Ekati and Diavik Diamond Mines

2014 Final Lac de Gras Regional Grizzly Bear DNA Report

RioTinto

DOMINION DIAMOND

Dominion Diamond Ekati Corporation and Diavik Diamond Mines (2012) Inc.

EKATI AND DIAVIK DIAMOND MINES

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ERM Rescan
5120 49th Street, Suite 201
Yellowknife, NT
Canada X1A 1P8
T: (867) 920-2090
F: (867) 920-2015

EXECUTIVE SUMMARY

This report presents final results from the joint Ekati/Diavik Regional Grizzly Bear DNA study as part of the 2012-2013 wildlife monitoring programs. The objectives for the two year program were to establish a baseline for the long term regional monitoring of the relative abundance and distribution of grizzly bears over time.

A total of 1,902 hair samples were collected during the 2012 survey period. From these samples, a total of 112 grizzly bear individuals were identified through DNA hair analysis, including 42 males and 70 females. DNA from an additional five samples from 2012 was extracted in 2013, which identified four individuals (1 male and 3 females), two of which were new to the 2012 dataset (1 male and 1 female). During the 2013 field program, 4,709 samples were collected. A total of 136 grizzly bears were identified (60 males and 76 females), including 39 that had no previous detections in the regional database (22 males and 17 females). Eight grizzly bears identified in the study area were also detected in other DNA study areas in Nunavut.

For the combined DNA dataset, the mean capture probability in the DNA Study Area was 0.22 (range 0.14 – 0.35) in 2012, and 0.35 (range 0.28 – 0.43) in 2013. The total number of grizzly bears estimated to be in the DNA Study Area in 2012 was 91 females (95% CI 81 – 108) and 53 males (95% CI 47 – 66). In 2013, the superpopulation was estimated to be 83 females (95% CI 80 – 91) and 65 males (95% CI 62 – 72).

These results suggest a detection frequency of approximately 9-11 grizzly bears/1,000 km^2, higher than density estimates in Nunavut (7 grizzly bears / 1,000 km^2), and possibly indicating a stable or increasing population in the central barrens of the Northwest Territories since estimates for the Slave Geological Province in the late 1990's (3.5 grizzly bears / 1,000 km^2). Absolute density will likely be lower than the detection frequency; however, a density estimate for the DNA Study Area is not possible because the geographic distribution of the superpopulation, which lies outside the study grid, and individual residency times are both unknown parameters.

ACKNOWLEDGEMENTS

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GLOSSARY AND ABBREVIATIONS

Terminology used in this document is defined where it is first used. The following list will assist readers who may choose to review only portions of the document.

CESCC	Canadian Endangered Species Conservation Council
COSEWIC	Committee on the Status of Endangered Wildlife in Canada - A federal committee of experts that assesses and designates the level of threat to wildlife and vegetation species in Canada.
Carnivore	An animal that feeds on flesh
DNA	Deoxyribonucleic acid. A molecule that contains genetic information.
Ecosystem	A volume of earth-space that is composed of non-living parts (climate, geologic materials, groundwater, and soils) and living or biotic parts, which are all constantly in a state of motion, transformation, and development. No size or scale is inferred.
Ecozone	The ecozone lies at the top of the ecological hierarchy, and therefore it defines, on a subcontinental scale, the major physiographic features of the country
GPS	Global Positioning System
Habitat	Land and water surface used by wildlife. This may include biotic and abiotic aspects such as vegetation, exposed bedrock, water and topography.
Hectare (ha)	10,000 m^2 or 0.01 km^2 or 2.47 acres
NWMB	Nunavut Wildlife Management Board
NWT	Northwest Territories
Topography	The configuration of a surface, including its relief and the position of its natural and person-made features

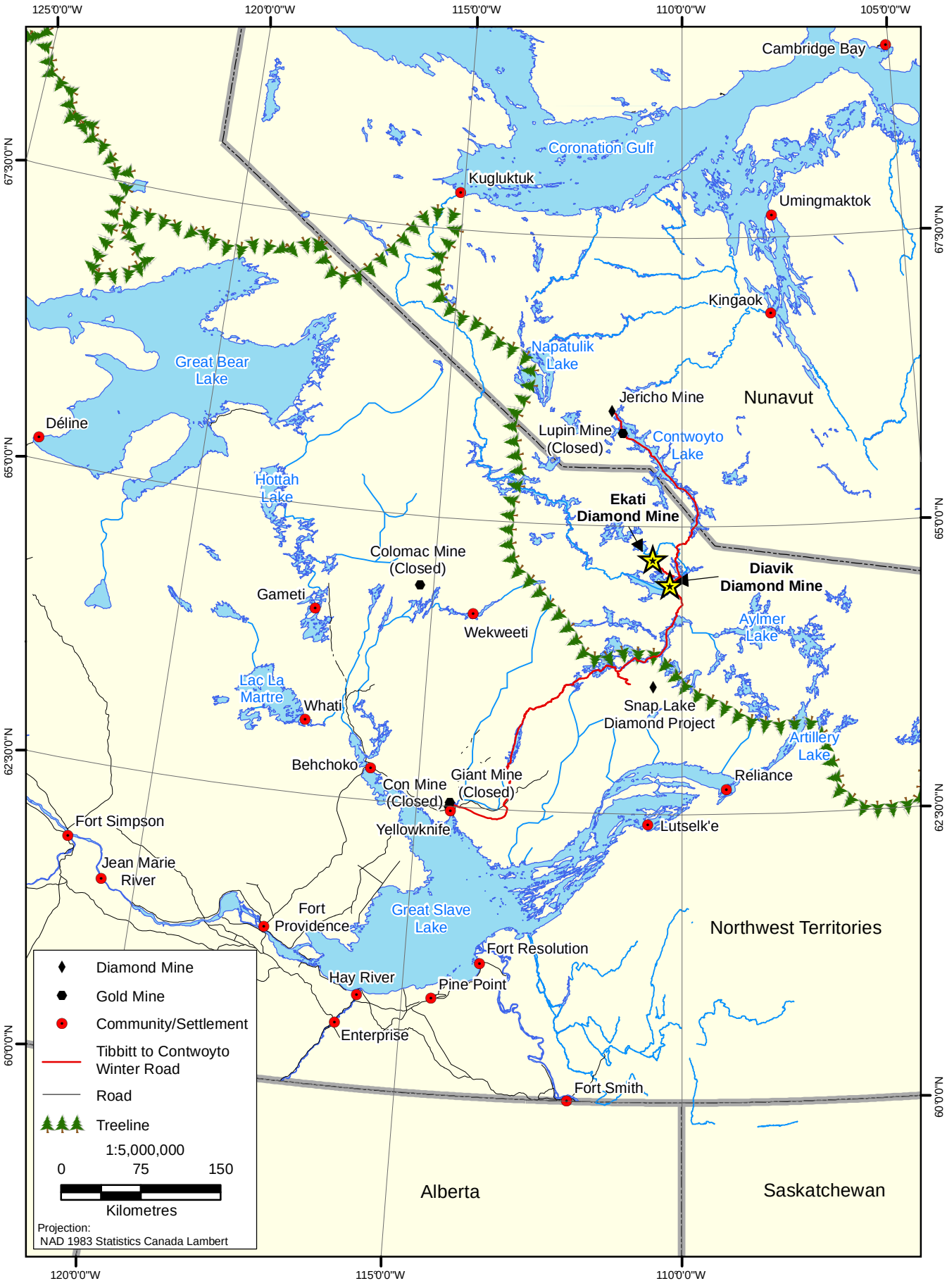
1. BACKGROUND

The Ekati Diamond Mine (Ekati), owned and operated by Dominion Diamond Ekati Corporation (DDEC), is located in the Slave Geological Province of the Northwest Territories, approximately 300 km northeast of Yellowknife between Yamba Lake and Lac de Gras (Figure 1-1). Ekati began construction in 1997 and officially opened in October 1998. Currently, Ekati has two operational pits throughout the year (Fox and Misery Pits), and two underground mines (Koala Underground and Koala North Underground).

The Diavik Diamond Mine (Diavik) is located approximately 30 km southeast of Ekati on a 20 square kilometre island, informally called East Island, in Lac de Gras (Figure 1-1). The Diavik Diamond Mine is an unincorporated joint venture between Diavik Diamond Mines (2012) Inc. (60%) (DDMI) and Dominion Diamond Diavik Limited Partnership (40%) (DDDLP). Both are headquartered in Yellowknife, Northwest Territories, Canada. DDMI is a wholly owned subsidiary of Rio Tinto plc of London, England and DDDLP is wholly owned by Dominion Diamond Corporation of Toronto, Canada. DDMI manages the operation of the mine, which officially opened in 2003. Diavik open-pit mined three kimberlite pipes, called A154 North, A154 South, and A418 from 2003 to 2012 when the transition to an all underground mine was completed.

The Slave Geological Province is semi-arid with short, cool summers and long, cold winters. Ekati is approximately 150 km north of the treeline where the predominant vegetation type is heath tundra. Several large eskers in the study area provide travel routes for caribou and denning habitat for wolves and grizzly bears. Numerous grass and sedge wetland areas provide food for grizzly bears in the spring and breeding habitat for migrating shorebirds, waterfowl, and some songbird species. Rocky cliffs and outcrops near lakes provide nesting areas for falcons and hawks. Other species known to inhabit the study area throughout or part of the year include wolverine, Arctic ground squirrel, fox (Arctic and red), lemming, hare, ptarmigan, and occasionally muskox and moose.

Potential impacts to barren-ground grizzly bears associated with mining activities are predicted to be minimal, but without detailed information about population status, testing this prediction is difficult. At technical and community workshops held on June 28, 2010 and October 5-6, 2010, it was determined that an important objective for grizzly bear monitoring was to determine the abundance and distribution of grizzly bears in a larger regional context. It was agreed at these meetings that a DNA mark-recapture design was the best approach to meet this objective. Regulators, monitoring agencies, and community members recommended that the mining industry collaborate on a large scale regional grizzly bear program to assess population status and monitor trends over the long term. In response, DDEC and DDMI agreed to work together on a large scale, long term grizzly bear mark-recapture study surrounding their diamond mine properties in the central barrens of the Northwest Territories. At a technical workshop in November, 2011, DDEC and DDMI introduced a study design for a joint regional DNA-based grizzly bear population estimate. This program was implemented in 2012, and concluded in 2013. This report summarizes the final results from the two year program.



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Location of the Ekati and Diavik Diamond Mines, Northwest Territories

Figure 1-1

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1.1 INTRODUCTION

The grizzly bear (*Ursus arctos*) is federally considered a species of Special Concern by the Committee on the Status of Endangered Wildlife in Canada (COSEWIC 2012). In the Northwest Territories, the grizzly bear is not listed under the *Species at Risk (NWT) Act (2009)* and is scheduled for assessment in 2015 by the NWT Species at Risk Committee (GNWT ENR 2012). Barren-ground grizzly bears occur at low densities and roam over larger areas. Home ranges average 2,100 km^2 for females and 7,200 km^2 for males, which are the largest home ranges for grizzly bears in North America (McLoughlin et al. 1999; McLoughlin et al. 2003). In general, barren-ground grizzly bears select home ranges with a large proportion of eskers for denning (McLoughlin et al. 2003).The esker dens typically are associated with adjacent tussock tundra, lichen veneer, birch seep, and tall shrub plant communities that can provide suitable forage. Barren-ground grizzly bears can also be carnivorous and caribou (*Rangifer tarandus*) can make up a large part of their annual diet (Gau 1998). Other available protein sources in the region are northern red-backed voles (*Myodes rutilus*), ptarmigan (*Lagopus* spp.), Arctic ground squirrel (*Uroceitellus parryii*), and fish. The bears supplement their diet with succulent vegetation in early summer and berries in the late summer and fall (Gau 1998).

Barren-ground grizzly bears are at the most northern and eastern limits of the continental grizzly bear range, thereby reducing overall population connectivity (McLoughlin and Messier 2001). Genetic diversity has been demonstrated to be comparatively low for grizzly bears in the NWT as a result of this relative isolation from other bears (Paetkau et al. 1998). Furthermore, the Arctic tundra environment consists of harsh climates and low productivity that contribute to low reproductive rates and smaller average litter sizes (McLoughlin and Messier 2001; McLoughlin et al. 2003), which may make northern grizzly bear populations particularly sensitive to human disturbance.

In order to census bears, researchers have used live captures to mark bears and then recaptured bears using camera stations (Mace 1994), aerial surveys (Larsen and Markel 1989), and hair removal and deoxyribonucleic acid (DNA) fingerprinting analysis (Proctor et al. 2005). Most recently, hair removal and DNA fingerprinting have been used to mark and recapture bears (Woods et al. 1999; Mowat and Strobeck 2000; Poole, Mowat, and Fear 2001; Boulanger et al. 2002; Proctor et al. 2005; Apps and McLellan 2006; Rescan 2011). This latter method has several benefits because live capture of bears is unnecessary, individuals can be identified with a small risk of error, and hair removal sites are faster to set up and are checked less often than live-capture sites (Mowat and Strobeck 2000). Roots of mammalian hair contain sufficient DNA for analysis (Higuchi et al. 1988). In mark-recapture studies, an initial population sample is captured, marked, and released. The population is then resampled during ≥ 1 additional sessions (Woods et al. 1999). The ratio of newly captured animals to recaptures is then used to compute a population estimate (White et al. 1982).

Bears can traverse in and out of study areas during sampling, which violates the assumption of geographic closure in most studies that use mark-recapture or related methods (Miller et al. 1997). Abundance estimates derived from mark-recapture correspond to the "superpopulation" if movement is random across grid boundaries (Kendall 1999). In the context of mark-recapture DNA studies, the superpopulation is defined as the number of animals that inhabit the sampling grid and surrounding area (as opposed to the grid alone; Boulanger et al. 2004). While the superpopulation estimate represents the number of animals that traverse an area, the estimate is compromised by the

undefined sampling area and therefore cannot be used to estimate density (Boulanger et al. 2004). Under a trend monitoring objective, however, an absolute abundance or density estimate is not necessary, and the assumptions of population closure can be relaxed (Apps 2010). In this case, the initial superpopulation estimate can be used as the basis for monitoring relative changes over the long term.

This report presents final results from the two year grizzly bear DNA study as part of the 2012 and 2013 wildlife baseline program.

1.2 OBJECTIVES

The objectives of the DNA program are to:

- Generate a superpopulation estimate of grizzly bears for the DNA Study Area as baseline data for trend monitoring;
- Describe the spatial and temporal distribution of grizzly bears in the DNA Study Area;
- Identify overlap with grizzly bears that were sampled in areas outside of the DNA Study Area by other surveys; and,
- Provide recommendations regarding a standard grizzly bear monitoring protocol for the NWT.

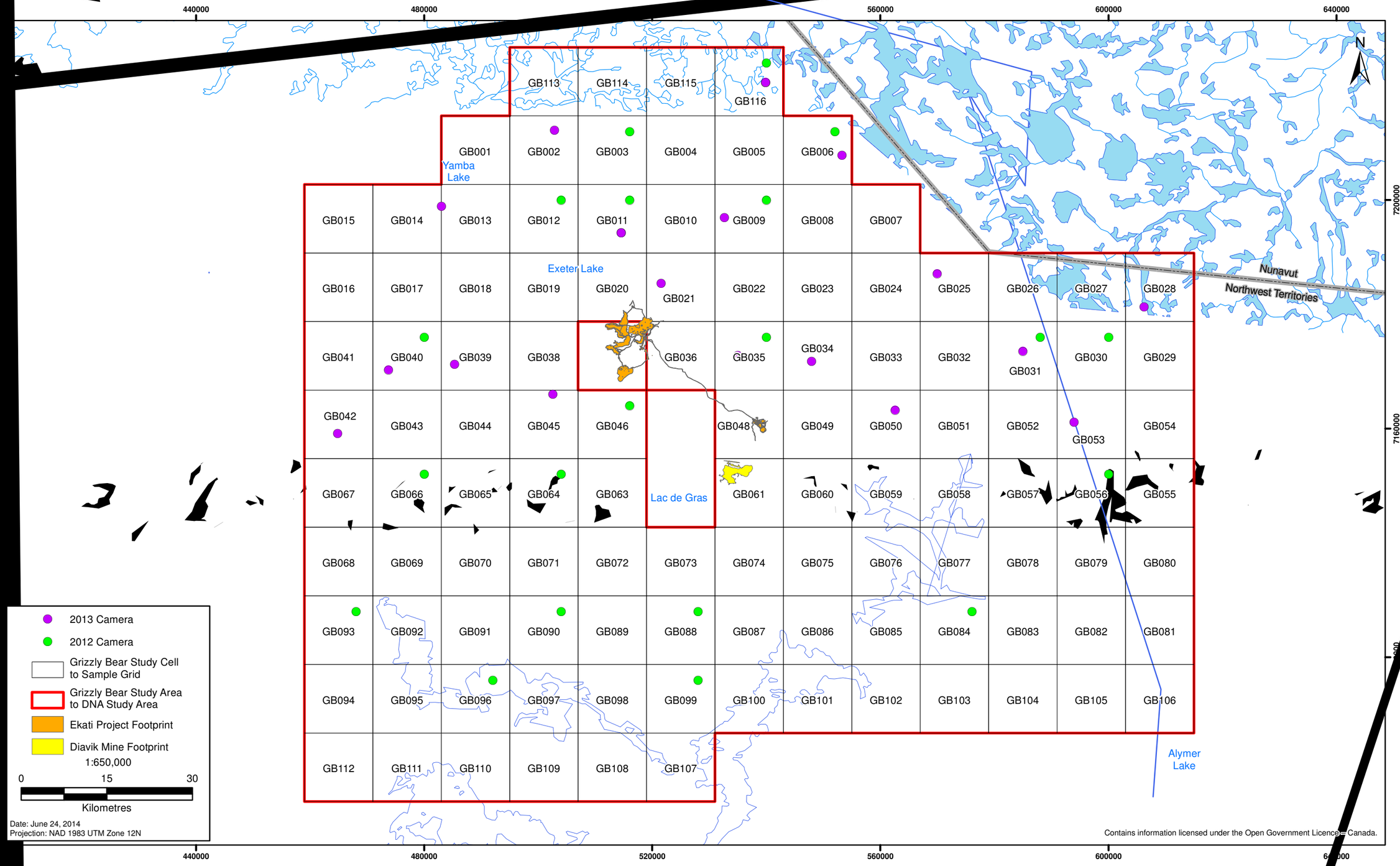
2. STUDY AREA

Within the DNA Study Area, 113 cells were sampled for grizzly bear hair (Figure 2-1). Each cell was 12 km by 12 km (144 km^2) for a total study area size of 16,272 km^2. Cell size was dependent on several factors, including the need to maximize capture probabilities (i.e., the likelihood of obtaining a hair sample), minimizing capture heterogeneity (i.e., variation in capture rates by sex and age class), and logistics. The cell size was chosen so that it was not larger than the expected area used by an individual bear over a sampling period, and it was assumed that a bear traveling through a cell had an equal probability of encountering a tripod as any other bear (Apps 2010).

2.1 REGIONAL SETTING OF WILDLIFE STUDY AREAS

The study area is located within the Southern Arctic Ecozone, which extends across much of the southern portion of continental Nunavut, and is bordered by the Northern Arctic Ecozone to the north. The northern area of the Southern Arctic Ecozone is characterized By stunted forms of tree species, such as dwarf birch (*Betula nana*) and green alder (*Alnus viridis* spp. *crispa*). Many species of willow (*Salix* sp.) grow throughout the ecozone, with stunted white (*Picea glauca*) and black spruce (*P. mariana*) present more towards the south. Much of the area is dominated by sedge fens, cottongrass tussock tundra, and heath. Sparsely vegetated areas, such as the wind-swept crests of eskers, are also common (NRC 2007).

Grizzly Bear DNA Study Area, 2012-2013



3. METHODS

3.1 TRADITIONAL KNOWLEDGE

Elders, land users, and youth from Kugluktuk, Lutsel K'e Dene, Yellowknives Dene, and the North Slave Metis Alliance participated in several site visits during the initial planning phases of the grizzly bear DNA program. During these visits, they were invited to share their information regarding grizzly bear habitat preferences and movement patterns to inform the overall study design.

In September, 2010, Ekati established a pilot grid of eight 10x10 km cells surrounding the mine site. To maximize capture probabilities, site locations were initially based on a desktop exercise that examined seasonal habitat suitability models (see Rescan 2010). Community members were taken to these sites to confirm that each location was suitable to detect grizzly bears. If community members felt a sampling site was not suitable, they were asked to select an alternate location.

In 2010, barbed-wire tripods were relocated between each of three sessions. Different scented lures (combinations of commercial bear bait, fish oil, beaver castor, anise oil, and vanilla extract) were tried during each session. In 2011, the pilot study was expanded to 13 10x10 km cells. There were six sampling sessions between June 18 and August 27. Once again, posts were relocated between most sessions and the same lures that were used in 2010 were applied in 2011.

Elders and land users tended to focus sampling sites along eskers as favored movement paths or in riparian areas that contain high quality forage and access to fish resources. In cells where these locations were limited, recommended sites included upland meadows and heath tundra areas away from extensive boulder fields. This information was additionally used during the design of the regional Ekati/Diavik grizzly bear DNA program as site selection criteria. As with the pilot programs, community members were invited during implementation and participated in site selection. Community members also participated during the hair collection sessions.

3.2 HAIR COLLECTION

One wooden tripod wrapped in barbed wire was used to collect grizzly bear hair (Plate 3.2-1) in a given cell, and the tripod remained at that location for the duration of the sampling season. Tripod locations were recorded by a handheld GPS. Within each cell, the tripod was located in an area of high quality grizzly bear habitat (e.g., esker, riparian area, upland meadow, wetland meadow) to increase the likelihood of "capturing" a bear. Short-distance, non-reward lures (e.g., cured cow's blood, fish oil, castor oil, and sweeter scents like anise oil and bergamot oil) were used to attract bears to the tripods. The lures were poured on the top of the tripods, down the legs (posts), and in the centre on the ground to encourage a bear to squeeze between the legs.

There were six sampling periods (sessions) at approximately 10-day intervals. Most studies in British Columbia opt for three to four sessions (Apps 2010); however, given the relatively low densities of grizzly bears in the Arctic, and their large home ranges (~2,000 km^2 for females) and movement

patterns, it was decided that more sessions were required to provide sufficient captures and recaptures of individuals for population analyses.

Plate 3.2-1. Example of barbed wire tripod used to collect grizzly bear hairs during DNA study.

During field sample collection, the barbed wire along the posts of the tripod, the ground under the tripod, and vegetation adjacent to the tripod were all searched for bear hair. Each clump of hair that was found was placed in a separate labelled coin envelope. Samples were then air dried for 48 hours and stored in paper bags for subsequent analysis. For each tripod, the three posts were arbitrarily selected as post 1, 2, or 3. Hair samples were labelled according to which post they were found on, or if they were collected off the ground. For subsampling purposes, hair samples along a post were grouped into clusters. A cluster is defined as a series of hair samples from consecutive barbs and a new cluster is identified following an empty barb.

After hair samples were collected, all barbs on which hair was found were burned with a propane torch to prevent double counting in the following session. In addition, tripods were moved a few metres after the check if hair had been collected from the ground so that grizzly hair from the current session would not contaminate future session samples.

Studies have suggested that relocating tripods to an alternate area within a cell every session improves precision in population estimates (Boulanger et al. 2004). The new location should be at least 1 km from the previous location, continuing to focus on high quality habitat. Relocating sampling stations between sessions was attempted during a pilot study at Ekati in 2010 (8 cells) and 2011 (13 cells) (see Rescan 2012) and it was determined that it was not logistically feasible to move stations in larger northern study areas. As a result, tripods were re-baited with a novel scent lure after each collection event to minimize acclimation by bears to sampling locations.

3.3 REMOTE CAMERA STATIONS

Reconyx PC800 Professional digital cameras were placed facing the DNA tripods in 19 of the cells in the DNA study area in 2012, and 20 cells in 2013 (Figure 2-1). Remote cameras were used to determine capture failure (i.e., whether some grizzly bears visiting a tripod were not leaving behind hair samples), and for those posts with hair samples, to determine whether DNA analyses were recording the correct number of grizzly bears visiting tripods (i.e., number of individuals identified by DNA matched the number observed by camera to have rubbed against the posts).

Remote cameras were mounted on 2x4" wooden posts and anchored to a five-gallon bucket that was filled with rocks. Energizer® Ultimate Lithium batteries were used to maintain camera performance at low-temperatures. Motion in front of the camera would trigger the camera to take 10 photos at 1-second intervals. Along with each photo, the cameras would record the date, time, type of trigger (i.e., time [T] or motion [M]), number of triggered photos taken (i.e., 1/10 - 10/10), temperature, and camera number. Cameras were programmed to immediately record a second set of 10 photos upon re-triggering. Remote cameras and DNA tripods were set-up at the same time. During each hair sample check, the cameras were also examined to ensure they were properly working.

3.4 LABORATORY ANALYSIS

3.4.1 Database Management and DNA Extraction

Genetic analyses on collected hair samples were conducted by Wildlife Genetics International (WGI) in Nelson, British Columbia. Sub-selection rules were provided that attempted to balance budgetary considerations with sample size and hair sample quality. Three criteria were used to exclude samples from DNA extraction. First, samples containing less than two guard hair roots and/or less than 30 underfur hairs were excluded. This is a higher quality threshold than is typically used, and was applied in response to the lower extraction success rates in other northern projects. Second, a sub-selection rule was applied, where the analysis was limited to one of every three samples from a series of adjacent samples, biasing towards samples of higher quality (2012), or the three best samples per post from separate clusters and one ground sample (2013). Finally, samples with an appearance inconsistent with grizzly bear hair were excluded. Leftover hair was archived at WGI.

DNA was extracted using QIAGEN's DNeasy Tissue kits, and followed the manufacturer's instructions (for details see http://www.qiagen.com). WGI aimed to use 10 guard hair roots where available. When underfurs were used, the number of roots used in the analysis was an estimate because entire clumps of whole underfur were extracted rather than clipping individual roots.

3.4.2 Microsatellite Genotyping

The analysis of individual identity was based on eight microsatellite markers that have been used in other northern grizzly bear projects in Nunavut and the NWT, and an additional gender marker. The 8-locus analysis of individual identity followed a 3-phase approach, which started with a first pass of all nine markers on all extracted samples. After the first pass, mixed and hopeless samples were set aside, with 'hopeless' being defined as having produced high-confidence data scores for less than four of eight markers during the first pass. The first pass was followed by a clean-up phase

in which data points that were weak or difficult to read the first time were re-analyzed. In some cases multiple rounds of re-analysis were used when it appeared that there was potential to upgrade a sample to a high-confidence 8-locus score.

The last phase of analysis was error-checking, which followed published protocol for selective data re-analysis (Paetkau 2003). Genotyping errors, which can lead to false individuals being recognized, normally create pairs of genotypes that match at all but one or two markers. Typically, such 1MM- and 2MM-pairs are sought out, and rule out genotyping error by re-analyzing the mismatching markers in each pair.

3.5 POPULATION ANALYSIS

Grizzly bear capture information from 2013 was combined with data from 2012 to generate a population estimate for the combined DNA Study Area. The superpopulation (N^) was modelled using a robust design with a Huggins estimator in program MARK. The superpopulation is the total number of bears that are expected to use the study area over the sampling period and is based on the relative probabilities of detecting and recapturing individuals. The robust design assumes that the active sampling period within a season or year (i.e., secondary sessions) is short enough to approximate closed population dynamics (no births, deaths, immigration, or emigration), but an open population dynamic is assumed during the interval between sampling years (i.e., primary sessions). In addition to the superpopulation, the Huggins estimator also provides estimates of survival and emigration parameters between primary sessions.

Precision in population estimates require that all individuals have an equal likelihood of being detected, and that detection probabilities are sufficiently high to ensure an adequate portion of the target population is being sampled. For grizzly bears, the target detection probability is 0.20, although reliable abundance estimates can be obtained with an overall capture probability of 0.10 for the sampled individuals (White et al. 1982). However, each individual is unique and likely to have a unique capture probability. Behavioural differences, social status, age, sex, and other innate characteristics can make an individual more or less likely to be captured. Inclusion of capture heterogeneity in this study was limited to dividing the dataset into males and females. Information about additional individual covariates that may influence individual capture rates (e.g., age, reproductive status) were unavailable and not incorporated into the models. While unobservable heterogeneity can be estimated by the Huggins models, this suite of models can perform less well than models without covariates if heterogeneity effects are not fully explained by the covariates (Chao and Huggins 2005). Accounting for capture heterogeneity may be more important in low density populations with extremely low capture probabilities (< 0.10) (Harmsen et al. 2010), or when the most recent and unbiased survival estimates from long term data sets are required for management purposes (Abadi et al. 2013).

Candidate models were assessed for providing the best population estimate using Akaike's Information Criterion adjusted for small sample sizes (AIC_c), a metric that provides the relative likelihood of any model given the available data (Burnham and Anderson 2002).

4. RESULTS

4.1 SUMMARY OF 2012 FIELD PROGRAM

Samples were collected in the field during six sessions from July 6 to September 4, 2012. A total of 1,902 hair samples were collected (Table 4.1-1), all of which were submitted to WGI for DNA analysis (Plate 4.1-1). Of the 1,902 samples collected, 649 (34%) were successfully extracted and assigned to 112 grizzly bear individuals, 42 males and 70 females. The 112 individuals included 19 (10M, 9F) with detections in other study areas, including 14 (8M, 6F) from the adjacent Courageous Lake study area, four (2M, 2F) from the Hackett River study area, and one female from the Izok study area in Nunavut. One male was detected at both Izok and Courageous Lake.

Table 4.1-1. Summary of Grizzly Bear Hair Samples Collected in the Field, 2012

Session	Collection Date Range	Type of Bait Used	Number of Cells with a Capture # (%)	Number of Samples Taken
Set-up tripods	June 23 - 29		-	-
Session #1	July 6 - 13	Blood	31 (27%)	195
Session #2	July 16 – 24	Fish oil	23 (20%)	149
Session #3	July 27 – Aug 6	Blood	49 (43%)	280
Session #4	Aug 6 -15	Fish oil + Anise	40 (35%)	358
Session #5	Aug 17 – 25	Blood	50 (44%)	515
Session #6	Aug 29 – Sept 4	Cherry oil, bergamot oil,	32 (28%)	371
Total			-	1,902

4.1.1 DNA Data Quality

The 1,902 records in the 2012 bear database were classified as follows:

1. Successful samples (34%): 649 samples that were assigned to individuals.
2. Inadequate samples (23%): 444 samples that lacked material suitable for DNA extraction.
3. Sub-selected samples (25%): 481 samples that were excluded due to sub-selection rules.
4. Bombed samples (15%): 284 samples that failed during microsatellite analysis.
5. Mixed samples (1%): 25 samples that showed evidence of ≥ 3 alleles per marker.
6. Non-target samples (1%): 19 samples did not appear to be from bears.

Plate 4.1-1. Example of a hair cluster sample collected during DNA surveys.

Successful DNA extraction of the Ekati-Diavik samples was moderate (68%) and lower compared to other barren-ground grizzly bear work in the Northwest Territories and Nunavut that had success rates around 80%. The stringent quality threshold, which resulted in an average of 7.0 guard hairs per extraction would be expected to produce a success rate closer to 80%. One underfur was treated as the equivalent to 0.2 guard hairs.

The success of extracts from underfur alone (59%) was poor in comparison to the extracts that used ≥2 guard hair roots (73%). Variation in success rates was also noted between specific sessions. This relationship between success rate and collection date suggests a potential environmental influence.

4.1.2 DNA Analysis Results

The 649 successful samples were assigned to 112 grizzly bears (42M, 70F) (Plate 4.1-2). There were many bears that were detected across multiple sampling sessions. Fifty-four individuals were recaptured at least once. Of the 54, six bears were detected in four sessions, 14 bears in three sessions, and 34 bears were detected in two sessions. Twelve individuals (3 females and 9 males) were new captures during the last sampling session.

Cell 48, on a northeast shoreline on Lac de Gras, and cell 58, on a northern shoreline west of Afridi Lake, detected the largest number of grizzly bears overall (N = 7) (Figure 4.1-1). Cells 2, 9, 61, and 82 had the second largest number of grizzly bears detected (N = 6).

Figure 4.1-1
Detection of Individual Grizzly Bears in the DNA Study Area, 2012

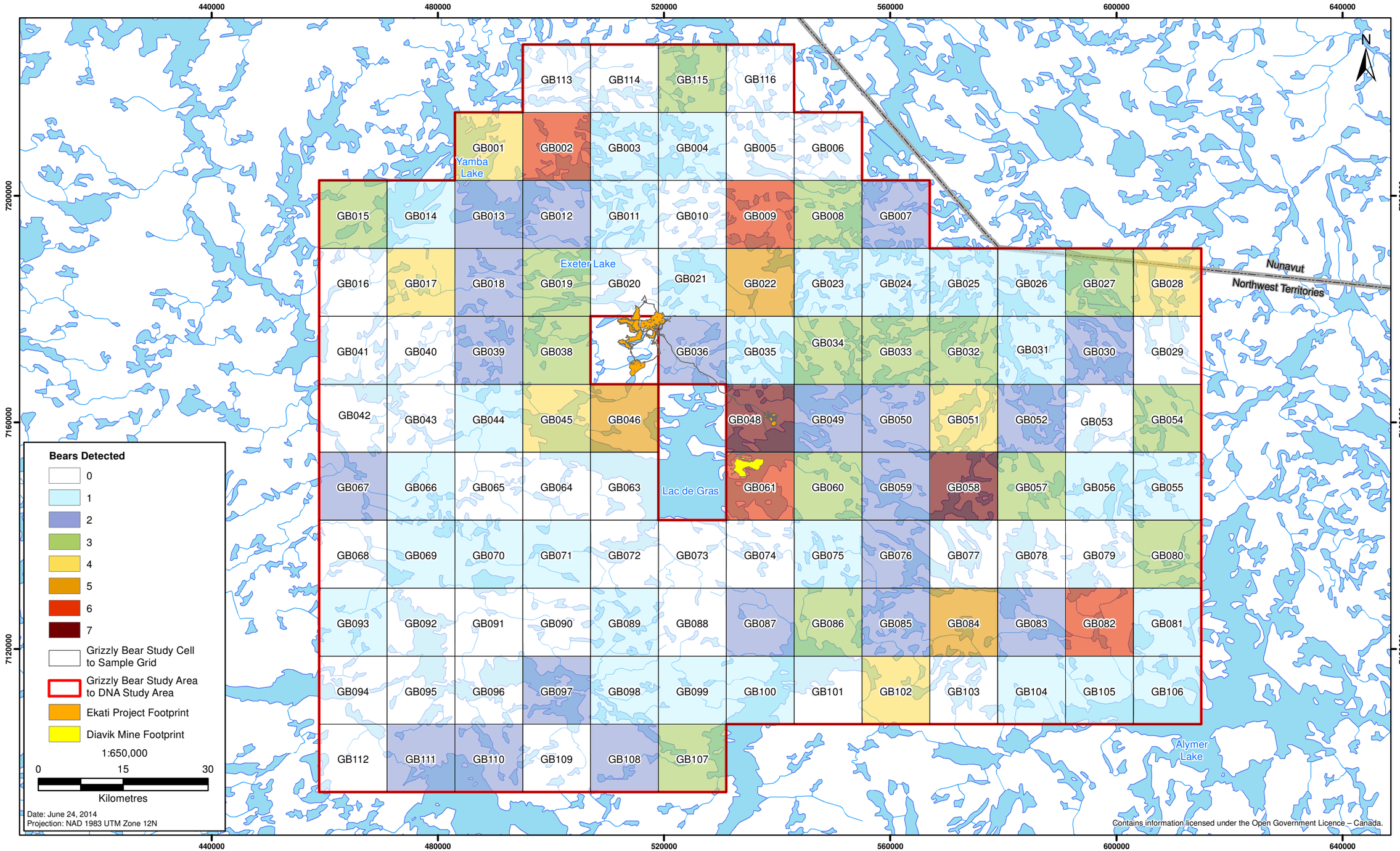



Plate 4.1-2. Photos of grizzly bears at tripod stations taken by remote cameras.

Some grizzly bears were detected in the same one or two sampling cells on multiple occasions. For example, one female (2011-158) was detected in adjacent cells 22 and 36 over four sessions. Similarly, female 2011-32 was detected in cells 46 and 48 and female 2012-1433 was detected in cells 82 and 83 over four sessions. Female 2011-25 was only detected in cell 46 and female 2012-229 was only detected in cell 1 over three sessions. Several grizzly bears were detected in the same cell in two different sessions. These multiple recaptures are possibly indicative of high habitat value in these cells within the respective grizzly bear home ranges.

Overall, the highest grizzly bear capture frequencies tend to occur in the northeast half of the study area, corresponding to a higher coverage of water and extensive esker systems that are prevalent throughout the area. This pattern was consistent across sessions (Figures 4.1-2a to f). The highest capture frequencies in the southwest portion of the study area occurred during sessions two (Figure 4.1-2b) and three (Figure 4.1-2c) with grizzly bears detected in five cells.

Most grizzly bears that were detected at least twice during the same session were detected in adjacent cells, or within two cells; however, some exceptional movements were noted. For example, female 2012-1826 moved between cells 58, 76, and 82 during session six, covering a straight line distance of approximately 58 km over 11 days. Females 2012-368 and 2012-49 covered approximately 55 km over 13 days between cells 8 and 45 during session five, and female 2012-711 travelled 40 km over 10 days between cells 22 and 115 during session four. Amongst males, the top movements were by male 2012-470 that travelled approximately 73 km between cells 48 and 54 during session five. The locations and distance travelled by grizzly bears per session is illustrated in Figures 4.1-2a to f. Given the topography and presence of water bodies between many of the cells, the actual distances travelled between points are likely considerably higher.

Some grizzly bears were detected at the same cells during the same session, indicating possible family groups. For example, females 2012-551 and 2012-561 were detected at cells 84 and 102 during session three, and females 2012-711, 2012-714, and 2012-725 were all detected at cells 2 and 9 during session six. Camera data provide additional information regarding the success of detecting family groups and potential bias in population estimates.

Figure 4.1-2a
Grizzly Bear DNA Results, Session 1, 2012

ERM

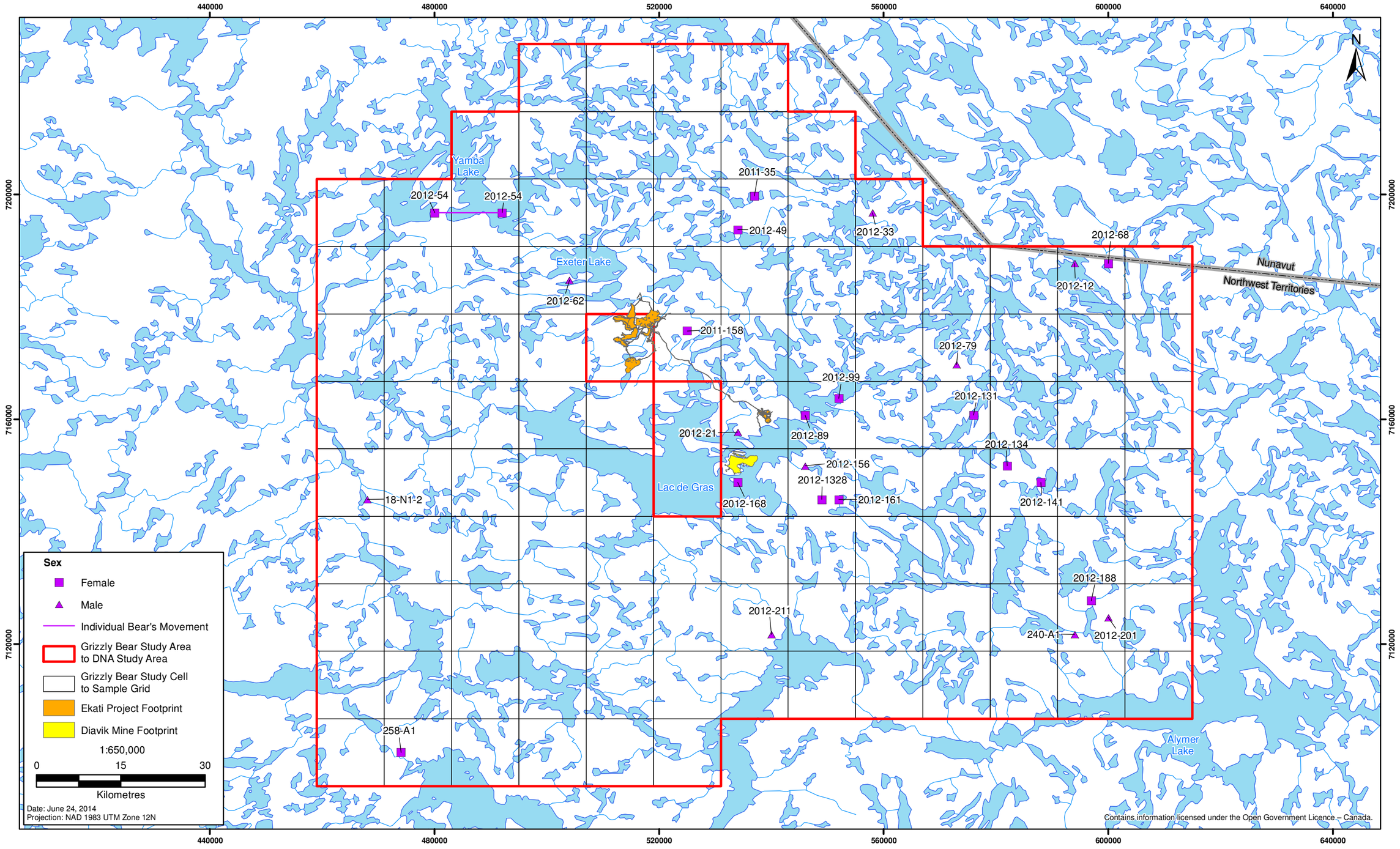


Figure 4.1-2b
Grizzly Bear DNA Results, Session 2, 2012

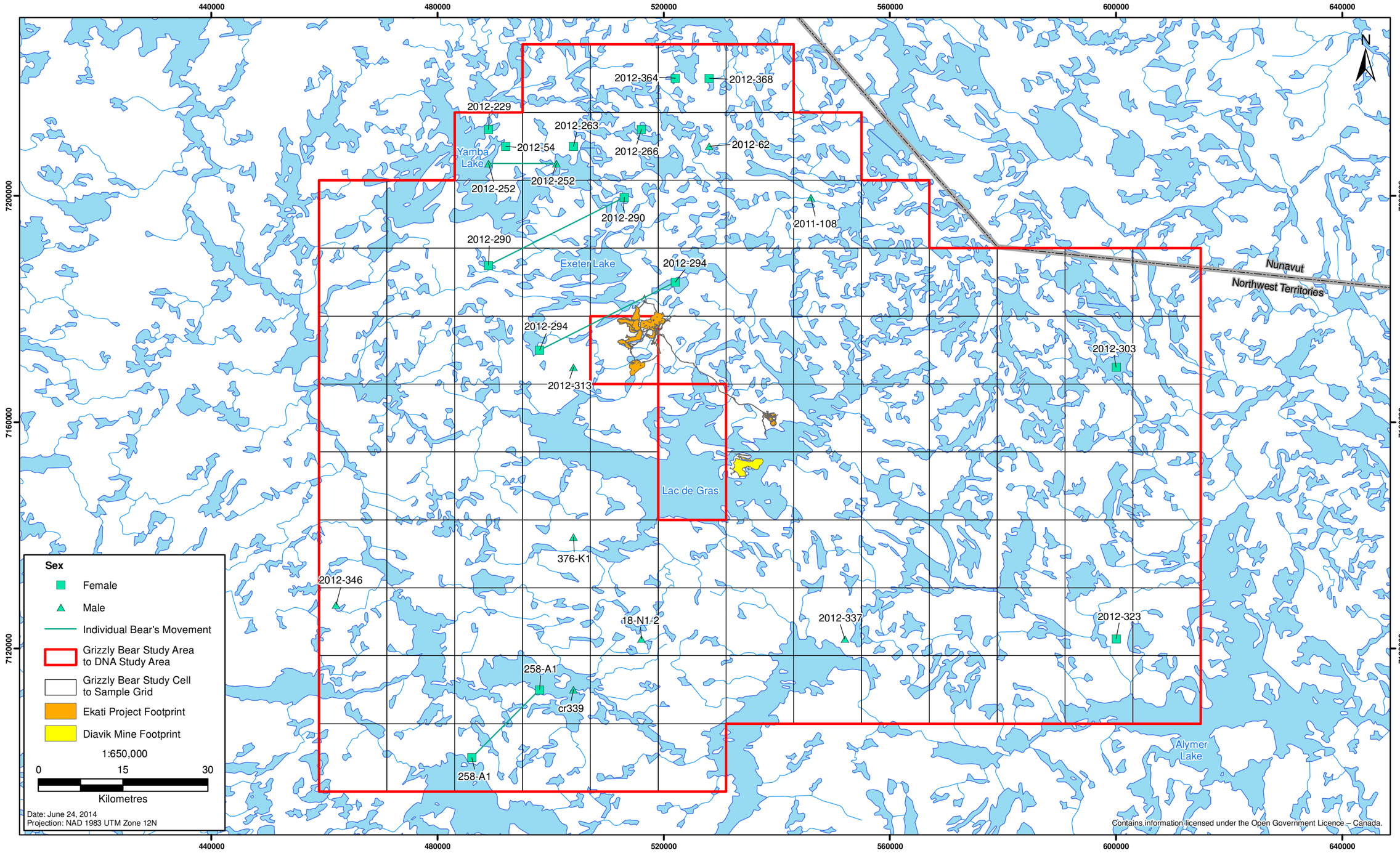


Figure 4.1-2c
Grizzly Bear DNA Results, Session 3, 2012

ERM

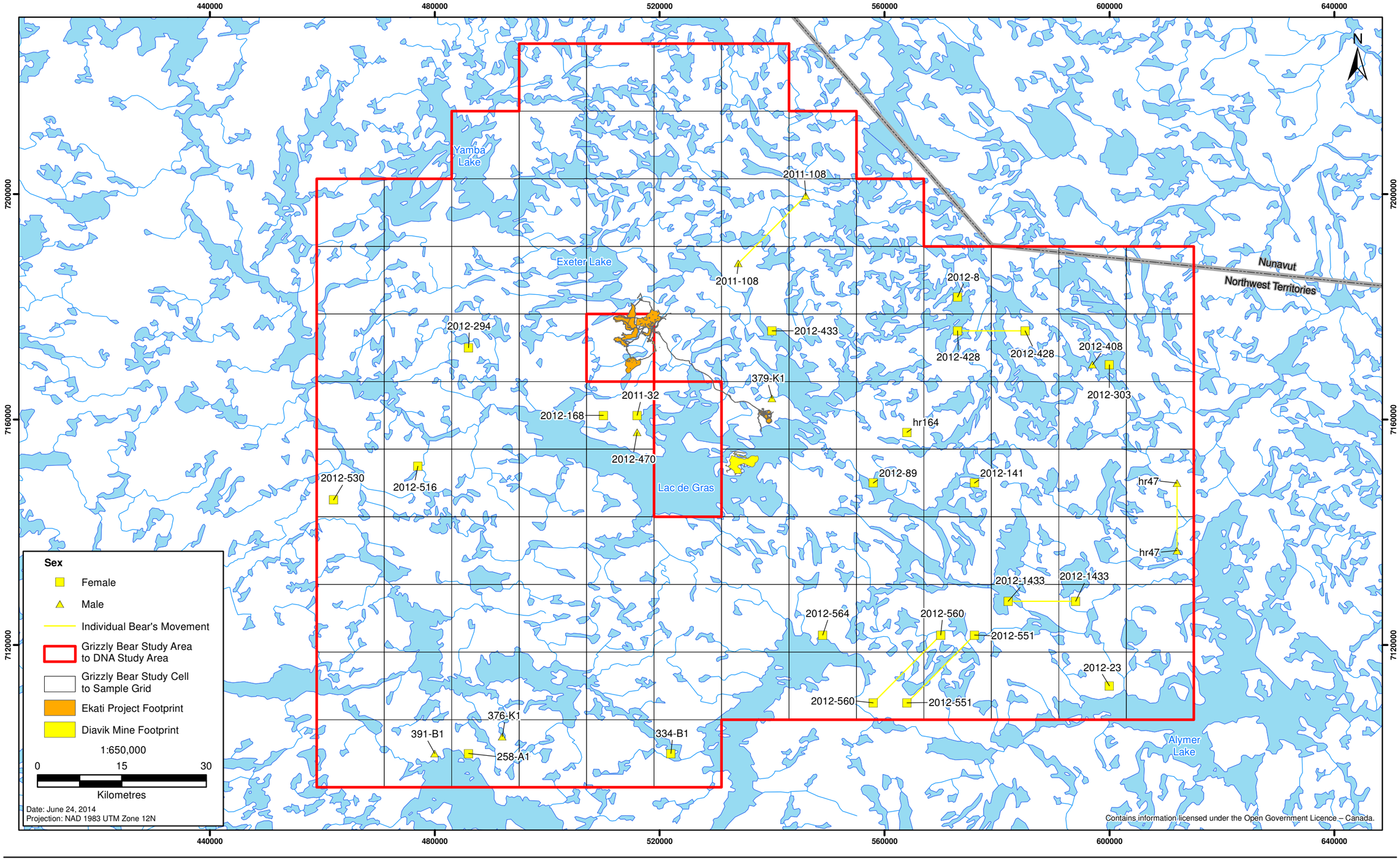


Figure 4.1-2d
Grizzly Bear DNA Results, Session 4, 2012

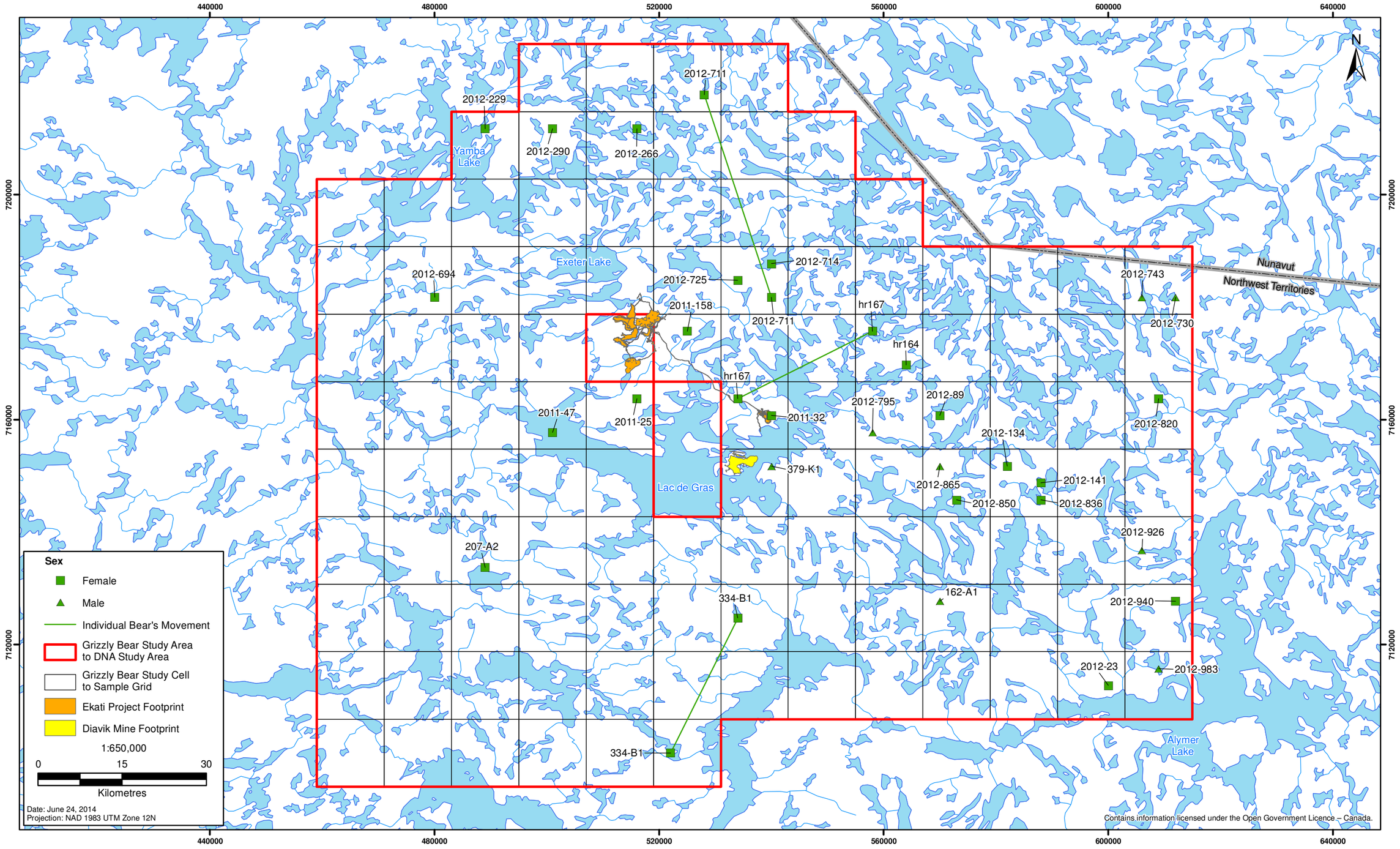


Figure 4.1-2e
Grizzly Bear DNA Results, Session 5, 2012

ERM

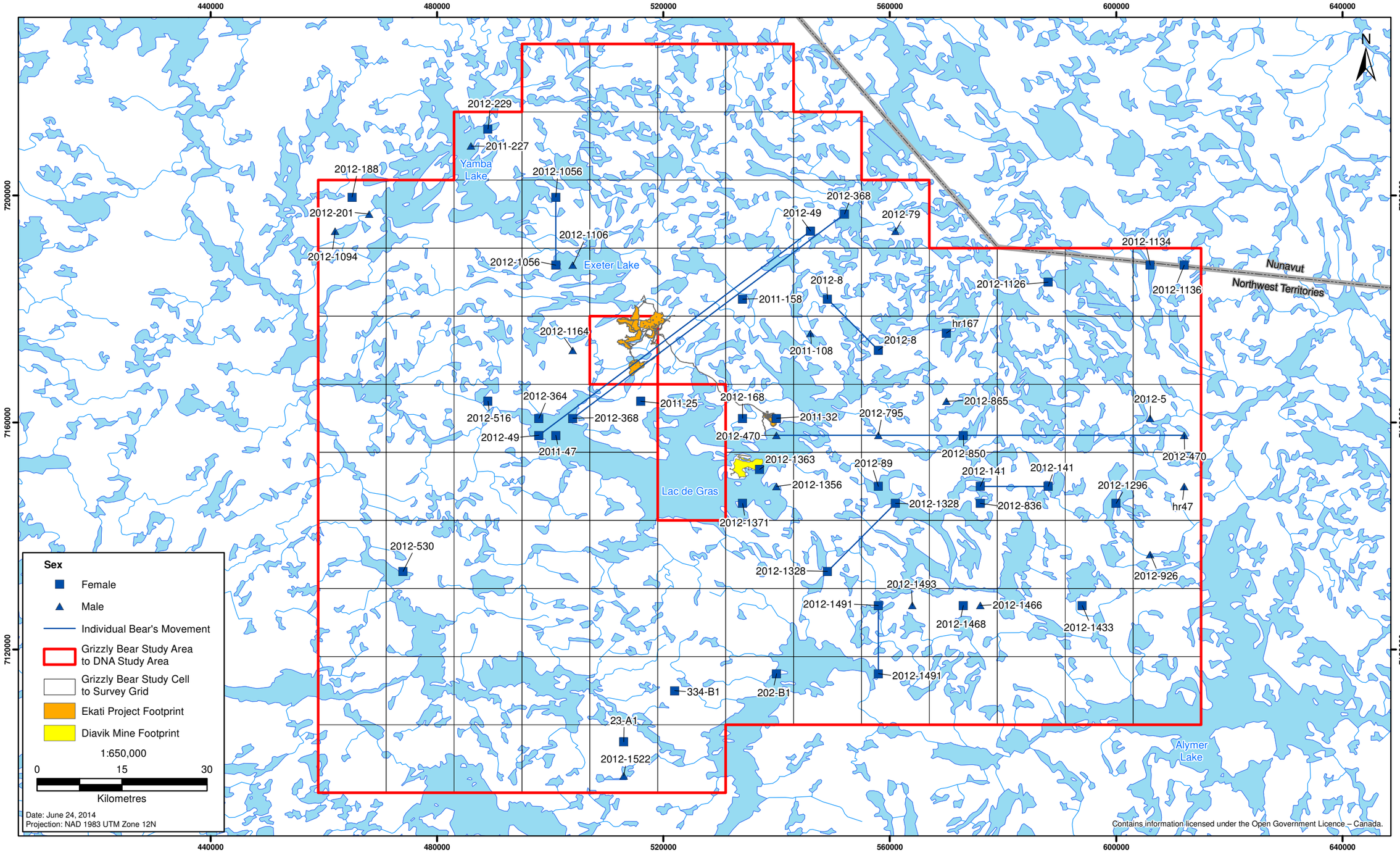
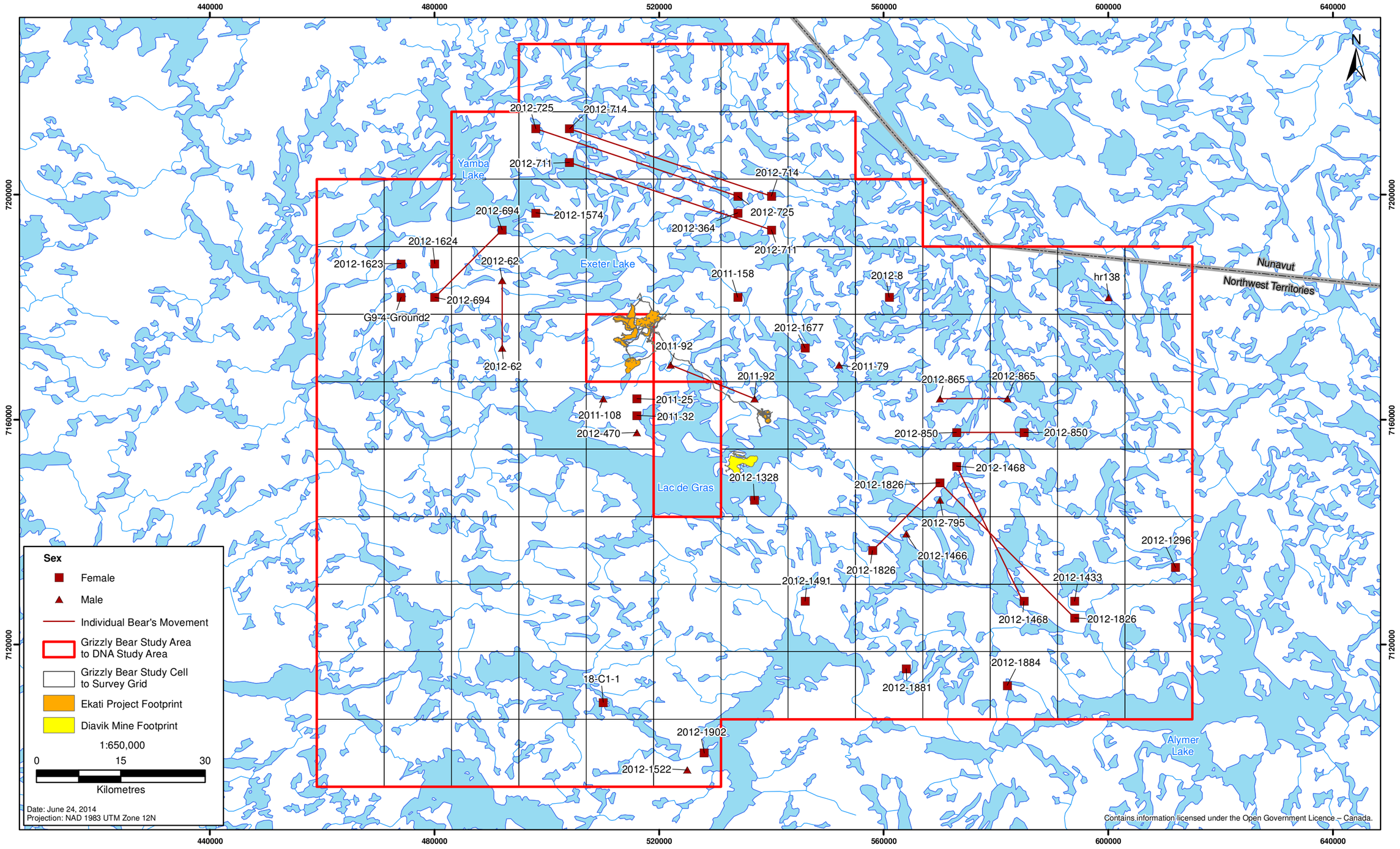


Figure 4.1-2f
Grizzly Bear DNA Results, Session 6, 2012



4.2 SUMMARY OF THE 2013 FIELD PROGRAM

Samples were collected in the field during six sessions from June 20 to August 21, 2013. A total of 4,709 hair samples were collected (Table 4.2-1), all of which were submitted to WGI for DNA analysis. Of the 4,709 samples collected, 1,180 (25%) were successfully extracted and assigned to 136 grizzly bear individuals (60M, 76F), including 39 that had no previous detections in the regional database (22M:17F). Camera data from 2012 indicated that some grizzly bears may have been missed from the database. As a result, DNA from an additional five samples from 2012 was successfully extracted, which identified 4 individuals (1M, 3F), including two that were recaptures and two that were new (1M, 1F) to the regional database. Some grizzly bears had detections in adjacent study areas, including two from Izok, four from Hackett River, and 20 from Courageous Lake.

Table 4.2-1. Summary of Grizzly Bear Hair Samples Collected in the Field, 2013

Session	Collection Date Range	Type of Bait Used	Number of Cells with a Capture # (%)	Number of Samples Taken
Set-up tripods	June 10 - 19		-	-
Session #1	June 20 – July 1	Blood	39 (35%)	610
Session #2	July 7 – 12	Fish oil	53 (47%)	816
Session #3	July 17 – 21	Blood	60 (53%)	704
Session #4	July 27 – 31	Seal oil	60 (53%)	789
Session #5	August 6 – 11	Blood	64 (57%)	1,005
Session #6	August 16 - 21	Sweet synthetics	52 (46%)	785
Total			-	4,709

4.2.1 DNA Data Quality

The 4,709 records in the 2013 bear database were classified as follows:

1. Successful samples (25%): 1,180 samples that were assigned to individuals.
2. Inadequate samples (25%): 1,197 samples that lacked material suitable for DNA extraction.
3. Sub-selected samples (38%): 1,791 samples that were excluded due to sub-selection rules.
4. Bombed samples (11%): 503 samples that failed during microsatellite analysis.
5. Mixed samples (0%): 1 samples that showed evidence of ≥ 3 alleles per marker.
6. Non-target samples (1%): 37 samples did not appear to be from bears.

Successful DNA extraction of the Ekati-Diavik samples in 2013 (70%) was similar to 2012 (68%). The sample quality was also similar, with a mean of 7.1 guard hairs per extraction, compared to 7.0 in 2012. One underfur was treated as the equivalent to 0.2 guard hairs.

The success of extracts from underfur alone (61%) was poor in comparison to the extracts that used ≥2 guard hair roots (78%). Limiting analysis of ground samples to those with ≥ 2 guard hairs

produced a marked increase in success (75%) over ground samples from 2012 (57%). Success rates also varied over time, ranging from 61% in session one to 77% in session four.

4.2.2 DNA Analysis Results

The 1,180 successful samples were assigned to 136 grizzly bears; 60 males and 76 females. There were many bears that were detected across multiple sampling sessions, including 117 individuals that were recaptured at least once. Of the 117, two bears were detected in all six sessions, seven bears were detected in five sessions, 14 bears were detected in four sessions, 26 bears in three sessions, and 43 bears were detected in two sessions. Five individuals (4 males and 1 female) were new captures during the last sampling session.

As in 2012, cell 58, on a northern shoreline west of Afridi Lake, detected the largest number of grizzly bears overall (N = 6), along with cells 9, 10, 30, 52, 53, and 110 (Figure 4.2-1). Eight cells had five grizzly bears detected and 15 cells detected four grizzly bears. There were 14 cells that did not detect any grizzly bears.

As in 2012, the highest grizzly bear capture frequencies tended to occur in the northeast half of the study area, corresponding to a higher coverage of water and extensive esker systems that are prevalent throughout the area. This pattern was consistent across sessions (Figures 4.2-2a to f). The highest capture frequency in the southwest portion of the study area occurred during session three (Figure 4.2-2c).

Most grizzly bears that were detected at least twice during the same session were detected in adjacent cells, or within two cells; however, some exceptional movements were noted. Amongst males, 2011-79 moved between cells 34 and 115 during session four, covering a straight line distance of approximately 65 km over 10 days. Male 2011-92 covered approximately 85 km over 10 days between cells 16 and 35 during session five. The longest detectable female movements in 2013 covered approximately 30 to 45 km during the 10 day sessions. The locations and distance travelled by grizzly bears per session are illustrated in Figures 4.2-2a to f. Given the topography and presence of water bodies between many of the cells, the actual distances travelled between points are likely considerably higher.

Family groups were not as readily identifiable in the 2013 dataset as compared to 2012. Camera data provide additional information regarding the success of detecting family groups and potential bias in population estimates.

Figure 4.2-1
Detection of Individual Grizzly Bears in the DNA Study Area, 2013

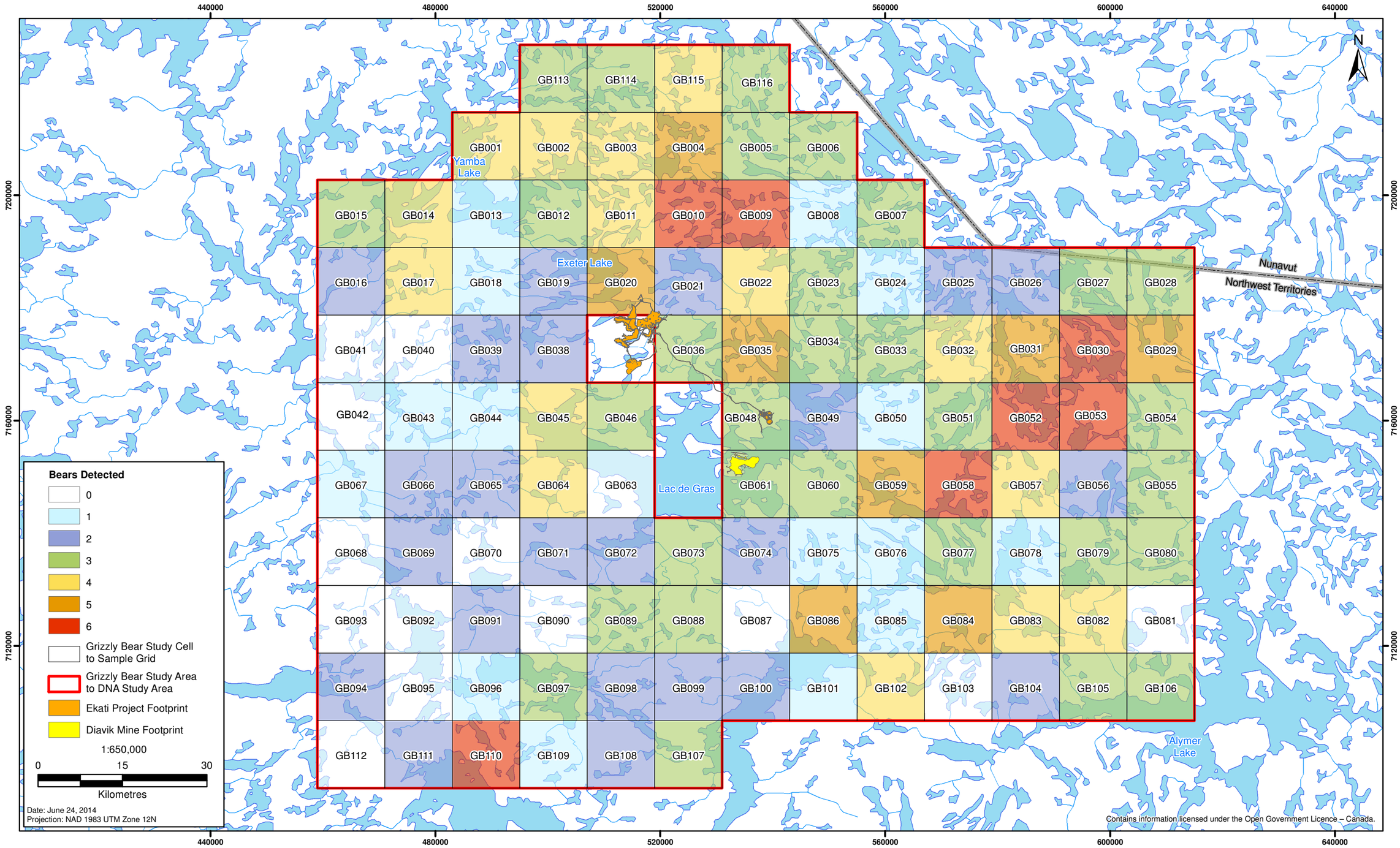


Figure 4.2-2a
Grizzly Bear DNA Results, Session 1, 2013

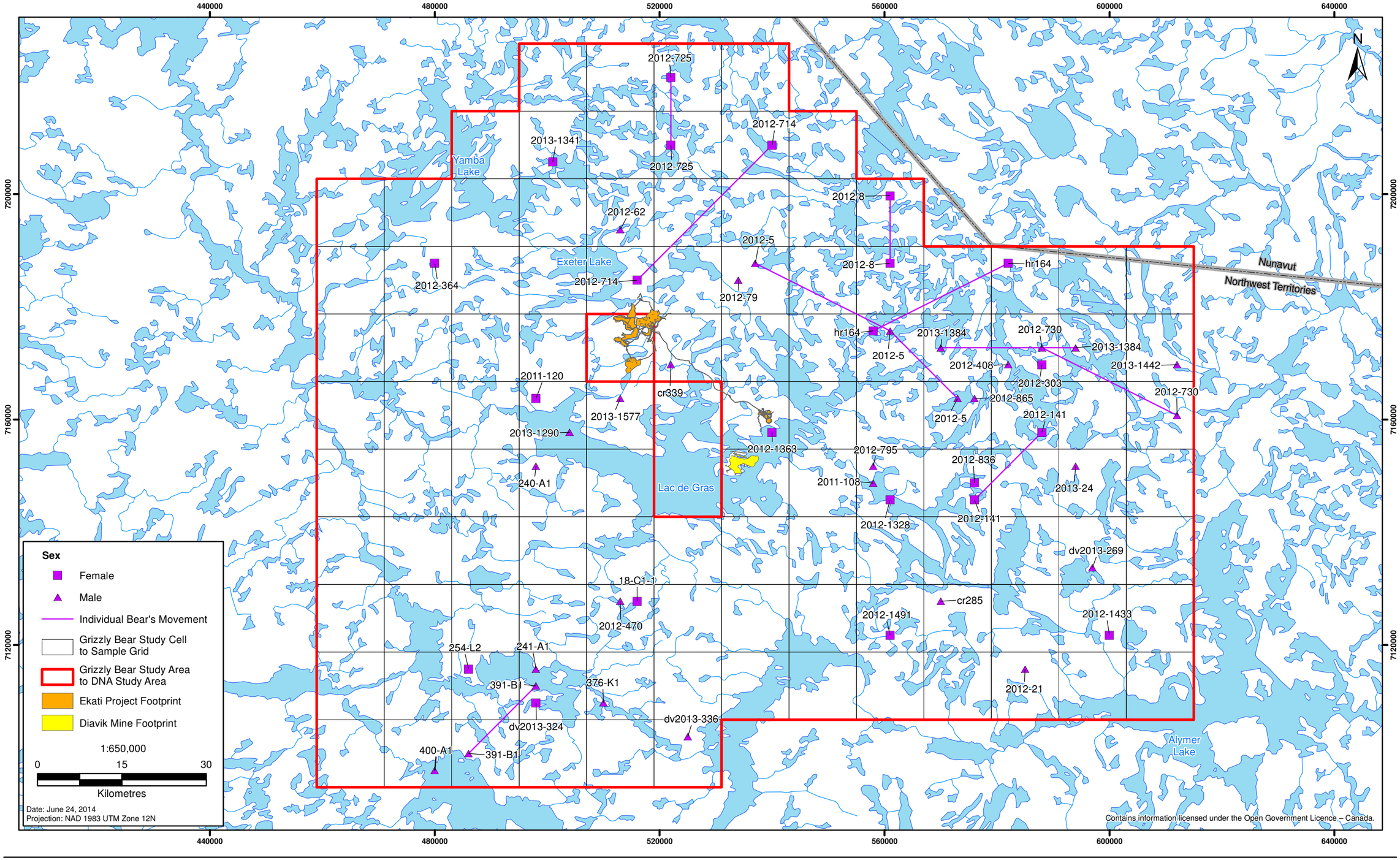


Figure 4.2-2b
Grizzly Bear DNA Results, Session 2, 2013

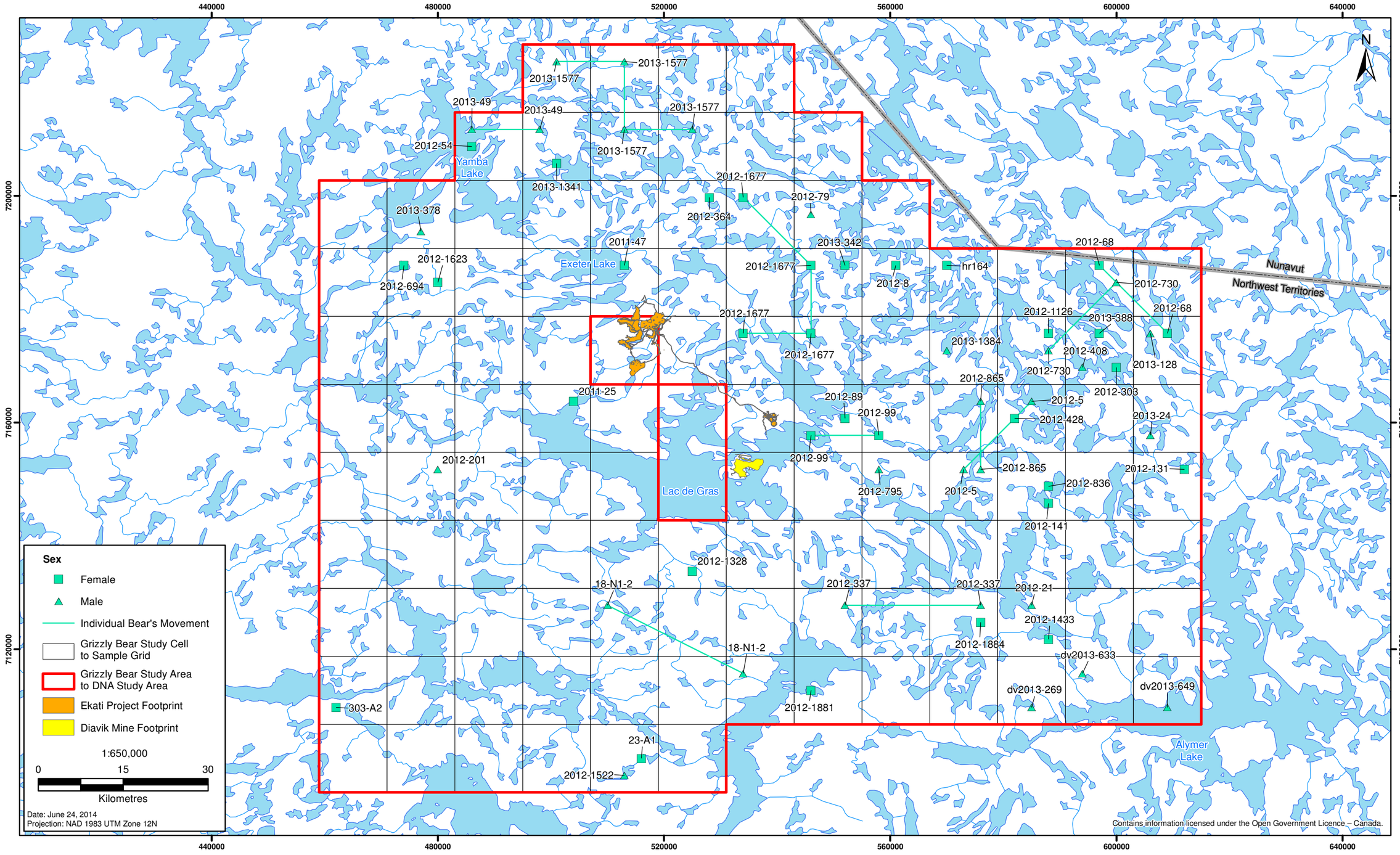


Figure 4.2-2c
Grizzly Bear DNA Results, Session 3, 2013

ERM

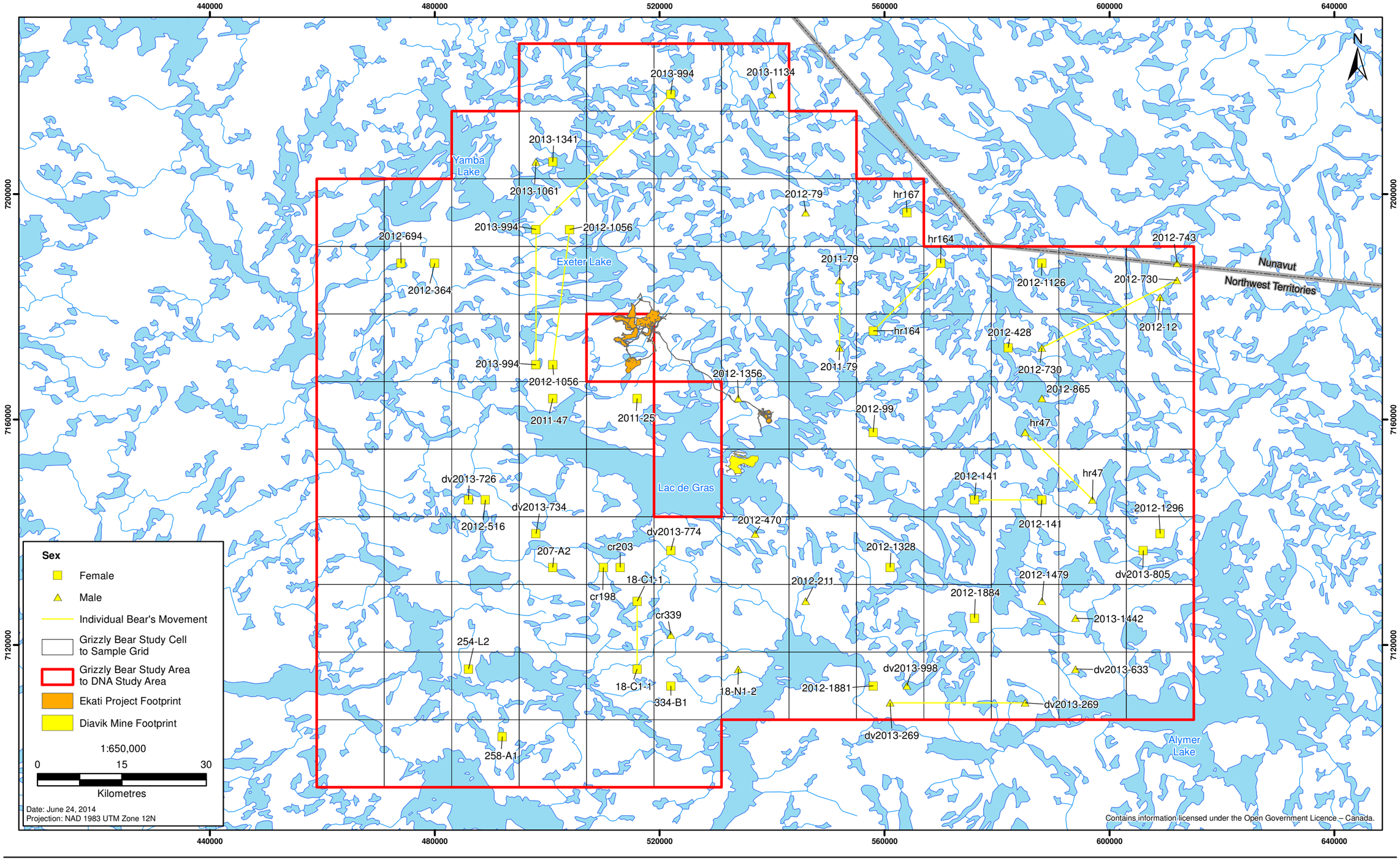


Figure 4.2-2d
Grizzly Bear DNA Results, Session 4, 2013

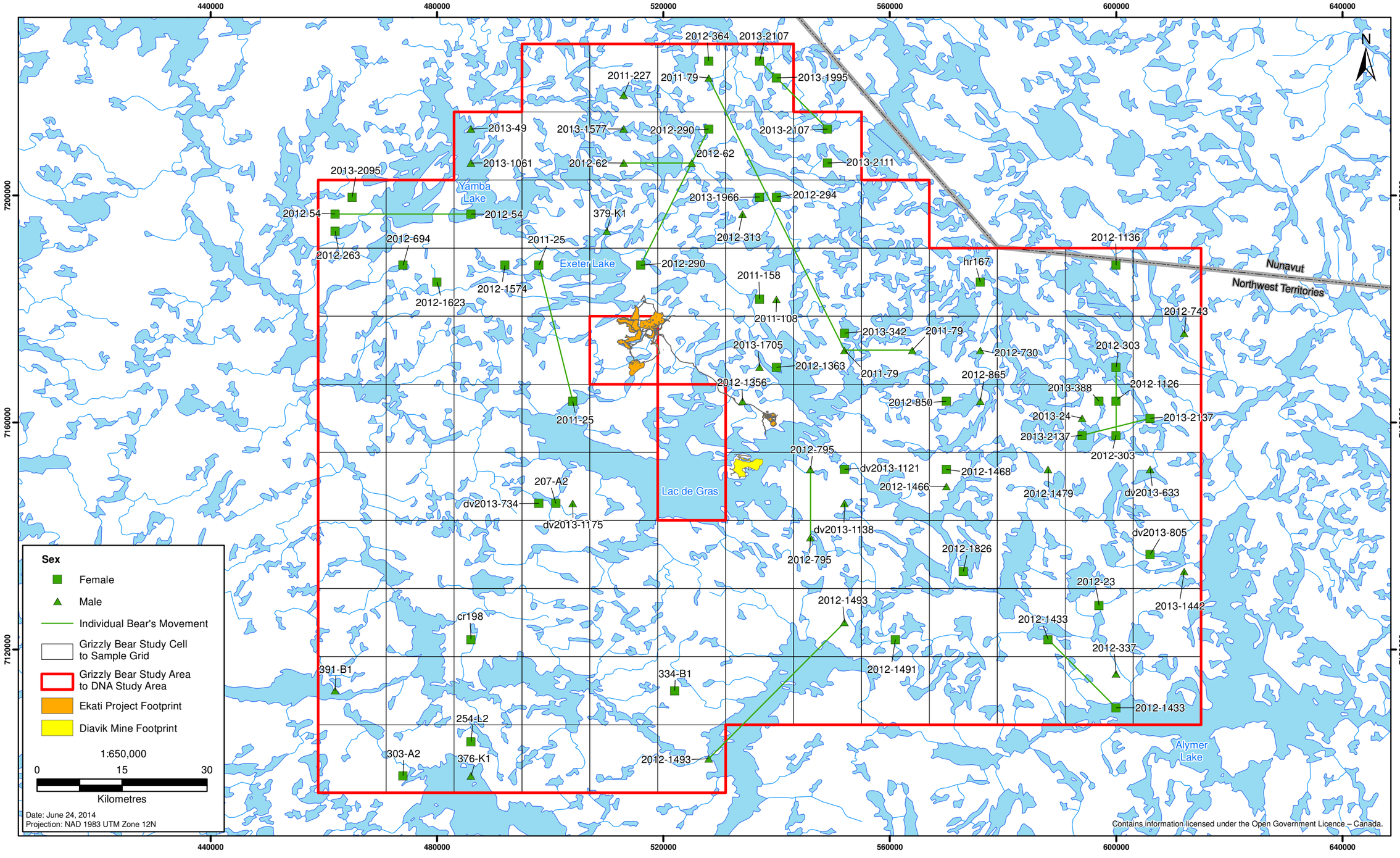


Figure 4.2-2e
Grizzly Bear DNA Results, Session 5, 2013

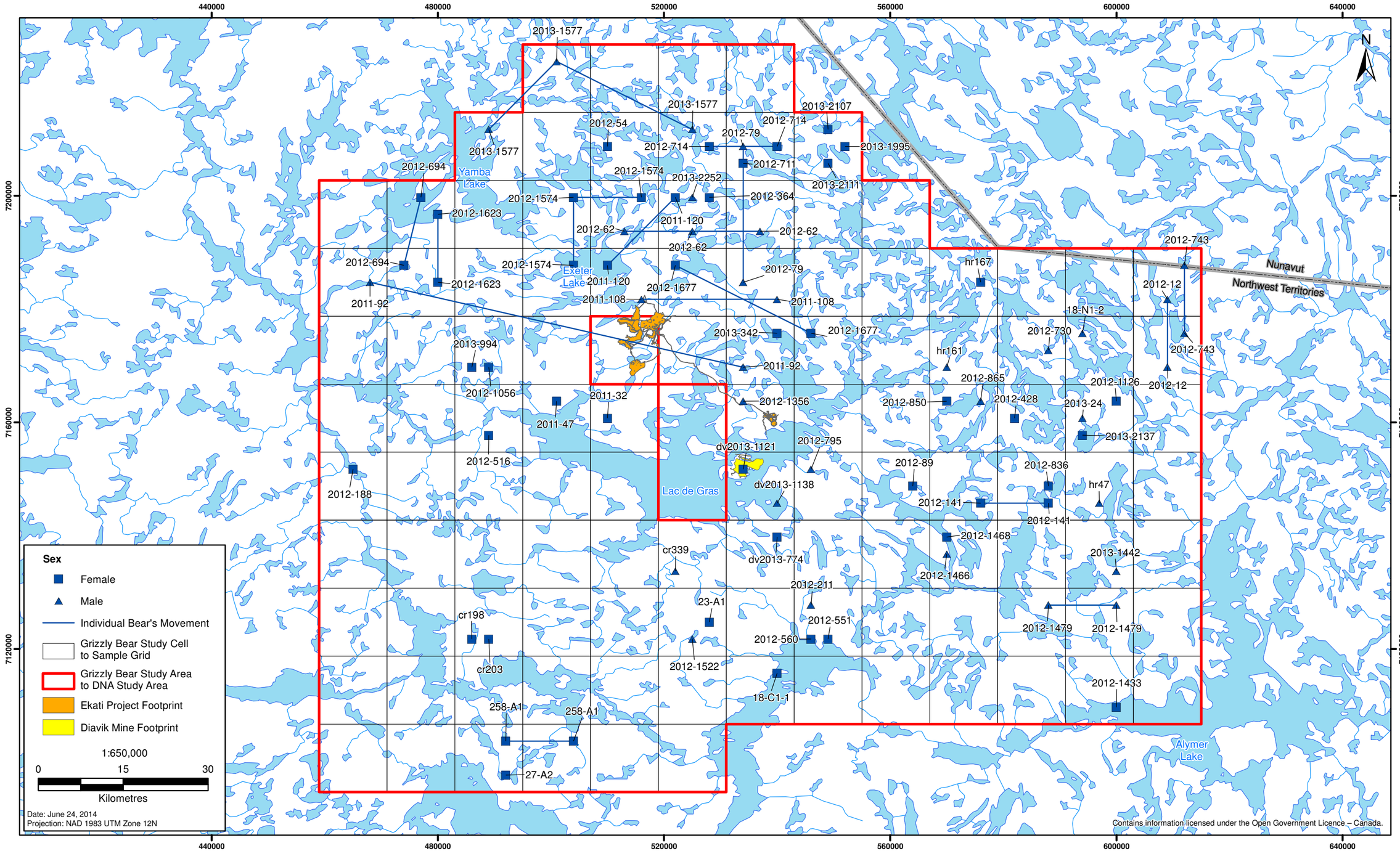
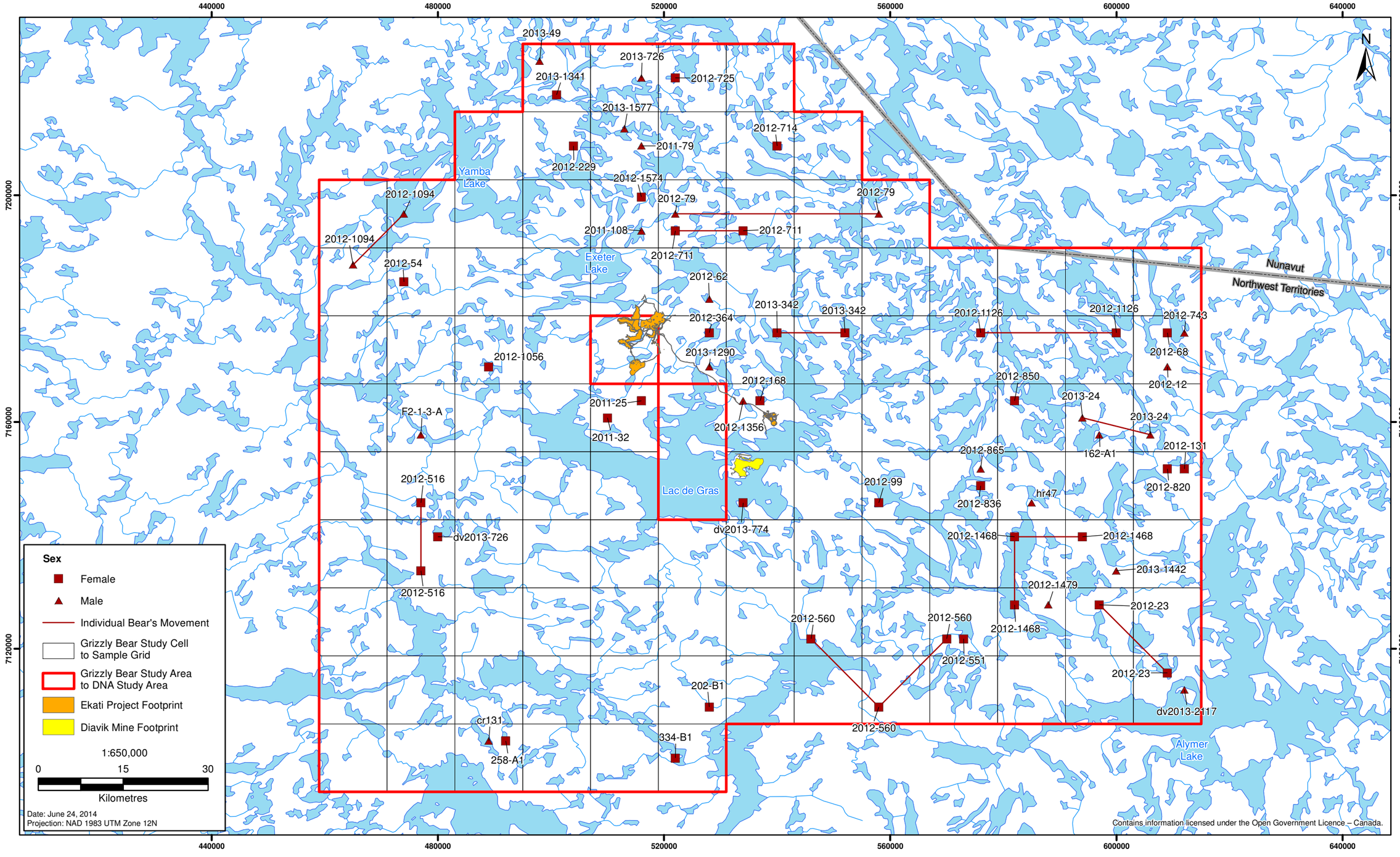


Figure 4.2-2f
Grizzly Bear DNA Results, Session 6, 2013



4.3 REMOTE CAMERA DATA

4.3.1 2012

Remote cameras were positioned facing grizzly bear tripods in 20 sampling cells. Remote cameras recorded 57 grizzly bears on 37 photo events. Some individuals may have been repeat visitors between sessions compared to 33 grizzly bears that were detected by DNA analyses for the corresponding sampling session (Table 4.3-1). There were 17 occasions where cameras took pictures of grizzly bears but DNA analysis did not identify all the potential grizzly bears. Much of this discrepancy involved family groups, particularly females accompanied by cubs of the year. There were four cases where DNA analysis identified more grizzly bears than were photographed during the corresponding sampling session.

Table 4.3-1. Summary of Remote Camera Data at Grizzly Bear Sampling Stations, 2012

Cell	Photo Date	Photo Result	DNA Result	Photo Bears	DNA Bears
3	13-Jul-13	F + 3coy	F2012-266	4	1
	1-Aug-13	single	F2012-266	1	1
	2-Aug-13	single	F2012-266?	1	?
	14-Aug-13	single	x	1	0
6	23-Jun-13	single	x	1	0
	2-Jul-13	single	x	1	0
9	23-Jun-13	F + 2x3yr	F2011-35, F2012-49	3	2
	25-Jun-13	single	unk	1	Unk
	27-Aug-13	2 bears	F2012-711, F2012-714, F2012-725	2	3
11	13-Jul-13	single	F2012-290	1	1
	15-Jul-13	single	unk	1	Unk
12	9-Aug-13	F + 2x1yr	F2012-1056	3	1
	20-Aug-13	single	F2012-1574	1	1
30	17-Jul-13	single	F2012-303	1	1
31	25-Jun-13	single	x	1	0
	16-Jul-13	single	x	1	0
35	18-Jul-13	F + 3x1yr	F2012-433	4	1
46	18-Jul-13	F + 2x2yr	F2011-32, F2012-168, M2012-470	3	3
	6-Aug-13	single	F2011-25	1	1
	18-Aug-13	single	F2011-25	1	1
	21-Aug-13	single	F2011-25?	1	?
	25-Aug-13	single	F2011-25, F2011-32, M2012-470, M2011-108	1	4
58	20-Jul-13	F + 2coy	F2012-141	3	1
	4-Aug-13	single	F2012-850, M2012-865	1	2
	17-Aug-13	single	F2012-141, F2012-836	1	2
66	27-Jun-13	single	X	1	0
	29-Jun-13	single	X	1	0
	29-Jun-13	F + 2x2yr	X	3	0
84	30-Jun-13	single	X	1	0
	23-Jul-13	F + 1x1yr	F2012-560, F2012-551	2	2
	26-Jul-13	single	unk	1	Unk

(continued)

Table 4.3-1. Summary of Remote Camera Data at Grizzly Bear Sampling Stations, 2012 (completed)

Cell	Photo Date	Photo Result	DNA Result	Photo Bears	DNA Bears
84	7-Aug-13	single	M162-A1	1	1
	17-Aug-13	F + 2x2yr	F2012-1468, M2012-1466	3	2
93	17-Jul-13	single	M2012-346	1	1
96	17-Aug-13	single	x	1	0
99	17-Aug-13	single	F354-B1	1	1
116	17-Jul-13	single	x	1	0
40	-	-	-	0	0
64	-	-	-	0	0
88	-	-	-	0	0
90	-	-	-	0	0
Total				**57**	**33**

unk denotes that it is unknown whether the photographed bear is the same as the previously identified bear, or represents a new bear not detected by DNA analysis.
coy refers to cubs of the year
1yr and 2yr refer to 1 year olds and 2 year olds

Ten family groups (30 individuals) were recorded by remote cameras during the survey period. Family units were mainly a mother and two cubs; a mother with three cubs was observed twice and a mother with a single cub was observed once. Two grizzly bear individuals were recorded together; however, picture quality did not allow age to be determined (i.e., whether they were cubs or yearlings).

4.3.2 2013

In 2013, remote cameras recorded 84 individual grizzly bears on 58 photo events (some may have been repeat visitors between sessions compared to 85 grizzly bears that were detected by DNA analyses for the corresponding sampling session (Table 4.3-2). There were 16 occasions where cameras took pictures of grizzly bears but DNA analysis did not identify all the potential grizzly bears; however, in contrast to 2012, there were 19 cases where DNA analysis identified more grizzly bears than were photographed during the corresponding sampling session.

Table 4.3-2. Summary of Remote Camera Data at Grizzly Bear Sampling Stations, 2013

Cell	Photo Date	Photo Result	DNA Result	Photo Bears	DNA Bears
2	26-Jun-13	F + 2x1yr	2013-1341	3	1
	4-Jul-13	F + 2x2yr	2013-1341; 2013-49	3	2
	12-Jul-13	F + 2x1yr	2013-1341; 2013-1061	3	2
	13-Aug-13	single	2012-229	1	1
6	25-Jun-13	F + 3coy	X	4	0
	23-Jul-13	F + 3coy	2013-2107; 2013-2111	4	2
	30-Jul-13	F + 3coy	2013-2107; 2013-2111; 2013-1995	4	3
9	10-Jul-13	single*	2012-1677	1	1
	11-Jul-13	single	X	1	0
	21-Jul-13	F + 2x2yr	2012-313; 2012-294; 2013-1966	3	3

(continued)

Table 4.3-2. Summary of Remote Camera Data at Grizzly Bear Sampling Stations, 2013 (continued)

Cell	Photo Date	Photo Result	DNA Result	Photo Bears	DNA Bears
9	8-Aug-13	single	2012-62	1	1
	9-Aug-13	single	2012-62	1	1
	X	X	2012-711	0	1
11	23-Jun-13	single	2012-62	1	1
	25-Jul-13	single	379-K1	1	1
	28-Jul-13	2 x single	?	2	unk
	30-Jul-13	single	?	1	unk
	1-Aug-13	single	2012-62	1	1
	7-Aug-13	single	2012-1574	1	1
	15-Aug-13	single	2012-108	1	1
	17-Aug-13	single	2012-1574	1	1
12	13-Jul-13	single	2012-1056; 2013-994	1	2
	5-Aug-13	single	2012-1574	1	1
14	3-Jul-13	single	2013-378	1	1
	5-Jul-13	single	?	1	?
	6-Aug-13	single	2012-1623	1	1
	8-Aug-13	single	2012-694	1	1
	20-Aug-13	single	2012-1094	1	1
21	19-Jul-13	single	X	1	0
	2-Aug-13	single	2012-1677	1	1
	X	X	2012-62	0	1
25	7-Jul-13	single	hr-164	1	1
	check 3	X	hr-164	0	1
	24-Jul-13	single	hr-167	1	1
	check 5	X	hr 167	0	1
28	check 3	X	2012-12; 2012-730; 2012-743	0	3
	30-Jul-13	single	X	1	0
	check 5	X	2012-12; 2012-743	0	2
31	check 1	X	2012-303; 2012-408; 2012-730	0	3
	4-Jul-13	single	2012-1126; 2012-730	1	2
	29-Jul-13	single	X	1	0
	check 5	X	2012-730	0	1
	18-Aug-13	single	X	1	0
34	6-Jul-13	single	2012-1677	1	1
	check 3	X	2011-79	0	1
	26-Jul-13	single	2011-79	1	1
	29-Jul-13	single	2013-342	1	1
	10-Aug-13	single	2012-1677	1	1

(continued)

Table 4.3-2. Summary of Remote Camera Data at Grizzly Bear Sampling Stations, 2013 (completed)

Cell	Photo Date	Photo Result	DNA Result	Photo Bears	DNA Bears
35	1-Jul-13	single	2012-1677	1	1
	27-Jul-13	single	2012-1363; 2013-1705	1	2
	31-Jul-13	F + 2x2yr	2011-92; 2013-342	3	2
	check 6	X	2013-342	0	1
39	7-Aug-13	single	2012-1056; 2013-994	1	2
	check 6	X	2012-1056	0	1
40	X	X	X	0	0
42	X	X	X	0	0
45	check 1	X	2013-1290; 2011-120	0	2
	6-Jul-13	single	2011-25	1	1
	19-Jul-13	single	2011-47	1	1
	10-Aug-13	F + 1x2yr	2011-25; 2011-47	2	2
	13-Aug-13	single	X	1	0
50	check 2	X	2012-99	0	1
	14-Jul-13	single	2012-99	1	1
53	20-Jul-13	F + 2x2yr	2013-24; 2013-388; 2012-1126	3	3
	26-Jul-13	single	2012-1126	1	1
	29-Jul-13	single	2012-303	1	1
	check 5	X	2013-24; 2013-2137; 2012-1126	0	3
	15-Aug-13	single	162-A1; 2013-24	1	2
116	16-Jul-13	single	2013-1134	1	1
	27-Jul-13	single	2013-2107	1	1
	28-Jul-13	F + 3x1yr	2013-1995; 2013-2107	4	2
	10-Aug-13	single	X	1	0
	18-Aug-13	single	X	1	0
Total				**84**	**85**

unk denotes that it is unknown whether the photographed bear is the same as the previously identified bear, or represents a new bear not detected by DNA analysis.
coy refers to cubs of the year
1yr and 2yr refer to 1 year olds and 2 year olds

Eleven family groups (36 grizzly bears) were recorded by remote cameras during the survey period. Family units were mainly a mother with yearlings or juveniles; a mother with three cubs of the year was observed three times in cell 6.

4.4 POPULATION ANALYSIS

A total of 12 candidate models were ranked using AIC_c (Burnham and Anderson 2002). The top three models are listed in Table 4.4-1. The top model was a time dependent model where capture probabilities (p) were assumed equal to recapture probabilities (c) across individuals and varied

across sessions and years, but no difference between males and females. The model is of the general form $N^{\wedge}_{(t)}\ \{ p_{(t)} = c_{(t)} \}$. Model parameters were not averaged due to strong support for the top model.

Table 4.4-1. Top Candidate Models for the Estimation of the Superpopulation in the DNA Study Area

Model	AIC_c	Delta(Δ) AIC_c	AIC_c Weight	Model Likelihood	No. Parameters
$N^{\wedge}_{(t)}\ \{p_{(m)(t)}=c_{(m)(t)}=p_{(f)(t)}=c_{(f)(t)}, G_{(m)}=G_{(f)}, S_{(m)}=S_{(f)}\}$	1929.27	0.00	0.71	1.00	13
$N^{\wedge}_{(t)}\ \{p_{(m)(t)}=c_{(m)(t)}=p_{(f)(t)}=c_{(f)(t)}, G_{(m)}\neq G_{(f)}, S_{(m)}\neq S_{(f)}\}$	1931.38	2.11	0.26	0.35	14
$N^{\wedge}_{(t)}\ \{p_{(.)},c_{(.)}, p_{(1)}=p_{(2)}, c_{(1)}=c_{(2)}, p\neq c, m\neq f, G_{(m)}\neq G_{(f)}, S_{(m)}\neq S_{(f)}\}$	1938.76	9.48	0.006	0.009	4

(t) denotes model parameter varies with time.
(.) denotes model parameter is constant over time.
N^ = superpopulation estimate.
m = males.
f = females.
S = survival parameter.
G = emigration parameter.

For the combined DNA dataset, the mean capture probability in the DNA Study Area was 0.22 (range 0.14 – 0.35) in 2012, and 0.35 (range 0.28 – 0.43) in 2013. The total number of grizzly bears estimated to be in the DNA Study Area in 2012 was 91 females (95% CI 81 – 108) and 53 males (95% CI 47 – 66; Table 4.4-1). In 2013, the superpopulation was estimated to be 83 females (95% CI 80 – 91) and 65 males (95% CI 62 – 72; Table 4.4-2).

Table 4.4-2. Number of Female and Male Grizzly Bears Estimated in the DNA Study Area Using Mark-Recapture Analysis

Sex	Year	$\widehat{N}$	S.E.	Lower 95% CI	Upper 95% CI
Females	2012	91	6.6	81	108
Males	2012	53	4.6	47	66
Females	2013	83	2.8	80	91
Males	2013	65	2.4	62	72

$\widehat{N}$ represents super-population estimate

These results suggest a detection frequency of approximately 9-11 grizzly bears/1,000 km^2. A true density estimate is not possible because the geographic distribution of the superpopulation, which lies outside the study grid, and individual residency times are both unknown parameters.

5. DISCUSSION

The objective of the two year DNA study was to establish a baseline to support the long term monitoring of trends in the relative abundance and distribution of grizzly bears over time, as established by wildlife technical and community sessions in Yellowknife from 2009 to 2011. In addition, these data can support cumulative effects assessment and population management by the Government of the Northwest Territories – Department of Environment and Natural Resources. DNA analyses identified 114 grizzly bears (42 males and 72 females) in 2012 and 136 grizzly bears (60 males and 76 females) in 2013 within the 16,272 km^2 study area. Eight of these grizzly bears were also detected in study areas in Nunavut, demonstrating the large movement of barren-ground grizzly bears and the large home ranges they may utilize in a given year (or portions thereof over multiple years).

Sub-selection rules were applied only to high quality DNA samples that remained in each cluster after pre-screening. In 2012, the best sample from each cluster (approximately 1 in 3 samples overall) was analyzed to genotype. This reduced the potential to miss individuals due to sampling bias, and hence potentially underestimated the number of animals on the study area. In 2013, due to a 2.5-fold increase in the number of samples collected, the sub-sampling protocol changed to three samples per post and one ground sample for a total of 10 samples per post per session. The change in protocol did not appear to negatively bias individual detections as more bears were detected in 2013 compared to 2012, including 39 that were new to the regional database. In both years, the overall rate of successful DNA extraction was moderate (68-70%) compared to other grizzly bear work in similar areas (~80%). The strict quality thresholds used to pre-screen samples for analysis were expected to increase the success rates. The low success rate is potentially because of exposure to sunlight or moisture, which can degrade DNA samples. In 2012, every effort was made to ensure session duration was kept to approximately 10-11 days, but in some cases cells were left active for 12-15 days, which may have contributed to some sample degradation. However, in 2013, sample sessions were all approximately 10 days with little improvement in success rates. Nevertheless, the moderate success rates did not appear to impact the ability to detect individual grizzly bears.

The success rate of extracting DNA from underfur samples was poor in comparison to samples that used ≥2 guard hair roots. Underfur has a finer structure than guard hairs, which may make them more susceptible to environmental conditions. Furthermore, new underfur growth does not generally occur until late summer or fall, such that underfur collected in the spring or early summer are remnants from the previous year that may have naturally degraded.

To date, other studies in Nunavut utilized a 10x10 km study design (for example, the West Kitikmeot study across 40,000 km^2; M. Dumond, GN DOE, unpublished data). As a means to maximize study area size while maintaining cost efficiencies and simplifying logistics, this study implemented a 12x12 km grid cell size. During technical and community workshops hosted by ENR in Yellowknife from 2009 to 2011, there was uncertainty expressed over whether a 12x12 km study design would yield sufficient capture probabilities to provide precise estimates. The metric for success is a capture probability of 0.20. The mean capture probabilities were 0.22 and 0.35 in 2012 and 2013, respectively. On a session basis, only the first three sessions in 2012 had capture probabilities below 0.20, and one of these was likely due to a poor batch of fish oil. In addition, Apps

(2010) recommends a minimum of 50 grizzly bears to support a trend monitoring objective, with 100 grizzly bears suggested as the ideal threshold, which has been met in this study.

Incorporating traditional knowledge was a key element to the success of the program. Prioritizing the locations of sampling stations in areas that were identified by elders and experienced land users as high value habitat for grizzly bears increased the likelihood of encountering grizzly bears. Relocating sampling stations that were not successful at detecting grizzly bears in 2012 to new higher value habitats in 2013 may have also in part resulted in improved detection rates. It cannot be discounted that experience in running the program in terms of bait application and sample processing may have contributed to the substantial 2.5 fold increase in samples collected in 2013. The detection of 22 more grizzly bears and the addition of 39 new grizzly bears to the regional database resulted in improvements to capture probabilities during the latter half of 2012 and throughout 2013.

Barren-ground grizzly bears exhibit extensive movement patterns, which were observed for some grizzly bears in this study, and have the lowest densities and utilize the largest home ranges of all grizzly bear populations. The result is that grizzly bears may only visit portions of their annual range in any given year, which is difficult to account for in heterogeneity based models during an initial baseline inventory. An additional study design element that was utilized to address this dynamic of low densities and large movement rates was implementing six sessions per year over two years. The standard in British Columbia is three to four sessions, typically in one year (Apps 2010). In the West Kitikmeot, a design of two sessions per year over a period of five years was used. The number of new captures at the end of 2012, the rate of recaptures in 2013, and the addition of new grizzly bears to the regional database all contributed to higher capture probabilities, and demonstrate the success of this approach. Additionally, in a concurrent program southwest of Bathurst Inlet in Nunavut over a similar sized study area and utilizing the same study design (two years, six sessions per year, 12x12 km grid cells), 112 individual grizzly bears were identified, resulting in capture probabilities over 0.20 and detection frequencies of 7-9 grizzly bears per 1,000 km^2 (Rescan 2014a).

Photographic evidence suggests that DNA analysis may be underestimating the number of grizzly bears using the study area during the sampling period. Much of this discrepancy results from the incomplete detection of family groups. In 2012, camera data suggest at least 10 family groups were detected, compared to three possible family groups identified by DNA analysis. In 2013, four family groups were photographed but were all partially detected by DNA analysis. Hair from cubs and yearlings may not snag on the barbed wire as easily as adult hair, which could explain why camera data identified family units where DNA analysis did not. In cases where lone grizzly bears were not detected by DNA analysis, there were some events where the grizzly bear approached the post but did not scratch against it, and others where the sampling interval exceeded 12 days, which may have resulted in the degradation of the sample.

In both years, grizzly bears appeared to be concentrated in the northeastern half of the study area, in a band that extended from Yamba Lake in the northwest, along the north shore of Lac de Gas, and to Aylmer Lake in the southeast. Grizzly bear tripods were not placed near the mine sites in order to reduce the potential for human and bear interactions; however, incidental observations of grizzly bears are recorded at both sites and included in their respective annual wildlife monitoring reports.

The high frequency of grizzly bear detections correspond to a higher prevalence of water compared to the southwest portion of the study area. The extensive distribution of water bodies of varying sizes may provide extensive forage. Water may also afford some thermal relief for grizzly bears during warmer periods in the summer. In addition to water, there are extensive esker systems distributed throughout the same region of the study area, which facilitate movement across the landscape and contain ground squirrel burrows, another important prey item for grizzly bears (McLoughlin et al. 1999). Results from habitat modeling conducted for the summer range of the Bathurst herd indicate that this area contains high quality habitat for caribou during the post-calving and summer periods, which corresponds to the timing of the sampling period (Rescan 2014b, in prep). Significant predation of caribou by grizzly bears in the Arctic has been speculated, but currently not fully understood and warrants further investigation.

The maximum distance travelled by a male grizzly bear (85 km or 8.5 km/day) during the 2013 survey period was 30% higher than the maximum for a female bear calculated in 2012 (58 km or 5.3 km/day). A small sample size precluded in-depth analysis. Male movement rates are typically higher than females and may average an extra 2-3 km/day during the summer and late summer periods (McLoughlin et al. 1999).

This DNA study suggests that the central barrens of the Northwest Territories are productive for grizzly bears. The Lac de Gras region supports a large number of grizzly bears, potentially because of the prevalence of esker habitats for secure denning, seasonal access to caribou, fish resources in the abundant lakes and streams in the area, productive forage in riparian zones, and the relatively low level of hunting in this area. The density of barren-ground grizzly bears was estimated to be 3.5 bears per 1,000 km^2 for the central barrens of mainland Nunavut and the Northwest Territories (McLoughlin and Messier 2001), and up to seven bears per 1,000 km^2 in the Kitikmeot region of western Nunavut (M. Dumond, Government of Nunavut Department of Environment, pers. comm.) and a detection frequency of 7-9 grizzly bears per 1,000 km^2 (Rescan 2014a). In this study, detection rates were approximately 9-11 grizzly bears per 1,000 km^2. The calculation of an absolute density is likely to be lower as closure rules would necessitate the removal of transients and individuals at the periphery of the study area. Under a trend monitoring objective, assumptions regarding population closure are relaxed, and the focus is on the total number of grizzly bears that may use the study area during the sampling period ("superpopulation"). Bearing in mind the potential underestimate of grizzly bears in the DNA analysis, these results suggest that grizzly bear numbers appear to be at the upper range of those previously reported, and are stable and possibly increasing since estimates from the late 1990's.

6. RECOMMENDATIONS

The overall goal of the two year DNA program was to estimate the number of grizzly bears that are likely to occur in the Grizzly Bear DNA Study Area as a baseline for long term trend monitoring. There is interest amongst communities, regulators, and industry in developing a protocol for regional grizzly bear monitoring, given that site specific monitoring is ineffective at addressing population level effects due to the large movement patterns and low densities of barren-ground grizzly bears. Based on the results of this study, the following protocol is recommended as part of a long term monitoring strategy for grizzly bears in the NWT:

1. These programs are expensive and logistically challenging. They can only operate effectively and efficiently by establishing regional partnerships amongst industry, government, and communities.
2. The initial baseline inventory requires intensive effort to fully characterize the regional superpopulation. In future sampling efforts under a long term trend monitoring objective, the study area should remain the same to avoid sampling different segments of the superpopulation, but the sampling effort can be reduced. The change in effort can be addressed in subsequent modeling exercises, but the effects of changing the study area boundary cannot be quantified.
3. The Ekati/Diavik study area was an appropriate size to estimate the regional grizzly bear population, providing information that can inform management and cumulative effects assessment. Depending on density, these results suggest that a study area size of approximately 15,000 km^2 is required to detect 100 grizzly bears recommended as the basis for long term monitoring.
4. For northern grizzly bear populations that are at naturally low densities with individuals that range over vast distances, multiple sampling sessions across multiple years may be required to attain adequate data for statistical analyses as accurate population estimates are dependent on sufficiently high recapture rates (Proctor et al. 2010). Results in this study and a parallel study in Nunavut (Rescan 2014) suggest that six sessions per year over a two year study will yield a sufficient number of individuals and capture probabilities for statistical analysis.
5. A 12x12 km grid cell size is an appropriate size to successfully conduct a large scale grizzly bear mark-recapture DNA program. A 12x12 km grid cell size roughly corresponds to the 10-day range use of a female grizzly bear, and provides an effective trade-off in terms of study area size, cost, and logistics while achieving the requirement for capture probabilities above 0.20.
6. Relocating sampling stations every session is not recommended at this scale. Instead, introducing novel baits each session is an effective alternative to continuously attract bears to the sampling post.
7. Considerable upfront work is needed to identify areas to locate posts. The incorporation of traditional knowledge to develop a set of criteria for placing posts within cells will reduce the intensity of the desktop phase, and will increase capture success. As a general guide and

in order of priority, key areas include eskers, riparian areas, upland meadows, and heath tundra. If sampling stations are relocated within a cell, it is recommended that they be moved at least 2 km from the previous location, and are located at least 5 km from a sampling station in an adjacent cell.

8. The deployment of motion detection cameras throughout the study area is an effective means to monitor grizzly bear activity at the sampling posts, and provides a way to assess the sampling protocol and DNA analyses.
9. It is an expensive process to extract DNA and all hair samples cannot be analyzed. A number of sub-sampling protocols are available, including a 1-in-3 if sample sizes are not prohibitive. Given the possibility of multiple bears interacting with a post during a single session, three samples per post plus a ground sample will maximize detections in the case of large sample sizes. If budgets are constrained, two samples per post from the upper and lower half can be considered.
10. A robust design in MARK is the most appropriate to generate a population estimate for a multi-year grizzly bear DNA mark-recapture program. Options to examine heterogeneity and individual covariates can be explored to improve precision, if necessary.

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Definitions of the acronyms and abbreviations used in this reference list can be found in the Glossary and Abbreviations section.

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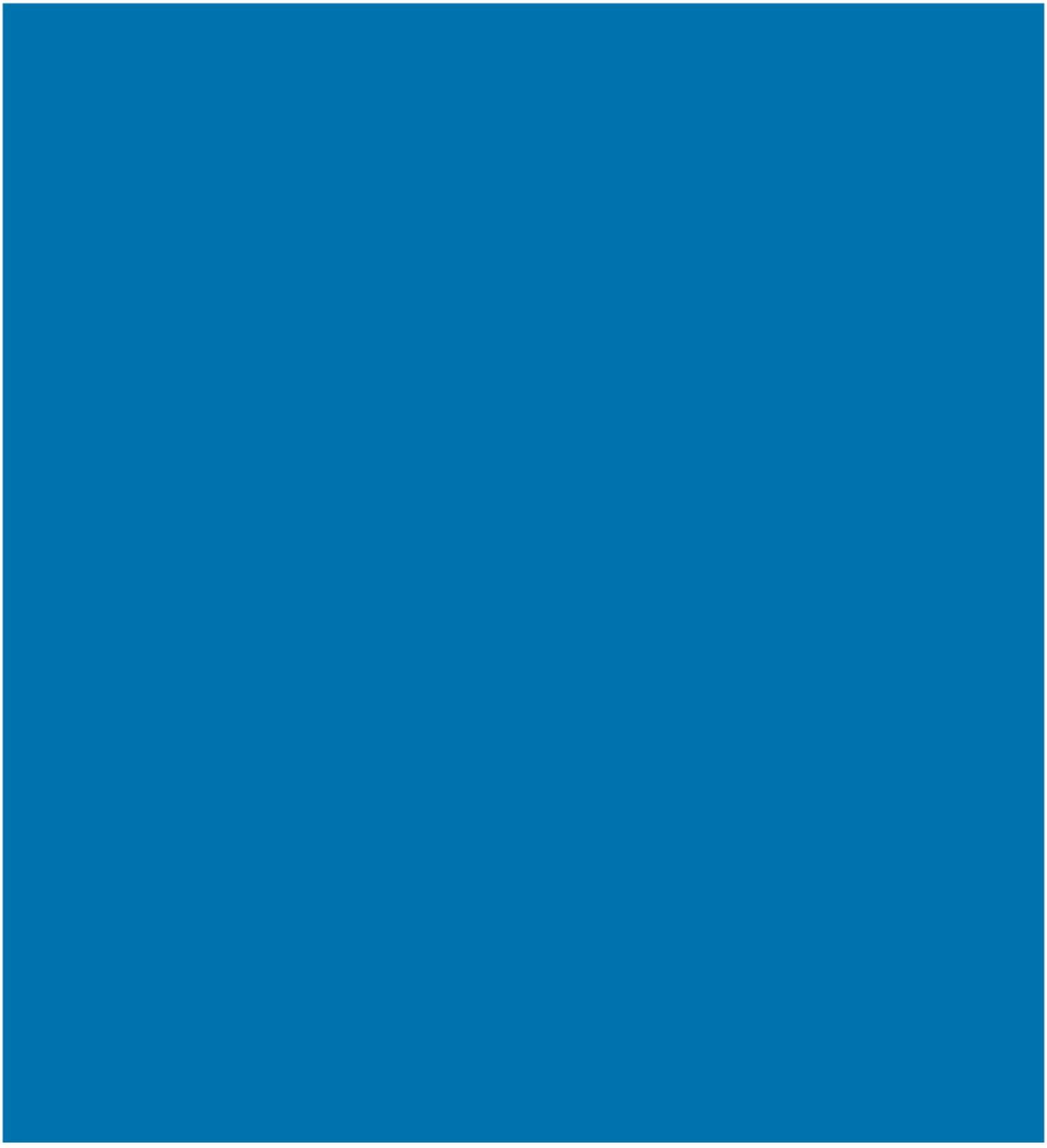

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#1102 – 4920 52nd Street, Yellowknife, NT, Canada X1A 3T1 T 867.669.6100 F 867.669.9293 www.ddcorp.ca