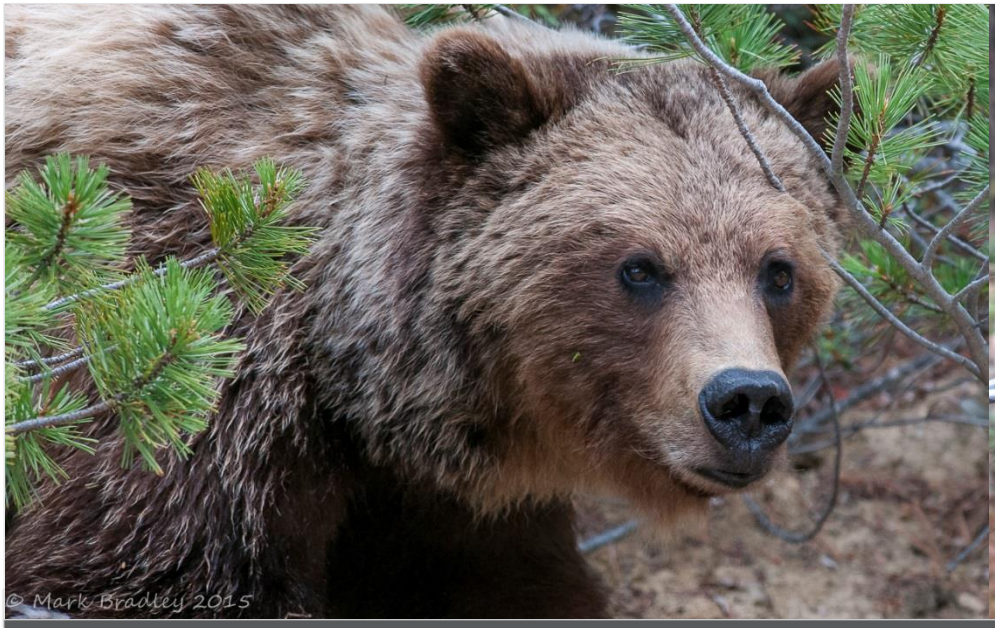

FINAL REPORT

Estimates of Grizzly Bear Population Size and Density for the Alberta Clearwater Population Unit (BMA 4) in 2018 with Comparisons to 2005 Data

Prepared for

Alberta Environment and Parks, Spray Lakes Sawmills, West Fraser Timber and The Forest Resource Improvement Association of Alberta

November 2020
Final Report

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FORWARD

This document represents the achievements and results from the 2018 grizzly bear population inventory project conducted in the Clearwater Bear Management Area (BMA 4). The focus of this project was to complete a DNA inventory in this BMA to provide both a new population estimate and to determine what changes had occurred in the area since the first population inventory was undertaken in 2005. These analyses required DNA laboratory results from the genetic samples collected in 2018, however, project funding was on hold for over a year and a half. With funding provided in 2020, we were able to complete the genetic laboratory work, the statistical analysis, and prepare this final report.

EXECUTIVE SUMMARY

The first grizzly bear DNA population inventory conducted in the Clearwater Bear Management Area (BMA 4) took place in 2005. In 2018, thirteen years following this first assessment, funding and support was provided by two regional forest management tenure holders, and the provincial government, to conduct a second grizzly bear population inventory in BMA 4.

The primary objectives of the 2018 inventory were to obtain an up-to-date estimate of grizzly bear abundance, distribution and density in BMA 4, to compare these findings with the 2005 inventory results, and to investigate the utility of newly created provincial genetic datasets to contribute to grizzly bear population monitoring efforts. We designed sampling and analysis approaches to allow for comparisons between the two time periods. The findings in this report are from the genetic analysis (DNA) of grizzly bear hair collected using non-invasive barb wire techniques and employed scent lures at sampling sites.

The 2018 BMA 4 survey detected 64 bears (35 males and 29 females) compared to 42 bears (17 males and 25 females) in 2005. The 2018 inventory had lower grizzly bear detection success rates than in 2005, which had the highest detection rates out of all grizzly bear DNA inventories in Alberta to date.

As was the case in 2005, the 2018 results showed that many detections occurred along the western side of the study area with a declining density gradient to the east. Most bears were detected in core habitat areas, but bears were also found in secondary habitat areas. Existing modelling tools (Resource Selection Functions [RSFs] and mortality risk [RISK]), which are currently used to guide management practices, proved useful as parameters to model grizzly bear habitat selection within the sampling grid. We found RSF to be a better predictor of grizzly bear densities than mortality risk. Higher densities of grizzly bears occurred in higher RSF areas, particularly in the core zone, where generally lower road densities are found. However, higher bear densities were also found in some low RSF habitats that also had lower RISK. These areas corresponded to some of the mountainous areas along the eastern boundary of Banff National Park.

The spatially explicit capture-recapture (SECR) analysis indicates that the population estimate for BMA 4 is 88 grizzly bears (CI = 59–130) while the population estimate in 2005 was 42 bears (CI = 32–50). Density estimates for this population in 2018 were 9.64 grizzly bears/1000 km^2 (CI= 6.54–14.27) while the 2005 densities were 4.39 grizzly bears/1000 km^2 (CI= 3.52–5.48). These new population and density estimates indicate an increasing population of grizzly bears in BMA 4, which has more than doubled in size since the previous population inventory work in 2005.

Open model analysis of the data also found relatively high apparent survival for female bears 0.96 (CI=0.86–0.99) which further supports the documented demographic increase. This rate of survival should be treated cautiously given that it is based on bears detected in the 2005 and 2018 surveys and therefore it assumes a constant survival rate for the 13-year period between surveys.

A comparison of estimates of density and abundance between 2005 and 2018 suggest increases in both core and secondary habitats with the largest relative increase occurring in secondary areas. This finding has important management implications.

Analysis of home range centers of detected bears using base detection models revealed that most home range centers were in the core area with only 4 of 17 male and 1 of 25 female home range centers falling in the secondary area. The home range centers for bears detected in both 2005 and 2018 also revealed a high level of fidelity for females with minimal change in home range centers, however, male bears showed lower fidelity. From a distribution perspective, the data also suggests that female bears are spreading eastward over time while male bears continue to occupy similar areas.

Long-term provincial genetic data sets, when coupled with DNA inventory data, proved their utility by allowing a greater understanding of bear survival, reproduction and movements of bears within this bear management unit (and provincially) and for the purposes of monitoring these population elements over time. The delay in processing scat samples that were also collected during field sampling sessions may have negatively impacted the genetic laboratory extraction rates. We had no individual scat sample results to use in the population estimation work.

Our findings represent an annual population rate of increase in BMA 4 over a 13-year period of approximately 6%, which is higher than commonly seen in most interior grizzly bear populations in North America. However, this rate of population increase was similar to that found in 2014 within the adjacent Yellowhead BMA 3 population unit to the north. Determination of the reasons for these observed rates of population increase are important for ongoing management decisions but are currently unclear and require additional investigation and analysis to determine how current and past management actions are contributing to this rate of increase.

Grizzly Bear DNA SECR Mark-Recapture Inventory for Bear Management Area 4

Introduction

As part of ongoing provincial grizzly bear recovery efforts, it has been widely recognized that there is an ongoing need to determine population status and trend within the various provincial grizzly bear management areas. In the 2008 it was recommended that population inventory work should be undertaken at five-year intervals within each of the 7 provincial BMAs (Alberta Grizzly Bear Recovery Team 2008). Although this has not taken place in every BMA, one bear management area (BMA 3) has had two inventories completed. The first taking place in 2004 and the second in 2014 (Stenhouse et al. 2015), which found that the population had doubled in size during the 10-year time period.

In an effort to determine grizzly bear population status in other BMAs, a collaborative project was undertaken between regional forest tenure holders and the Alberta Government in 2018 to assess grizzly bear populations in both BMA 7 (Swan Hills) and BMA 4 (Clearwater). This report details the results of our spatially explicit based (SECR) mark-recapture population inventory of grizzly bears in the Clearwater Bear Management Area (BMA) 4. This area was previously surveyed by our research team in 2005 (Boulanger et al. 2005) with an estimated population size of 45 bears (coefficient of variation (CV = 8.9%) using a closed population model analysis. In the first year of the current FRIAA supported project, this data set was re-analyzed using SECR models with a resulting estimate of 43 bears (CV = 15.7%). In both analyses, the resulting density estimate was approximately 5 bears per 1000 km^2 for the grid area.

Since the population inventory in 2005, management boundaries within the BMA have been further designated into core and secondary conservation areas (combined as recovery zone) that now provide a guideline for assessment of populations relative to habitat states and anthropogenic risks (Nielsen et al. 2009). The primary current management emphasis is recovery of grizzly bears within these recovery zones that consist of higher quality habitat with lower road densities. The core and secondary conservation areas provide a management-based stratification of BMA areas as well as a delineation of core habitat areas that should harbor the highest densities of bears within BMA areas (Nielsen et al. 2006). Therefore, sampling consideration of core and secondary areas was of primary consideration in the design of the BMA 4 2018 inventory with an emphasis being on estimation of densities within these areas. The study design for this project incorporated our current knowledge of the study areas and resident bear populations, previously used spatially explicit capture recapture methods, and relied on DNA hair sampling methodologies that use non-invasive approaches.

The objectives of this BMA 4 inventory were to:

1. Provide an estimate of the current population size within this BMA

2. Obtain a current (2018) estimate of abundance, spatial distribution and density that can be compared to the 2005 inventory estimates.
3. Assess changes in the distribution relative to core, and secondary areas, including a statistical comparison of point estimates of density as well as distribution of bears across the BMA area.

Study Area

The 2018 DNA inventory of BMA 4 consisted of a systematic sampling grid with 148, 49 km^2 grid cells covering approximately 7252 km^2 of the eastern foothills of Alberta's Rocky Mountains (Figure 1). Because population closure is an important assumption of our population estimators, we designed the sampling of the study area to minimize the movement of bears across the boundaries. Our study area encompassed almost all habitat designated as core and secondary grizzly bear conservation areas in BMA 4. The sampling area was bounded by Highways 1 and 11, providing relative closure to the south and north respectively. To the east, the area extended into land minimally occupied or unoccupied by grizzly bears, and to the west it reached into portions of Banff National Park. The sampling design mimicked that used in the 2005 inventory to allow direct comparisons between the sampling years (see Appendix 1 for full 2005 study design details).

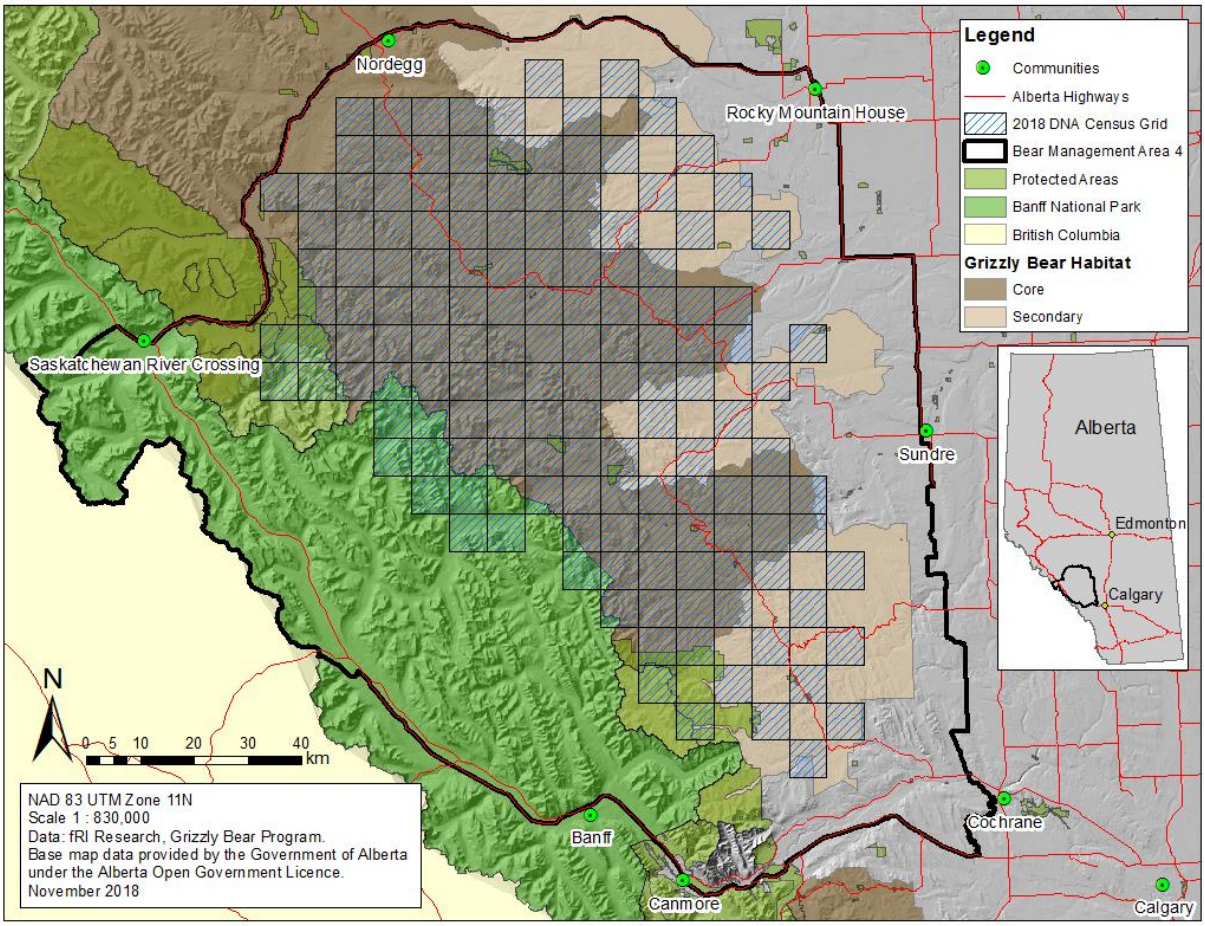


Figure 1: The Clearwater Bear Management Area (BMA 4), including provincial lands, Banff National Park, and the core and secondary grizzly bear habitat areas.

Elevation ranged from 800 m to 3500 m and included a diversity of habitats. Sub-alpine areas consisted primarily of Engelmann spruce (*Picea engelmannii*) and sub-alpine fir (*Abies lasiocarpa*) whereas upland forests consisted of aspen (*Populus tremuloides*), white spruce (*Picea glauca*), and open stands of lodgepole pine (*Pinus contorta*). Lowland forests were characterized by mixed forests of black spruce (*Picea mariana*), tamarack (*Larix laricina*), and lodgepole pine while wetlands and riparian areas were dominated by willow (*Salix spp*.) and shrub-graminoid communities. Important grizzly bear foods occurring in the area include buffaloberry (*Shepherdia canadensis*), alpine sweet vetch (*Hedysarum alpinum*), cow parsnip (*Heracleum lanatum*), and various blueberry species (*Vaccinum spp*.; Munro et al., 2006). Other large predators in the region are black bears (*Ursus americanus*), wolf (*Canine lupus*), and cougar (*Puma concolor*).

Several different types of landuse activities occur within BMA 4 including forestry, oil and gas exploration and development, and extensive outdoor recreation. Protected areas within BMA 4 include Banff National

Park, Kootenay Plains Ecological Reserve, Siffleur Wilderness Area, Ghost River Wilderness Area, and Don Ghetty Provincial Park. Linear features such as roads, pipelines, seismic lines, and all-terrain vehicle (ATV) trails are widespread on the landscape making most of the study area accessible by vehicle and foot, though some areas required helicopter support for access, including the vast majority of Banff National Park.

METHODS

Barb wire hair-snag sampling of grizzly bears in western Canada is usually based on spatial sampling design that places one or more hair snag sites in each cell of an arbitrary square grid (Woods et al. 1999, Proctor et al. 2010, Boulanger et al. 2018). This ensures sufficient spatial coverage while allowing some latitude for the placement of hair snags within each cell. Overall sampling intensity is governed by the grid cell size, the number of sites per cell, and the duration of sampling.

Field Data Collection

Site Selection

We selected 2018 site locations based on the 173-cell 7 km × 7 km grid system applied to BMA 4 during the 2005 grizzly bear DNA inventory. By maintaining close consistency between 2005 and 2018 study design and sampling strategies, we aimed to allow for comparisons between these two data sets. We modified the 2018 grid, however, to better reflect core and secondary grizzly bear conservation areas (Nielsen et al. 2009), which were not established or mapped during the 2005 DNA inventory. The northern tip of BMA 4 was not sampled due to high recreational traffic in the area and difficulties with placement of hair snag sites. We continued to sample every cell in the core areas, while systematically sampling the secondary areas (every other cell) therefore allowing a robust estimate of density. The sampling design is also similar to that employed in the 2014 BMA 3 population inventory (Boulanger and Efford 2014; Stenhouse et al. 2015). Our final grid in 2018 consisted of 148 cells (Figure 2).

One hair snag site was placed in each grid cell. Sites were not moved throughout the field season since spatially explicit methods are theoretically more robust to heterogeneity caused by site placement relative to home range centers (Boulanger and Efford 2014; Stenhouse et al. 2015). Where possible, we used the same within-cell locations as in the previous survey (2005) DNA site locations. Where necessary, we generated new site locations in a geographic information system (GIS) prior to fieldwork using a grizzly bear resource selection function (RSF) model (Nielsen et al. 2002), aerial photographs, and expert opinion. Preference was given to areas of high RSF and reasonable access for field crews. In the field, we targeted site locations near riparian areas, linear clearings, natural meadows, and forestry cutblocks. Research has shown that placing sites in these areas is important for maximizing detection at fixed hair snag sites (Rovang et al. 2015). To minimize the risk of bear-human encounters and to address public safety concerns, sites locations were also placed at least 200 m from roads, pipelines and heavily used seismic

lines (i.e. ATV trails), and 500 m from facilities (e.g. wellsites, industrial camps, trapper cabins, campgrounds, or private homes).

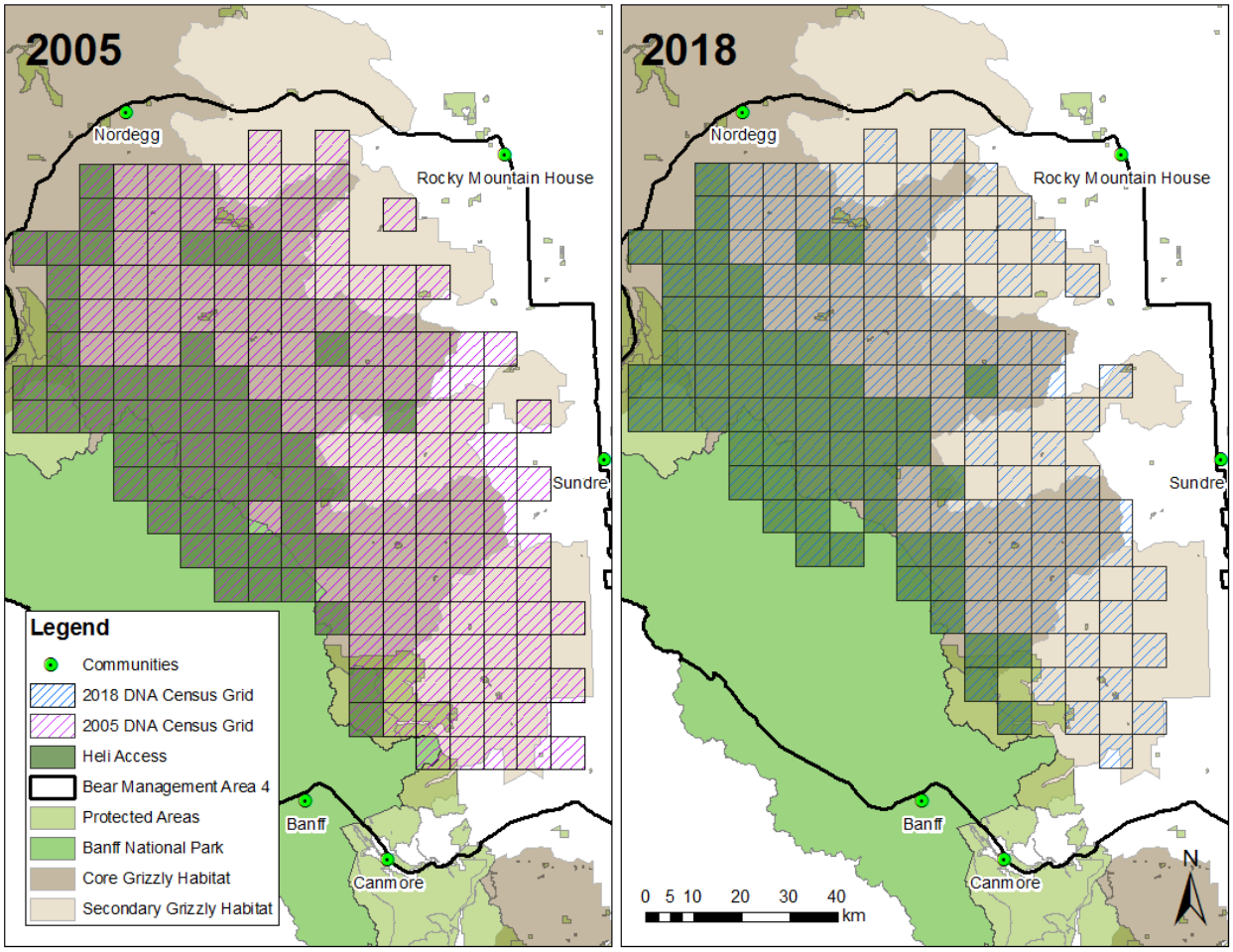


Figure 2: DNA sampling grids used in the grizzly bear population inventory of the Clearwater Bear Management Area (BMA 4) in 2005 (173-cells) and 2018 (148-cells). Green highlighted cells depict cells that required helicopter access.

Site Set-Up and Sampling

We built hair snag sites (corrals) using approximately 30 m of barbed wire strung around 3-6 trees at a height of 55 cm above ground following protocols adapted from previous studies (Woods et al. 1999, Boulanger et al. 2005, 2006). We constructed a scent lure pile in the center of the corral using branches, rotten wood, and other forest debris, topped with a thick layer of moss or other absorbent material available at the site. Corrals were large enough so that the lure pile could be reached only when a bear crossed over or under the barbed wire. Uneven ground (low or high spots) below the wire was filled or obstructed to prevent bears from entering the corral without coming into contact with the wire. During site setup and every two weeks thereafter, we baited the site with 2.5 L of scent lure (2 L of aged cattle

blood mixed with 500 mL of canola oil), topped with conifer branches to protect the lure from rain. Each site was set up with caution tape and a warning sign to deter the public from entering the sampling area.

Our field season consisted of 5 field sessions from May 22nd to July 25th 2018. Following our first shift of site set-up with no hair collection (Session 0), we checked sites for hair every 14 days for 4 sampling periods (Sessions 1, 2, 3, and 4; with hair collection). Three helicopter access cells were not set up due to a prescribed fire along the Panther River during the set-up shift (cells 459, 487, and 486, Session 0). An additional helicopter access cell was not set up due to challenging access from steep slopes, persistent wind, and difficult terrain (cell 430, Session 0). Two truck access sites were not established until the first hair collection session (Session 1) due a black bear encounter (site 319B) and time constraints (site 409E) in Session 0. One site (607E) was replaced and relocated (as 607G) in Session 1 after unintentionally being set up in a grazing lease.

Once sites were established, every site was sampled each session. Hair samples were collected and placed in paper envelopes. Each barb on the wire with hair was treated as a single sample that was placed into its own envelope. Hair samples on adjacent barbs were labelled as a group, and groupings were split by one or more empty barbs. Samples from the ground, trees, shrubs and the bait pile were considered as separate groupings. Samples on the wire (but not on a barb) were also a separate grouping, unless known to be immediately adjacent to a barb. Based on these designated groupings, we selected the best hair sample in each group.

During the field season, we implemented a sub-sampling protocol for hair samples which staff could identify as black bear with a high degree of confidence, due to the abundance of black bears at sites and the time required for sampling. As of June 20th 2018 (Session 2), barb groups with 2 or more adjacent black bear samples, regardless of the total number of samples at a site, were sub-sampled. We selected the best sample for each set of three black bear samples within a barb group. All grizzly bear samples were always collected, as well as any samples that crews suspected had the slightest possibility of being grizzly bear.

We collected data regarding sample location, adjacency to other samples, and sample quality to facilitate the final sub-selection of hair samples for DNA analysis. Following collection of samples, we burned the barbed wire to confirm no hair was inadvertently left behind, ensuring that hair found during subsequent visits was from the correct sampling session. Throughout the field season, hair samples were stored with silica desiccant both in the field and in the office.

Once all hair samples were collected, a 25 m radius from the site center was searched for bear signs (e.g., digging, anting, foraging on vegetation or berry bushes, beds, or scat). Any suspected bear scat found at hair snag sites was collected and documented with additional information (e.g., likelihood of the same bear for multiple scats, scat contents, etc.). Bear scat was sampled using a wooden sampling stick to collect 1 cm^3 of scat. Samples were stored in vials containing silica desiccant. Scat samples were also collected opportunistically during the walk to and from sites and well as while driving along the roads within the

grid sampling area. If scat samples were located on a road, after sampling the remaining scat was cleared off the road to prevent duplicate samples.

All field data collected was entered directly into a tablet using the Device Magic Mobile Forms Software and Data Collection App for consistent data entry. Separate forms were used for site set-up information, site habitat and photo information, scat collection and hair collection.

As part of ongoing research, there were also active culvert trapping sites where grizzly bear capture and collaring work took place before the DNA inventory data collection period began. To avoid having other scent lures in the sampling area which had the potential to affect hair capture rates, all capture and collaring work concluded before barbed wire sites were set up.

Sub-Selection of Samples for DNA Analysis

As is the case in most large-scale grizzly bear inventory projects and recognizing budget constraints, it was not possible to genotype all hair samples collected during 2018. To select a sub-sample of hair for the DNA analysis, we followed a series of sub-selection criteria based on those previously used for DNA surveys in Alberta (Stenhouse et al. 2015). The sub-sampling criteria have been shown to result in a minimal reduction in the number of individual bears identified. Initial screening of hair samples excluded those identified as non-bear species, and those with a high confidence of species identified as black bear. In some cases, it was possible to confirm bear species using wildlife camera data from the hair snag site. Previous research (David Paetkau, pers. comm.) indicates that for successful genotyping, bear hair samples must include either 1) at least one guard hair, or 2) five or more underfur hairs. Samples that did not meet these minimum criteria were excluded based on the likelihood that they did not contain sufficient genetic material.

For hair snag sites, we reviewed each site and session separately, and further criteria were only applied to samples not excluded by the initial screening criteria. At a minimum, we selected the best sample for each site/session, as indicated by field data, hair sample size, and probability of grizzly bear species. In addition, we selected 1 in every 3 from adjacent samples, starting with the best sample in each barb group. If there were more than 3 samples in a barb group, for the remaining samples, greater preference was given to samples with a greater number of guard hairs and samples with greater confidence in grizzly bear species identification. Less preference was given to samples with unknown species, samples with black bear and grizzly bear hair on the same barb, and directly adjacent samples.

Bear scat found on roads, on the way to and at hair snag sites during site set-up and collection sessions were sampled and sent for genetic analysis.

Lab Methods

We sent our hair samples to Wildlife Genetics International (WGI), Nelson, Canada, for genotyping to identify species, gender and individual bears. We did not analyze samples that lacked suitable material for analysis (no guard hair roots and less than 5 underfurs), samples that contained other species hair (e.g., ungulate), or samples with uniform jet-black colouration associated with black bears. The DNA from the

remaining samples was purified using QIAGEN DNeasy Blood and Tissue kits, with the tissue protocol. The lab aimed to use 10 clipped guard hair roots, if available, or up to 30 whole underfurs, if needed to supplement guard hairs. Multilocus genotyping was used to analyze the DNA extracts with the established set of 8 'Alberta grizzly bear' markers (7 microsatellites plus [G10B, G10H, G10J, G10M, G10P, G1A, G1D] a ZFX/ZFY sex marker) to identify unique individuals. The samples went through multiple passes and error checking during genotyping (Paetkau 2003). An individual was defined for each unique multilocus genotype using the 8-locus analysis to produce full genotypes. The sample that provided the best result for each bear had an additional 13 microsatellites run (CPH9, CXX110, CXX20, G10C, G10L, G10U, G10X, MSUT2, MU23, MU50, MU51, MU59, REN145P07), so each bear had a final genotype consisting of 20 microsatellites plus a sex marker.

For scat, we sent our samples to the DNA lab at the Norwegian Institute of Bioeconomy Research (NIBIO), Ås, Norway to determine the species, identity and gender of individuals using STR markers. DNA was extracted from the samples and each sample underwent a mitochondrial DNA (mtDNA) species-specific differentiate grizzly from black bear scat. For all samples identified as grizzly bear, genotypes were determined based on 12 STR markers (G10B, G10J, G10L, G1A, G1D, MU50, G10P, Mu23, Mu51, Mu59, G10X and G10U) and one sex-specific marker (BIK-F XY). Samples with unique profiles included the analysis of 9 additional STR-markers (GIOH, G10M, G10C, REN145P07, CPH9, CXX20, MSUT2, MSUT6 and CXX110).

For both lab methods, identified individual profiles were compared with known individuals in our fRI provincial reference database.

Data Analysis

Spatially explicit capture-recapture (SECR) methods (Efford et al. 2004, 2009, Efford 2004, 2011) estimate population density allowing for the spatial scale of movement, estimated from the detection sites of bears that are detected repeatedly. Unlike closed models that pooled data from multiple hair snag sites within each session for each bear, the SECR method used multiple detections of bears at unique hair snag sites within a session to model bear movements and detection probabilities. Using this information, the detection probabilities of grizzly bears at their home range center (g_0), spatial scale of grizzly bear movements (σ) around the home range center, and bear density were estimated.

An assumption of this method is that grizzly bear home range can be approximated by a circular symmetrical distribution of use (Efford 2004), but the method is robust to deviations from circularity (Efford 2019b). The configuration of the sampling sites is used in the process of estimating the scale of movements and density, and lack of geographic closure (incursion of bears centered outside the grid) is modeled directly. There is therefore no need to adjust for study-area size and closure violation as with previous closed models.

SECR models detections of bears with home ranges centered either directly on the sampling grid or in adjoining habitat; the grid and adjoining habitat together comprise the habitat 'mask'. Considering too little adjoining habitat as the potential source of detected bears can cause positive bias in density

estimates. An initial analysis was conducted with sexes combined to determine the size of the mask (relative to study area size) needed to control bias in density estimates. The *esa.plot* and *suggest.buffer* functions of the R package 'secr' were run for a g_0(sex) σ(sex) conditional likelihood model. These suggested a buffer width of 35 km would give unbiased estimates; estimation is also expected to be unbiased with a wider buffer, but computation is then slower for a given spatial resolution. Subsequent analyses were run separately for male and female grizzly bears to test for variation in detection probability at the home range center and scale of movements.

Spatially explicit capture recapture model fitting had three phases: 1) tests for temporal, behavioural, and individual variation in g_0 and σ to establish a 'baseline' model of detection. 2) Addition of site covariates to baseline model to describe heterogeneity induced by site placement. 3) Using the most supported model from step 2, strata-specific and other density covariate models were fit.

Terrain ruggedness index and canopy closure were used as site covariates and evaluated at two spatial scales as potential predictors influencing detection probability parameters (g_0 and σ; Table 1: Site habitat and sampling covariates used to describe scale of movement and detection of bears; (Boulanger et al. 2009). The two scales ('site' and 'home-range') corresponded respectively to the distance at which bears encountered (i.e., responded to) hair snags and the typical home-range radius. We used 1.96 km as the site scale, based on estimates by (Boulanger et al. 2004), and 10 km as the home range scale, corresponding to bear home range areas (Nielsen et al. 2004). Humans often plan and influence land use activities approximately on the scale of bear home ranges (i.e., the township). In most cases site scale was used as a covariate for detection probabilities (g_0) and home range scale was used as a covariate for the σ scale parameter. For this phase of the analysis, density was assumed constant across the extent of the survey area.

Table 1: Site habitat and sampling covariates used to describe scale of movement and detection of bears

Habitat Variable	Description
TRI	Terrain ruggedness index (Riley et al. 1999)
CC	Percent canopy cover

Strata were defined based on a-priori boundaries of management interest as well as likely difference in density and sampling intensity (

Table 2 and Figure 2). Banff National Park was minimally sampled and the strata area listed in

Table 2 corresponds to the area covered by DNA cells rather than the entirety of Banff National Park.

Table 2: Strata used in spatially explicit capture-recapture analysis. Habitat area is defined by the total area minus area of barren landcover of greater than 2000 m elevation.

Strata	Defined By	Sampling Design	Area (km^2) & Total %	
			Total	Habitat
BMA 4 Core	BMA 4 grizzly bear zone	One site per 7x7 km cell 4 sessions	5934.0 (56.7%)	5151.7 (56.7%)
BMA 4 Secondary	BMA 4 grizzly bear zone	One site per 10x10 km cell 4 sessions	3823.8 (36.8%)	3609.7 (39.7%)
Banff	Cells in mountainous/ protected areas	One site per 7x7 km cell 4 sessions	622.3 (6.0%)	326.7 (3.6%)

Some sites were not sampled in all sessions and the resulting temporal variation was represented with a binary 'usage' matrix—a series of 1s and 0s for each site indicating the sessions in which it was active (1) or non-active (0). The habitat mask for the SECR analysis used a discrete cell size (i.e., mask spacing) of 3 km for all analyses. A sensitivity analysis of mask spacing suggested 3 km was a good compromise between processing time and minimizing bias in estimates (no change in density [D] with spacing of 3.5–2.5 km). Mask cells were categorized according the stratum of their centroid. Centroids outside of the grid area (where no sites were sampled) were assigned to the stratum of the nearest BMA 4 cell. Many of the sampling grids contained substantial areas of barren rock and ice which was not considered suitable habitat for grizzly bears (Figure 5). Barren land cover above 2000 m was excluded from the habitat mask in the SECR analysis, as in previous habitat analyses using DNA mark-recapture data (Boulanger 2015, Stenhouse et al. 2015).

Estimates of home range center, and potentially density, are sensitive to differences in sampling intensity in core and second strata. The effect of sampling intensity on density was further tested using a "site density" model that grouped the Banff and core strata (1 site per 7x7 km cell) and the secondary (1 site per 10x10 km cell). This model was used for baseline density estimates as well as estimation of home range centers. The issue of site layout was not prevalent in the 2005 project where all cells on the sampling grid were sampled equally with one site per session that was moved between sessions.

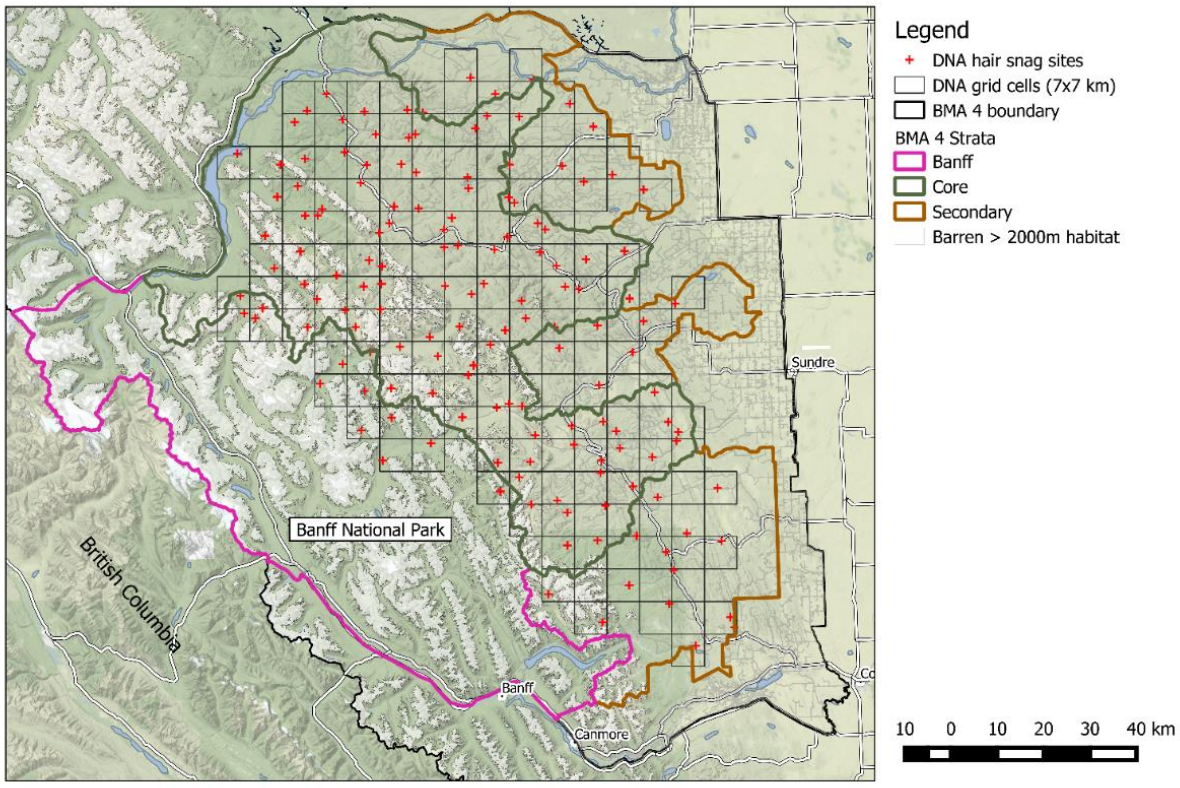


Figure 3: Layout of DNA sampling grid cells and sites in Clearwater BMA 4. Each site was sampled for 4 sessions.

One potential challenge with estimating density for the BMA 4 grid was that it Park on the west and the foothills/plains to the east, which likely created a SECR methods are reasonably robust to heterogenous densities within sampling however, it was likely that there might be sensitivity of estimates to placement relative to Banff National Park. Defining Banff as a stand-alone stratum for the complicated by the very small proportion of habitat in Banff (3.6% of total habitat area;

Table 2) that was sampled which resulted in imprecise estimates if modelling Banff as a stratum. To confront this issue and explore factors influencing density on the grid, surface models were run with habitat value (Resource Selection Function, RSF) and mortality risk as predictors of density across the SECR mask. This general approach was used previously with the BMA 4 data set to also assess relative factors influencing density in BMA 4 (Boulanger et al. 2018). Figure 3 illustrates the values of RISK and RSF for the SECR mask used in the analysis. The distribution of these metrics from west to east, as indexed by the distance from the B.C. border illustrates the spatial gradient in RSF and RISK with increasing RISK and decreasing RSF from west to east (Figure 5).

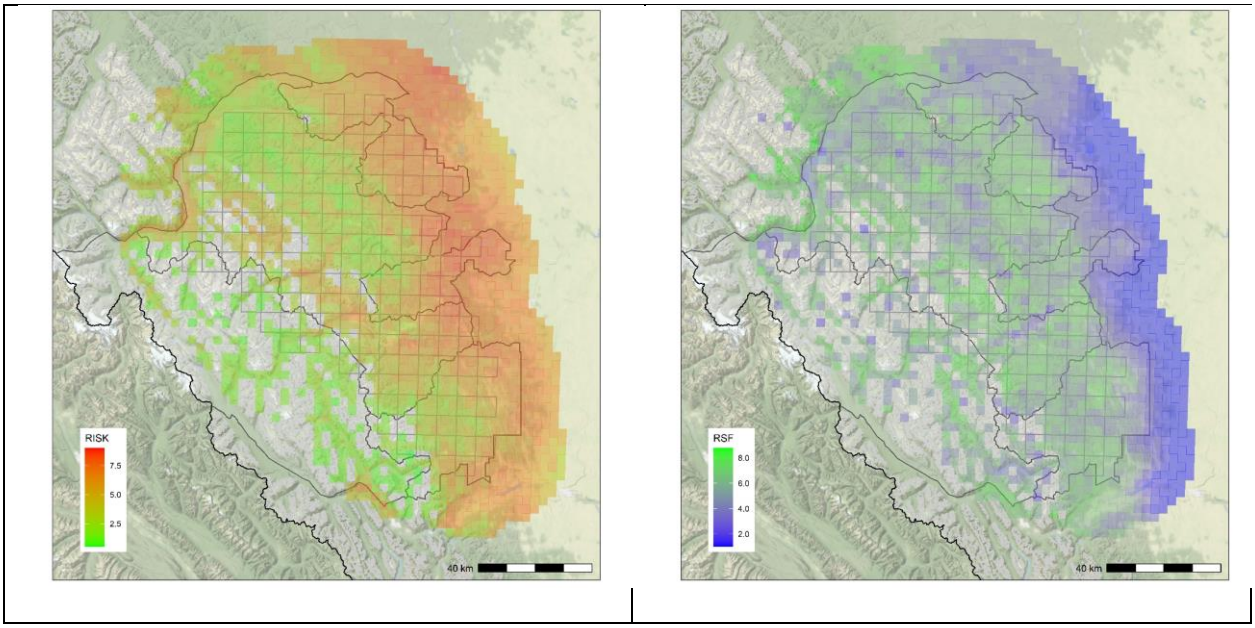


Figure 4: RISK and RSF surfaces used for density surface modelling.

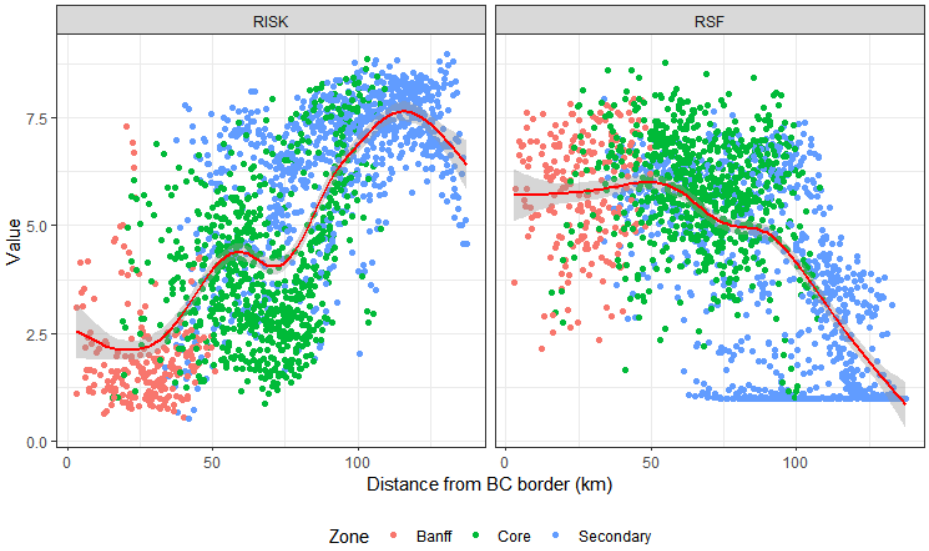


Figure 5: Scores of RISK and RSF covariates as a function of distance from the Alberta/British Columbia border as an illustration of spatial gradients in habitat value (RSF) and RISK going from West to East in the study area. Points are also coded by zone in which they occurred.

Expected population size and density estimates were derived from the most
sex and stratum combination. Estimates of grizzly bears on the entire sampling
protected areas within each sampling grid (

Table 2) were produced. Expected population size is the expected number of bears that would be contained within the study area or regional area at one time (Efford and Fewster 2013). It is analogous to the average number of bears on the sampling grid given in previous survey reports. Density is then estimated as the expected number of grizzly bears divided by the entire area of the grid, or the habitat area within the grid. Log based confidence intervals on expected population size and density were generated using formulas from Efford and Fewster (2013). The precision of SECR estimates is primarily related to the number of bears on the sampling grid and the number of recaptures during sampling (Efford and Boulanger 2019). It is indexed by the coefficient of variation (CV_d), which is the standard error of an estimate divided by the estimate. One central question in study design is whether precision of estimates is limited by the number of bears on the sampling grid or estimation of detection parameters, which relates to recaptures and the complexity of detection models. To explore this question, we dichotomized estimate precision into binomial variation caused by the number of bears detected on the sampling grid (CV_n) in contrast to the variance caused by estimation of effective sampling area and related detection parameters (CV_a). These two components add up to the CV of the density estimate using the equation $\mathrm{CV_d} = \sqrt{\mathrm{CV_n^2} + \mathrm{CV_a^2}}$ (Huggins 1991, Borchers and Efford 2008, Efford 2019b).

Estimates from BMA 4 were compared to assess overall change and annual change (λ) for males, females, and pooled estimates for core, secondary, core+secondary, Banff, and the total sampling grid. The gross change was then scaled to an annual change (λ: under the assumption of constant exponential increase) as the 13th root of gross change. This basically assumes a constant annual rate of change so that annual λ values are multiplied together to equal overall change. For example, the change from 2005 to 2007 would be $\lambda_{2005\text{-}6}$*$\lambda_{2006\text{-}7}$. This sequence could then be repeated up to 2018 to obtain the gross change estimate. The log-normal (skewed to the right) shape of the distribution of abundance and density estimates was accounted for when estimating trend using a simulation approach where 1000 samples were drawn from the log-normal distributions of estimates for each year and 1000 estimates of gross change and λ used to calculate percentile based 95% confidence limits (2.5th and 97.5th percentiles) for gross change and λ.

In addition, a cursory open model analysis (Pradel 1996, Boulanger et al. 2004, Efford 2019b) was conducted to cross-validate estimates of λ from ratios of estimates as well as provide estimates of apparent survival (ϕ: probability that a bear that was present in 2005 was still present in 2018 in the sampled area) if adequate sample sizes (recaptures of bears from 2005 in 2018) occurred. The long-time interval between years of sampling precluded detailed open model analyses.

All spatially explicit analyses were done in package *secr* (Efford 2014a) and *openCR* (Efford 2019a) in the R statistical software (R Development Core Team 2020). Map and data figures were produced using program *QGIS* (QGIS Development Team 2020), *ggplot* (Wickham 2016) and *ggmap* (Kahle and Wickham 2013) R packages.

RESULTS

DNA Sample Extraction Rates

The lab results show there was a difference in the success of confirming the species and identifying unique individuals from DNA samples depending on the biological sample used (Table 3).

Of the 706 sub-selected hair samples sent to the genetics laboratory 8% (57/706) were not analyzed as they were visually determined as not grizzly bear species and 13% (90/706) lacked material suitable for analysis. One sample came from more than one animal and was not analyzed. Of the 559 remaining samples analyzed, 93% (518/559) of the samples were successfully identified to the bear species level, with 60% (310/518) determined as grizzly bear and 40% (208/518) were black bear (*Ursus americanus*). From the 310 grizzly bear samples, 271 samples were assigned to 63 individual grizzly bears, with an 87% (271/310) success rate to the individual level.

Of the 88 scat samples sent to the lab, 19% (17/88) were negative for bear DNA in the species-specific test, while 81% (71/88) were successfully identified as a bear species. Twenty-five percent of bear species samples (18/71) were grizzly bear and 75% were black bear (53/71). Sixty-one percent of the grizzly bear samples (11/18) were positive in the microsatellite analysis, however, none of these samples were successfully assigned an identity.

Table 3: Extraction rate comparisons between hair sampling and scat sampling techniques for species and individual level analyses.

	Hair Sampling	Scat Sampling
Number of Samples Sent to the Lab	706	86
Number of Samples Analyzed	559	86
Percentage of Samples Identified to Bear Species	93% (518/559)	81% (71/88)
Percentage of Samples Determined Grizzly Bear	60% (310/518)	25% (18/71)
Percentage of Samples Determined Black Bear	40% (208/518)	75% (53/71)
Percentage of Grizzly Bear Samples Identified to Individual	87% (271/310)	0% (0/88)
Number of Individual Grizzly Bears	63	0

Sampling and Distribution of Bear Species in BMA 4

Of the 148 sites in BMA 4, 75% of sites had hair samples found at least once during the hair collection sessions and 25% of sites had no hair found. The bear species detected in 2018 show some variation in the location of grizzly bears within BMA 4 compared to those detected in 2005 (Figure 6).

For scat samples, we found suspected bear scat at 21% of sites, while there was no scat found at 79% of sites. Additional scat samples were encountered and collected along the path to hair snag sites, ATV trails and roads within the study area (Figure 7).

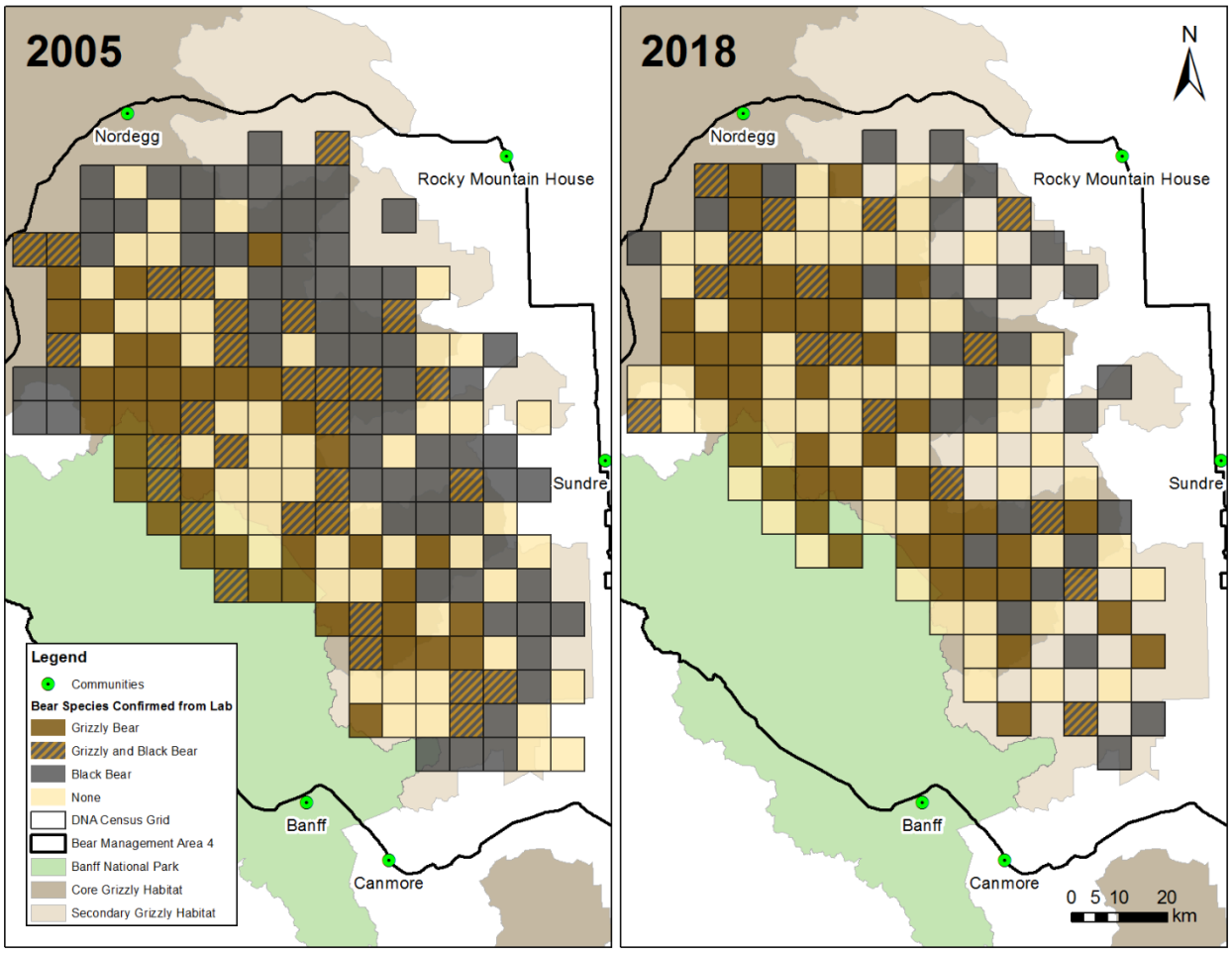


Figure 6: Comparison of bear species locations confirmed in the lab from hair samples in 2005 and 2018 during the DNA inventories of the Clearwater Bear Management Area (BMA 4). Note that this excludes black bear hair visually determined in the field and in the lab.

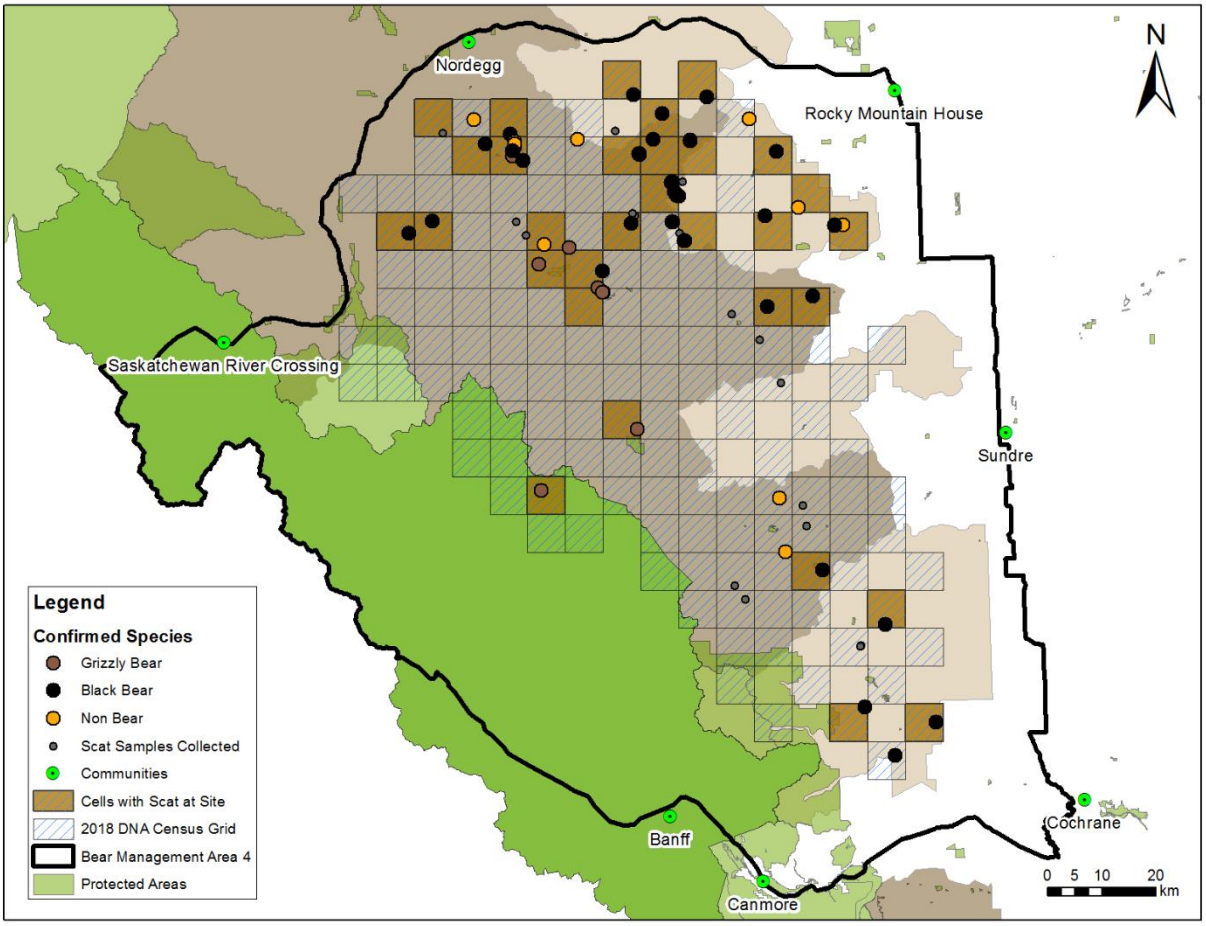


Figure 7: Location of scat samples found and cells with scat samples found at hair snag sites in 2018 during the DNA inventory of the Clearwater Bear Management Area (BMA 4).

Data Summary for Population Analysis – Hair

Sampling occurred across 4 sessions from June to the end of July with a mean sampling interval of 14.1 days (std=0.67, min=12, max=17, n=590). Sampling was synchronized with equal gaps between sessions (Figure 8). The actual number of sites active per session varied from 146 to 148 sites (Table 4). The number of individuals detected per session varied from 18 in session 1 to 31 in session 4.

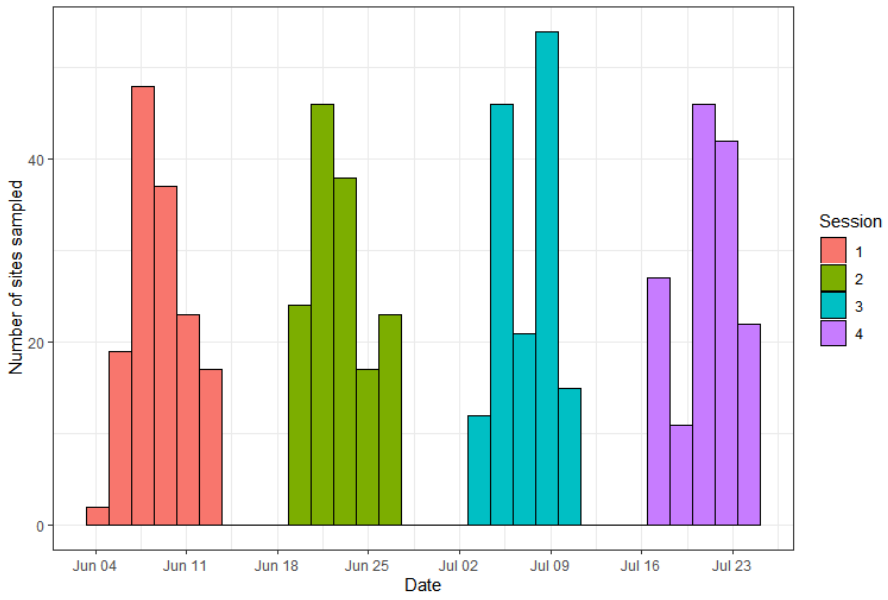


Figure 8: Timing of survey sessions for the BMA 4 inventory. The number of sites sampled by date and session are shown.

Table 4: Summary statistics for BMA 4 Inventory project.

Statistic	Session				
	1	2	3	4	Total
Females + Males					
Animals caught (n_j)	18	13	27	31	89
Newly caught (u_j)	18	10	19	17	64
Total individuals caught (M_j)	18	28	47	64	64
Detection frequencies (f)	46	11	7	0	64
Unique detections	20	16	32	41	109
Detectors visited	16	14	22	29	81
Females					
Animals caught (n_j)	5	5	11	17	38
Newly caught (u_j)	5	4	9	11	29
Total individuals caught (M_j)	5	9	18	29	29
Detection frequencies (f)	22	5	2	0	29
Unique detections	5	6	13	20	44
Detectors visited	5	5	12	15	37
Males					
Animals caught (n_j)	13	8	16	14	51
Newly caught (u_j)	13	6	10	6	35
Total individuals caught (M_j)	13	19	29	35	35
Detection frequencies (f)	24	6	5	0	35
Unique detections	15	10	19	21	65
Detectors visited	14	10	14	20	58
Detectors employed	146	148	148	148	590

Overall, 64 bears (29 females, 35 males) were detected. The proportion of new bears detected (Figure 9) did decrease with session, however, in session 4 55% of bears detected were new bears suggesting sampling was moderately effective in detecting all the bears on the sampling grid. In comparison, the proportion new bears detected in the 2005 BMA 4 survey was 7% (Figure 9). Detection frequencies, which is the number of sessions individual bears were detected, was moderate for both males and females with a proportion of bears being detected in up to three different sessions.

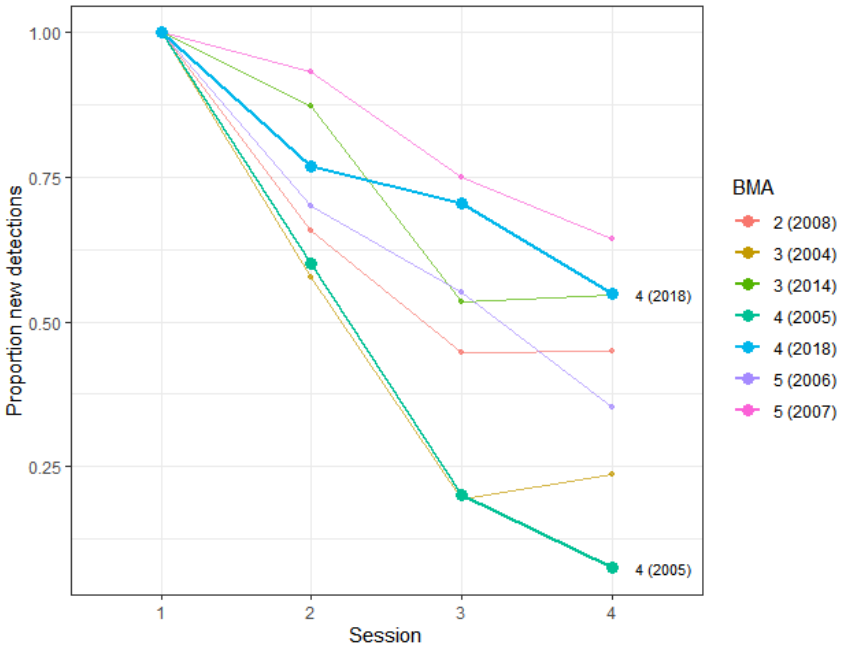


Figure 9: Proportion new bears detected by session for the BMA 4 (2005 and 2018) compared to each other and other inventory projects. BMA 4 inventories lines are bolded and labelled.

The spatial spread of detections by session (Figure 10) shows that most bears were detected in core areas and the cells that occurred in Banff National Park, however detections did occur in secondary areas in all sessions except session 3. Some sites had up to 4 individual bears detected which were potentially family groups. As with the 2005 survey, many detections occurred on the western edge of the grid in Banff National Park.

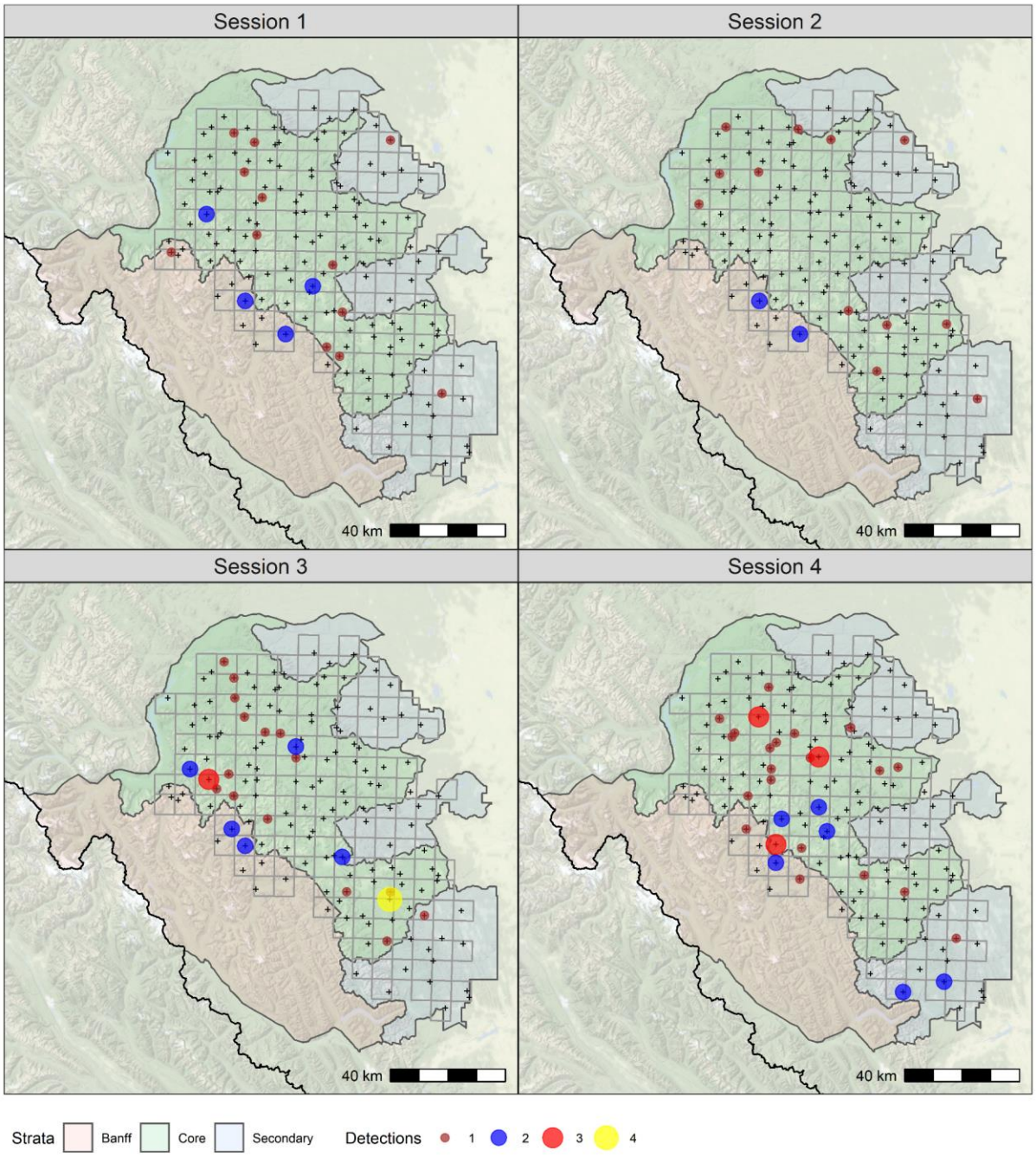


Figure 10: Spatial distribution of hair snag sites (+ signs) and frequencies of bears detected at sites for each sampling session.

The location of male and female detections suggests similar distribution for males and females. However, movement of males was much more widespread with 3 males venturing into the secondary strata along with 2 only detected in the secondary strata. In contrast, two females were detected in the secondary strata (Figure 11).

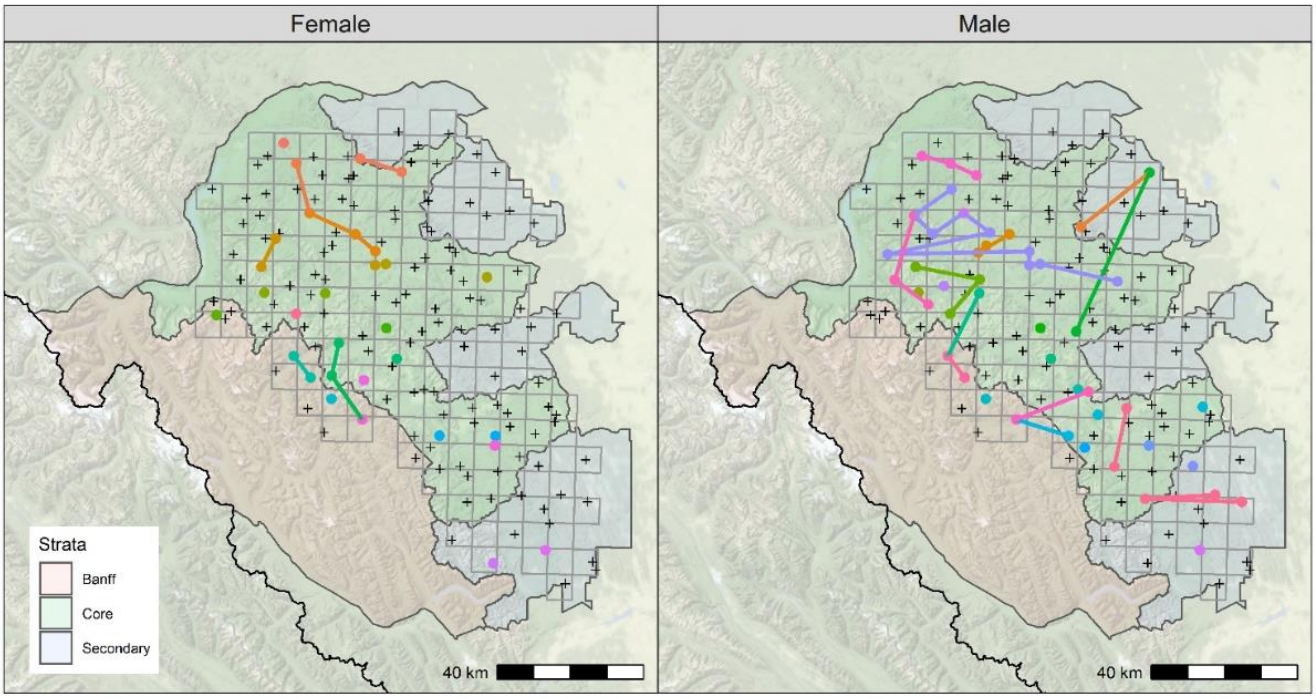


Figure 11: Detections of individual female and male bears. Multiple detections for individual bears are connected by lines indicating potential paths of travel. The order of paths is approximate given that the time of detections of bears within sessions is unknown.

Four bears were collared during sampling, however, of these only G355 had locations on the sampling grid during sampling (Figure 12). One female (G354) had locations on the grid prior to the survey on the east side of the grid but was then detected on the grid on the west side of the grid. The two other collared bears did not have locations on the grid and were not detected during DNA sampling. The low sample size of collared bears on the sampling grid during sampling precluded further inclusion of collared bears in the analysis.

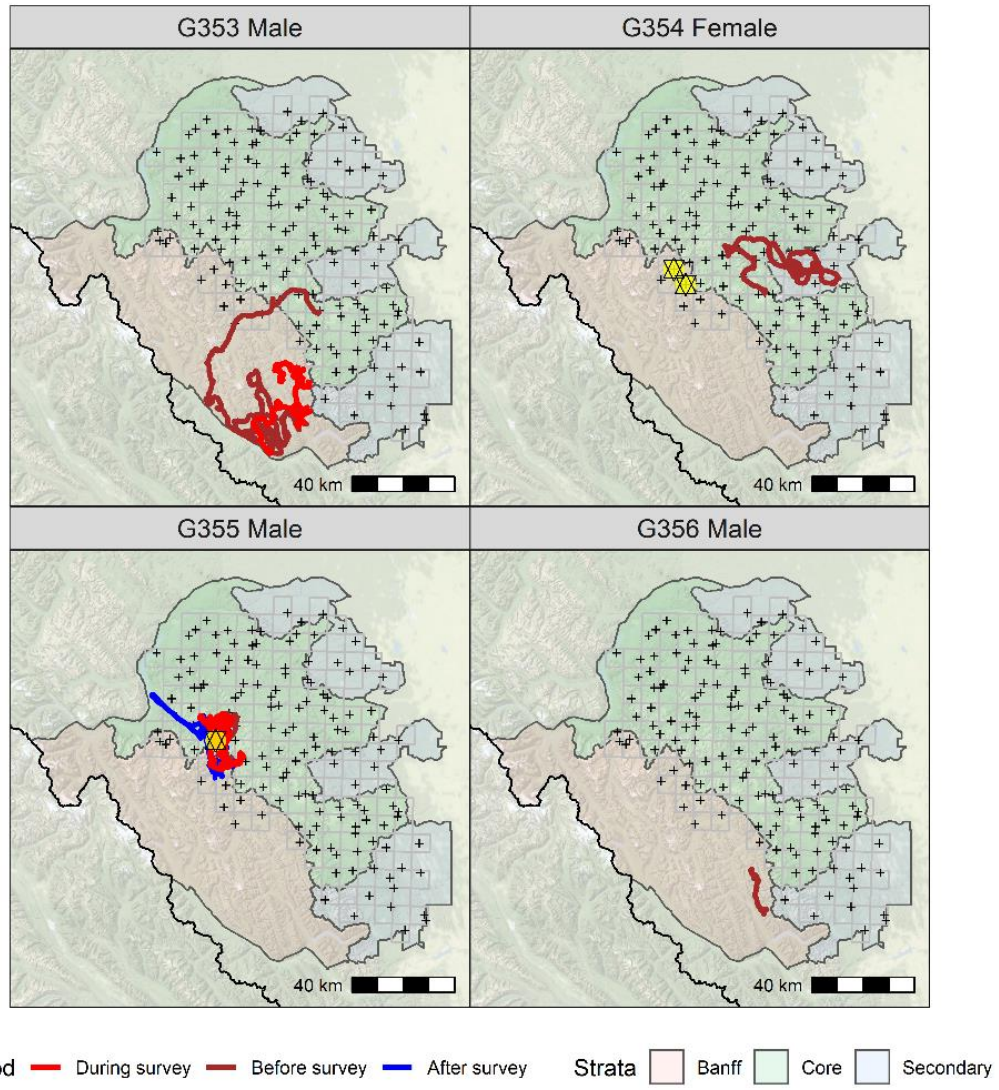


Figure 12: Tracks of grizzly bears collared during 2018 with period indicating whether the GPS track occurred before, during or after DNA sampling. A yellow star indicates a DNA hair-snag site where a bear was detected.

Model selection

Females

Base model selection for females indicated that detection at home range center was influenced by terrain ruggedness (TRI; Table 5, model 6) with some support for a model with a linear trend in detection function (Table 5, model 9). These 2 base models were then considered with density surface models. Of the density models, models with density varying as an interaction of RSF and RISK (Table 5, model 1) and RISK (model 2) were supported with ΔAICc values of less than 2. The base model for these models had detection at home range center increasing with session as modelled by the trend term.

Table 5: Model selection for females. AIC_c = sample size adjusted Akaike Information Criterion, ΔAIC_c = the difference in AIC_c between the model and the most supported model, AIC_c weight = w_i, K, the number of model parameters and log-likelihood (LL) are given. Baseline constant models are shaded for reference with covariate models. A half-normal detection function was used for the analysis.

No	Density	Detection at HR center (g_0)	Scale (σ)	AIC_c	ΔAIC_c	w_i	K	LL
1	RSF*Risk	trend	constant	390.44	0.00	0.52	7	-185.6
2	RISK	trend	constant	391.42	0.97	0.32	5	-189.4
3	RSF+Risk	trend	constant	394.25	3.81	0.08	6	-189.2
4	Site density	trend	constant	395.57	5.13	0.04	5	-191.5
5	RSF	trend	constant	398.90	8.46	0.01	5	-193.1
6	Constant	TRI	constant	399.09	8.64	0.01	4	-194.7
7	Risk	TRI	constant	399.62	9.17	0.01	5	-193.5
8	Site density	TRI	constant	399.71	9.26	0.01	5	-193.5
9	Constant	trend	constant	400.89	10.44	0.00	4	-195.6
10	Constant	constant	trend	401.04	10.60	0.00	4	-195.7
11	Constant	constant	TRI	401.05	10.61	0.00	4	-195.7
12	RSF*Risk	TRI	constant	401.13	10.69	0.00	7	-190.9
13	RSF	TRI	constant	401.32	10.88	0.00	5	-194.4
14	Constant	CC	constant	401.34	10.90	0.00	5	-194.4
15	RSF+Risk	TRI	constant	402.47	12.03	0.00	6	-193.3
16	Constant	bk	constant	404.31	13.87	0.00	4	-197.3
17	Strata	constant	constant	405.57	15.12	0.00	4	-197.9
18	Constant	constant	session	406.23	15.79	0.00	6	-195.2
19	Constant	constant	site-specific (bk)	406.30	15.85	0.00	4	-198.3
20	Constant	session	constant	406.62	16.18	0.00	6	-195.4
21	Constant	CC	constant	407.89	17.45	0.00	4	-199.1
22	Constant	constant	bear-specific (b)	408.41	17.97	0.00	4	-199.4
23	Constant	b	constant	408.42	17.97	0.00	4	-199.4
24	Constant	constant	CC	410.58	20.14	0.00	4	-200.5
25	Constant	constant	constant	411.13	20.68	0.00	3	-202.1

A plot of the detection function from model 6 (Table 5) shows that females are more detectable in areas of higher terrain ruggedness which would correspond to higher elevation areas (Figure 13). In addition, detection increased with session as indicated by predictions from model 9. Interestingly, density surface models with linear trend in detection probabilities were more supported than TRI models once habitat factors were accounted for.

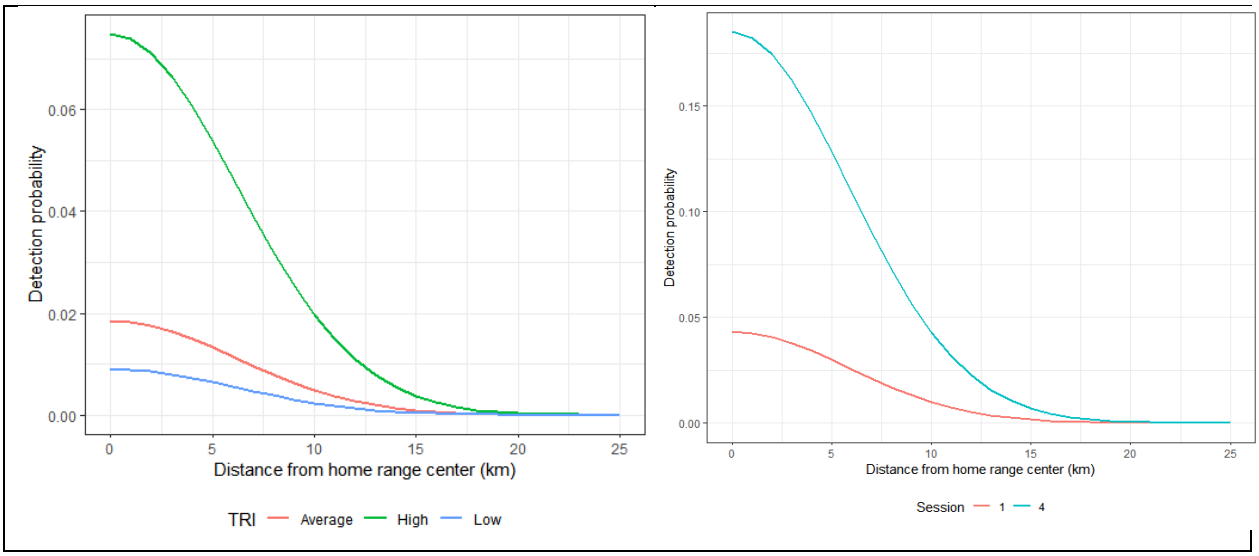


Figure 13: Detection function for females as function of terrain ruggedness from model 6, (Table 5) on the left. In the right plot. Detection functions are shown as a function of sampling sessions 1 and 4 (model 9).

A plot of estimated home range centers from the site density model (Table 5, model 4) and predicted density from the RISK x RISK model (Table 5, model 1) suggests a higher density of bears on the western edge of the grid, with 9 of 29 bears in Banff National Park or on the border of the core and Banff strata. The rest of the bears were evenly distributed in the core area with home range centers and density restricted to areas of low to moderate risk (Figure 14). Higher densities were predicted in Banff National Park, however, these results should be interpreted cautiously given that only a small proportion of Banff was sampled.

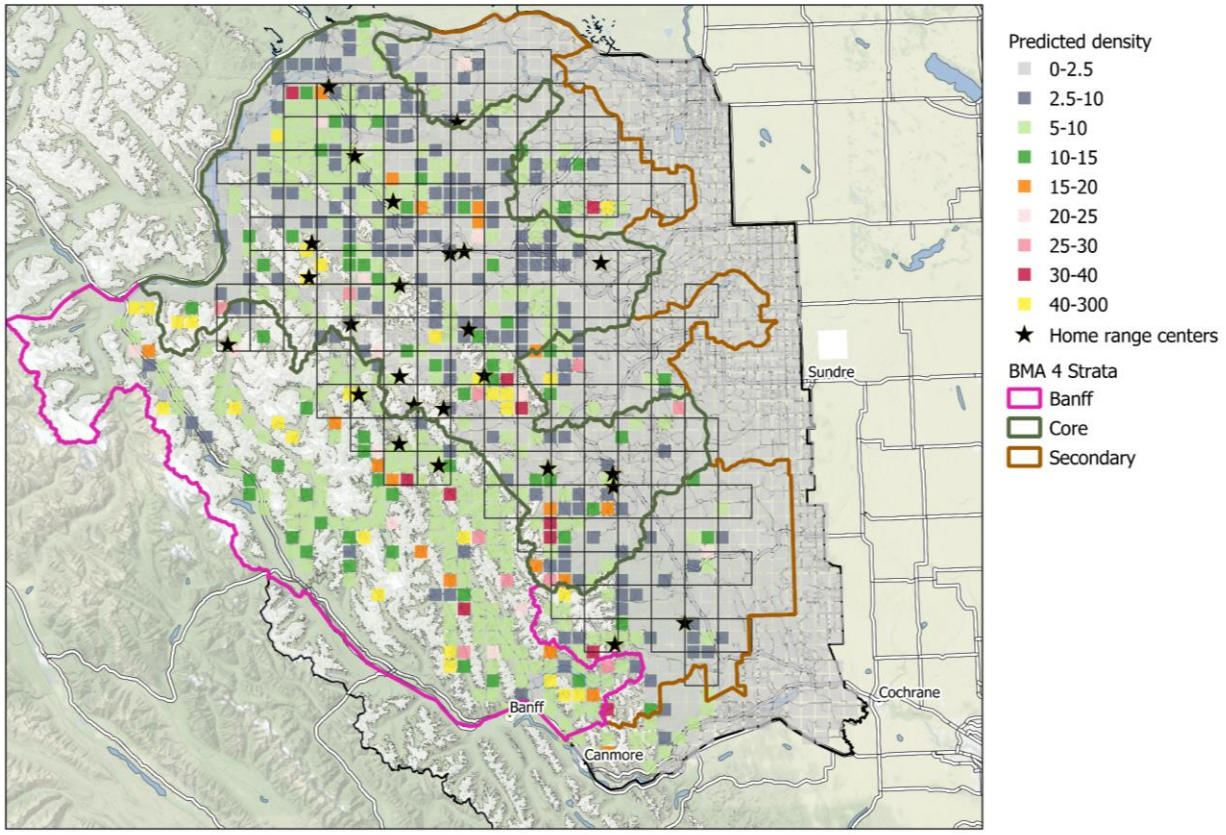


*Figure 14: Estimated female home range centers from the site density model (Table 5, model 7) along with predicted density from the RSF*RISK model (Table 5, model 1). The site density model was used to estimate home range centers given potential sensitivity of home range center estimates to site density.*

Predictions from the RSF and RISK model by zone in comparison to spatial gradients in RSF and RISK (Figure 5) are displayed in Figure 15. It can be seen that in general higher density is estimated in higher RSF habitats, particularly in the core zone, where generally lower road densities are found. However, higher bear densities are also predicted in low RSF habitats that also are lower RISK. These would correspond to some of the mountainous areas in Banff National Park.

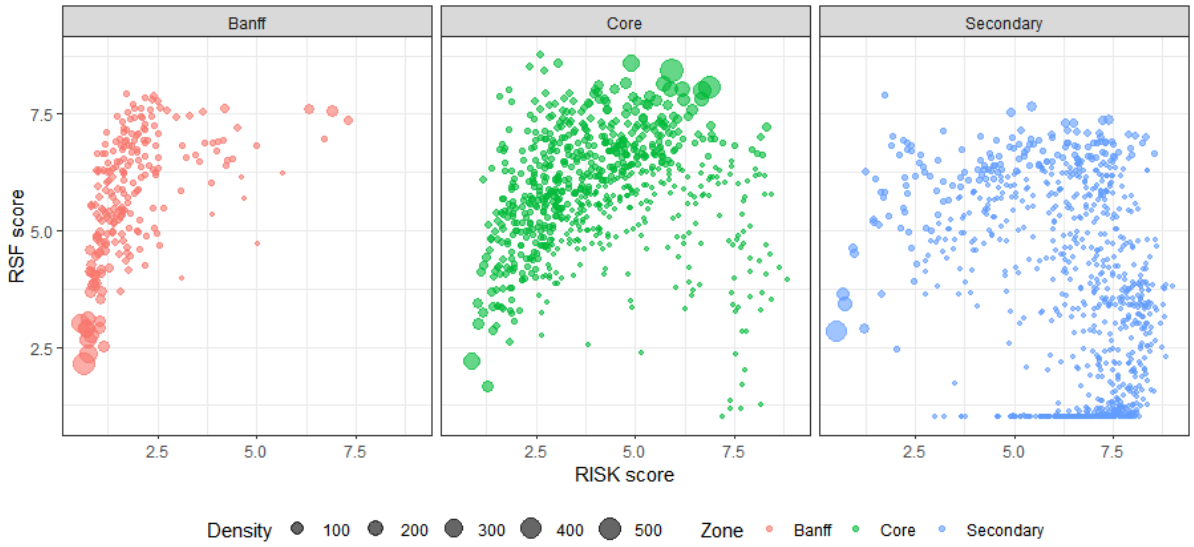


Figure 15: Predicted density based on RSF and RISK scores for females in the three zones of the BMA 4 mask based on the D (RSF x Risk) model (Table 5, model 1).

Males

One issue with the male data set was longer distances of movement for a subset of males that potentially influenced the detection function. To confront this issue an exponential detection function, which is less sensitive to outlier values of movement (Murray Efford, per. comm.), was considered in unison with the half normal detection function. Using a constant model, the exponential detection function was more supported by 3.8 AIC_c units and was therefore used for estimates.

Of the constant density models, a model with no covariates for detection probability was most supported (Table 6, model 7). Of the density surface models, a model with RSF as a predictor of density was most supported (Table 6, model 1). This model had strong support as indicated by ΔAIC_c values greater than 2 for other candidate models.

Table 6: Model selection for males. AIC_c = sample size adjusted Akaike Information Criterion, ΔAIC_c = the difference in AIC_c between the model and the most supported model, AIC_c weight = w_i, K, the number of model parameters and log-likelihood (LL) are given. Baseline constant models are shaded for reference with covariate models. An exponential detection function was used for the analysis.

No	Density	Detection at HR center (g_0)	Scale (σ)	AIC_c	ΔAIC_c	w_i	K	LL
1	RSF	constant	constant	619.12	0.00	0.69	4	-304.9
2	RSF+Risk	constant	constant	621.31	2.18	0.23	5	-304.6
4	RSF*Risk	constant	constant	624.06	4.94	0.06	6	-304.5
5	Risk	constant	constant	627.96	8.83	0.01	4	-309.3
6	Site density	constant	constant	629.72	10.60	0.00	4	-310.2
7	constant	constant	constant	630.91	11.79	0.00	3	-312.1
8	constant	Trend	constant	631.28	12.16	0.00	4	-311.0
9	constant	constant	CC	631.30	12.17	0.00	4	-311.0
10	constant	CC	constant	631.72	12.59	0.00	4	-311.2
11	constant	TRI	constant	631.76	12.63	0.00	4	-311.2
12	constant	constant	trend	631.77	12.64	0.00	4	-311.2
13	constant	Trend	CC	631.85	12.73	0.00	5	-309.9
14	constant	site-specific (bk)	constant	631.96	12.84	0.00	4	-311.3
15	constant	constant	site-specific (bk)	632.23	13.10	0.00	4	-311.4
16	constant	constant	TRI	632.57	13.45	0.00	4	-311.6
17	constant	bear-specific (b)	constant	632.73	13.60	0.00	4	-311.7
18	constant	constant	bear-specific (B)	632.75	13.63	0.00	4	-311.7
19	constant	CC	TRI	634.03	14.91	0.00	5	-311.0
20	constant	Trend	constant	634.46	15.34	0.00	6	-309.7
21	constant	constant	constant	634.68	15.56	0.00	3	-314.0
22	constant	constant	session	635.68	16.56	0.00	6	-310.3

A plot of the detection function for the covariate model of closest support to the constant model (model 9) suggests minimal influence of canopy cover on scale of movement (Figure 16), further suggesting that the constant model is the best description of detection for male bears.

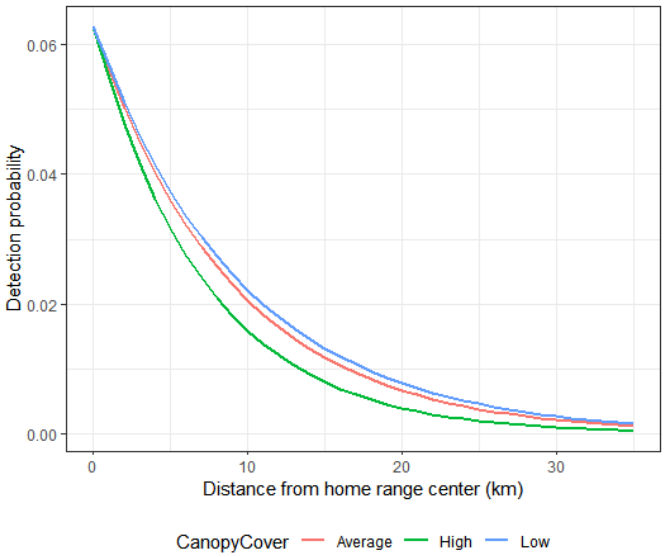


Figure 16: Detection function for male bears as a function of canopy cover.

Estimates of home range center and prediction of density (Figure 17) suggest that males selected areas of high RSF value including areas in the secondary strata. Male home ranges were also clustered around the Banff and core boundary with 8 bears being in Banff National Park or on the border.

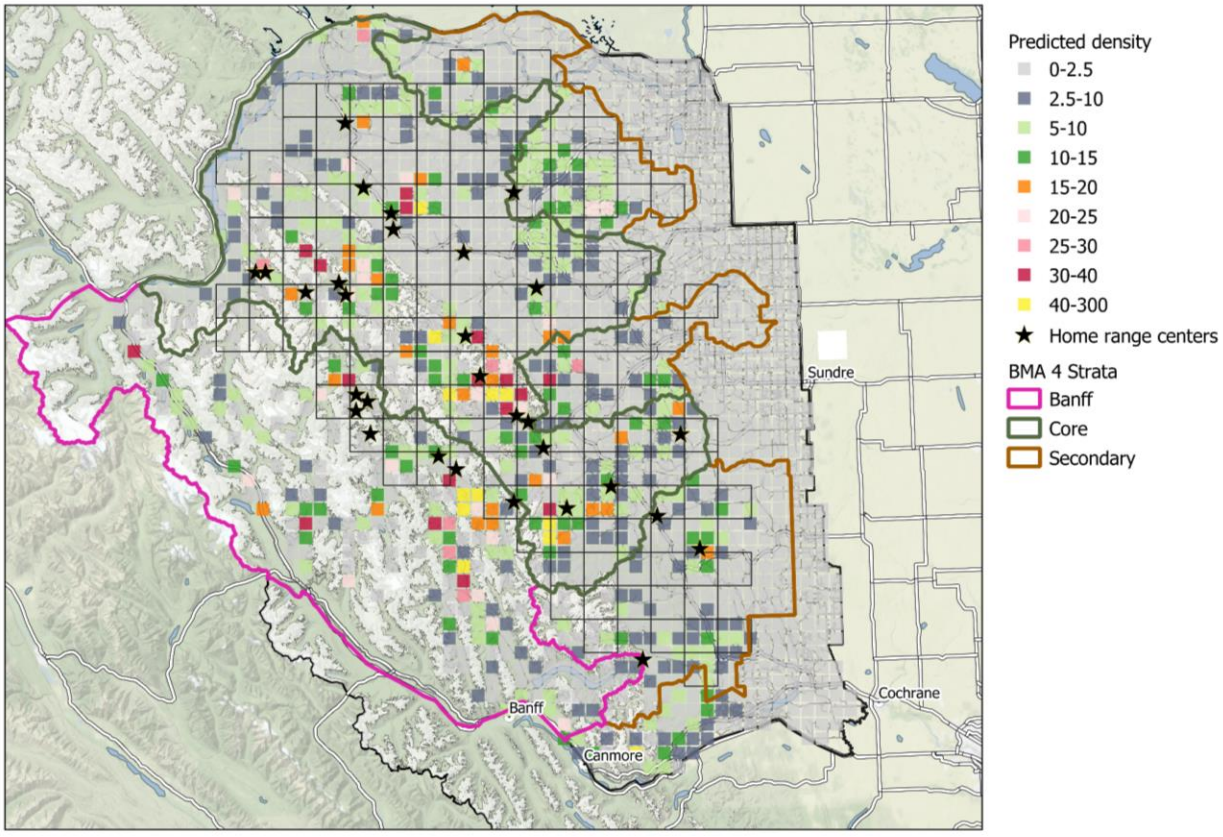


Figure 17: Male home range centers from the site density model (Table 6, model 6) compared to predictions of density from the RSF density surface model (Table 6, model 1). The site density model was used to estimate home range centers, given potential sensitivity of home range center estimates to site density.

A plot of predicted density by RSF, RISK and zone, as was done for females (Figure 18) demonstrates how the D (RSF) male model predicts higher densities as a function of RSF regardless of RISK score.

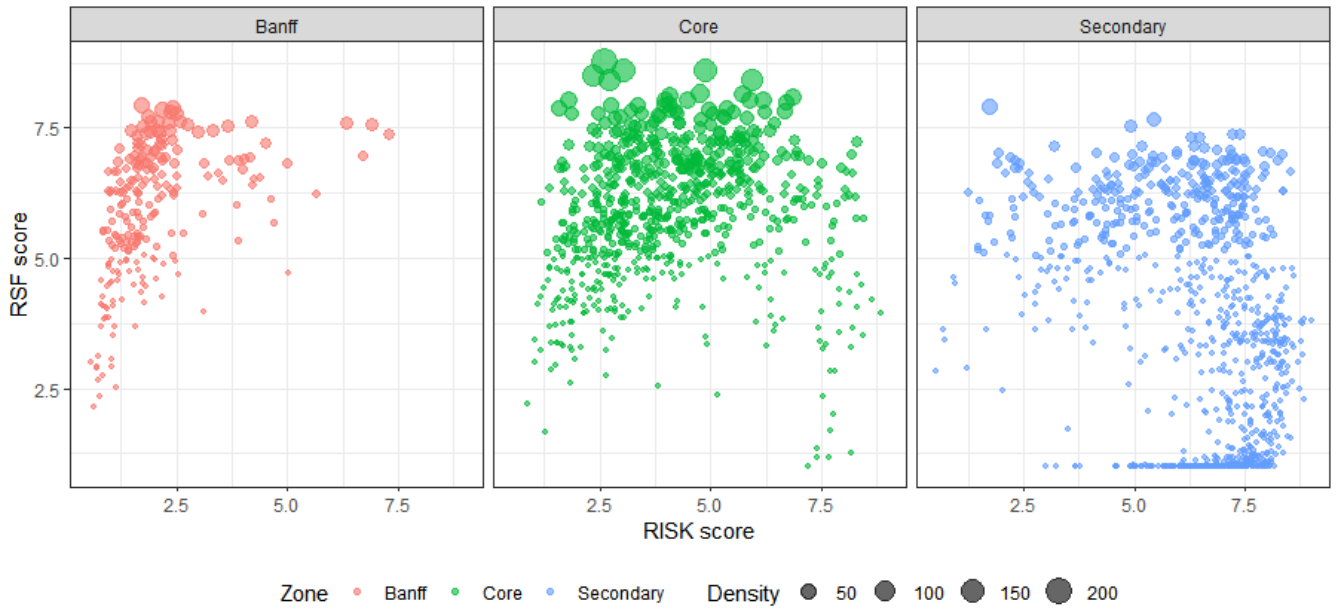


Figure 18: Predicted density from the D (RSF) model for males as a function of RSF and RISK score of SECR mask points.

Estimates

Estimates of average numbers of bears and density of bears from the most supported sex-specific SECR models (Table 5 and Table 6) in each strata illustrate higher densities in the cells in Banff National Park and core areas for both males and females. Estimates of density for Banff National Park should be interpreted cautiously given the small area that was sampled.

The precision of female estimates was relatively low compared to males. Precision of the overall estimates for core and secondary areas was acceptable (CV=14.6%; Table 7). Analysis of the components of precision for females suggest that the CV of 23% was equally due to binomial variation in the number of bears detected on the sampling grid (CV_n=16%) and estimation of detection parameters (CV_a=16%). Precision of males was higher (CV=17%), which was due to a larger number of males detected (35 males compared to 29 female individuals) that reduced the CV due to binomial variation (CV_n=13%). In addition, detection rates for males were higher with 31% (11/35) detected more than once compared to females where 24% (7/29) were detected more than once, which resulted in a lower CV due to detection parameters (CV_a=11%).

Table 7: Estimates of average N and density for grizzly bears in BMA 4 from the inventory. Estimates are given by sex of bears and sexes combined. Densities are based on habitat area (as listed in

Table 2) not total area.

Sex		Abundance (Average N on grid)				Density (N/habitat area*1000)			
Area	N	SE (N)	Confidence limit		CV	D	SE (D)	Confidence limit	
Females (29 individuals detected; D(RSF*Risk), g_0(trend) σ (.))									
Core	31.0	7.5	19.5	49.4	24.1%	6.02	1.45	3.78	9.59
Secondary	11.6	3.4	6.6	20.4	29.3%	3.22	0.94	1.83	5.65
Core + Secondary	42.7	9.9	27.2	66.8	23.2%	4.87	1.13	3.11	7.63
Banff	4.1	1.5	2.0	8.1	36.1%	12.43	4.48	6.26	24.67
Grid total	46.7	10.8	29.9	73.0	23.1%	5.14	1.19	3.29	8.04
Males (35 individuals detected; D(RSF), g_0(.) σ (.))									
Core	28.9	4.7	21.0	39.8	16.4%	5.62	0.92	4.08	7.73
Secondary	9.2	2.3	5.7	15.0	25.1%	2.56	0.64	1.58	4.15
Core + Secondary	38.2	6.4	27.5	53.0	16.8%	4.36	0.73	3.14	6.05
Banff	2.7	0.4	2.0	3.8	16.4%	8.35	1.37	6.06	11.50
Grid total	40.9	6.8	29.5	56.7	16.7%	4.50	0.75	3.25	6.23
Females + Males									
Core	60.0	8.8	40.5	89.2	14.7%	11.64	1.72	7.87	17.32
Secondary	20.9	4.1	12.3	35.4	19.7%	5.78	1.14	3.41	9.80
Core + Secondary	80.8	11.8	54.7	119.8	14.6%	9.23	1.35	6.25	13.67
Banff	6.8	1.5	4.0	11.8	22.6%	20.78	4.69	12.32	36.17
Grid total	87.6	12.8	59.4	129.7	14.6%	9.64	1.41	6.54	14.27

Estimates from other supported models for the core-secondary areas are displayed in Table 8. In general, estimates were similar for the most supported models with estimates for females ranging from 40 to 43 bears and males ranging from 34 to 38 bears. Models that assumed constant density and detection throughout the survey area were also included for comparison with constrained models. In both cases estimates were higher especially for females. This result illustrates the need for models that account for varying sampling intensity as well as accounting for the directional declining gradient in density (from West to East) in the study area, in this case the most supported sex-specific SECR models.

Table 8: Sensitivity of abundance estimates to model specification for female and male grizzly bears.

No	Model Selection (full list in Tables 4 and 5)						Abundance (core-secondary strata)				
	Density	Detection at HR center (g_0)	Scale (σ)	AIC_c	ΔAIC_c	w_i	N	SE	lcl	ucl	CV
Females											
1	RSF*Risk	trend	constant	390.44	0.00	0.52	44.4	9.9	28.9	68.2	22.2%
2	RISK	trend	constant	391.42	0.97	0.32	40.7	9.4	26.1	63.5	23.0%
3	RSF+Risk	trend	constant	394.25	3.81	0.08	39.9	9.5	25.2	63.1	23.7%
4	Site density	trend	constant	395.57	5.13	0.04	42.7	8.9	28.5	64.0	23.2%
25	Constant	constant	constant	411.13	20.68	0.00	53.4	11.9	34.6	82.3	22.4%
Males											
1	RSF	constant	constant	619.12	0.00	0.69	38.2	6.4	27.5	53.0	16.8%
2	RSF+Risk	constant	constant	621.31	2.18	0.23	34.3	6.7	23.5	50.0	19.4%
4	RSF*Risk	constant	constant	624.06	4.94	0.06	36.1	6.9	24.9	52.4	19.2%
5	Risk	constant	constant	627.96	8.83	0.01	35.0	7.3	23.4	52.4	20.8%
5	Site density	constant	constant	629.72	10.60	0.00	38.3	6.1	28.0	52.3	16.0%
21	constant	constant	constant	634.68	15.56	0.00	40.8	7.1	29.1	57.1	17.3%

Re-analysis of the 2005 DNA Inventory Data Using Spatially Explicit Capture-Recapture Methods

The 2005 inventory data set was re-analyzed to allow direct comparison of population estimates between 2005 and 2018 inventory periods, estimation of densities of bears in protected areas within the BMA (Boulanger 2015) as well as to assess larger-scale factors influencing distribution of bears within Alberta BMAs (Boulanger et al. 2017). Details of this analysis are given in Appendix 1.

The 2005 inventory sampled the same general grid area as the 2018 inventory, however, 2005 sites were moved each session which increases the spatial coverage of sampling. In addition, the secondary zone was sampled more intensively in 2005, with even sampling throughout the entire grid (Figure 19). However, neither of these differences precluded comparison of the 2005 to 2018 results.

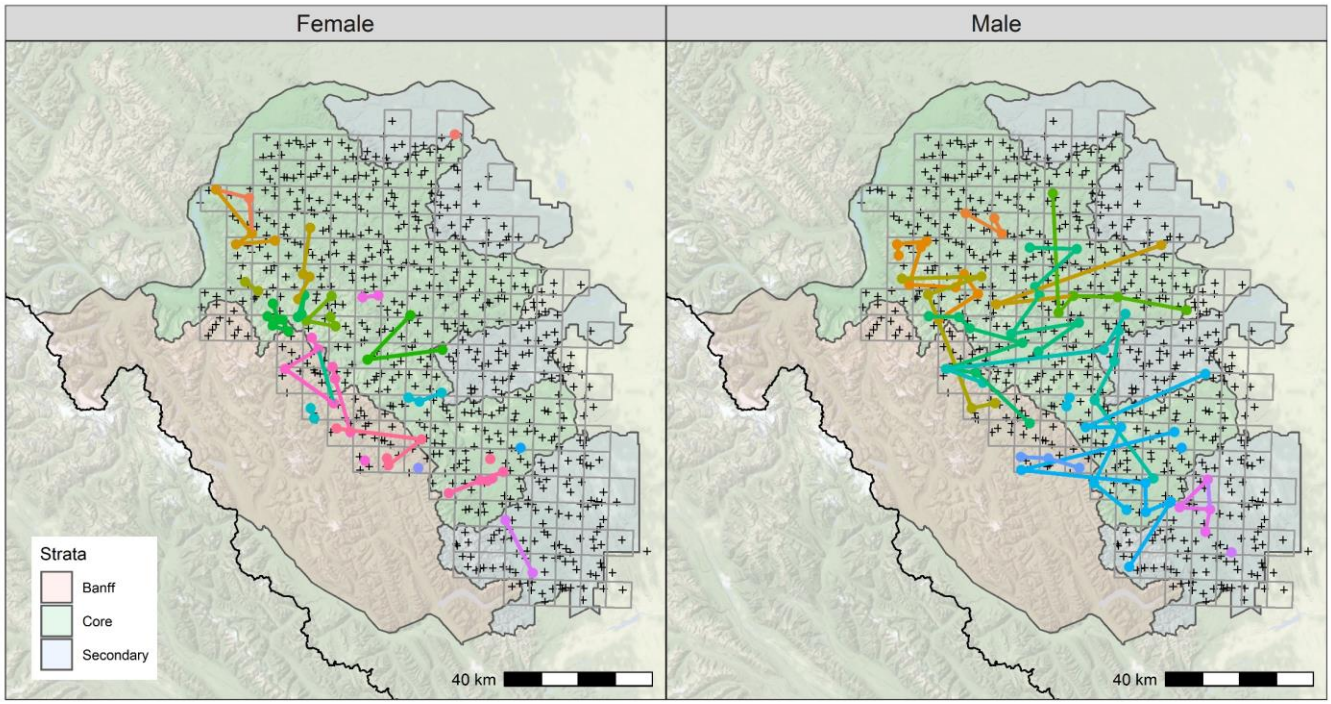


Figure 19: Movements based on detections of bears detected during the 2005 BMA 4 inventory. Each + sign indicates a site which was present during 1 session of sampling. Therefore, the map represents the cumulative rather than per-session sampling coverage.

One of the first steps of the analysis was estimation of home range centers of detected bears using base detection models. This revealed that most home range centers were in the core area, with only 4 of 17 male and 1 of 25 female home range centers falling in the secondary area. In addition, 7 of 25 female and 2 of 17 home range centers were estimated to fall in Banff National Park, which is outside the BMA 4 core area (Figure 20). Substantive model fitting of base models was conducted, as detailed in Appendix 1 of this report.

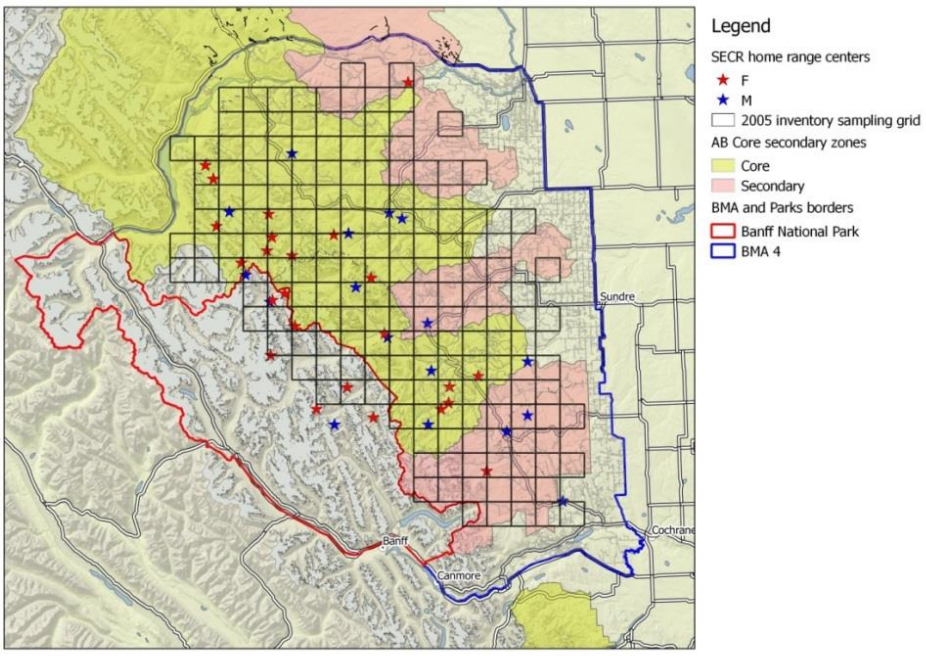


Figure 20: Estimated home range centers relative to core, secondary, and Banff National Park during the 2005 inventory.

A focus of the SECR re-analysis was density surface modelling of male and female densities on the 2005 grid. In this analysis, models tested the association of RSF, RISK (Nielsen et al. 2006) and the interaction of RSF and RISK to determine larger-scale factors influencing distribution. The analysis aimed to test the hypothesis that home range centers would more likely be located in areas of higher habitat value and lower risk. For both females and males, RSF was determined to be a better predictor of density than risk.

Models with strata-specific densities (core, secondary and Banff) were also considered for males and females. For females the strata-specific model was less supported than the most supported RSF model (ΔAICc=7.79) but more supported than a constant density model (ΔAICc=11.87; Appendix 1, Table 14) suggesting that female density was associated with core and secondary areas but strata models (that assume a constant density in core, secondary, and Banff areas) were not as good of an overall predictor of density as RSF score. For males, strata was not associated with density with the strata model showing lower support than a model that assumed constant density across all strata (Appendix 1, Table 15).

Predicted maps of density were then produced for males and females for the most supported RSF density surface models (Figure 21). These maps provide a model-based prediction of densities on the sampling grid as well as the mask surface that extended beyond the sampling grid into Banff National Park (Figure 4).

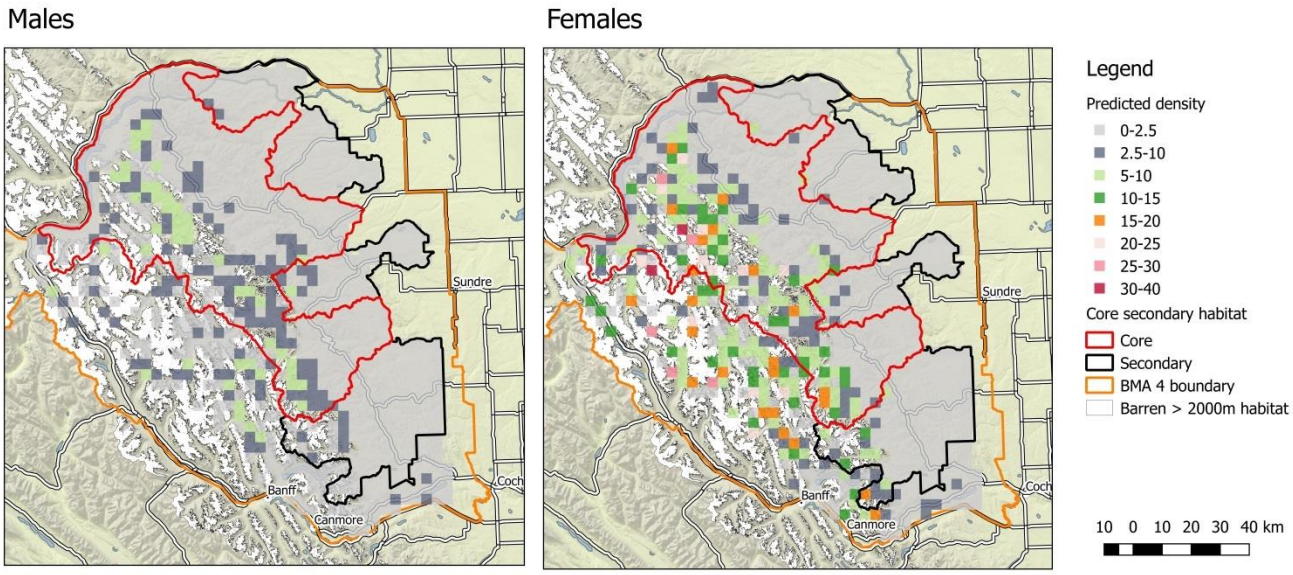


Figure 21: Density surface model predictions of density (grizzly bears per 1000 km^2) for males and females. In both cases densities were predicted by RSF score. More details about the analysis can be found in Appendix 1.

Both male and female analyses estimate the highest densities occurring on the western border of the sampling grid with lower densities in secondary areas to the east. The RSF density surface model was then used to estimate density and abundance for core, secondary, and Banff National Park (Table 9). Estimates of the Banff National Park area were only for the area contained within the sampling grid, whereas estimates of core and secondary were for the entire core and secondary regions some of which extended beyond the grid boundaries (Figure 20). For this reason, estimates of density for Banff National Park should be interpreted cautiously given the relatively small area that was sampled. We note that the estimates in Table 9 for the entire sampling grid (39.9) differ slightly from previous estimates for BMA 4 (35-45) bears (Boulanger et al. 2005, 2018) due to the slight change in grid area used for estimates (to make estimates completely similar to the area sampled in 2018).

Table 9: Estimates of expected population size and density core, secondary, and areas contained within the 2005 sampling grid for BMA 4 using RSF density are based on habitat area (as listed in

Table 2) not total area.

Sex	Abundance (Average N on grid)				Density (N/habitat area*1000)			
Area	N	SE (N)	Confidence limit	CV	D	SE(D)	Confidence limit	
Females (25 individuals detected; D(RSF) g_0(TRI) σ (T))								
Core	19.3	2.29	15.3	24.3	11.9%	3.74	0.45	2.97	4.72
Secondary	4.2	1.44	2.2	8.1	34.2%	1.16	0.40	0.61	2.23
Core + Secondary	23.5	2.99	18.3	30.1	12.7%	2.68	0.34	2.09	3.44
Banff	1.4	0.17	1.1	1.8	12.2%	4.24	0.52	3.34	5.37
Grid total	25.7	3.16	20.3	32.7	12.3%	2.83	0.35	2.23	3.60
Males (17 individuals detected; D(RSF) g_0(TRI) σ (.))								
Core	10.1	1.19	8.0	12.7	11.9%	1.95	0.23	1.55	2.46
Secondary	3.0	0.93	1.7	5.5	30.4%	0.84	0.26	0.47	1.51
Core + Secondary	13.1	1.29	10.8	15.9	9.9%	1.50	0.15	1.23	1.81
Banff	0.7	0.10	0.5	0.9	13.8%	2.16	0.30	1.65	2.83
Grid total	14.2	1.38	11.7	17.1	9.8%	1.56	0.15	1.29	1.88
Males + Females								
Core	29.3	2.59	23.3	37.0	8.8%	5.69	0.50	4.51	7.18
Secondary	7.2	1.71	3.9	13.5	23.6%	2.01	0.47	1.08	3.75
Core + Secondary	36.6	3.26	29.1	46.0	8.9%	4.18	0.37	3.32	5.25
Banff	2.1	0.19	1.6	2.7	9.3%	6.40	0.60	4.99	8.20
Grid total	39.9	3.45	32.0	49.8	8.6%	4.39	0.38	3.52	5.48

Trends from 2005 and 2018 Surveys

The 2018 BMA 4 survey detected 64 bears (35 males and 29 females) compared to 42 bears (17 males and 25 females) in 2005, with overall estimates of average number of bears on the sampling grid of 39.9 (Table 9: CI=32–49.8) in 2005 and 87.6 bears (Table 7: CI=59.4–129.7) in 2018. The sampling intensity in 2005 was higher with sites being moved each session which increased detection probabilities (Boulanger et al. 2006). Higher detection success is illustrated by plotting the proportion of new bears detected each session (Figure 9) as well as detection function plots for each year (Figure 22). Another metric for comparison is the ratio of the number of bears detected once to the total number of bears detected. In this case, it is 40% (17/42) for 2005 and 72% (46/64) for 2018, further illustrating the relatively low redetection rates in 2018.

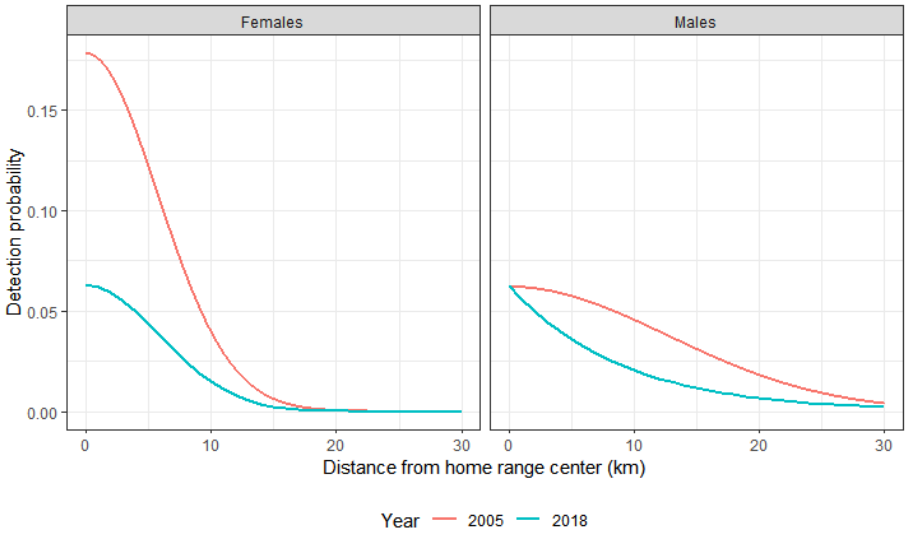


Figure 22: Comparison of detection functions for female and male bears from the 2005 and 2018 DNA surveys. Detection functions were generated at mean levels of covariates.

A comparison of estimates of density and abundance between 2005 and 2018 suggest increases in all areas, with the largest relative increase in secondary areas. In this case, density was very low in 2005 (<2 bears/1000 km^2), increasing up to 5 bears/1000 km^2 in 2018 with the highest increase with females (Figure 23).

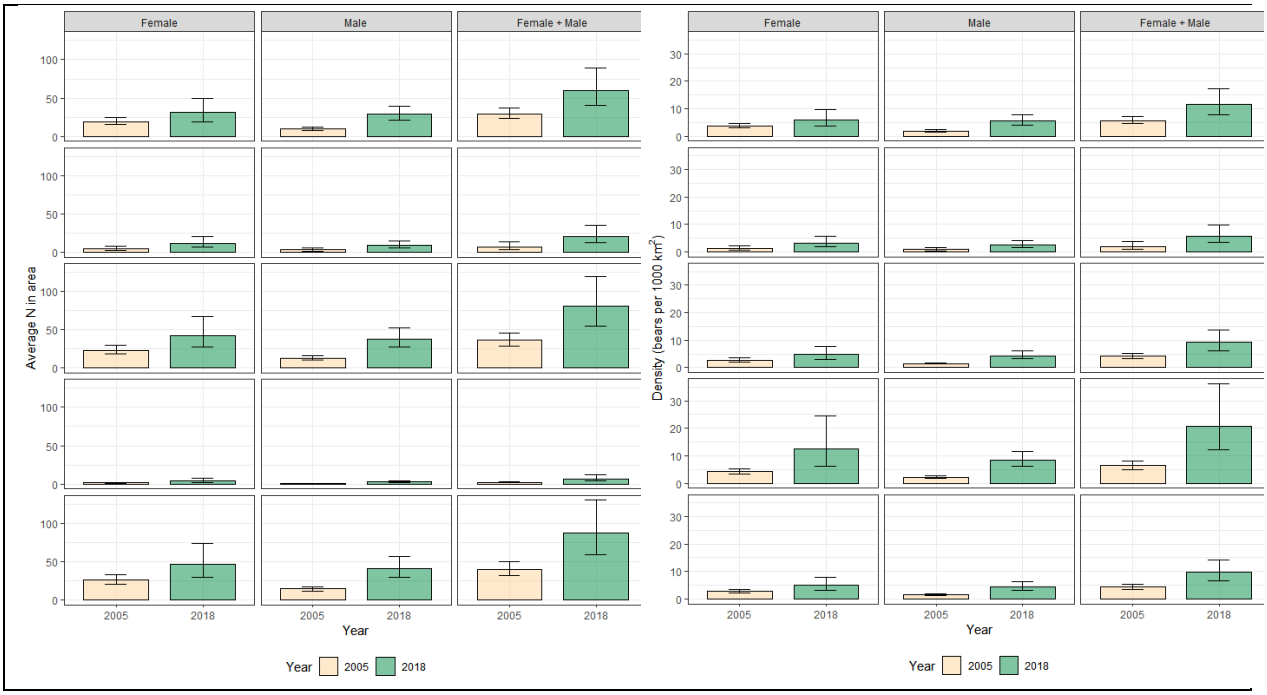


Figure 23: Comparison of Average N and density estimates for male, female, and pooled sex estimates by strata of grid.

One attribute of the 2005 and 2018 data sets was the higher precision of the 2005 data set (CV=9% for core/secondary estimates) compared to 2018 (CV=15% for core/secondary). The difference in precision is illustrated by the simulated densities of the core/secondary estimates used to estimate confidence intervals for change between the surveys (Figure 24). The overlap between the distributions was very low (<0.01%) resulting in relatively precise estimates of rate of change.

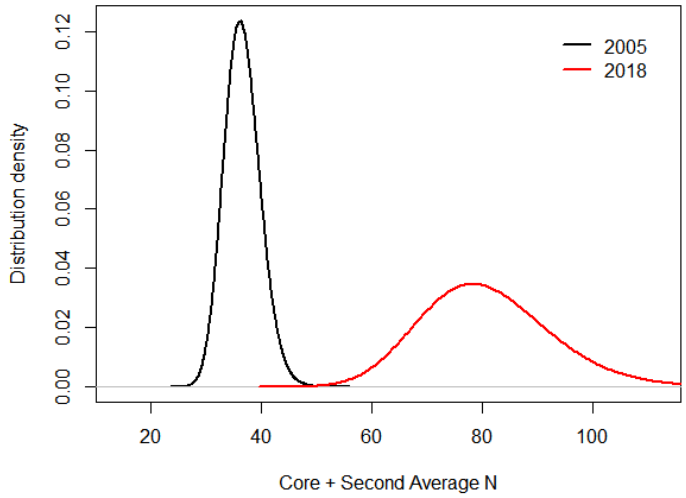


Figure 24: Simulated log-normal distributions of the core/secondary, male/female estimates for the 2005 and 2018 surveys.

The annual rate of change for the core/secondary area for females, males, and pooled male/females was 1.05, 1.09, and 1.06, suggesting annual increases of 5–9% (Table 10). Confidence limits for λ did not overlap 1 in all cases, except for females in the core area, suggesting a significant increase in most cases. The overall increase for males and females with confidence limits is 6% (CI=4–9%).

Table 10: Estimates of gross and annual change from comparison of the 2018 and 2005 DNA surveys of BMA 4. We note that estimates of trend based on the ratios of abundance or density estimates will be identical given that the area used to estimate N was identical for 2005 and 2018.

Sex	Gross change (N_{2018}/N_{2005})				Annual change ($\lambda=N_{t+1}/N_t=(N_{2018}/N_{2005})^{(1/13)}$)			
Area	Estimate	SE	Confidence limit		λ	SE	Confidence limit	
Females								
Core	1.61	0.44	0.94	2.65	1.04	0.02	1.00	1.08
Secondary	2.76	1.43	1.18	6.65	1.08	0.04	1.01	1.16
Core + Secondary	1.82	0.49	1.07	2.98	1.05	0.02	1.01	1.09
Banff	2.93	1.14	1.35	5.75	1.09	0.03	1.02	1.14
Total grid	1.81	0.48	1.07	2.95	1.05	0.02	1.01	1.09
Males								
Core	2.88	0.59	1.93	4.24	1.08	0.02	1.05	1.12
Secondary	3.03	1.33	1.44	6.56	1.09	0.03	1.03	1.16
Core + Secondary	2.91	0.58	1.97	4.22	1.09	0.02	1.05	1.12
Banff	3.86	0.85	2.53	5.85	1.11	0.02	1.07	1.15
Total grid	2.89	0.57	1.96	4.18	1.09	0.02	1.05	1.12
Males + Females								
Core	2.04	0.35	1.45	2.84	1.06	0.01	1.03	1.08
Secondary	2.88	0.94	1.60	5.26	1.08	0.03	1.04	1.14
Core + Secondary	2.21	0.38	1.57	3.06	1.06	0.01	1.04	1.09
Banff	3.25	0.80	1.98	5.11	1.09	0.02	1.05	1.13
Total grid	2.20	0.38	1.57	3.03	1.06	0.01	1.04	1.09

A graphic representation of annual estimates shows that the most certainty was increase in the core and core + secondary areas (Figure 25).

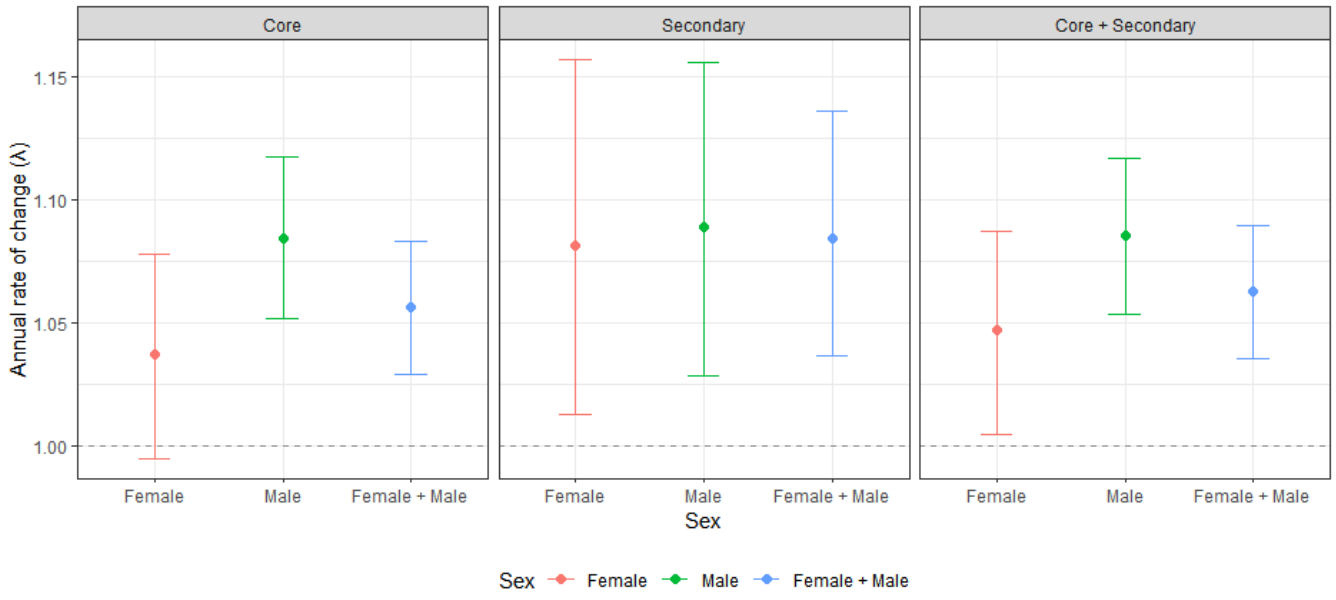


Figure 25: Comparison of estimates of annual change for the core, secondary, and core + secondary.

The change in abundance is also reflected in a shift in distribution for females as revealed by plots of estimated home range centers from sex-specific SECR models from 2005 and 2018 (Figure 26). In 2005, female home range centers mainly occurred within 20 km of the Banff National Park border, whereas in 2018 home range centers extended up to the edge of the core area. Patterns for males were less obvious with a general filling in of areas occupied in 2005.

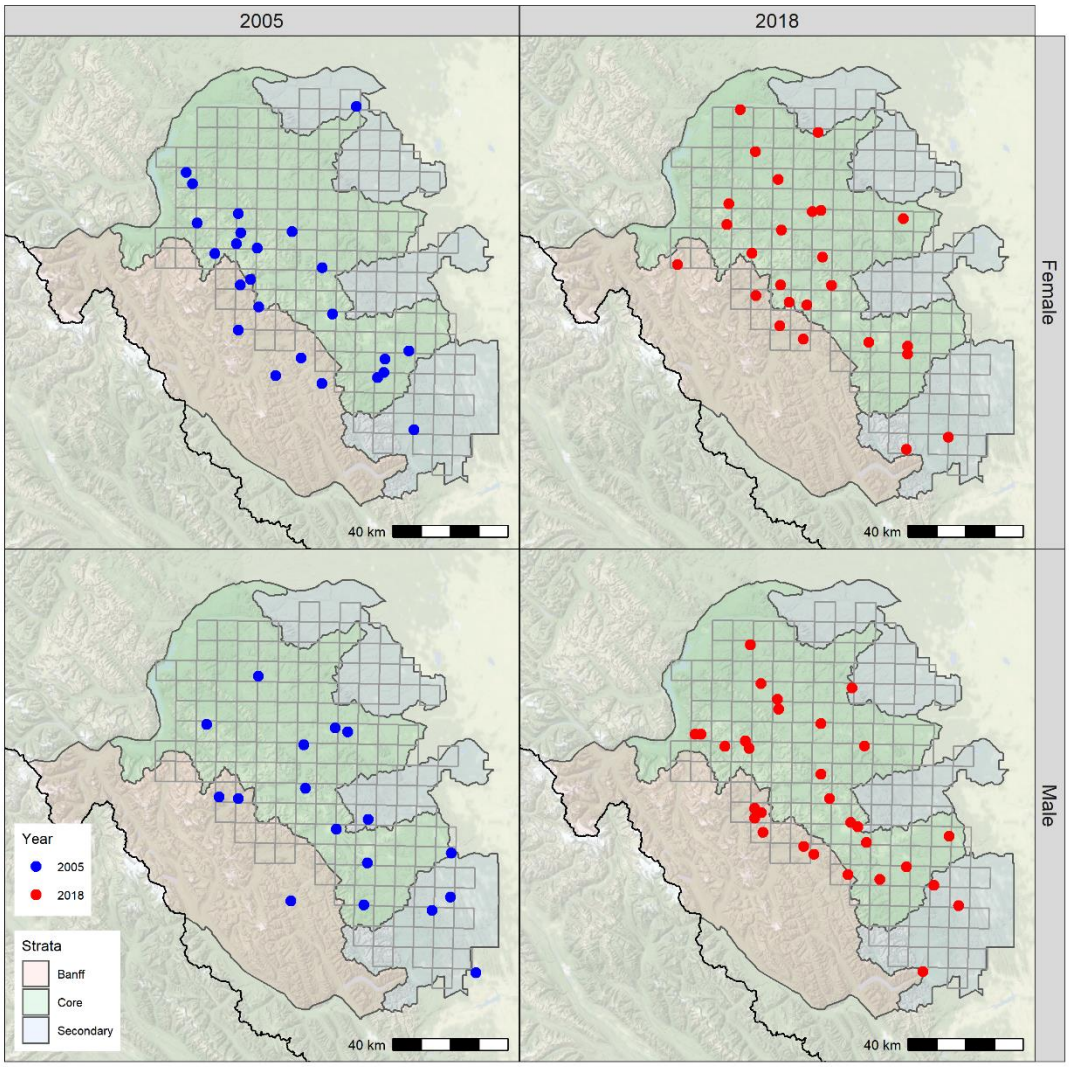


Figure 26: Estimated home range centers for female and male bears in 2005 and 2018 from the most supported constant density models in 2005 and the D (strata) models in 2018 (as also shown in Figures 11, 14 and 17).

Open Model Analysis

A brief open model analysis was undertaken to cross-validate λ estimates based on ratios of abundance estimates and obtain estimates of rates of addition (*f*: number of new bears each year per bear in the previous year) and apparent survival (ϕ: probability that a bear that is in the sampling area one year will be on the sampling area the next year). In review, apparent survival and rates of addition add together to provide an estimate of trend (λ). Estimates were scaled by the survey interval (13 years between 2005 and 2018) to allow estimates on the annual scale. A "robust design" open model type (Pollock and Otto 1983) was used which used sessions to estimate year-specific detection rates with the assumption of population closure within each sampling year.

Overall, 46 females were detected in the 2005 and 2018 surveys with 25 individuals detected in 2005 and 29 individuals detected in 2018, 8 of which were detected in both surveys. Details about bears detected are given in Table 12. For males, 50 individuals were detected in both surveys with 17 detected in 2005 and 35 detected in 2018 of which 2 were detected in both surveys.

An open model was run for both sexes and sexes combined with year-specific detection probabilities (Table 11). For females, estimates of apparent survival were very high (0.96) with moderate rates of addition (0.10) which added up to an overall trend (λ) of 1.06 (CI=1.01–1.11), which was similar to that of the estimate from ratios of abundance estimates for the full grid (Table 10: 1.05, CI=1.01–1.09). For males, estimates of apparent survival were lower than females (0.87) with higher rates of addition (0.21) which added up to an overall trend (λ) of 1.09 (CI=1.04–1.14), which was similar to that of the estimate from ratios of abundance estimates for the full grid (Table 10: 1.09, CI=1.05–1.12). The combined male and female estimates were an average of males and females leading to an overall estimate of trend of 1.07 (CI=1.03–1.10), which was similar to the full grid ratio-based estimate of 1.06 (Table 10: CI=1.04–1.09).

Table 11: Estimates of demographic parameters from the Pradel open model analysis (Pradel 1996).

Sex/parameter	Estimate	SE	Confidence Limits	
Females				
Apparent survival (ϕ)	0.96	0.03	0.86	0.99
Rates of addition (f)	0.10	0.02	0.06	0.15
Population rate of change (ϕ + f= λ)	1.06	0.03	1.01	1.11
Males				
Apparent survival (ϕ)	0.87	0.05	0.76	0.94
Rates of addition (f)	0.21	0.05	0.14	0.33
Population rate of change (ϕ + f= λ)	1.09	0.03	1.04	1.14
Females + Males				
Apparent survival (ϕ)	0.93	0.02	0.87	0.96
Rates of addition (f)	0.14	0.02	0.10	0.19
Population rate of change (ϕ + f= λ)	1.07	0.02	1.03	1.10

Estimates of demographic parameters from the open models provide some inference on the dynamics of male and females in BMA 4. Female dynamics were driven by higher survival rates, whereas male dynamics were driven by moderate survival rates but also higher rates of addition potentially due to immigration of bears from adjacent areas given that the sex ratio of bears at birth is likely to be 50:50 (Figure 27).

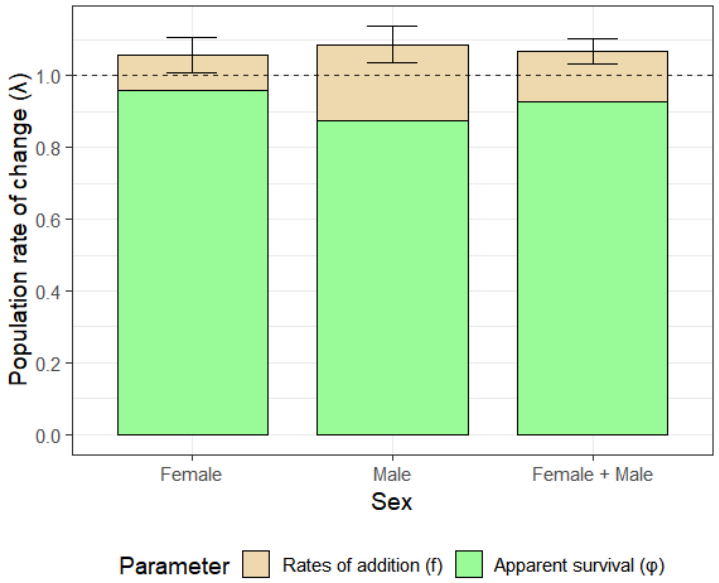


Figure 27: A graphical representation of demographic parameters based on the open model analysis of 2005 and 2018 BMA 4 survey data. The parameter values are listed in Table 11. The dashed line indicates a λ value of 1 where the population would be stable.

A plot of home range centers for bears detected in both 2005 and 2018 reveals a high level of fidelity for females with minimal change in home range centers (Figure 28). Males showed lower fidelity which may partially explain the lower apparent survival (due to emigration and mortality) and higher rates of addition (which would be influenced by movement of bears into the sampling area as well as births).

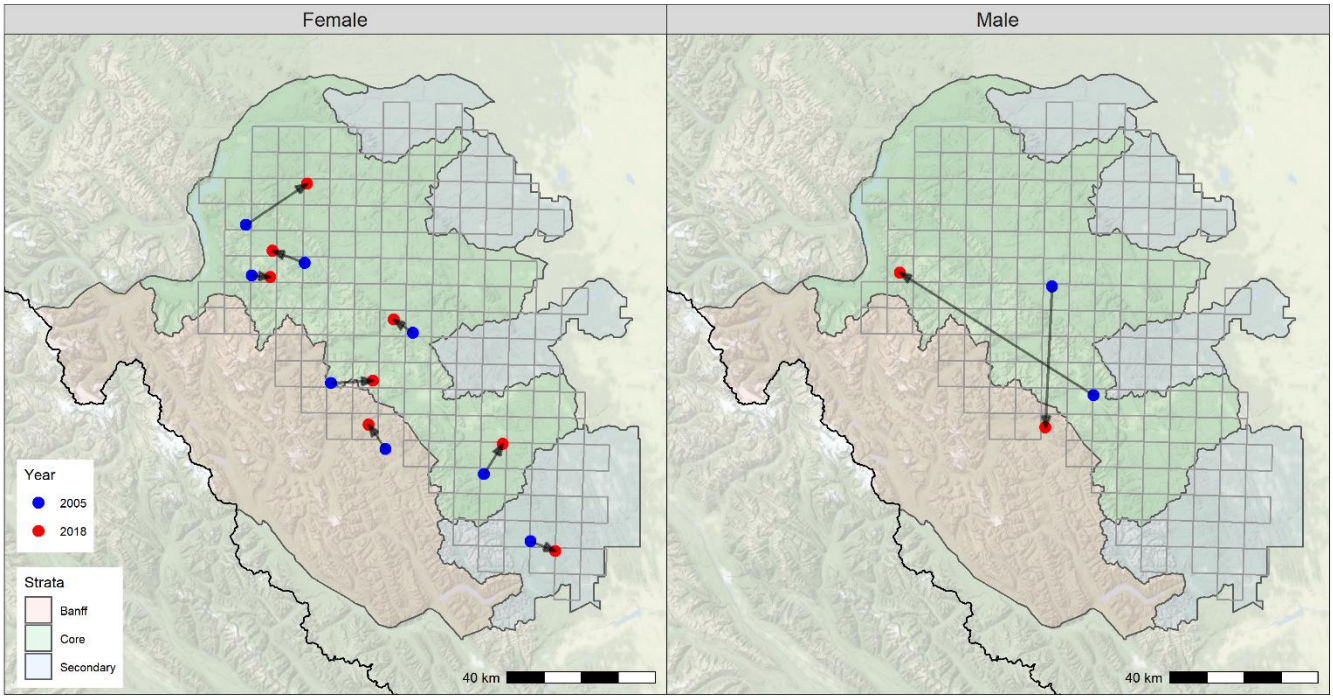


Figure 28: Estimated home range centers for bears detected in 2005 and 2018. Eight female and two male bears were detected in both 2005 and 2018. Figure 23 shows all home range centers for each year of sampling.

Alberta Grizzly Bear Genetic Dataset Comparison

Since 2004, when the first DNA based grizzly bear population inventory was undertaken, there have been similar inventory efforts carried out in all 7 provincial BMAs, including areas within adjacent national parks. In addition, genetic samples have been obtained from ongoing research capture and collaring efforts along with samples from grizzly bear translocations and mortality events. The genetic data from these various long term collection efforts have recently been combined into a single province wide grizzly bear genetic database. This newly created database was used, for the first time, to evaluate additional information that could be gleaned from the genetic samples gathered in this 2018 BMA 4 population inventory project.

For this evaluation, we compared the 63 grizzly bear genotypes from the 2018 BMA 4 samples with all available genetic samples of grizzly bears from across the province (WGI unpublished data; Graham and Stenhouse 2019) to determine if any of these bears were previously known. There were 25 genetic matches: 10 bears were previously detected during the first inventory conducted in 2005 in BMA 4, of which four were also captured and collared by fRI Research biologists prior to 2018 (Table 12, see ‘a’); four were research bears captured and collared on BMA 4 in 2018 or 2019 by fRI Research biologists and detected during the 2018 BMA 4 census (Table 12, see ‘b’); four were detected in a 2006–2008 Banff census (Table 12, see ‘c’); four had been detected during the 2014 census of BMA 3 which is located

directly north of BMA 4 (Table 12, see 'd'); and three had been previously detected in southern Alberta in BMA 6 (Table 12, see 'e'). These three bears from BMA 6 were likely translocated grizzly bears moved by Alberta Environment and Parks conservation officers because of a conflict that occurred. We do not know where these bears were released or the reason for the translocation.

Table 12 illustrates the value of obtaining DNA samples over time. We can track survival, movements and reproduction using a long-term genetic database. These are important elements of grizzly bear population and trend monitoring efforts to support recovery efforts.

Table 12: Additional information on 25 individual grizzly bears (previously known) that were detected on the 2018 BMA 4 population inventory grid.

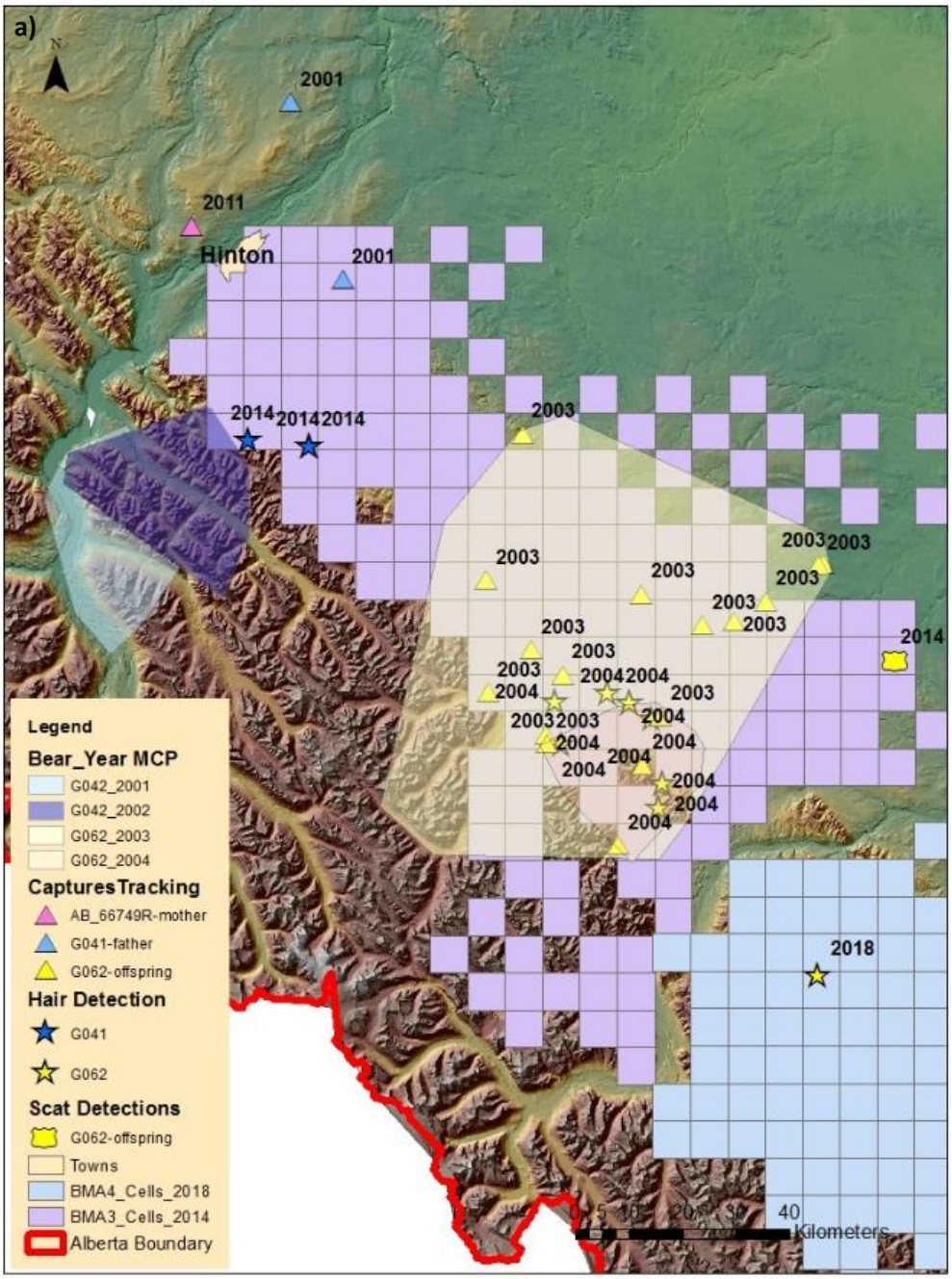
Bear[(i)]	Sex	Birth Year	Year First Detected	Other Detections	Year Last Detected
G062 (d)	M	1998	2003 capture BMA 3	2004 census BMA 3 2014 scat BMA 3	2018 census BMA4
G093 (a)	F	1996	2004 capture BMA 4	2005 census BMA 4	2018 census BMA 4
G095 (a)	F	1997	2004 capture BMA 4	2005 census BMA 4	2018 census BMA 4
G097 (a)	F	1995	2004 capture BMA 4	2005 census BMA 4	2018 census BMA 4
G165 (d)	M	2002	2013 census BMA 3	2014 census BMA 3 2015 capture BMA 3	2018 census BMA 4
G350 (b)	M	2011	2018 capture & census BMA 4		2019 capture BMA 4
G351 (a)	M	2002	2005 census BMA 4		2018 capture & census BMA 4
G352 (b)	M	2011	2018 capture & census BMA 4	2018 hair at a ranch	
G354 (c)	M	2005	2007 Banff	2008 Banff	2018 capture & census BMA 4
G355 (b)	F	2009	2018 capture & census BMA 4		
G358 (c)	M	2006	2006 Banff	2007 Banff 2018 census BMA 4	2019 capture BMA 4
G364 (b)	M	2009	2018 capture & census BMA 4		2019 capture BMA 4
550-3B-2 (d)	M	?	2014 census BMA 3		2018 census BMA 4
522-3C-2 (d)	M	?	2014 census BMA 3		2018 census BMA 4
318A-4C-2 (e)	M	?	2011 BMA 6	2013 BMA 6 2014 BMA 3	2018 census BMA 4
605C02x (a)	F	?	2005 census BMA 4		2018 census BMA 4
597625 (c)	F	?	2008 Banff		2018 census BMA 4
345A03a (a)	M	?	2005 census BMA 4		2018 census BMA 4
09580 (e)	M	?	2012 BMA 6	2013 BMA 6	2018 census BMA 4
579567 (e)	M	?	2008 Banff		2018 census BMA 4
320C03a (a)	F	?	2005 census BMA 4		2018 census BMA 4
314A02a (a)	F	?	2005 census BMA 4		2018 census BMA 4
287B04b (a)	F	?	2005 census BMA 4		2018 census BMA 4
258A01x (a)	F	?	2005 census BMA 4		2018 census BMA 4
SAR2003 (e)	F	?	2013 BMA 6	2014 BMA 6	2018 census BMA 4

[(i)] See text for details.

A parentage analysis using software Parente was performed by WGI on their full set of Alberta and southeast British Columbia genotypes, including the 2018 BMA 4 results (WGI, unpublished data). This is

a method used by the lab to check for possible errors in scoring. The program highlights perfect matches as mother-father-offspring triads, as well as triads that mismatch at 1 or 2 markers. Any mismatched markers were then double checked to ensure that a scoring error had not made.

Because the dataset used by WGI for the parentage analysis is made up of > 4700 unique individuals, the Parente program can output by chance some perfect triads of mother-farther-offspring that are incorrect. Therefore, each perfect triad must be scrutinized by gathering additional available information on these bears such as ages and locations. If the ages and locations seem appropriate, then we have greater confidence that the triads are true. Some interesting findings from the parentage analysis that are plausible include one male bear (G062) who was first captured in 2003 within BMA 3 by fRI grizzly bear program biologists. During capture, a premolar tooth was removed to obtain a birth year which was established to be 1998. He was detected again in 2004 during the BMA 3 census, and in 2014 via scat in BMA 3 and lastly in 2018, as a 20-year-old, during the BMA 4 census. The parentage analysis indicated that G062's mother was likely an adult female shot by a poacher(s) in 2011, 8 km north of Hinton, AB in BMA 2 and his father was likely research bear (G041) who was born in 1988 and had a home range within BMA 3 (Figure 29a). G062 is now the presumed father of a male offspring (G151) born in 2007 and lives in the south half of BMA 3 (Figure 29b). G062 mated with a female (551-12D-2) bear detected in 2014 on the BMA 3 grid (Figure 29b).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G042_2002
G062_2003
G062_2004
Captures Tracking
AB_66749R-mother
G041-father
G062-offspring
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G062-offspring
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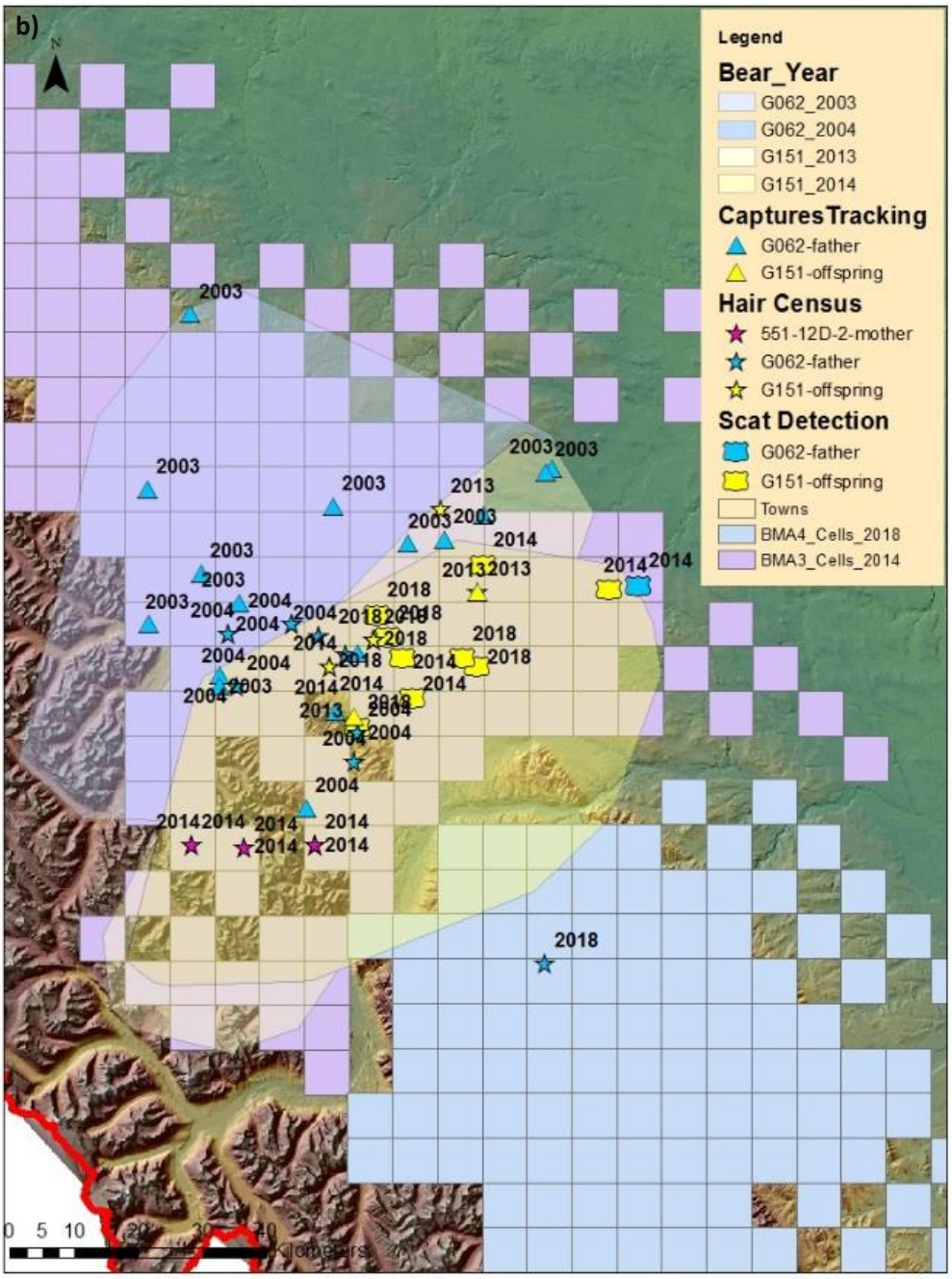

Figure 29. Maps showing a) G062's detections along with his presumed parents and b) G062's detections along with his presumed offspring and mate.

We have provided maps in Appendix 3 which provide the spatial and temporal data for each of the bears that were identified from the 2018 DNA hair data and had a previous known history as documented in the new genetic database. An impressive 40% of the bears found in the 2018 inventory had known history

largely due to long term research and monitoring efforts in Alberta. To highlight the results from looking at these genetic datasets we have presented two examples here.

The first is a male bear G354 (Figure 30) born in 2005 and therefore would have been a 13-year-old bear in 2018 when detected on the population inventory grid. This bear was first detected in Banff National Park in 2007 and then captured and collared by our research team in 2018 outside the park in core habitat within BMA north east of previously known locations. Although the collar information from this bears in 2018 was only available for May 2018 it did show movements to the eastern side of the BMA, however DNA data showed this bear was also using habitat within Banff National Park in the same year. Genetic data from this bear also showed another bear that G354 mated with and we found an offspring from G354 within the database showing successful reproduction from this bear.

The parentage analysis also suggests that two bears that were translocated from southern Alberta in BMA 6 successfully produced offspring after they were moved. A male grizzly bear first detected in 2011 and then again in 2013 in BMA 6 (Morehouse and Boyce 2016) was later detected within the BMA 3 sampling grid in 2014 and then on the BMA 4 sampling grid in 2018. His presumed offspring was also detected in 2018 on the BMA 4 grid. In addition, a female (SAR2003) first detected in 2013 and again in 2014 in BMA 6 (Morehouse and Boyce 2016) was detected in BMA 4 in 2018 and is the presumed mother to a male bear detected on the 2018 BMA 4 sampling grid (Figure 31). The presumed father was a known bear whom resided in BMA 4, so it is likely she bred with this male after her move, established a home range within the BMA and produced offspring. This is an example of the tremendous value of this new genetic database and for this translocated bears indicates survival over time, fate, the establishment of a new home range and successful breeding and cub production. It is also important to recognize the importance of obtaining complete records on the management movement of grizzly bears within the province.

There were also adult female bears with their presumed cub(s) detected together at the same site and sampling session. While this is not surprising, it gives us more confidence that the Parentage analysis is assigning parent offspring correctly.

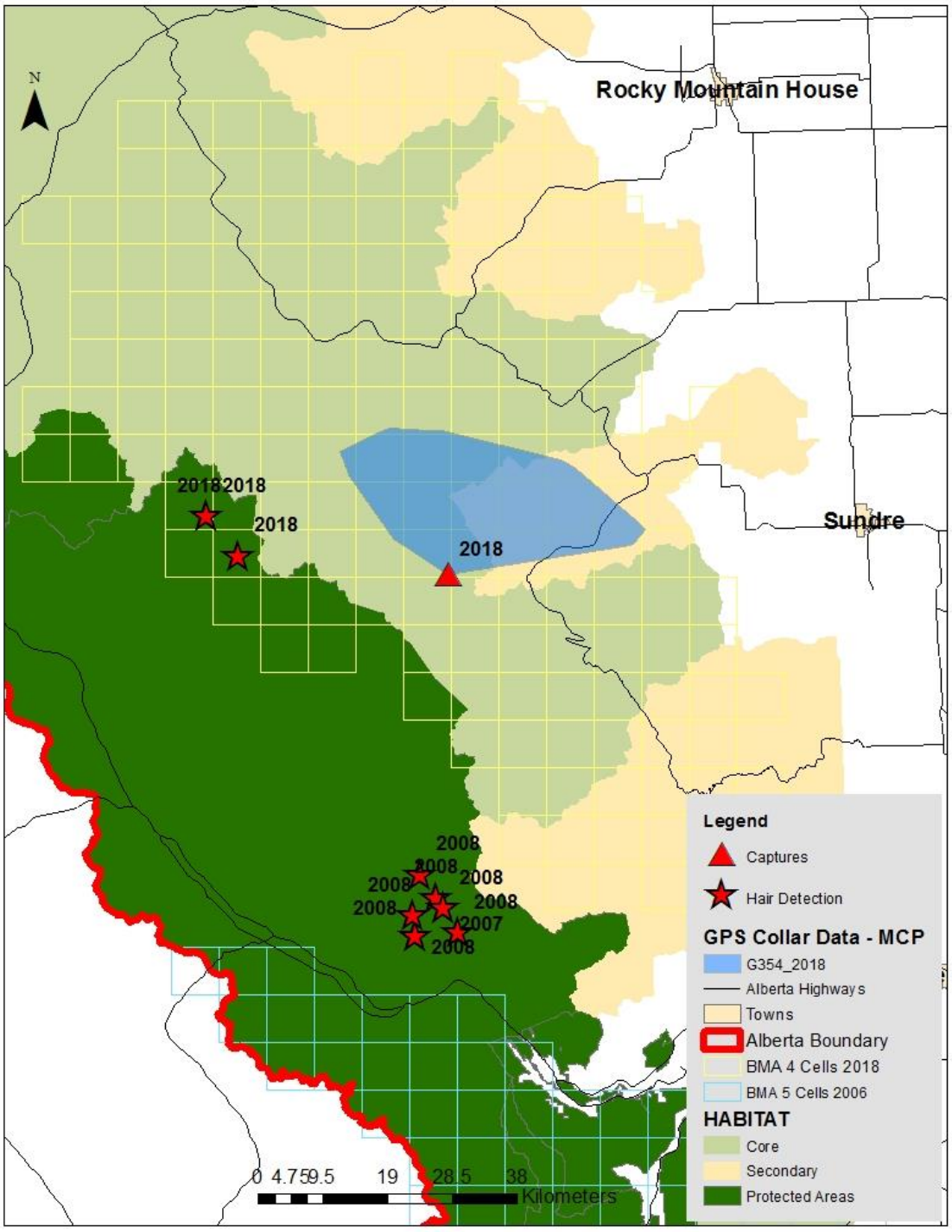

Figure 30: G354 male; born 2005; first detected 2007 and 2008 Banff census (NW of Lake Minnewanka); 2018 spring capture 40 km north of Banff detections. Collar data only for May 2018; 2018 BMA 4 grid further west of capture and collar data. Likely bred with 320C03a (=347C-1B-4 first detected 2005 BMA 4 grid; 2018 BMA 4 grid) to produce 347C-1G-4 (first detected 2018 BMA 4 grid with mom). Dispersal example, survival determination, home range establishment, and parentage documentation.

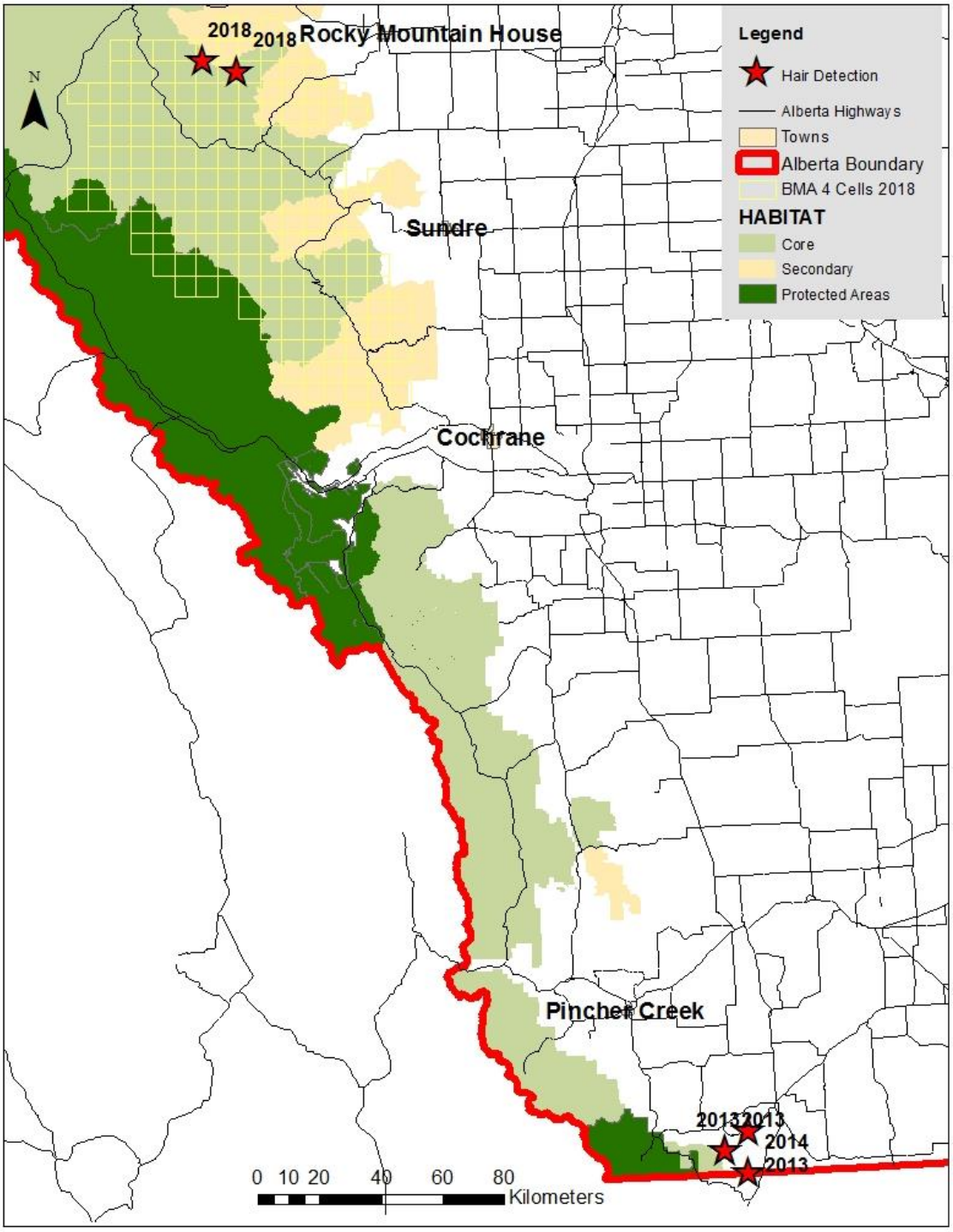

Figure 31: SAR2003=150B-1A-2: female; first detected 2013 Castle on a tree; 2014 Castle on a tree and opportunistically; 2018 BMA 4; Possible mother to 348A-1C-1 (male; first detected 2018 BMA 4) with father AB_6339 (relocated 2010 from Caroline area to Nordegg but still in BMA 4). Cub and mom not at same site and time. This means that the father survived after his move to have bred with 150B-1A-2 after she was presumably moved from Castle sometime between 2014 and 2017.

Agriculture Zone Bears

During the 2018 population inventory work our focus was on ensuring that the sampling design and field methodologies would allow a direct comparison with the results of our 2005 inventory project within this BMA. Although it is widely recognized that there are grizzly bears which are seen to the east of the sampling grid (Figure 32) in the agricultural zone, sampling was not directed to the eastern edge of this BMA. It was felt that bears along this eastern edge occurred at low density and would require a more intensive sampling regime and thus more resources. However, in 2019 the year following DNA inventory work, as part of ongoing research activities in BMA 4 there were 2 bears that were captured and GPS radio collared outside our DNA sampling grid along this eastern edge of the BMA. Telemetry data from these 2 bears showed that while they spent a great deal of time outside the sampling grid, there were times during the same DNA sampling time periods where these bears entered the DNA grid and hence had an opportunity for detection, but these bears were not identified in the 2018 sampling.

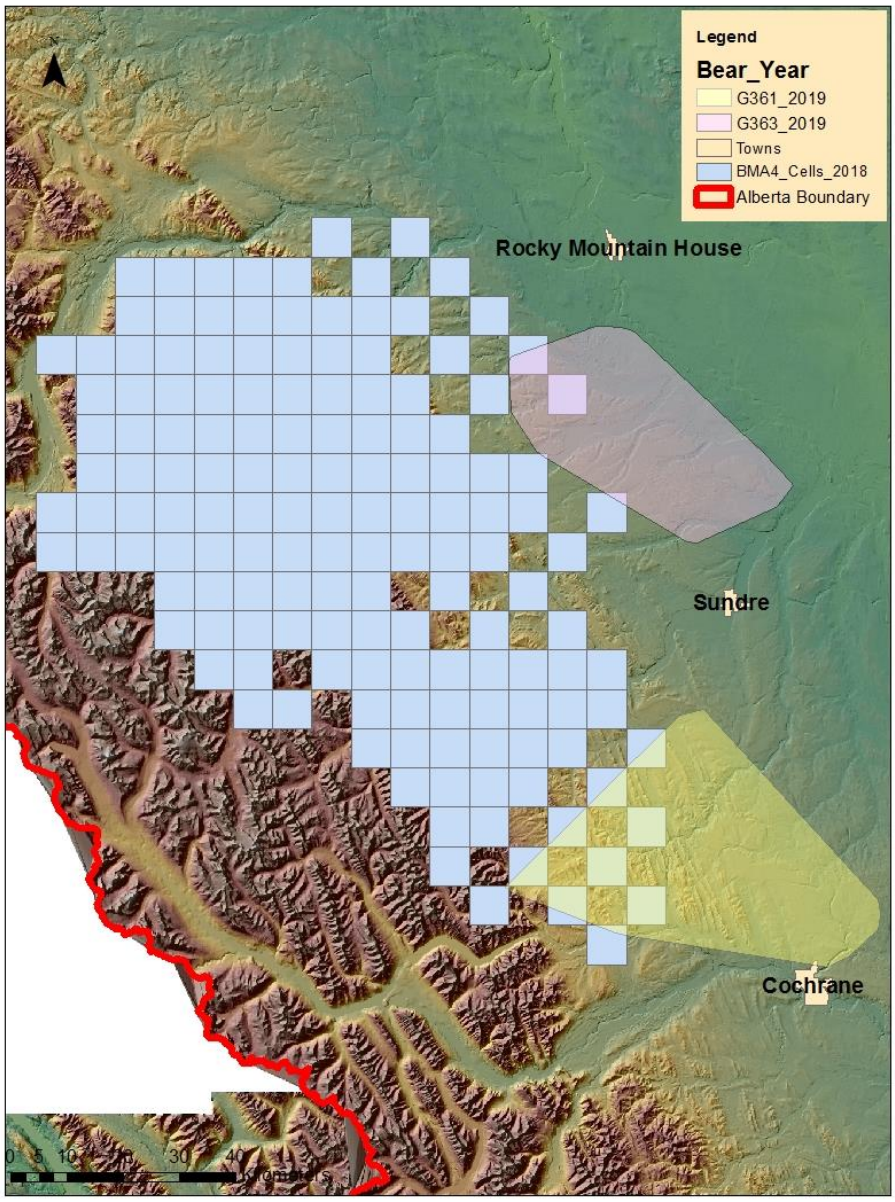

Figure 32. Two grizzly bear home ranges (2019 collar data) within the eastern agricultural zone in relation to the BMA 4 DNA inventory grid.

CONCLUSIONS

The 2018 population estimate for BMA 4 was 88 grizzly bears (CI= 59–130), while the inventory work conducted 13 years previously in 2005 had an estimate of 42 bears (CI=32–50). These results show that the population of grizzly bears in BMA 4 has increased substantially at an average rate of 6% (CI=5–9%) per year since the 2005 inventory based on the ratio of abundance estimates for the core and secondary areas (Table 9). This rate of increase is similar to that observed for the 2014 BMA 3 inventory, which

estimated an annual increase of 7% (Stenhouse et al. 2015). Other recent grizzly bear studies have also estimated increases in grizzly bear populations with an annual 4% increase in the Northern Continental Divide Ecosystem area of Montana (Kendall et al. 2019).

The relatively high apparent survival for female bears 0.96 (CI=0.86–0.99) from open model analyses (Table 11) further supports demographic increase. This rate of survival should be treated cautiously given that it is based on bears detected in the 2005 and 2018 surveys and therefore it assumes a constant survival rate for the 13 year period between surveys. However, other evidence, such as the apparent spread in distribution of females (Figure 25), as well as the similarity in λ estimates from the ratio of estimates (Table 9: λ=1.06 for the grid area) and open models (λ=1.07), indicate an increasing population. Further analysis that uses information from collared bears as well as detections of bears in other areas between surveys should be pursued to provide refined demographic estimates.

The main challenges with this analysis was the gradient in RSF, RISK, and bear density from West to East in the sampling area (Figure 4), which resulted in bear detections being most prevalent on the western edge of the sampling grid (Figures 7 and 8). To confront this issue, density surface models were used which also illustrated dominant factors affecting bear distribution. For female bears, RSF and RISK influenced distribution with females showing higher densities in lower RSF/lower RISK Banff National Park areas (Figures 11 and 12) with males being most influenced by RSF (Figures 14 and 15). his contrasts with 2005 BMA 4 results where both male and female distribution was most influenced by RSF (Boulanger et al. 2018). The actual mechanisms for change in observed bear densities could be investigated further. For example, female density did increase in secondary areas which had areas of higher RISK in 2018 compared to 2005 and therefore more spatial data was available to model the relationship between RISK and RSF as further indicated by shifts in home range centers from 2005 to 2018 (Figure 23). The high RSF and high RISK areas can be conceptualized as attractive sinks (if mortality sources are not managed) and higher densities in these areas could be due to success in managing bears and reducing mortality pressure, therefore allowing increases in density.

The overall detection success in 2018 was lower than 2005 as illustrated by the proportion of new detections by session (Figure 6) as well as the shapes of detection functions (Figure 19). The 2005 inventory had one of the highest detection probabilities with roughly 80% of bears detected (Table 9: 32 bears detected/Ave N on sampling grid of 40). In contrast, in 2018 approximately 72% of bears were detected (64 bears detected/Ave N of 88; Table 6). The reduction in detection success was likely due to stratification (secondary area sampled with less intensity) and not moving sites between sessions which reduces the ability to select seasonal habitat and can create behavioural responses to sampling (Boulanger et al. 2006). It is suggested that moving sites for one session (2 sessions at one location and 2 sessions at a new location) might be considered to offset reduction of detection probabilities due to not moving sites.

Previous work (Phoebus et al. 2020) has shown that although DNA extraction rates are much lower than from hair samples and thus do not provide a strong data set for population estimation, scat samples can

provide important information regarding the distribution and occurrence of bears on the landscape. It was unfortunate that the scat samples that were collected within this project in 2018 were not analyzed until 2020. We believe this delay allowed sample degradation which had a negative impact on DNA extraction rates from these samples. However, it is important to also recognize that despite the lack of individual bear identifications, the scat samples did provide data on species distribution which can be an important metric in grizzly bear recovery determination. We recommend that any scats collected be processed at the end of each sampling season.

The recently created (2019) provincial grizzly bear genetic database was used to explore the history of the unique grizzly bears that were identified on the population inventory grid cell using the hair samples collected. This dataset, which represents a huge investment of both time and resources, is now able to support recovery and management efforts by providing important data on: grizzly bear survival, site fidelity, bear movements between BMAs, fates of translocated bears, and productivity assessment through parentage analysis. We are unaware of any other jurisdiction in North America that has this type of dataset and hence the ability to monitor grizzly bear populations in this manner. It is recommended that the collection and laboratory analysis of all genetic samples obtained from grizzly bears continue with annual analysis and reporting. All bears that are handled for management actions, or mortalities, should have samples provided for this effort. We also believe that a co-ordinated program for genetic sample collection should include local landowners who reside on the eastern edges of BMAs. Active engagement of these landowners could add greatly to our knowledge base on regional population trends and therefore support data needs for recovery and management.

Alberta has a unique and important data set that can be used to successfully manage and recover grizzly bears. Additional analysis of these data to help understand the mechanisms that have led to the documented population increases over time should be a high priority in the future.

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APPENDICES

Appendix 1: Details on the 2005 BMA 4 SECR Analysis

This appendix details on the analysis of the 2005 BMA 4 data set. It is taken from the supplemental data issued as part of a Scientific Reports journal article on DNA mark-recapture sampling in Alberta (Boulanger et al. 2018). Estimates and spatial predictions are presented in the main report.

The Clearwater (BMA 4) area was sampled in 2005 (Figure 2 and Figure 19; Boulanger 2015). Initial analyses were conducted with sexes pooled to assess appropriate buffer distances to negate bias in density estimates due to movements from the grid area. A buffer size of 15 kilometers was estimated using the esa.plot and suggest.buffer functions in program SECR. As with other analyses 3.5 kilometer mask centroid spacing was used. Barren habitat at elevations of greater than 2000 m was considered as non-habitat in the analysis.

Overall, 42 bears were detected (17 males and 25 females) in the 2005 inventory. Summary statistics suggest that sampling was very efficient with the majority (40 of 42 bears) being detected prior to session 4 and 30 of 42 bears being detected in more than one session (Table 13).

Table 13: Summary statistics for the 2005 Alberta Clearwater (Bear Management BMA 4).

	Session				
Statistic	**1**	**2**	**3**	**4**	**Total**
Females					
Animals caught (n_j)	10	15	13	19	57
Newly caught (u_j)	10	9	4	2	25
Frequencies (f_j)	7	8	6	4	25
Total individuals caught (M_j)	10	19	23	25	25
Detections	11	18	18	22	69
Detectors visited	9	15	16	17	57
Detectors available	187	183	181	182	733
Males					
Animals caught (n_j)	7	15	12	8	42
Newly caught (u_j)	7	9	1	0	17
Frequencies (f_j)	5	2	7	3	17
Total individuals caught (M_j)	7	16	17	17	17
Detections	16	26	19	10	71
Detectors visited	14	24	19	10	67
Detectors available	187	183	181	182	733

Females

Model selection results suggested a temporal increasing trend in movement of grizzly bears with detection probabilities at the home range center being positivity related to terrain ruggedness (Table 14, model 1).

Of density surface models, a model with RSF was most related to density of grizzly bears on the sampling grid. A model with strata (model 3: core, secondary, and Parks) was less supported than the RSF model but more supported than a constant density model suggesting association of strata areas with bear density.

Table 14: Abridged model selection for female grizzly bear SECR analysis for Unit 4 (2005). AIC_c = sample size adjusted Akaike Information Criterion, ΔAIC_c = the difference in AIC_c between the model and the most supported model, AIC_c weight = w_i, K, the number of model parameters and log-likelihood are given. Baseline constant models are shaded for reference with covariate models.

No	Density	Detection	AICc	ΔAIC_c	w_i	K	LL
1	RSF	g_0(TRI) σ (T)	564.1	0.00	0.98	6	-273.70
2	RSF+Risk	g_0(TRI) σ (T)	568.0	3.89	0.02	7	-273.71
3	Strata (Parks, core, secondary)	g_0(TRI) σ (T)	571.9	7.79	0.00	7	-275.7
4	RSF+Risk+RSF*Risk	g_0(TRI) σ (T)	572.2	8.07	0.00	8	-273.6
5	constant	g_0(TRI) σ (T)	576.0	11.87	0.00	5	-281.4
6	Risk	g_0(TRI) σ (T)	579.5	15.37	0.00	6	-281.4
7	constant	g_0(CC) σ (T)	581.1	17.02	0.00	5	-284.0
8	constant	g_0 (.) σ (T+TRI)	581.2	17.13	0.00	5	-284.0
9	constant	g_0 (.) σ (T+CC)	581.6	17.49	0.00	5	-284.2
10	constant	g_0 (.) σ (T)	584.4	20.24	0.00	4	-287.2
11	constant	g_0 (T) σ (T)	586.4	22.31	0.00	5	-286.6
12	constant	g_0 (CC^2) σ (T)	586.7	22.59	0.00	5	-286.8
13	constant	g_0 (CC) σ (T)	586.8	22.67	0.00	5	-286.8
14	constant	g_0 (.) σ (T+TRI)	587.1	22.99	0.00	5	-287.0
15	constant	g_0 (K) σ (T)	587.3	23.19	0.00	5	-287.1
16	constant	g_0 (.) σ (T+CC)	587.5	23.34	0.00	5	-287.1
17	constant	g_0 (stream) σ (T)	587.5	23.35	0.00	5	-287.2
18	constant	g_0 (.) σ (T+h2)	588.2	24.09	0.00	6	-285.8
19	constant	g_0 (T) σ (.)	589.0	24.91	0.00	4	-289.5
20	constant	constant	589.4	25.30	0.00	3	-291.1

Males

Model selection results suggested that detection of male bears was positively related to terrain ruggedness with scale of movement being relatively constant (Table 15, model 2). Of density surface models, a model that associated density with RSF score was most supported (model 1). A model with strata-specific densities (model 8) was less supported.

Table 15: Abridged model selection for male grizzly bears for the Unit 4 (2005) inventory. AIC_c = sample size adjusted Akaike Information Criterion, ΔAIC_c = the difference in AIC_c between the model and the most supported model, AIC_c weight = w_i, K, the number of model parameters and log-likelihood are given. Baseline constant models are shaded for reference with covariate models.

No	Density	Detection	AICc	ΔAIC_c	w_i	K	LL
1	RSF	g_0(TRI) σ (.)	693.16	0	0.74	5	-338.9
2	constant	g_0(TRI) σ (.)	696.89	3.73	0.12	4	-342.8
3	RSF+Risk	g_0(TRI) σ (.)	697.84	4.69	0.07	6	-338.7
4	constant	g_0(TRI) σ (TRI)	699.90	6.75	0.03	4	-344.3
5	constant	g_0(TRI) σ (.)	701.50	8.35	0.01	4	-345.1
6	constant	g_0(.) σ (CC)	701.81	8.66	0.01	4	-345.2
7	constant	constant	702.33	9.18	0.01	3	-347.2
8	Strata (Parks, core, secondary)	g_0(TRI) σ (.)	703.68	10.52	0.00	6	-341.6
9	RSF+Risk+RSF*Risk	g_0(TRI) σ (.)	703.85	10.70	0.00	7	-338.7
10	constant	g_0(T) σ (.)	704.11	10.96	0.00	4	-346.4
11	constant	g_0(CC^2) σ (.)	705.39	12.23	0.00	4	-347.0
12	constant	g_0(.) σ (T)	705.40	12.25	0.00	4	-347.0
13	constant	g_0(CC) σ (.)	705.68	12.53	0.00	4	-347.2
14	constant	g_0(T) σ (.)	706.92	13.76	0.00	6	-343.3
15	constant	g_0(T) σ (T)	707.53	14.37	0.00	5	-346.0
16	constant	$g_0(h_2)$ σ (h_2)	709.52	16.37	0.00	5	-347.0
17	constant	g_0(.) σ (h_2)	709.94	16.78	0.00	5	-347.2
18	constant	g_0(.) σ (t)	712.71	19.55	0.00	6	-346.2

Appendix 2: Sampling Designs for 2018

This appendix details simulations used for the design of the 2018 survey. Of key interest was whether the precision of density estimates from potential designs would be similar to the 2005 survey design. For this reason, the 2005 design was simulated along with a design that utilized the 7x7 km cell sampling in core area and sampled every other cell in secondary areas. The rationale behind this design was that it would be comparable to the 2005 design given that it sampled the same cells and potential site locations within the core areas. In addition, it provided a systematic sample of the secondary areas therefore allowing a robust estimate of density. This design is similar to the design employed for the 2014 BMA Unit 3 inventory project (Boulanger and Efford 2014, Stenhouse et al. 2015) which employed 7x7 cells in core area and 10x10 cells in secondary areas All designs did not sample the northern tip of the BMA due to high recreational traffic in this area and difficulties with placement of hair snag sites (Figure 33).

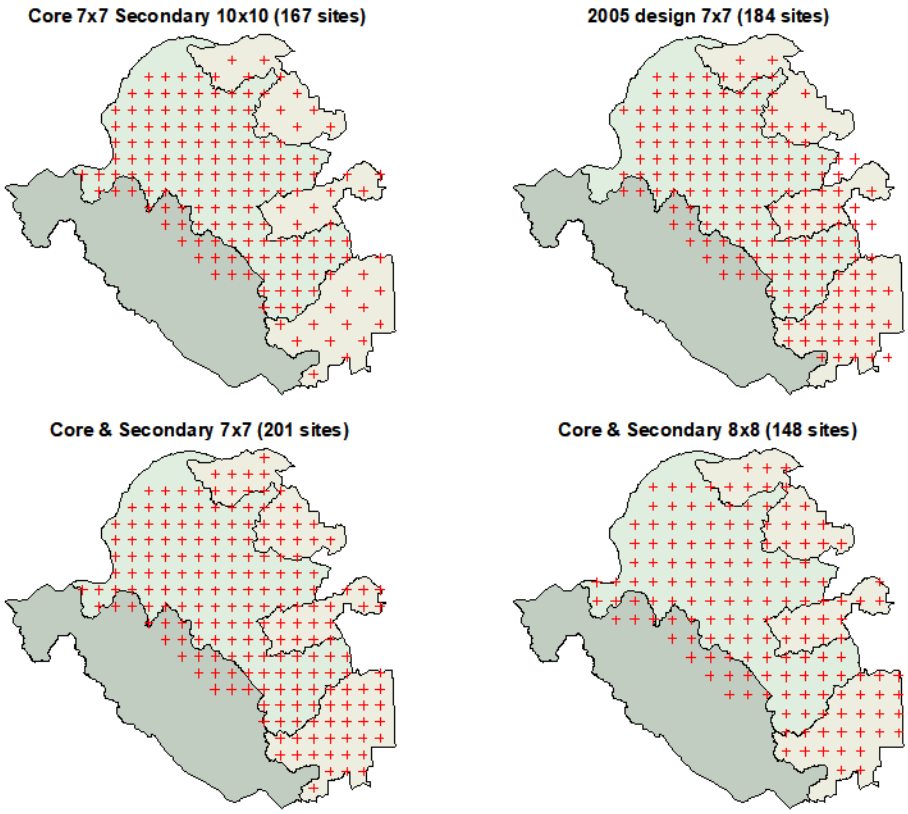


Figure 33: Potential designs considered in simulations. Park, core, and secondary areas are delineated along with sites (red + signs).

Simulation Methods and Results

In terms of study design, we were most concerned with detection and redetection of females which exhibit smaller home ranges than males and therefore simulation parameters were mainly based upon females. Detection parameters for females were taken from the 2005 survey with an estimate of detection at home range center (g_0) of 0.18 and spatial scale parameter (σ) of 5782 m. These values fall within the general range observed for previous inventories in Alberta (Figure 34).

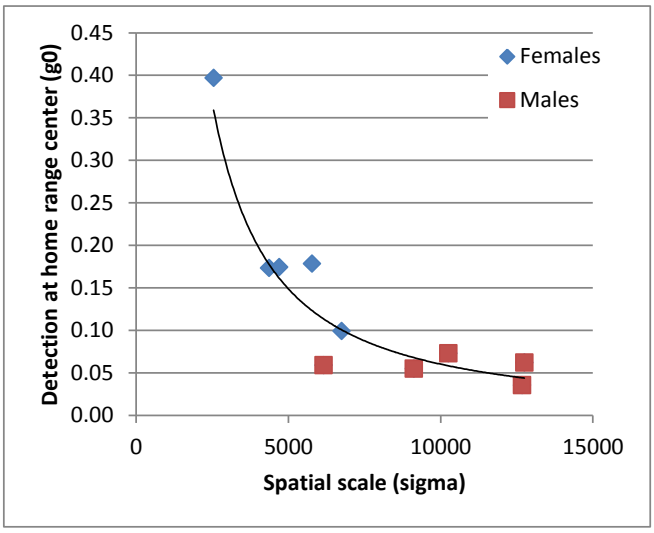


Figure 34: Relationship between detection at home range center (g_0) and spatial scale (sigma) from Alberta DNA mark-recapture projects (Boulanger et al. 2017; Table 1). A power curve was fit to the data ($g0=10058\sigma^{-1.3}$) was fit to describe the relationship between g0 and σ. More direct parameterizations between g0 and σ are available (Efford and Mowat 2014, Efford et al. 2016).

We simulated grizzly bear home range centers across a region (SECR mask) that was closed on all sides in the west where it extended 15 kilometers into Banff Park beyond the extent of traps. From the 2005 analyses we inferred that more distant bears were very unlikely to influence the estimates and could therefore be safely omitted from simulations. There was no need to consider bears with home range centers to the east because the area is heavily roaded and is believed to hold very few bears. The north and south borders were based on major highways that defined the BMA boundary based on genetic analysis (Proctor and Paetkau 2004), and simulations assumed bears did not cross the highways. Home range centers were assumed not to occur in barren habitat above 2000 m elevation.

The population was simulated using two approaches. First, we applied the 2005 RSF model (Figure 4) to predict population density in each cell of the mask. Second, we assumed uniform density within each of the park, core and secondary areas, using either the values observed in 2005 or the stratum-specific densities with an allowance for population increase (Figure 35). In the increase scenario we doubled the secondary densities and increased core and park densities by a factor of 1.75. The net effect of the increase scenario was to increase population size in the masked region by a factor of 1.56 over 2005, which is equivalent to an annual increase of 5% (λ = 1.05). The average number of bears simulated under the mask was 49, 46, and 86 for the RSF, core-secondary (2005 levels) and core-secondary (λ=1.05) scenarios.

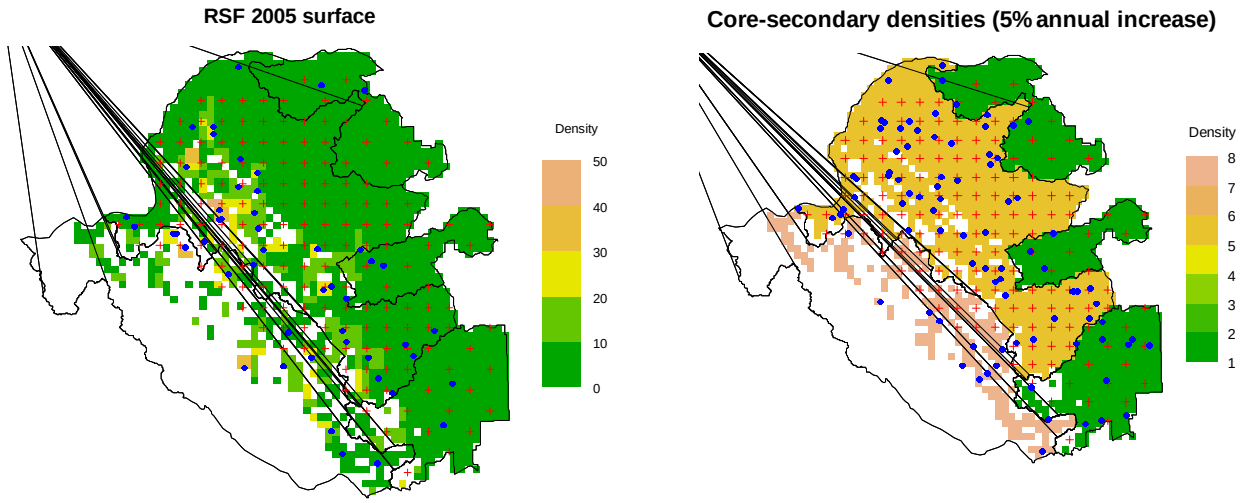


Figure 35: Simulated variation in density based upon density surface modelling of 2005 data set (left) and estimated densities in core and secondary areas (right). Home range centers were assumed to not occur in barren areas above 2000 m. Blue dots indicate home range centers from one simulation.

Simulations results were evaluated in terms of realized N estimates of abundance for the mask area which would be most sensitive to changes in density across the mask surface. Precision was evaluated using relative standard error (RSE) of estimates (estimate of standard error scaled by the point estimate). The RSE (also known as CV) allows comparison of precision across different levels of abundance. In addition, simulations were evaluated in terms of relative bias which is the difference between the point estimate and true value divided by the true value. Simulations were conducted in the *secrdesign* package (Efford 2015) with further analysis using the *secr* package (Efford 2014a) in program R.

Simulation results (Figure 36) suggested that all designs had reasonable precision which is not surprising given the relatively high detection probabilities of female bears during the 2005 survey (g_0=0.18/σ=5782 m) and subsequent higher precision of SECR estimates. The full 7x7 systematic design had the highest precision which was intuitive given that it had the highest level of effort. Precision was roughly equal for the 2005 design and the core 7x7/secondary 10x10 design. Precision was lowest for the 8x8 design for all scenarios, however, the difference was minimal for the core-secondary increase (λ=1.05) scenario. Differences between designs were most apparent with scenarios that set abundance at 2005 levels. Relative bias was less than +/- 5% for all designs, with all designs displaying confidence interval coverage at close to 95% levels.

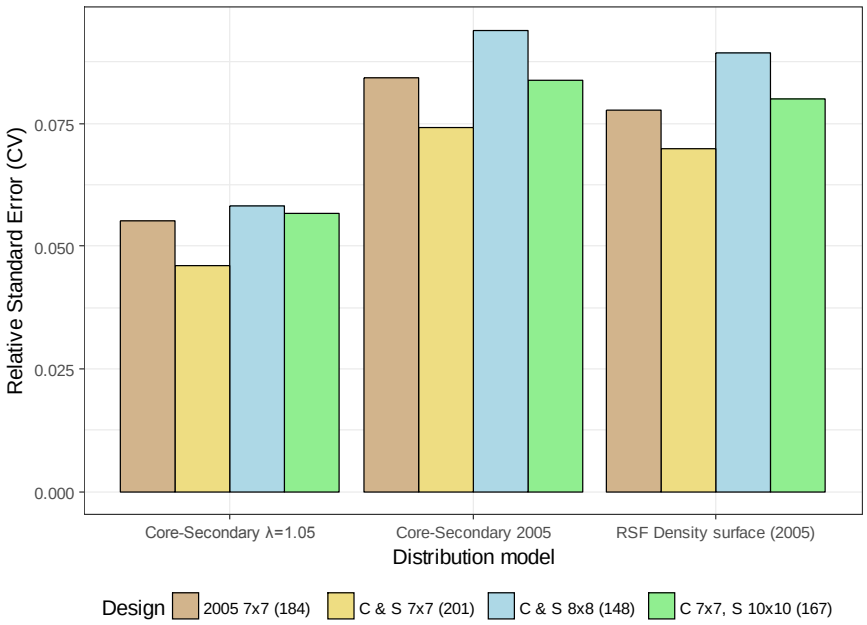


Figure 36: Precision as indicated by RSE for the 4 proposed sampling designs. The designs (C=core, S=Secondary) and the number of sites per design are given in parenthesis. Distribution models relate to the SECR mask used in simulations (Figure 9).

I suggest that the core (7x7)/secondary (10X10) design is optimal in that it allows a thorough systematic sample of the BMA while putting the most sampling effort in the core where the highest densities of bears occur. This recommendation is under the assumption that the relative distribution of bears in 2018 will be similar to 2005 with the majority of bears occurring in the core area. This design in cell form is shown in Figure 37.

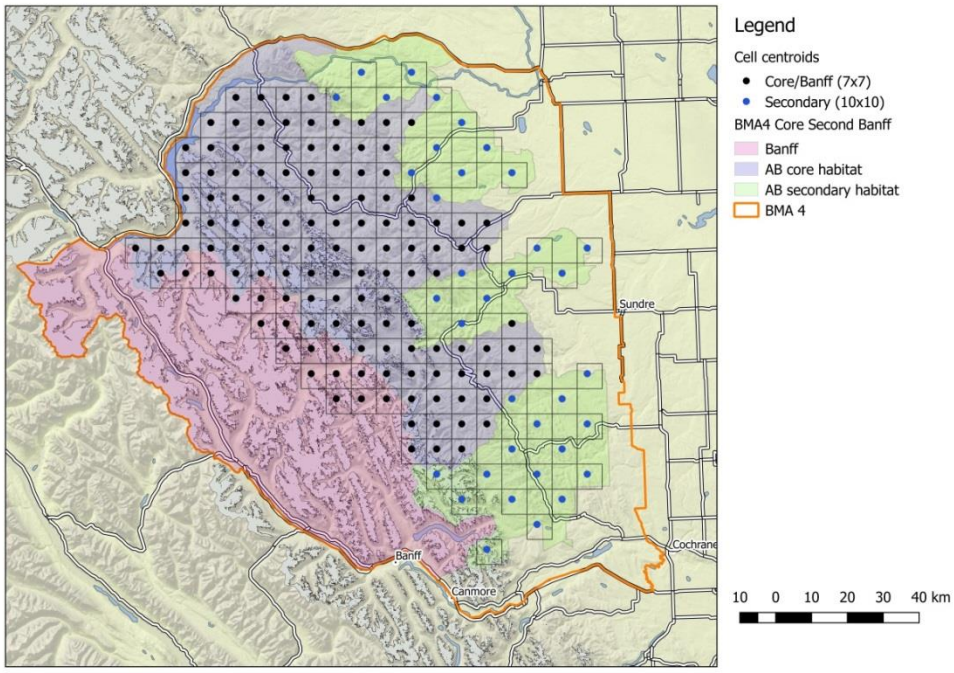


Figure 37: The core (7x7)/secondary (10X10) design with cells to be sampled designated by centroids in each cell.

If it is possible that a large increase has occurred in secondary area then a design that systematically samples the entire BMA may be optimal. This design will result in less precise overall estimates as well as less precise estimates in core areas but will allow a more precise estimate in secondary areas. For this design, the 8x8 km cell size could be used given that overall estimates with acceptable precision (but less precise then the core 7x7 km; secondary 10x10 km design) were obtained by the 8x8 km design in simulations (Figure 38).

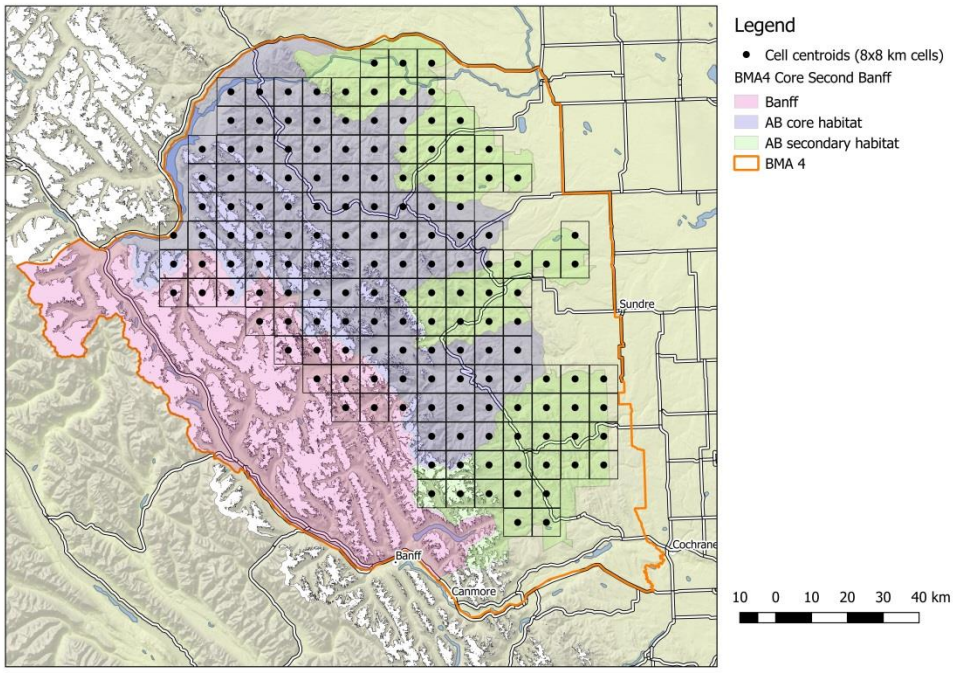


Figure 38: The non-stratified 8x8 km cell design to be considered if large increases in density in secondary areas are expected.

Discussion

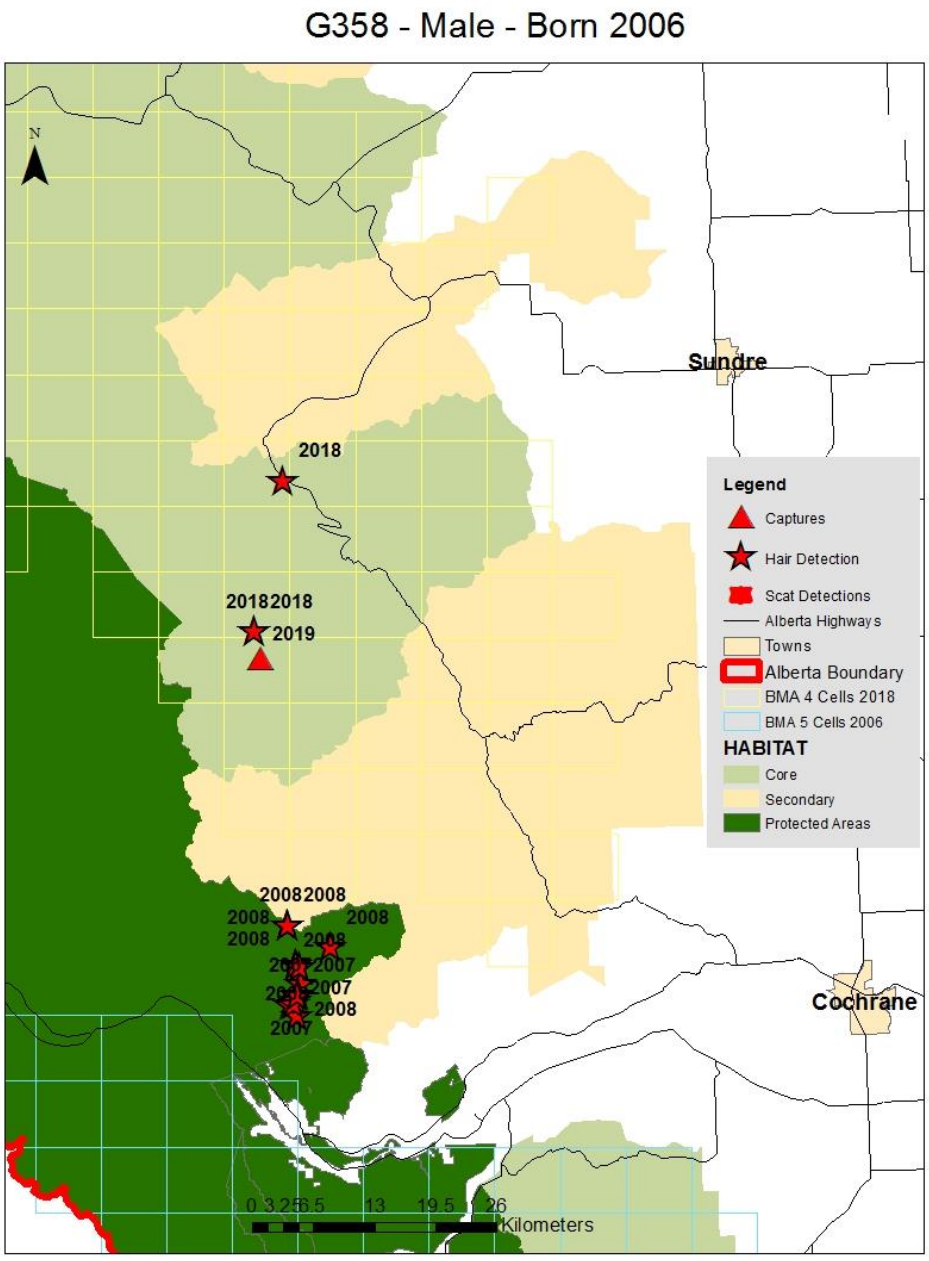
The main objective of the 2018 BMA 4 inventory is to allow an estimate of change in the bear population based on comparison with the 2005 survey. For this reason, the proposed design for 2018 closely mirrors the 2005 survey including the use of the same cells in core habitat areas where densities are highest. This approach allows a direct comparison of both distribution and estimates without the need for additional assumptions regarding study area extent. The 2018 design additionally systematically samples secondary habitat which should allow a stratified SECR analysis that estimates both core and secondary density and abundance as was done in the 2014 BMA 3 inventory (Stenhouse et al. 2015).

The main assumption behind the 2018 stratified design is that densities will be compared to secondary areas therefore justifying a stratified sampling reasons why this assumption is justified. First, analysis of the 2005 data set densities were 34% of core densities (

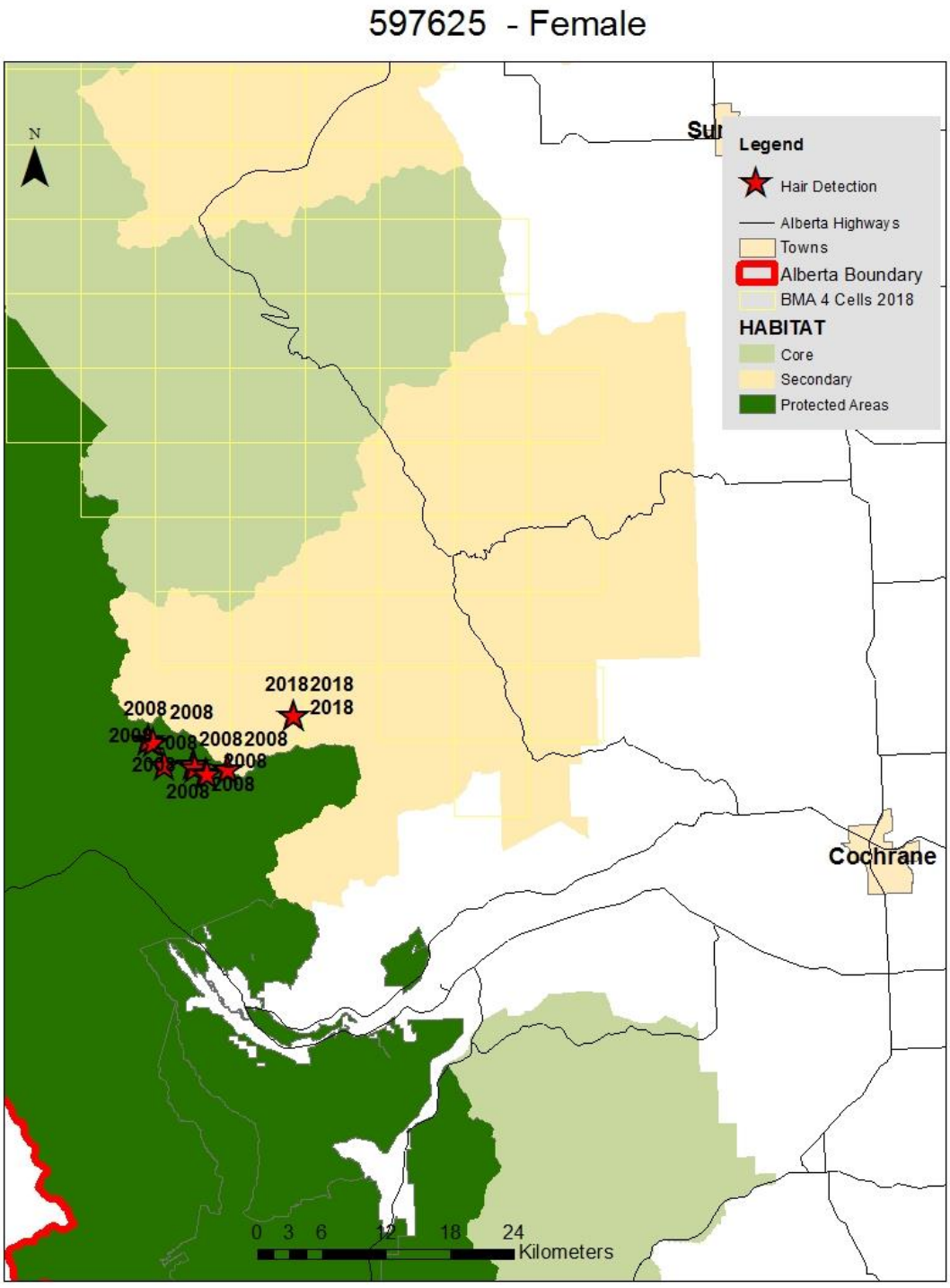
Table 2). It could be argued that increase is more likely to occur in the secondary compared to core habitats, but historically this does not appear to be the case. Comparison of the 2004 and 2014 BMA 3 inventory results suggests that core density approximately doubled between 2004 and 2014 (5.1 to 11.1 bears per 1000 km^2) whereas density remained stable in secondary habitats (1.26 to 1.15 bears per 1000 km^2). Given these results it is unlikely that densities will increase to the point where core and secondary densities are similar and a less stratified sampling design would be warranted. If an increase in secondary areas is suspected to be large then a non-stratified 8x8 km cell design (Figure 38) should be considered.

Appendix 3: Additional Maps Showing Histories of Individual Grizzly Bears in BMA 4

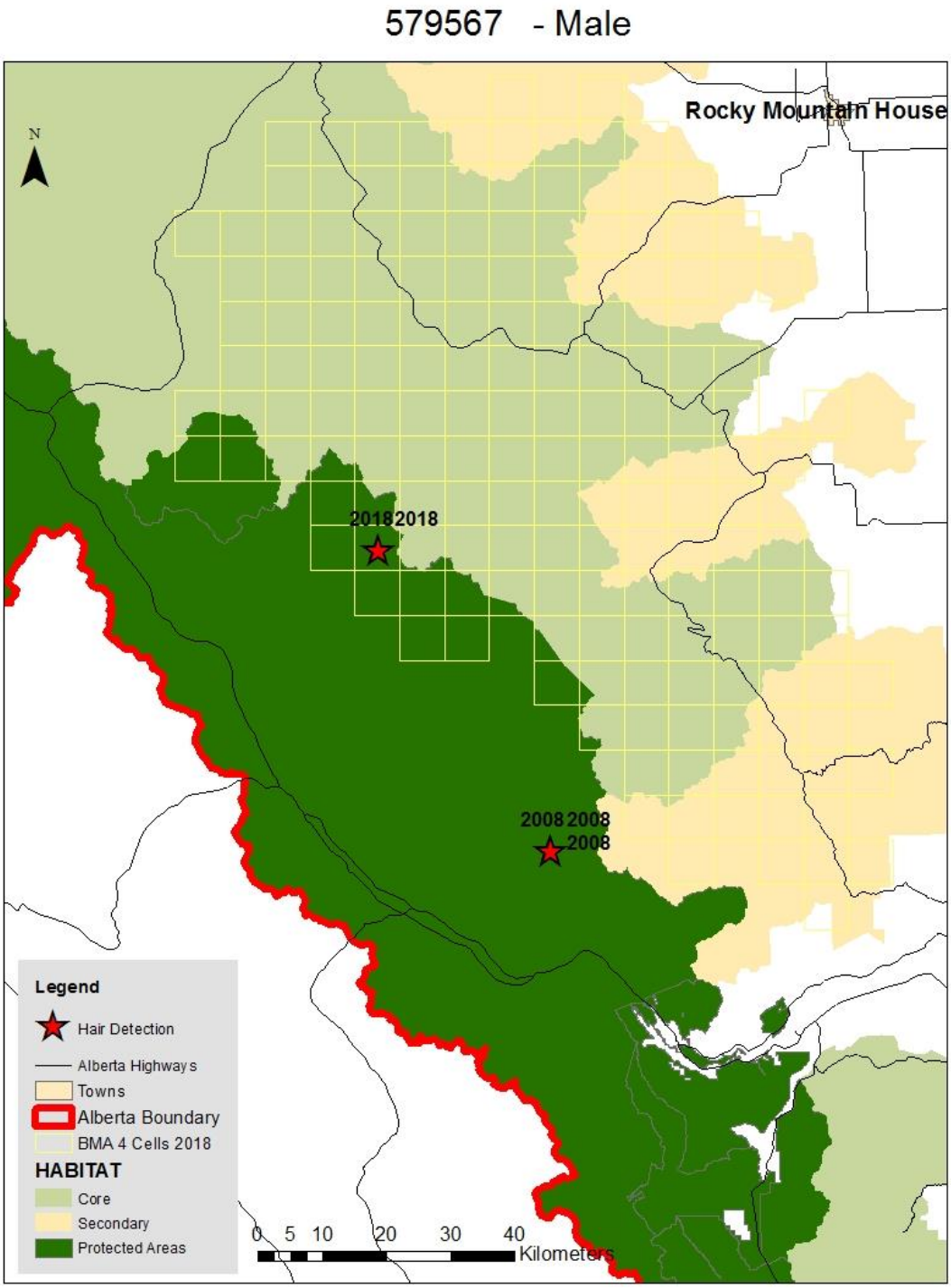
Bears with Prior Detection in Banff and on the 2018 BMA 4 Grid



G358: male; born 2006; first detected 2006 and 2007 Banff grid (south of Lake Minnewanka); 2008 Banff grid (north of Lake Minnewanka); 2018 BMA 4 grid (28 km north of previous detections); captured spring 2019 BMA 4 but no collar locations; likely bred with G095 (born 1997; spring 2004 capture; 2005 tracking; 2005 BMA 4 grid; 2018 BMA 4 grid) to produce 3 cubs of the year (491G-1H-3 & 491G-1I-3 & 491G-1J-3 detected 2018 BMA 4 grid with mom). Survival and parentage determination, park boundary movements.

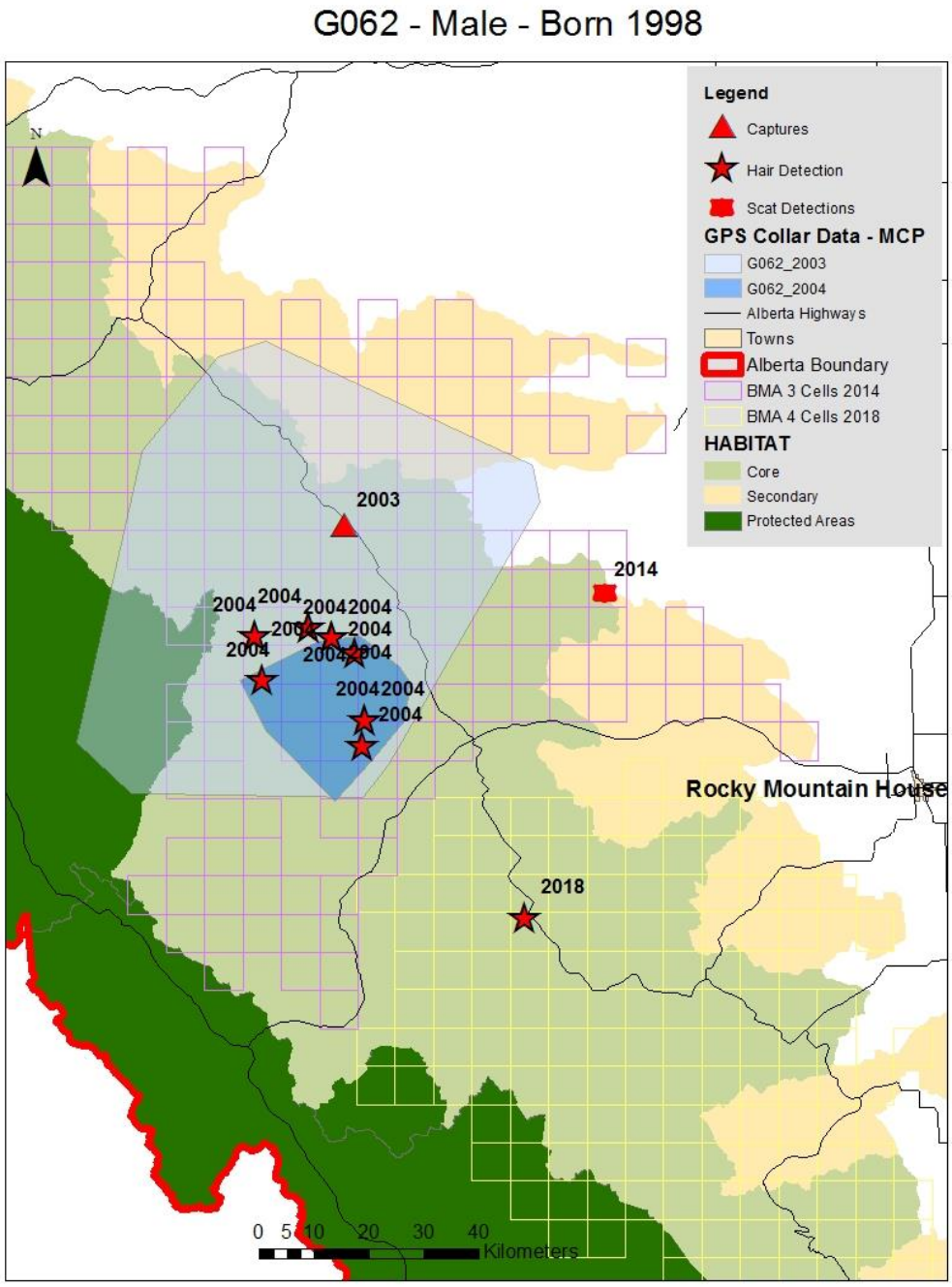


597625=603A-1D-4: female; first detected 2008 Banff grid; then 2018 BMA 4 grid; no mention in Parentage analysis. Survival of an adult female bear who moves between provincial lands and Banff National Park.

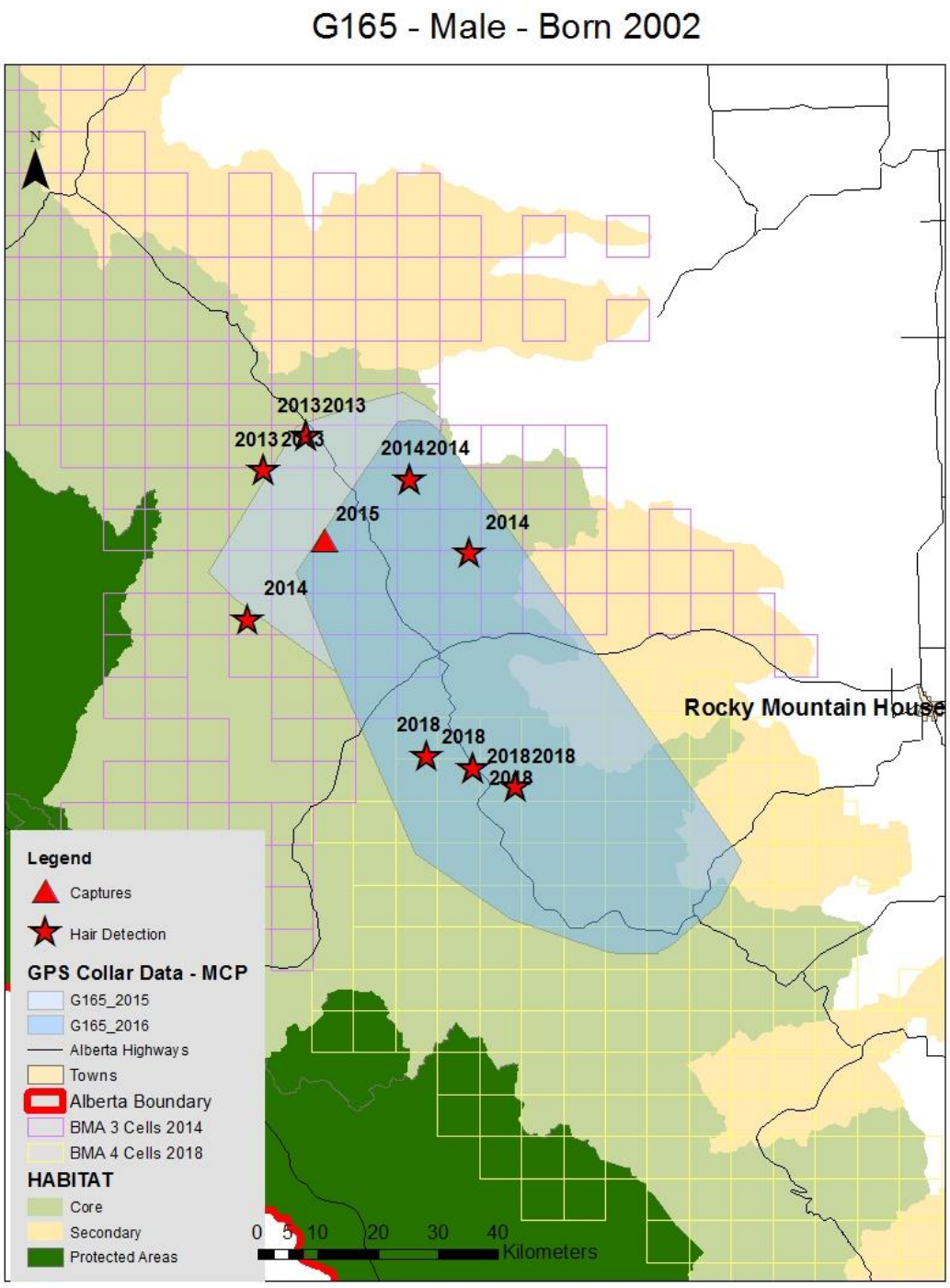


579567=400E-1C-3: male; first detected 2008 Banff grid; then 2018 BMA 4 grid; no mention in Parentage analysis. Survival and residency determination.

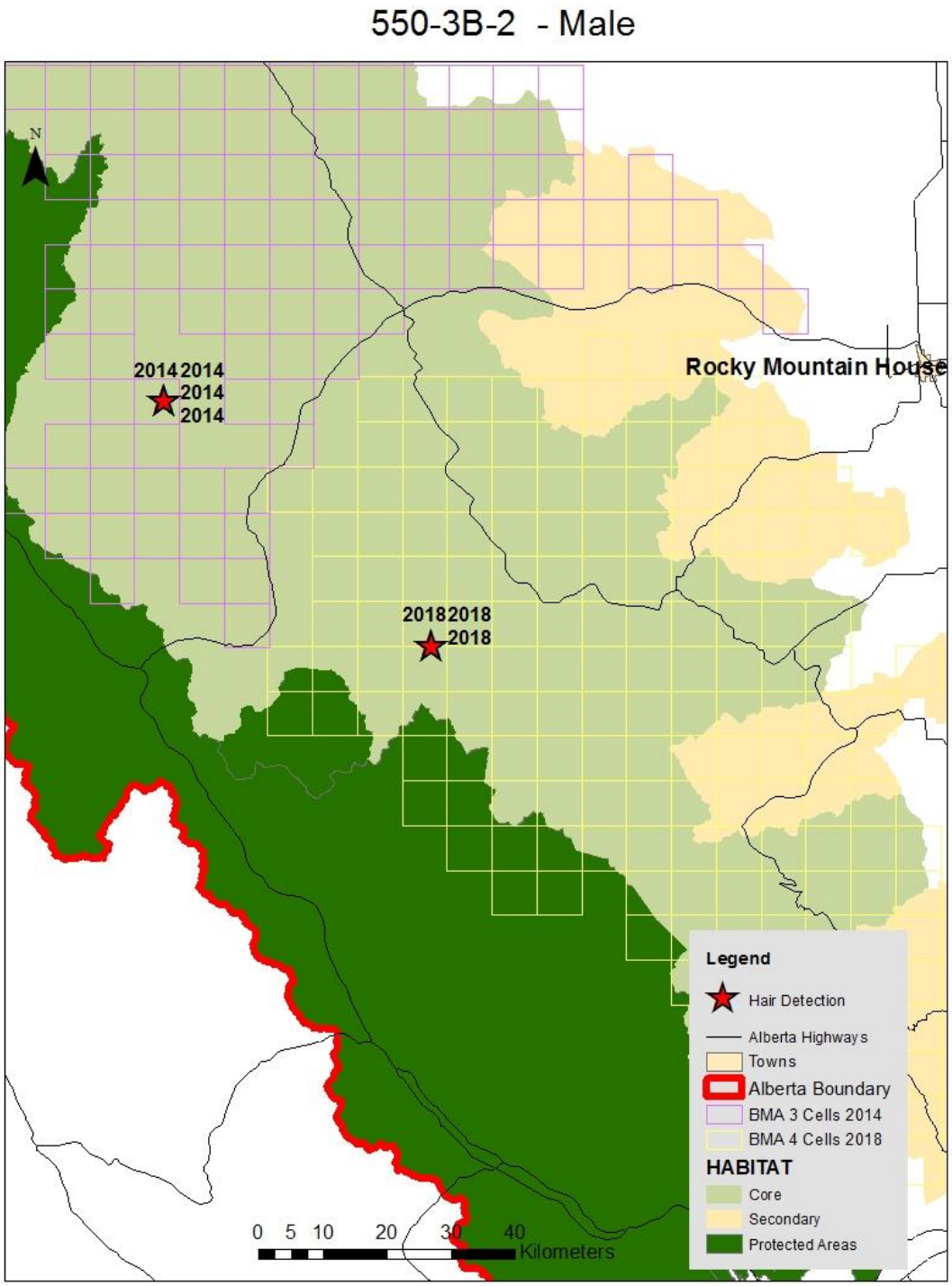
Bears with Prior Detection on the 2004 BMA 3 Grid and the 2018 BMA 4 Grid



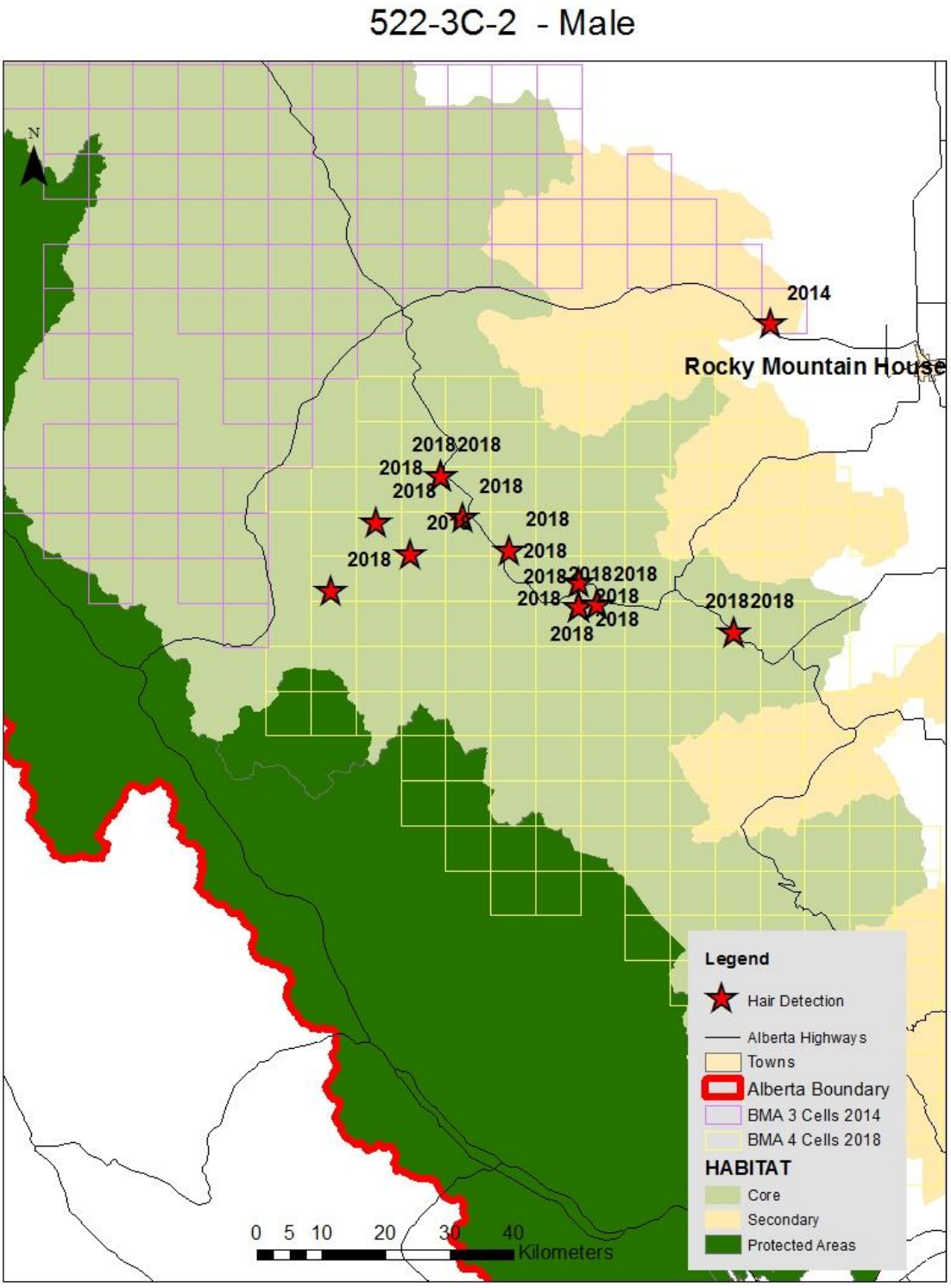
G062: male; born 1998; first detected spring 2003 capture BMA 3; detected 2004 BMA 3 grid; scat spring 2014 BMA 3; 2018 BMA 4. Possible parents are mother AB_66749R (first detected as a dead bear 2011) and father G041 (born 1988; first detected spring 2001 capture; detected 2014 BMA 3 grid). Possible father to G151 (born 2007; first detected spring 2013 capture; detected 2013 BMA 3 grid; 2014 BMA 3 grid; 2014 spring summer scat and 2018 BMA 3 hair and scat) with mother 551-12D-2 (first detected 2014 BMA3 grid). Long term survival, movement between BMA's, parentage and productivity.



G165: male; born 2002; first detected 2013 BMA 3 grid; 2014 BMA 3 grid; capture fall 2015; 2018 BMA 4 grid. Likely bred with 11166Ta1 (first detected 2004 BMA 3; 2013 BMA 3; 2014 BMA 3) for offspring 408D-1A-3 (first detected 2018 BMA 3). Long- term survival, movement between BMA's, parentage, and site fidelity by time period.

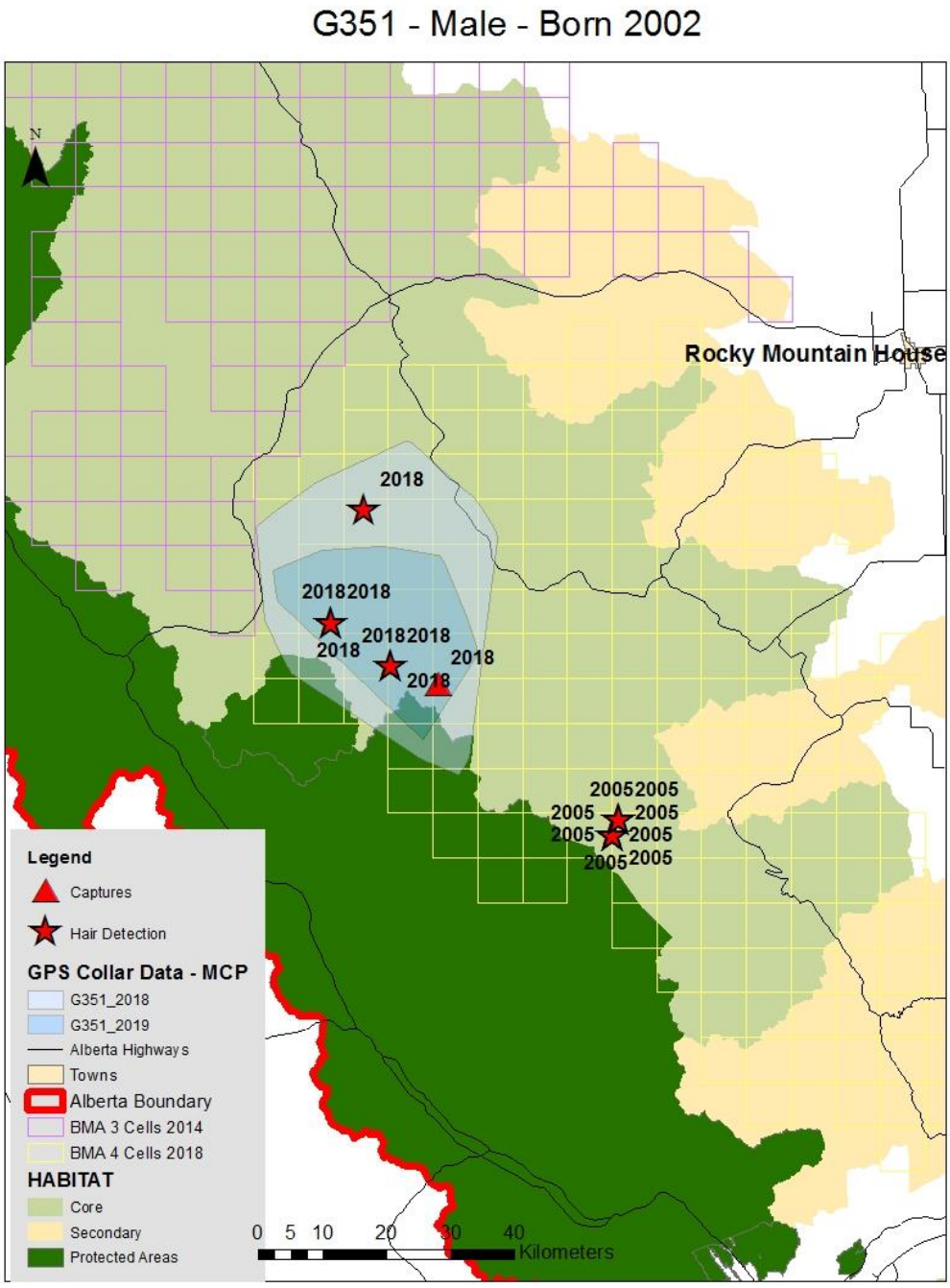


550-3B-2: male; cub in 2014; detected 2014 BMA 3 grid with sibling 550-23F-2 and mother 551-12D-2; father is G138 for both cubs (G138 born 2003; detected 2004 BMA 3 grid, 2014 BMA 3 grid, captured spring 2015 BMA 3); detected 2018 BMA 4 grid. Determination of survival, productivity, parentage and inter BMA movements.

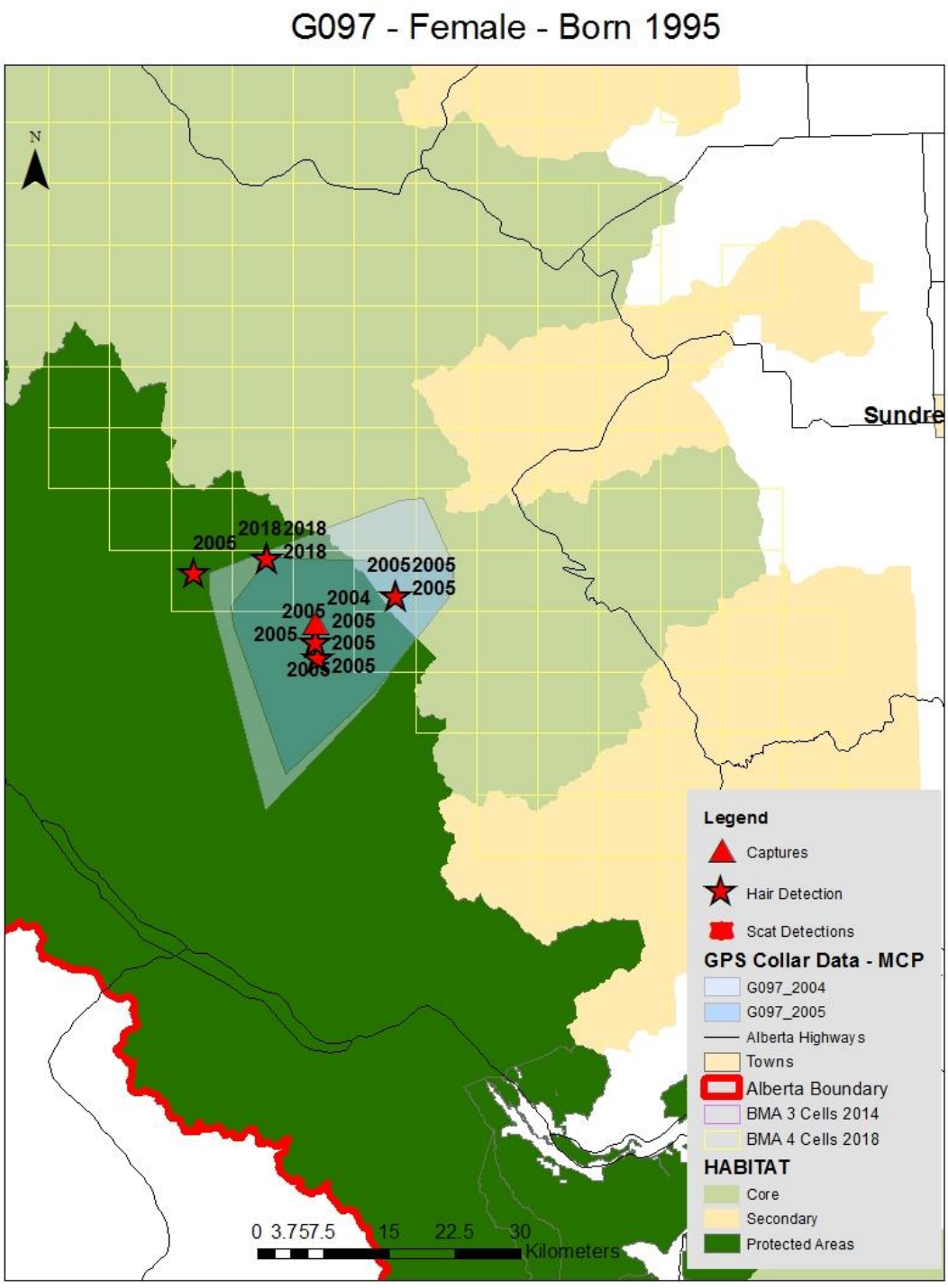


522-3C-2: male; first detected 2014 BMA 3 grid on south east edge; 2018 BMA 4 grid. No mention in Parentage analysis. Determination of survival, movement between BMA's.

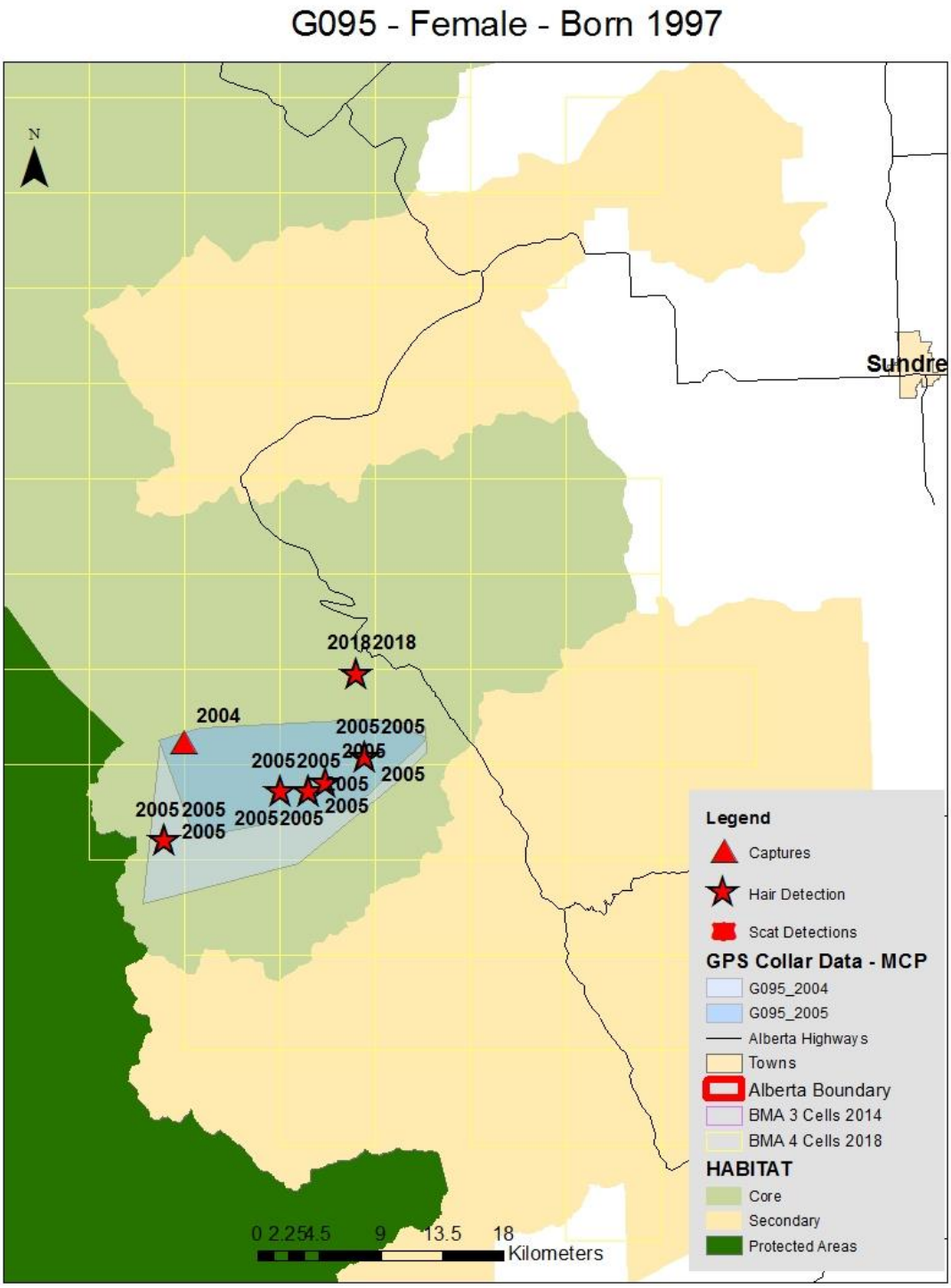
Bears with Prior Detection on the 2005 and the 2018 BMA 4 Grids



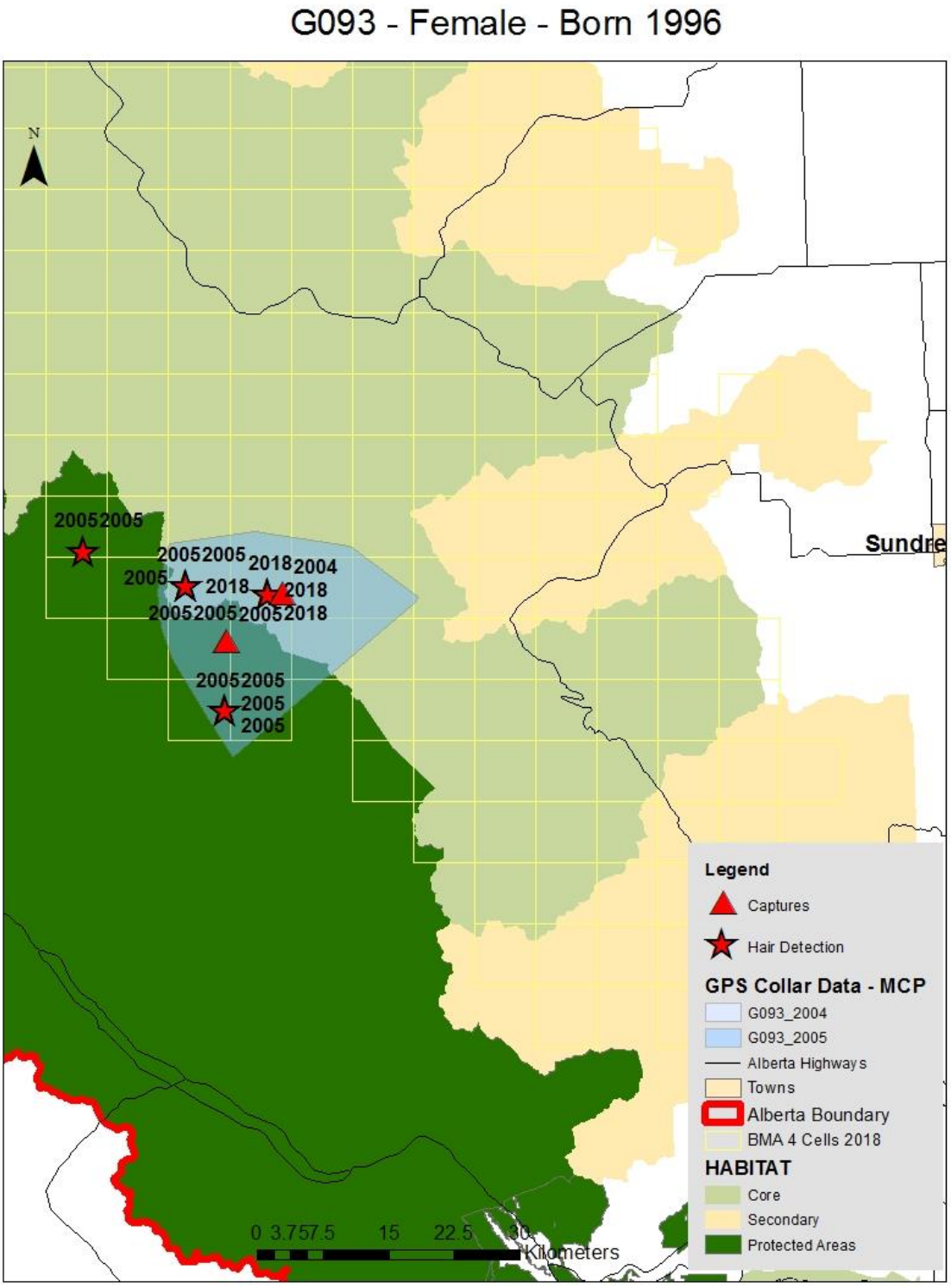
G351: male; born 2002; first detected 2005 BMA 4 census; 2018 spring capture; 2018 BMA 4 grid; collar data (May 2018-May 2019) and grid detections match. Likely bred with 314A02a (=314C-1A-3; first detected 2005 BMA 4 grid; 2018 BMA 4 grid) to produce two coy (314C-1C-3 & 314C-1H-3 first detected 2018 BMA 4 grid) detected with mother. Possibly bred with 373E-1B-4 (first detected 2018 BMA 4 grid) to produce 373E-1A-4 (first detected 2018 BMA 4 grid) detected with mother..



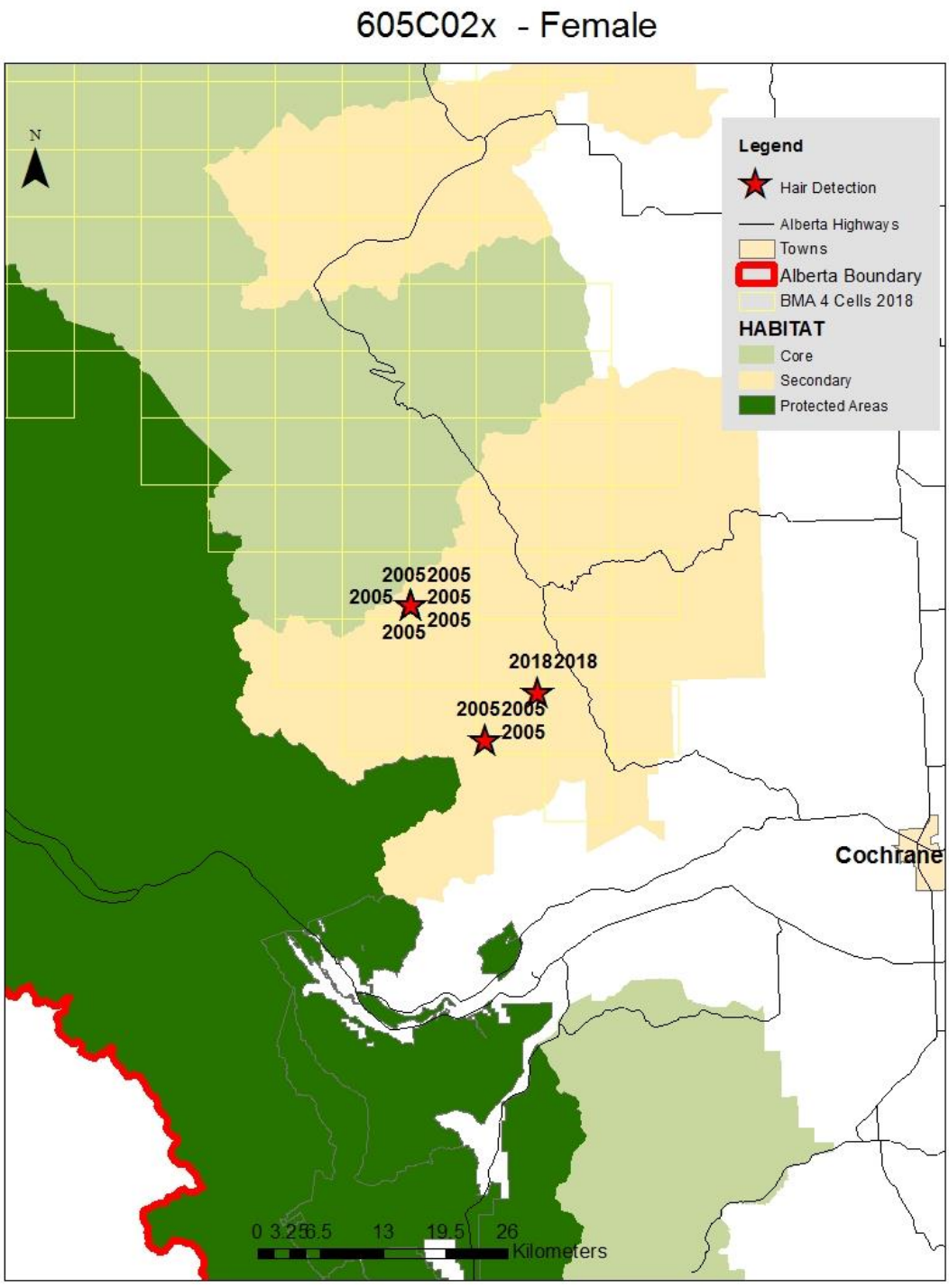
G097: female; born 1995; first detected spring capture 2004; tracking 2005; 2005 BMA 4 grid; 2018 BMA 4 grid. May have bred with G356 (male; born 2014?; age seems off as bear was captured in spring 2018 and weighed > 450 lbs and was matched to a bear detected in Banff in 2007; 2018 BMA 4 grid) to produce 461E-1B-3 (first detected 2018 BMA 4 grid). Collar data and grid detections correspond.



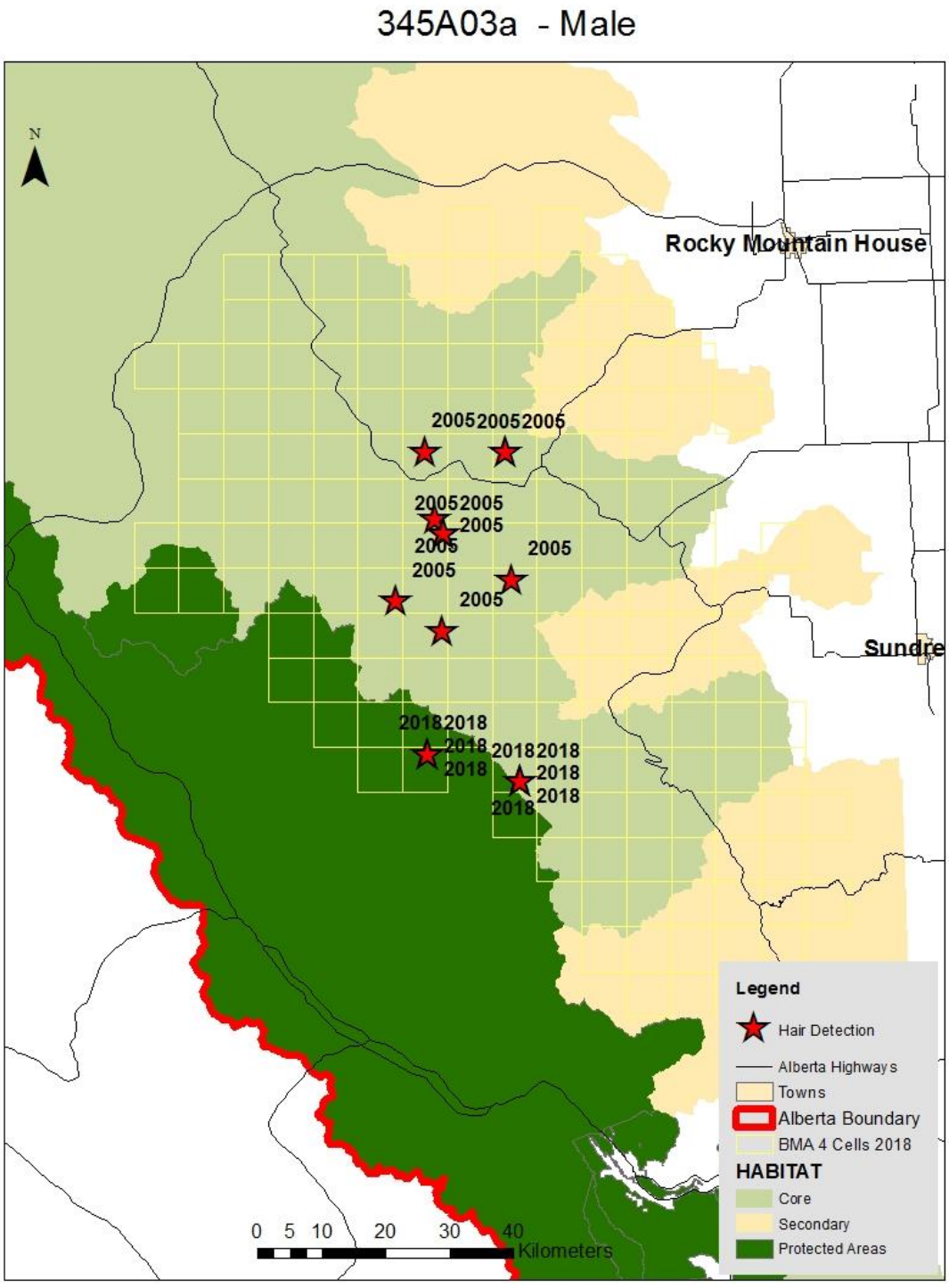
G095: female, born 1997; 2004 spring capture; 2005 BMA 4 grid; 2018 BMA 4 grid. Likely bred with G358 (male; born 2006; first detected 2006, 2007 & 2008 Banff grid; 2018 BMA 4 grid to produce 3 coy (491G-1H-3 & 491G-1I-3 & 491G-1J-3 detected 2018 BMA 4 grid with mother). See map of G358.



G093: female, born 1996; 2004 spring capture; 2005 BMA 4 grid; 2018 BMA4 grid. Collar data and grid detections correspond. No mention in Parentage analysis.

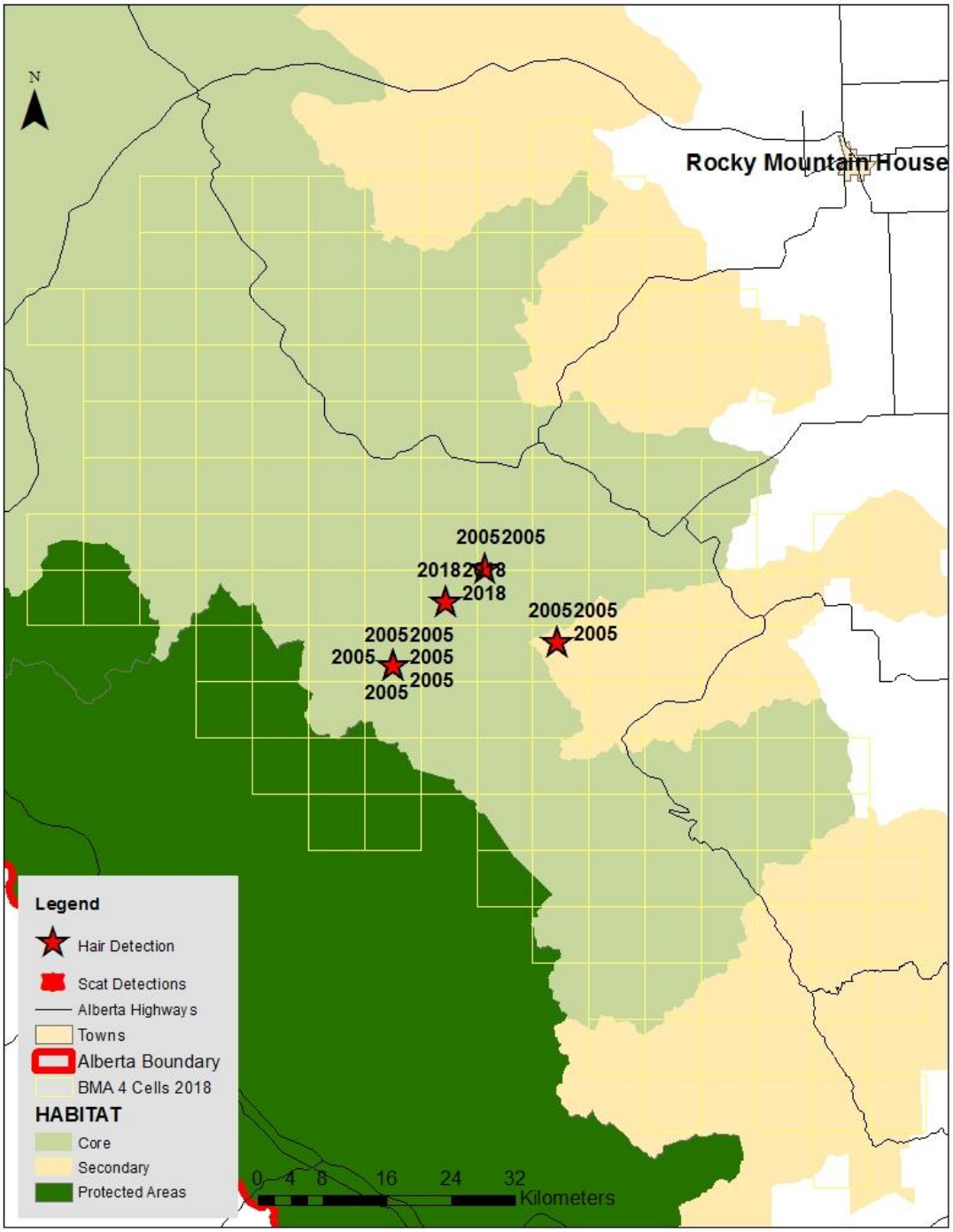


605C02x = 605F-1H-4: female; first detected 2005 BMA 4 grid; 2018 BMA 4 grid. Possible offspring of G095 (female, born 1997; 2004 spring capture; 2005 BMA 4 grid; 2018 BMA 4 grid) with 605F-1C-4 (first detected 2018 BMA 4 grid). Note: 605C02x was never detected with G095 at same site and time so likely older than a cub in 2005 if G095 is really mother.

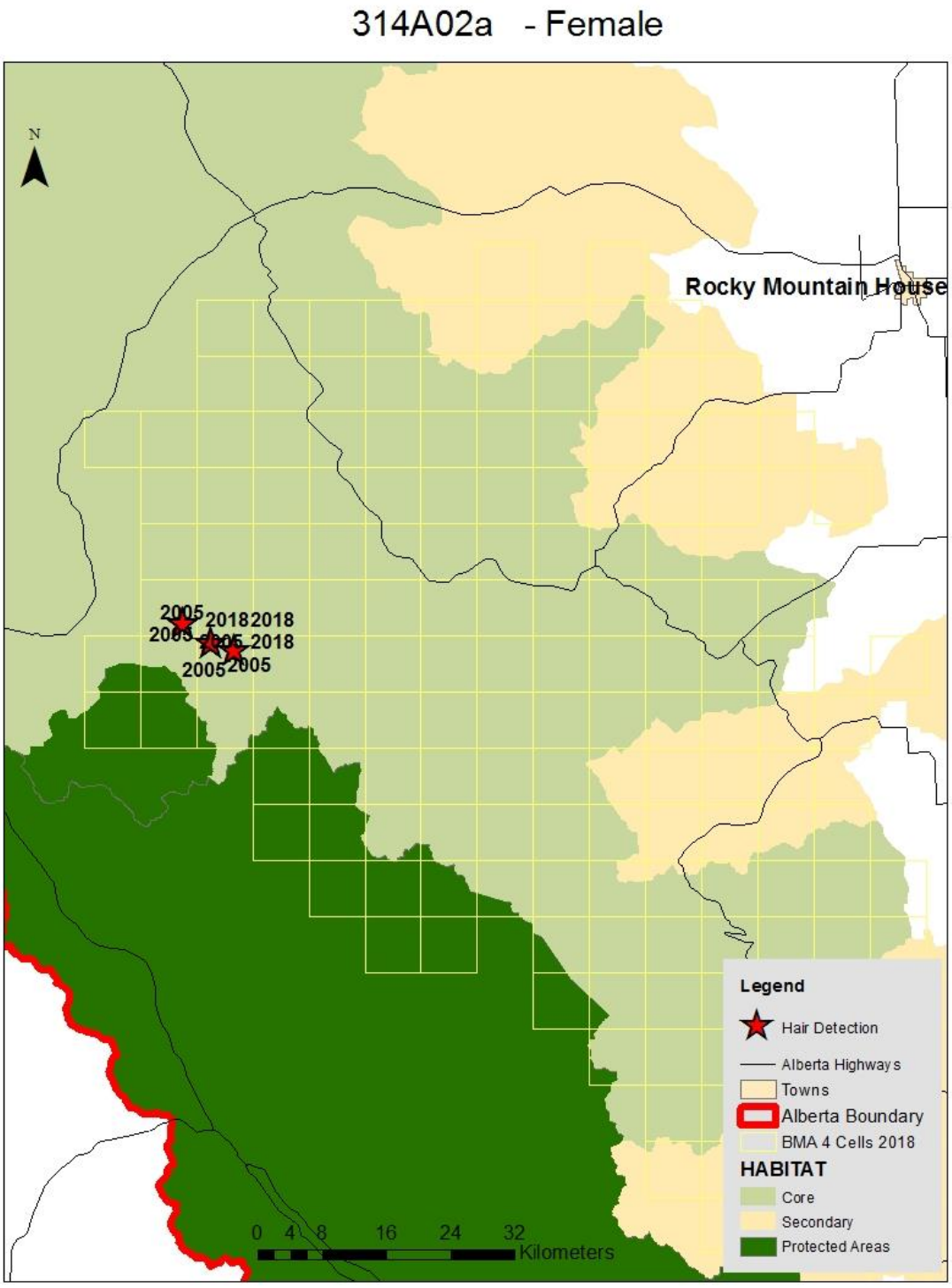


345A03a=458B-1C-1: male; first detected 2005 BMA 4; 2018 BMA 4. Possible father to 261F-1A-1 (male first detected 2018 BMA 4) with female 287B04b = 286B-1B-1 (first detected 2005 BMA 4; 2018 BMA 4); cub and female not detected together.

320C03a - Female

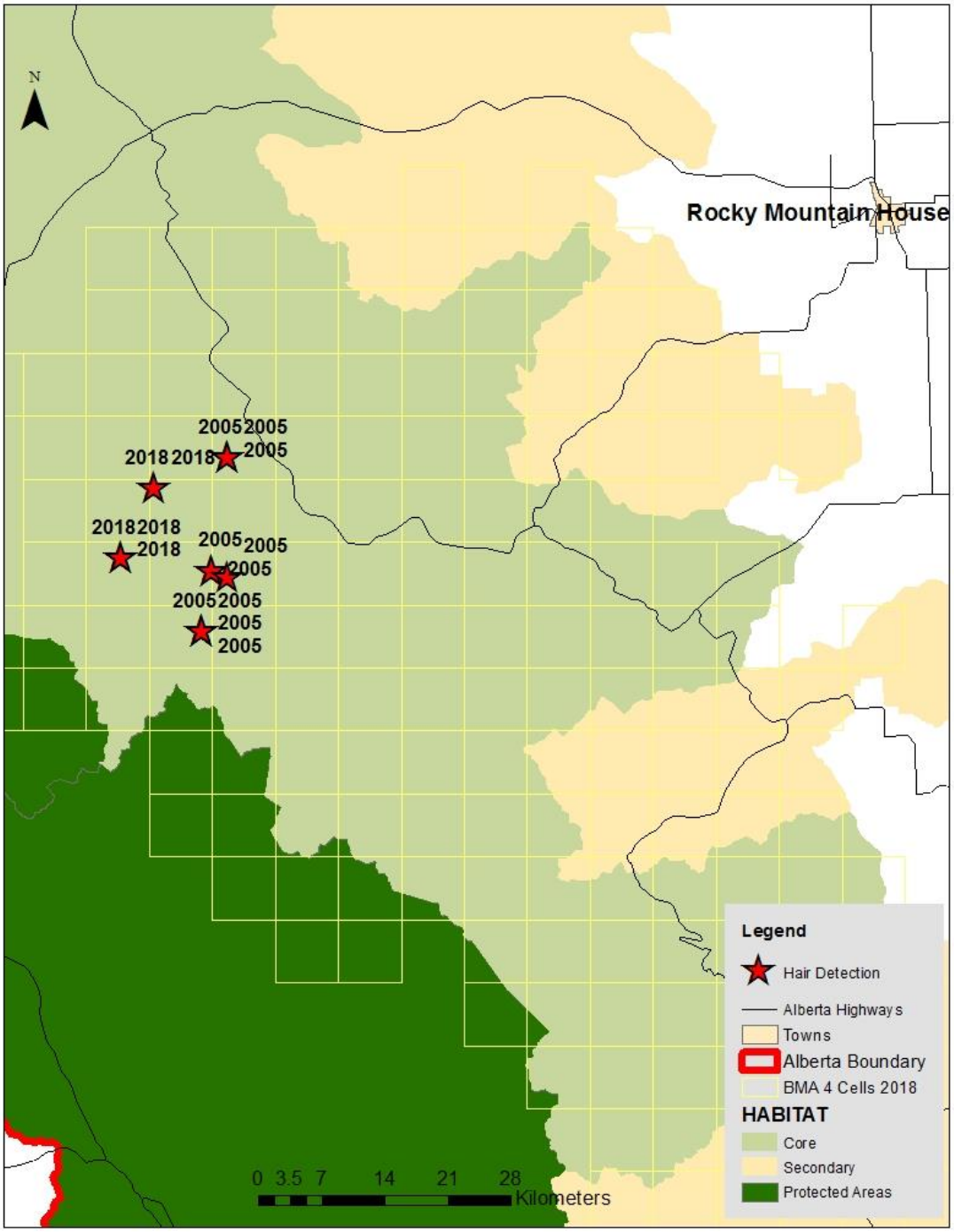


320C03a =347C-1B-4: female; first detected 2005 BMA4; 2018 BMA 4. Likely mother to 347C-1G-4 (first detected 2018 BMA 4 grid with mother at same site and time) with father G354 (born 2005; first detected 2007 Banff grid; 2008 Banff; 2018 BMA 4 grid). See map for G354.



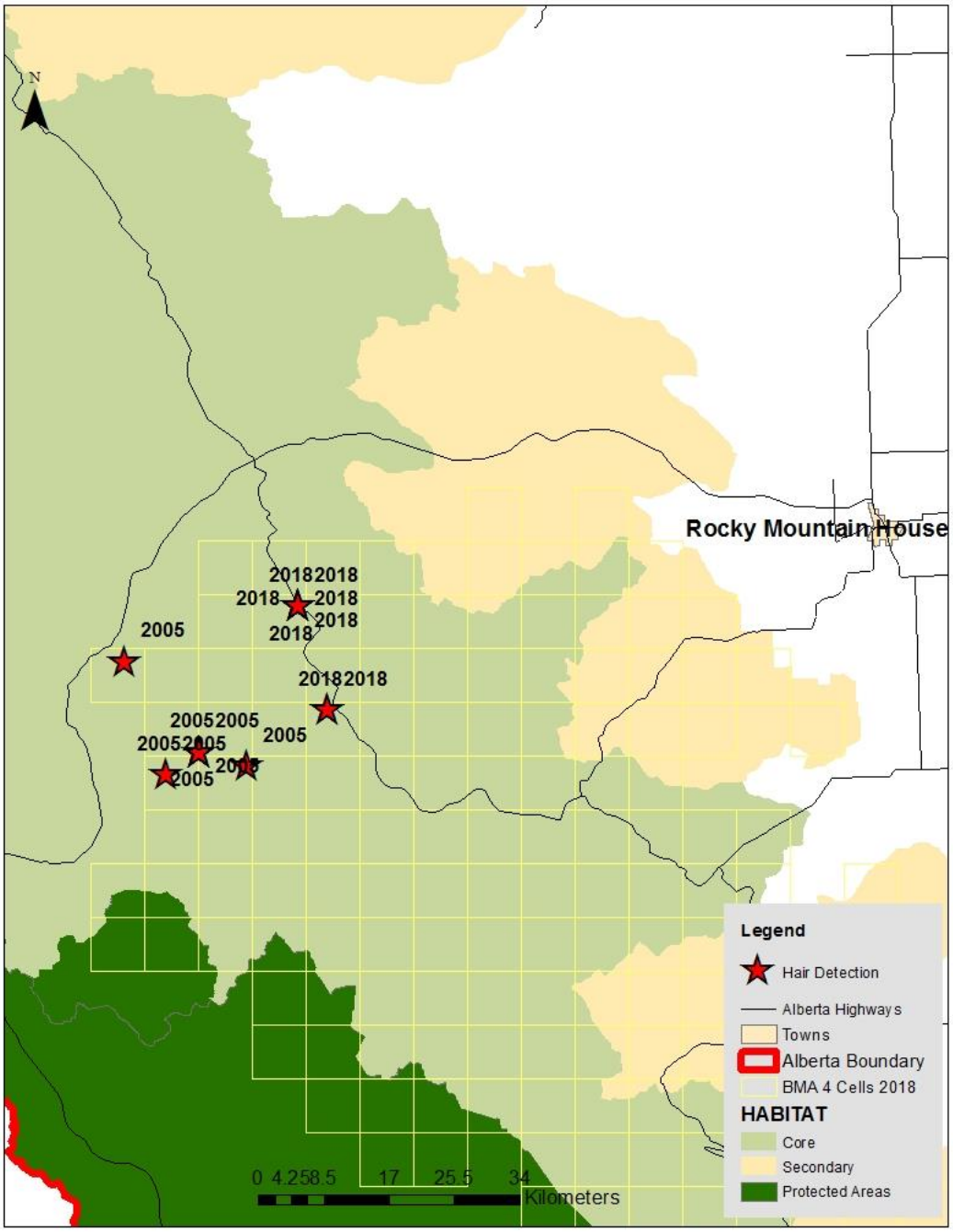
314A02a =314C-1A-3: female; first detected 2005 BMA 4 grid; 2018 BMA 4 grid. Likely mother to two cubs (314C-1C-3 & 314C-1H-3 first detected 2018 BMA 4 grid) detected with mother and G351. See map for G351.

287B04b - Female



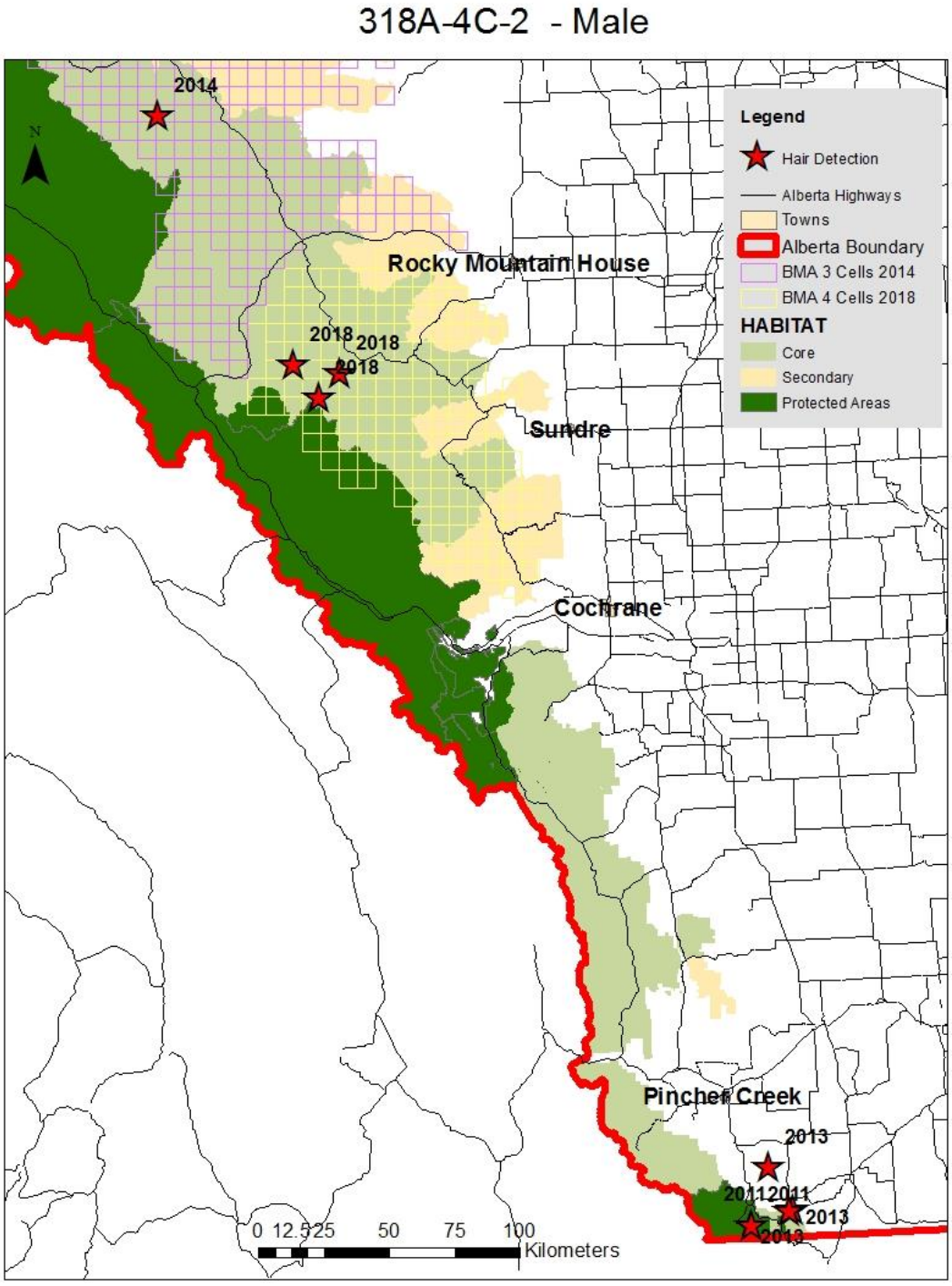
287B04b =286B-1B-1: female; first detected 2005 BMA 4; 2018 BMA 4. Possible mother to 261F-1A-1 (male first detected 2018 BMA 4) with 345A03a=458B-1C-1 (first detected 2005 BMA 4; 2018 BMA 4). Cub and female not detected together.

258A01x - Female

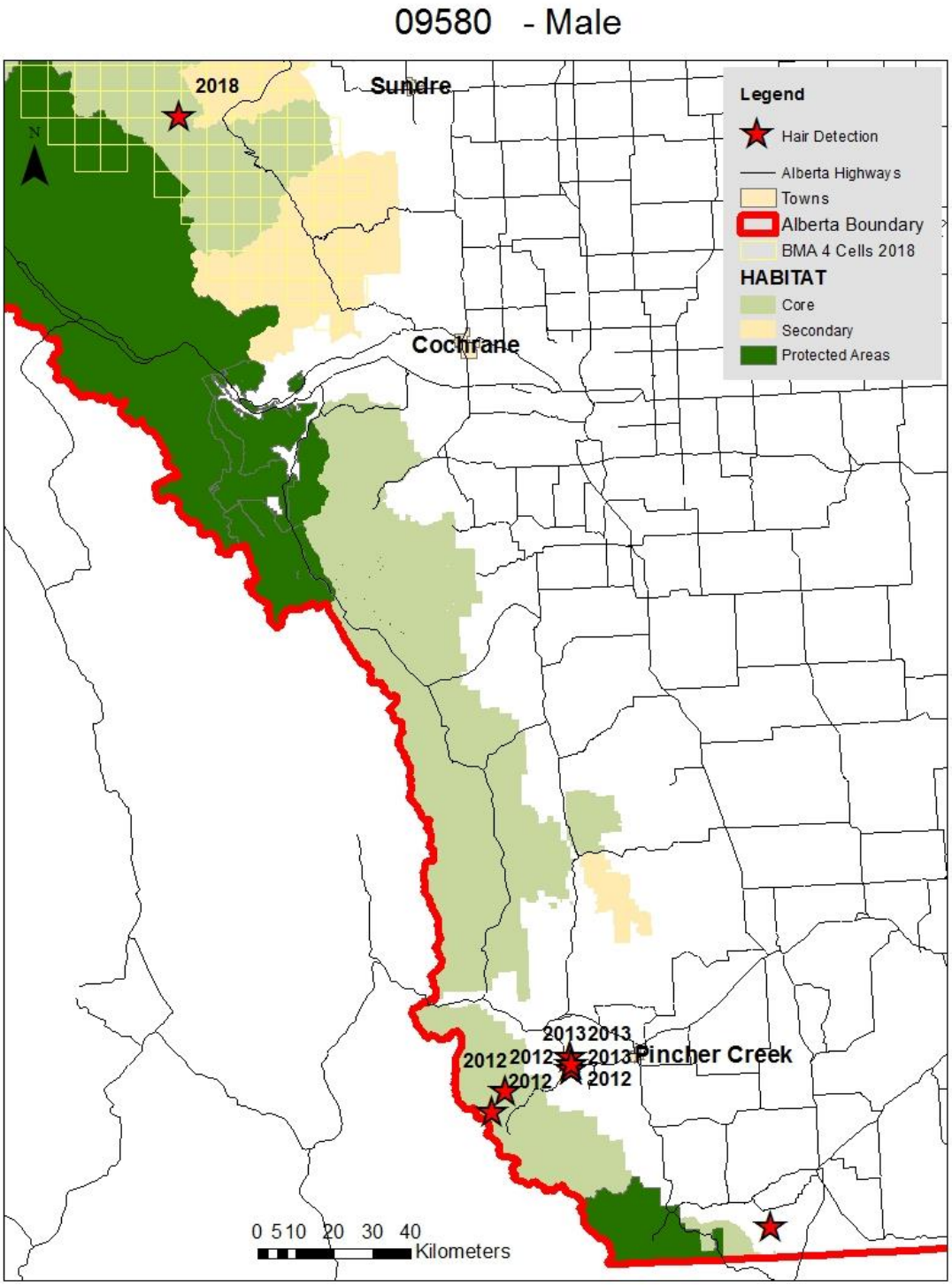


258A01x =175A-1A-3: female; first detected 2005 BMA 4; 2018 BMA 4. Possible mother to 232A-1A-2 (female; first detected 2018 BMA 4 with mother same time and place) with male AB_0959 (relocated from Caroline to Rock Lake 2012; may also be w9815 578B01x (2005 DNA) at 6 markers); so either this is an incorrect match or AB_0959 made it back and bred with 258A01x in 2016/2017 or their cub 232A-1A-2 checked out the same site as mother during the same session but they are independent now.

Bears with Prior Detection in BMA 6 and the 2018 BMA 4 Grid

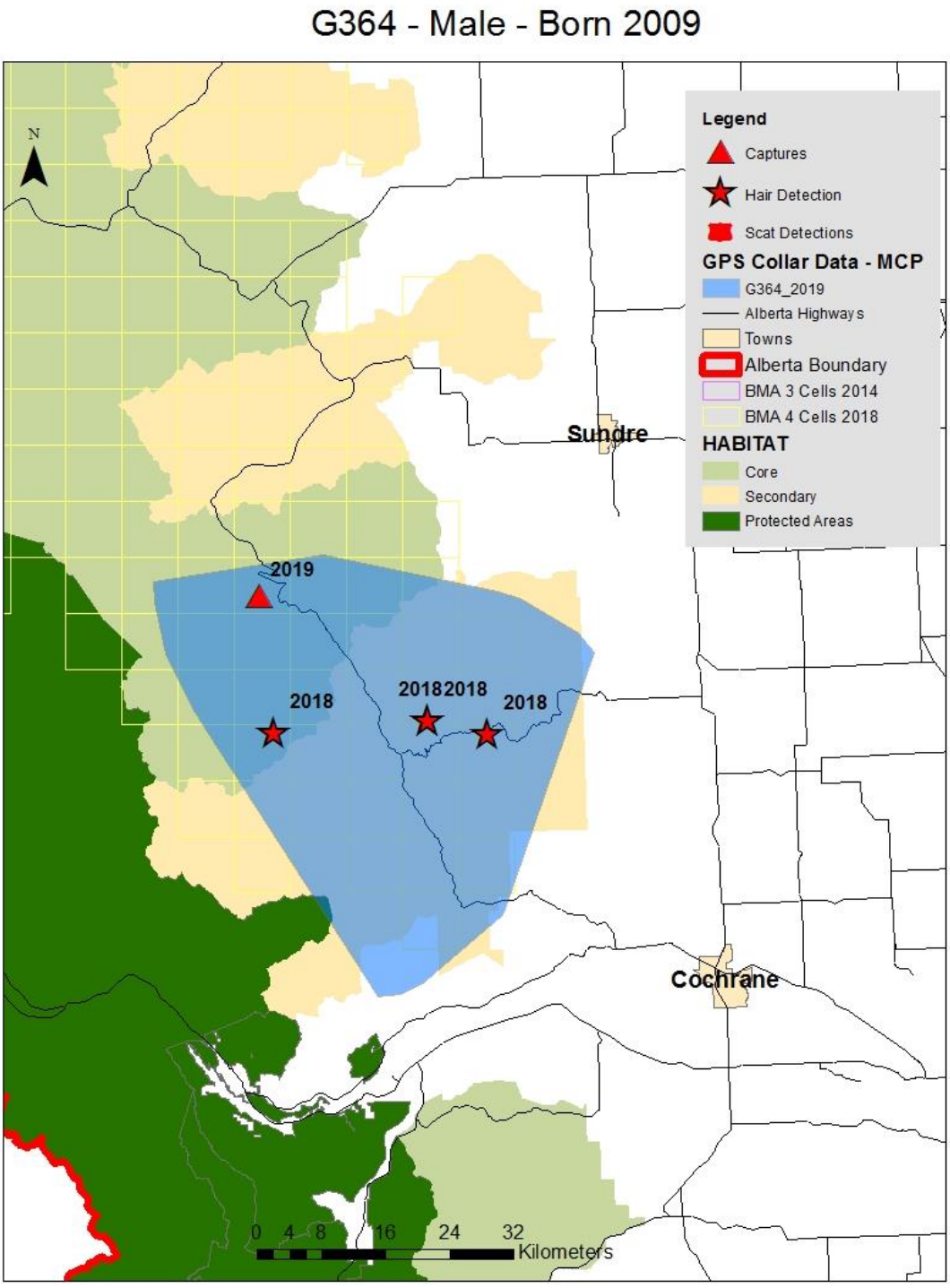


318A-4C-2=SA298: male; first detected 2011 by A. Morehouse in Castle on a tree; detected 2013 Castle on a tree and opportunistic; 2014 BMA 3, 2018 BMA 4; likely father to 291A-1B-4 (first detected 2018 BMA 4 grid) with female 291A-1C-4 (first detected 2018 BMA 4 grid).

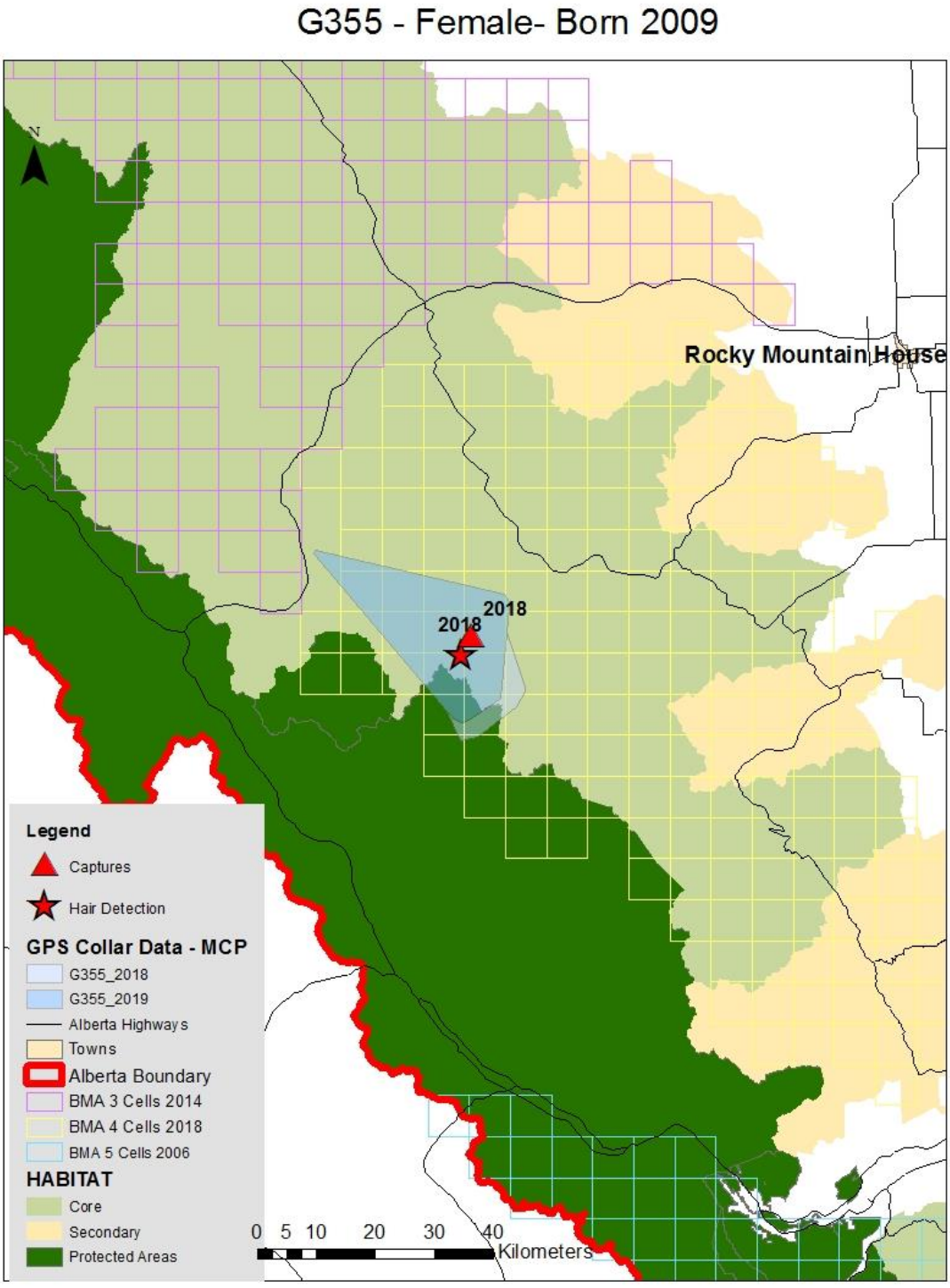


09580 =404C-1A-2: male; first detected 2012 Castle on a tree, fence and opportunistic; 2013 Castle opportunistic; 2018 BMA4. Note a biosample located in Castle without a year is called BMA5-R3339, so bear may have been also in BMA 5 at some point. No mention in Parentage analysis.

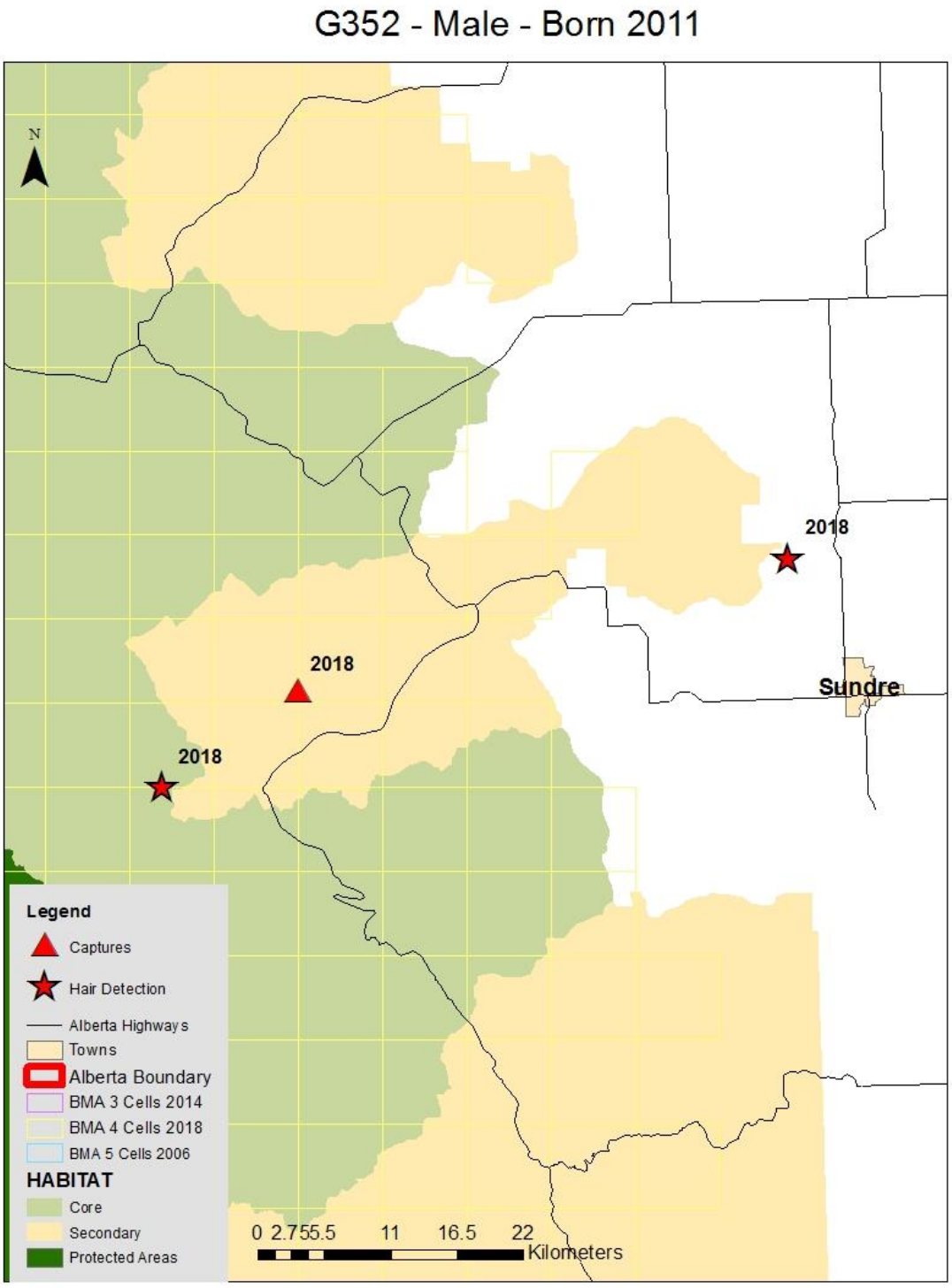
Bears Detected on the 2018 BMA 4 Grid and Captured



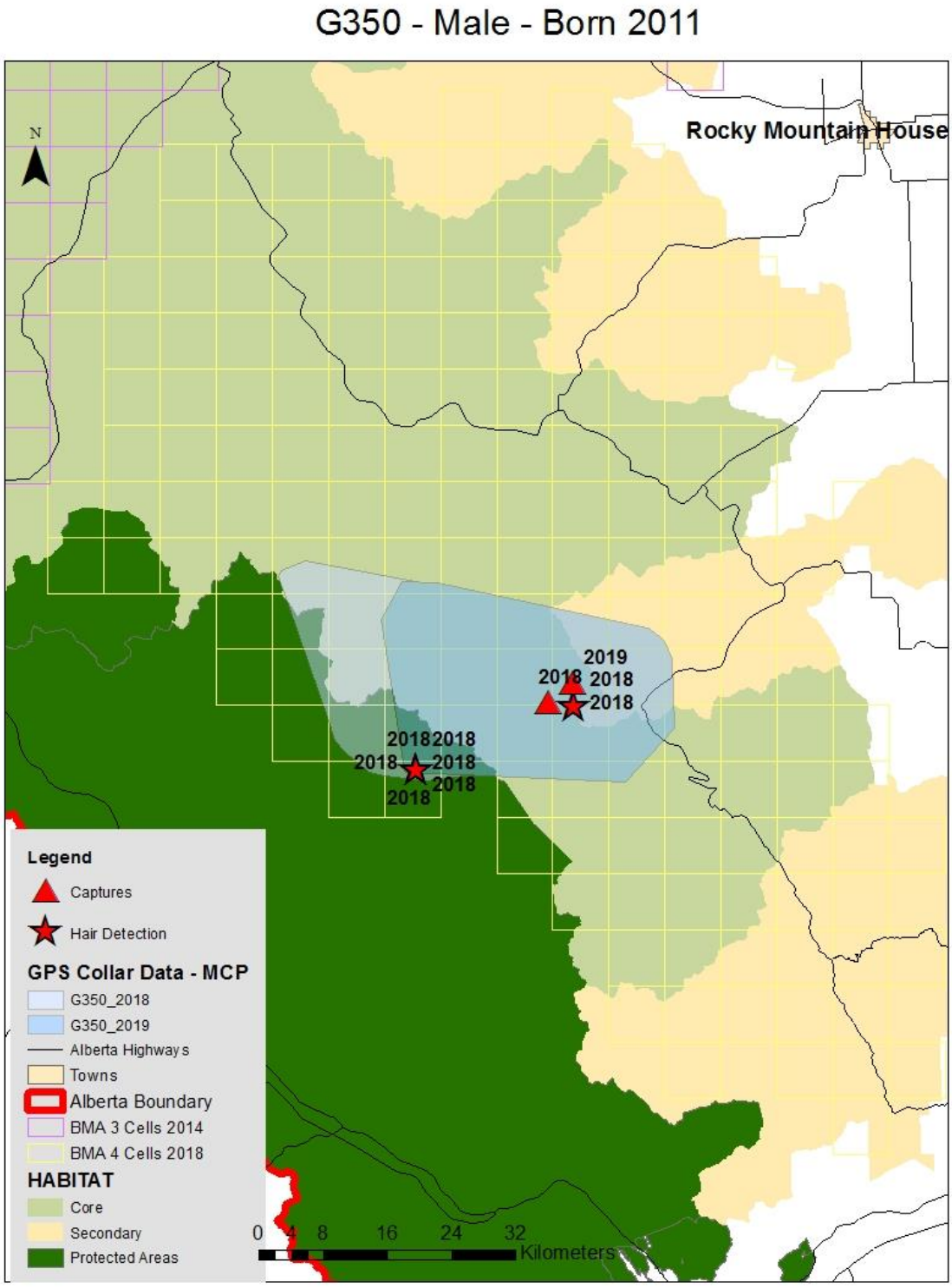
G364: male; born 2009; first detected on 2018 BMA 4 grid; captured spring 2019 BMA 4. Collar data and grid detections correspond. No mention in Parentage analysis.



G355: female; born 2009; first detected spring 2018 capture with 2 2-yr olds; 2018 BMA 4 grid. Collar data and grid detections correspond. No mention in Parentage analysis.



G352: male; born 2011; first detected 2018 spring capture, not collared because of size; 2018 hair collected at Peterson's Ranch NW of Sundre; 2018 BMA 4 grid. Capture and grid detections correspond. No mention in Parentage analysis.



G350: male; born 2011; first detection spring 2018 capture; 2019 spring capture. Collar data and grid detections correspond. No mention in Parentage analysis.