/ <i>AseI</i> -TAA																			
KK#	108	109	112	116	117	126	127	130	133	135	137	139	142	145	147	150	154	157	158
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1610	0	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	0
1611	0	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	0
1612	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	1	1	1	0
1559	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	0	1	1	0
1560	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	0	1	1	0
1561	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	0	1	1	0
1562	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	0	1	1	0
1563	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	0	1	1	0
1564	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	0	1	1	0
1565	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	0	1	1	0
1566	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	0	1	1	0
1567	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	0	1	1	0
1568	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	0	1	1	0
1569	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	0	1	1	0
1590	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	0	1	1	1
1591	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	0	1	1	1
1592	0	1	1	1	1	1	1	1	0	1	1	1	1	1	1	0	1	1	0
1619	0	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	0
1620	0	1	1	0	1	1	1	1	1	1	1	1	1	1	1	0	1	1	0
1621	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1
1622	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	1	1	1	0
1623	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	0	1	1	1
1493	0	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1
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1498	0	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	0
1499	0	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	0
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1501	0	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	0
1516	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	0	1	1	0
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1556	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	0	1	1	0
1557	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	0	1	1	0
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1596	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	0	1	1	0
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1599	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	0	1	1	0
1600	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	1	1	1	0
1601	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	0	1	1	0
1602	0	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0
1603	0	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0
1604	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	0	1	1	0
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1606	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	0	1	1	0
1509	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1
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1515	0	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1
1518	0	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
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1503	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	1	1	1	0
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1505	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	0	1	1	0
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1507	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	0	1	1	0
1508	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	0	1	1	1
54480	0	1	1	0	1	1	1	1	0	1	1	1	1	1	1	0	1	1	0

<i>EcoRI</i> -CAT/ <i>AseI</i> -TAA																			
KK#	161	164	167	170	173	174	178	179	183	184	185	186	188	189	193	194	196	198	205
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1535	1	1	1	1	1	1	1	1	1	0	1	1	1	1	0	1	0	0	0
1536	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	0	1	0	0
1537	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	0	1	0	0
1538	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	0	1	0	0
1539	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	0	1	0	0
1541	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	0	1	0	0
1542	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	0	1	0	0
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1544	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	0	1	0	0
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1490	1	1	1	1	1	1	1	1	1	0	1	1	1	1	0	0	0	0	0
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<i>EcoRI</i> -CAT/ <i>AseI</i> -TAA																			
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KK#	EcoRI-CAT/AseI-TAA																			
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1624	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	
1625	1	0	0	1	1	1	1	1	0	1	1	1	1	1	1	0	1	1	1	
1628	1	0	0	0	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	
1607	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	
1608	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	

<i>EcoRI</i> -CAT/ <i>AseI</i> -TAA																			
KK#	206	207	208	209	210	212	218	219	220	224	227	229	234	235	236	238	239	240	247
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1610	1	0	0	0	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1
1611	1	0	0	0	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1
1612	1	0	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1
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1507	0	0	0	0	1	1	1	1	0	1	1	1	1	1	1	0	1	1	1
1508	0	0	0	0	1	1	1	1	0	1	1	1	1	1	1	0	1	1	1
54480	1	0	0	1	1	1	1	1	0	1	1	1	1	1	1	0	1	0	1

<i>EcoRI-CAT/AseI-TAA</i>																			
KK#	252	255	257	261	264	269	270	271	272	273	275	277	278	279	280	282	284	289	289
1534	0	1	1	1	1	1	0	1	0	1	1	1	0	1	1	1	1	0	0
1535	0	1	1	1	1	1	0	1	0	1	1	1	0	0	1	1	1	1	0
1536	0	1	1	1	1	1	0	1	0	1	1	1	0	1	1	1	1	0	0
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1490	0	1	1	1	1	0	1	0	0	1	1	1	0	0	1	0	0	0	1
1491	0	1	1	0	1	1	0	1	0	1	1	1	0	0	1	1	1	0	0
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1522	0	1	1	1	1	1	0	1	0	1	1	1	0	1	1	1	1	0	1
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1525	0	1	1	0	1	1	0	1	0	1	1	1	0	1	1	1	1	0	0
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1607	0	0	1	1	1	1	1	1	0	1	1	1	1	1	1	0	0	0	1
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<i>EcoRI-CAT/AseI-TAA</i>																			
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1607	1	1	1	1	1	0	0	1	1	1	1	1	1	1	0	0	0	1	1
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<i>EcoRI-CAT/AseI-TTC</i>																			
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<i>EcoRI-CAT/AseI-TTC</i>																			
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1607	0	1	1	0	1	1	1	1	0	1	1	1	1	1	0	1	1	1	1
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<i>EcoRI</i> -CAT/ <i>AseI</i> -TTC																			
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<i>EcoRI-CAT/AseI-TTC</i>																			
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KK#	EcoRI-CAT/AseI-TTC		EcoRI-CAT/AseI-TTC																
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KK#	EcoRI-CAT/Ase1-TTC		EcoRI-CAT/Ase1-TTC																
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<i>EcoRI-CAT/AseI-TTC</i>															
KK#	341	345	347	349	352	352	354	356	358	359	360	364	367	373	374
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<i>EcoRI-CAT/AseI-TTC</i>															
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1600	0	1	1	0	1	1	1	1	0	1	0	1	1	1	1
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1508	0	1	1	0	0	1	1	1	0	1	0	1	1	1	1
54480	0	1	1	0	0	1	1	1	0	1	0	1	1	1	1

APPENDIX III

Kansas County Map

