2015 Translocation Plan for Sierra Nevada Bighorn Sheep: A Focus on Strategic Planning

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Executive Summary

Sierra Nevada bighorn sheep have increased from 100 to 600 animals between 1995 and present, yet numbers and distribution remain below recovery goals. Translocations are required to reoccupy historic habitat and ensure the persistence of Sierra Nevada bighorn, a federally endangered subspecies (USFWS 2007). Here we present 2 phases of translocations planned for the next 10-20 years. The first phase of translocations will ensure the long-term viability of herds (populations) and recovery units (metapopulations) with small population sizes and also ensure that recovery criteria are met. The second phase of translocations increases connectivity within and between recovery units. Many of phase 2 translocations are not necessary to meet recovery criteria; however, these translocations will build metapopulation dynamics to improve population viability and genetic diversity in the absence of future management intervention. We anticipate completing phase 1 translocations in 5-10 years and phase 2 translocations within 10-20 years.

We analyze the risks and the likelihood of success of planned translocations. Our analyses indicate the 4 largest herds of Sierra bighorn can sustain removals over 10 years to support planned reintroductions and augmentations in the absence of heavy mortality from predation, disease, or weather. In populations where phase 1 translocations are planned, the risks of disease and predation are low, and there is sufficient suitable habitat. Phase 2 translocations, which are designed to increase connectivity, are based on the current distribution of Sierra bighorn; many of these translocations are planned for areas that currently have higher risk of disease through contact with domestic sheep and goats. Prior to implementation of phase 2 translocations, we will re-evaluate the risk of disease and distribution of Sierra bighorn to ensure that these translocations are necessary to increase connectivity without unduly increasing disease risk.

Currently, 2 populations, Laurel Creek and Taboose Creek, considered essential for recovery are not inhabited by reproducing ewe populations. However, separate sightings of ewes in the Taboose Creek herd unit suggest colonization or range expansion from the neighboring Sawmill Canyon herd. Thus, we will allow time for further colonization to occur in the Taboose Creek herd unit and proceed with other phase 1 translocations. In 2015, we plan to reintroduce Sierra bighorn to Laurel Creek in the Kern Recovery Unit and the Cathedral Range, a new herd unit added to the Northern Recovery Unit. We also plan to augment the small herds at Mt. Gibbs and Olancha Peak.

The Laurel Creek herd unit in the Kern Recovery Unit was selected for immediate reintroduction because populations in this recovery unit are isolated both from other recovery units and domestic sheep grazing allotments; thus, this herd will serve as a reservoir should disease spread throughout the more connected herds along the Sierra crest. The Cathedral Range was selected for reintroduction in 2015 because the Northern Recovery Unit needs an additional herd to reach recovery criteria. Historic detections, excellent summer habitat, and separation from domestic sheep, which have the potential to transmit disease, suggest that bighorn will thrive in this new herd unit. Augmentations to Mt. Gibbs and Olancha Peak are planned to increase genetic diversity in these small herds. At Mt. Gibbs we plan to create a new deme of high heterozygosity ewes at Alger Creek, and at Olancha Peak, we plan to add high heterozygosity rams to decrease the likelihood of inbreeding.

Table of Contents

I. Strategic Planning

Introduction

Sierra Nevada bighorn sheep (*Ovis canadensis sierrae*, *hereafter* Sierra bighorn) are a subspecies of wild sheep that is native to the southern portion of the mountain range for which they are named. In 1999, the U.S. Fish and Wildlife Service granted emergency endangered status to Sierra bighorn sheep inhabiting the central and southern Sierra Nevada of California as a distinct population segment (USFWS 1999a, 1999b). The final rule granting endangered status to the population was published in 2000 (USFWS 2000). While the population has grown to 600 in recent years, the current size and geographic distribution does not meet yet recovery objectives; thus, the population is still under threat from factors such as disease, predation, and weather.

Recovery goals for Sierra bighorn include recovery unit population size thresholds and distribution criteria. The Recovery Plan stipulates that 305 adult and yearling females be distributed among 12 of 16 geographic areas, referred to as herd units (Map 1) (Downlisting Criterion A1 and Delisting Criterion B2; USFWS 2007). Meeting these goals will ensure long-term viability of this genetically unique subspecies. The 12 herd units needed for recovery are designated as critical habitat. Currently, 10 of the 12 herd units are occupied. Delisting Criterion B1 in the Recovery Plan for Sierra bighorn recommends that Sierra bighorn persist in the 12 herd units without intervention for at least 7 years (USFWS 2007).

Translocations to reoccupy historic habitat and to meet recovery goals are identified as high priority tasks in the Recovery Plan, which recommends the use of “the limited number of Sierra Nevada bighorn sheep available for translocations in a way that maximizes recovery of Sierra Nevada bighorn sheep in the shortest period”. In 2013, California Department of Fish and Wildlife (CDFW) reintroduced Sierra bighorn to the Olancha Peak herd unit. The creation of the Olancha Peak herd represents the first reintroduction of Sierra bighorn to historical habitat since 1988 (Map 2). In 2014, another portion of historic habitat was re-occupied by translocating Sierra bighorn to the Big Arroyo herd unit (Map 2). These reintroductions are the first in a series of translocations planned with the goal of meeting Recovery Plan criteria for delisting as quickly as possible.

This translocation plan analyzes reintroductions proposed for currently unoccupied habitat and augmentations to supplement small existing herds of Sierra bighorn. This plan is divided into two sections: strategic planning and operational planning. The strategic planning section analyses the necessity of translocation, outlines all foreseeable translocations needed to delist Sierra bighorn and enhance metapopulation processes, addresses the risks of these translocations, and the likelihood of successful restoration. The operational planning portion of this document addresses specific translocations proposed for 2015 and includes a summary of logistical constraints.

Necessity of Translocation

The current distribution of Sierra bighorn is fragmented. The fragmented population structure is a result of natural causes and human disturbances that led to listing Sierra bighorn as endangered. The complex topography and the vegetation structure of the southern and central Sierra landscape, coupled with the intrinsic biology and behavior of bighorn sheep, results in a naturally fragmented distribution of animals (Bleich et al. 1990b). Conservative philopatric behaviors (reluctance to disperse from their home range) make bighorn slow to colonize unoccupied habitat (Geist 1967, 1971). Since the 1950s, translocation of bighorn sheep has been the primary means of reintroducing populations to vacant historic habitat and of augmenting small existing populations.

Prior to listing in 1999, a series of translocations between 1979 and 1988 reestablished 4 populations of Sierra bighorn significantly expanding their range (Map 2). Subsequently, 2 natural colonizations have produced persistent herds in the Bubbs Creek and Convict Creek herd units (Map 2). The series of translocations outlined in this plan (below) will ensure the long-term viability of Sierra bighorn by further restoring Sierra bighorn to their historic range and enhancing the viability of small existing populations.

Long-Term Objectives and Justification

This plan outlines translocations CDFW plans to conduct over the course of the next 10 to 20 years. Translocations are organized into 2 phases and analyzed in Table 1. This table describes the location and sex of animals of proposed translocations (left group of columns) and lists the purposes of the translocations: meeting Recovery Plan goals, increasing connectivity, population viability, genetic diversity, and occupied habitat, and creating refugia from disease (middle left set of columns). The table also identifies issues with proposed translocations such as predation, disease risk, habitat quality, and genetic isolation (middle right group of columns) as well as logistical constraints of translocations such as required National Environmental Policy Act (NEPA) analyses and the need for a transport helicopter to move large groups of bighorn to distant release sites (far right columns).

The first phase of translocations (top half of Table 1) focuses on actions that increase viability of either individual populations (herd units) or metapopulations (recovery units). Phase 1 translocations will reintroduce bighorn sheep to historic and currently unoccupied habitat in Laurel Creek in Sequoia National Park and the Cathedral Range of Yosemite National Park (Map 3); reintroductions will enhance metapopulation processes in the Kern Recovery Unit and Northern Recovery Unit, respectively. Translocations in phase 1 will also augment small existing populations in the Big Arroyo, Olancha Peak, Taboose Creek, Convict Creek, Mt. Gibbs, and Mt. Warren herd units (Map 3), thereby increasing the viability of these populations.

We anticipate accomplishing phase 1 actions within 5-10 years. Phase 1 translocations that produce viable herds of bighorn will meet Downlisting Criterion A1 and Delisting Criterion B2 (USFWS 2007), which set the abundance and distribution goals stated in the introduction of this document. While the Recovery Plan delisting goals and designated critical habitat do not include the Cathedral Range as one of the 12 essential herd units (USFWS 2007 and 2008), the Recovery Plan does set a goal of “a minimum of 50 yearling and adult females exist in the Northern Recovery Unit” (Downlisting Criterion A1). Demographic data from the 2 occupied herd units over the last 25 years suggest that an additional herd is necessary to meet this goal. Yosemite’s Cathedral Range is a suitable location for a new herd because it has numerous historical detections (Wehausen and Jones 2014), superb summer habitat, separation from domestic sheep which pose the threat of disease, adequate forage, and potential for connectivity with the Mt. Gibbs herd. With the translocations outlined here, we will likely reach the abundance and distribution goals stated in the Recovery Plan within the next 10 years.

Phase 2 translocations (Table 1 and Map 3) will also expand the distribution of Sierra bighorn and serve one of two major purposes: increasing connectivity or increasing occupied habitat. While many of the herd units required for recovery are currently occupied, the distribution of Sierra bighorn within those herd units is incomplete (Map 4). In many cases this limits potential colonization and gene flow among herds that are required to prevent degradation of the already limited gene pool of Sierra bighorn. Phase 2 translocations proposed for the Olancha Peak, Mt. Langley, Mt. Williamson, and Mt. Warren herd units will attempt to increase connectivity by creating new demes of bighorn at Cartago and Ash Creeks, Cottonwood Creek, Symmes and Pinyon Creek, and Lee Vining Canyon, respectively (Map 4; see Table C-1 in the Recovery Plan). Translocations in phase 2 will also increase occupied habitat by reintroducing Sierra bighorn to the Black Divide area of Kings Canyon National Park, repopulating the Coyote Ridge herd unit, and augmenting the Wheeler Ridge and Convict Creek herd units to create a new demes at Mt. Tom and McGee Creek, respectively (Map 4).

All of these translocations are to areas included in existing herd units and listed as critical habitat (USFWS 2008) except the reintroduction to the Black Divide. There are many reasons why a new population in the Black Divide will likely thrive. Its remote location provides separation from domestic sheep which pose the threat of disease. The Black Divide has one of the largest contiguous areas of predicted winter range west of the Sierra crest and abundant alpine summer habitat. Finally, summer, winter, and lambing habitat exist in adjacent areas along a continuous elevation gradient.

In many cases phase 2 translocations are not necessary to achieve Recovery Plan Downlisting and Delisting Criteria. However, phase 2 translocations are designed to increase connectivity and will enhance gene flow between neighboring herd units and recovery units which will preserve genetic diversity in Sierra bighorn a stated goal of the Recovery Plan (Recovery Action 4, USFWS 2007). Translocations designed to increase occupied habitat will expand the distribution of Sierra bighorn and consequently overall abundance to meet Recovery Action 3 (USFWS 2007).

The translocations proposed in this plan create new populations or increase the size of existing populations, often aiming to expand their range. As the abundance and distribution of Sierra bighorn increases, the risk and consequence of a disease outbreak will also increase. Greater connectivity between populations increases probability of disease transmission occurring between populations of Sierra bighorn. Thus, it will be important, while implementing the translocations proposed here, to focus efforts to minimize the probability of bighorn sheep contracting disease by completing the actions outlined in Recovery Action 2.3 of the Recovery Plan (USFWS 2007). These actions include preventing contact between bighorn and domestic sheep and goats and developing a disease response plan. These actions will also meet Recovery Criterion A2 (USFWS 2007).

Description of Augmentation/Reintroduction				Purpose						Issues							Logistics	
Recovery unit	Herd Unit	Location	Sex	Meet basic R.P. goals	Increase connectivity	Increase pop. viability	Max. genetic diversity with high het. sheep	Increase occupied habitat	Potential refuge from disease	Lion predation	Nearby domestic sheep	Low elev. winter habitat	Mid. elev. winter habitat	High elev. winter habitat	Limited summer habitat	Potential small isolated herd (genetic problems)	NEPA required	Transport helicopter required
Phase 1: **Increase Pop. / Metapopulation Viability**																		
Kern	Big Arroyo		F	x		x		++	x				x					
			M	x		x	x						x					
	Laurel		F+M	x		x	x	++	x				x					x[#]
Southern	Olancha		F	?		x				x		x			x	x		
			M	?		x	x					x		?				
	Taboose		F	x		x		+		x			x	x				
Central	Convict	Esha Pk herd	F			x					x			x				
Northern	Gibbs	Alger Cr	F	x		x	x	++					x	x				
	Warren		F	x		x	x			x	x		x	x				
	New	Cathedral Range*	F+M	x		x	x	++	x				x			x	x[1]	x[#]
Phase 2:																		
Increase Connectivity																		
Southern	Olancha	Cartago/Ash Cr.	F+M		x			+				x			x			
	Langley	Cottonwood Cr	F		x			+		x		x		x				
	Williamson	Symmes/Pinyon	F		x			+		x			x					
Northern	Warren	Lee Vining Cyn	F	x	x	x	x	++		x	x		x	x				
Increase Occupied Habitat																		
Southern	New	Black Divide*	F+M		x		x	++	x				x			x	x[2]	x
	Coyote		F		x			++		x		x		x				
Central	Wheeler	Mt. Tom	F		x			++		x			x		x			
	Convict	N.McGee Cr	F	?	x	x		++			x		x	x				

[1] NEPA for Cathedral Range will likely be complete by March 2015.

[2] No plans to begin NEPA.

* CDFW will have discussions with the USFWS prior to moving animals to these locations.

[#] Yosemite is covering costs for a transport helicopter for the Cathedral Range reintroduction. Non-governmental organizations are providing funds for a transport helicopter for Kern Recovery Unit translocations.

Table 1.

The table is broken into four groups of columns. On the left are identifiers that describe proposed translocations such as recovery unit, herd unit, location, as well as the sex of the animals that might be moved. Note that two of these locations, the Cathedral Range and Black Divide, define new herd units not identified in the Recovery Plan.

In the middle left are a set of columns that identify the purposes for moving sheep to these locations. The first concerns simply meeting occupancy and population goals in the Recovery Plan. Question marks denote uncertainties. For instance, the Central Recovery Unit already meets the numerical and distribution goals, but with only a southern portion of the Convict Creek herd unit occupied. The second column concerns increasing connectivity within or between recovery units. In most cases this is for locations that will increase gene flow between herd units, something also called for in the Recovery Plan. The third column concerns increasing populations to a more viable size where, for varying reasons, populations are small. In many cases this relates to population goals in the Recovery Plan. The fourth column is action that will specifically address genetic diversity issues, i.e. genetic rescue or maximizing genetic diversity in reintroduced or recently colonized herd units. Checks in this column imply that animals will be chosen based on their heterozygosity levels. The fifth column is increased distribution of these bighorn; + denotes a small increase and ++ denotes a large increase. In some cases that relates to specific Recovery Plan goals and in others it does not. The sixth column is the creation of more isolated populations that would be least likely to be infected by a respiratory disease epizootic.

On the middle right are columns that identify issues with potential translocations. First is potential lion predation at the site. Second is nearby domestic sheep. Next are 3 columns that identify if low elevation, mid elevation, or high elevation wind swept habitat is available. This is followed by a column for areas where alpine summer range is limited in quantity and quality. The final column concerns the potential to create a small isolated population that may suffer from inbreeding and genetic drift.

On the far right are columns that identify logistical constraints of translocations, the need for NEPA and the need for a transport helicopter to move bighorn to distant release sites. More information relative to these constraints can be found in the footnotes of the table.

Risk Evaluation

This analysis addresses impacts to source populations of Sierra bighorn and considers potential effects to other sensitive species and the ecosystem as a whole.

Helicopter Net-Gun Captures

CDFW will use helicopter net-gunning to capture Sierra bighorn for translocation. The U.S. Fish and Wildlife Service issued a biological opinion analyzing the effects of activities listed under the CDFW's Federal Fish and Wildlife Permit (i.e., Recovery Permit) and determined that these activities and the methods used to carry out these activities, namely helicopter net-gun captures, would not jeopardize the continued existence of Sierra bighorn (USDI 2011). Guidelines provided by the Northern Wild Sheep and Goat Council and the Desert Bighorn Council describe the steps necessary for a successful capture and state that helicopter net-gunning is the most commonly used capture technique, followed by drop-nets, drive-nets, and darting (Foster 2005). Kock et al. (1987) compared the success rate of 4 capture methods (drop-net, drive-net, net-gun, and darting) on 644 bighorn sheep in the western United States. The net-gun was found to have considerable advantages over the use of ground nets and chemical immobilization, and the net-gun method had the lowest proportion of injured or killed bighorn sheep, had no capture myopathy (CM) mortality, and resulted in 2% (2/137) accidental mortality. Other studies (Jessup et al. 1988) and captures of Sierra bighorn have had similar results. Since October 2011 CDFW has contracted wildlife capture specialists Leading Edge Aviation, and the average capture-related mortality rate for Sierra bighorn was 3.4% (less than 1 individual per year; Stephenson et al. 2012). This mortality rate falls below the amount of take (3 bighorn / year) authorized under the Recovery Permit issued by the U.S. Fish and Wildlife Service. As mentioned previously, the U.S. Fish and Wildlife Service determined that this amount of take would not jeopardize the continued existence of the Sierra bighorn. Additionally, CDFW will cease any operations if they result in take that exceeds the amount identified in the U.S Fish and Wildlife Service's biological opinion and Recovery Permit pending re-initiation with the Service.

Population Viability Analysis: Source Populations

We performed population viability analyses to determine the effects of harvesting ewes for translocation from source populations. We constructed a stochastic, discrete time, stage-structured matrix model (Cahn 2011) and based estimates of demographic rates on data collected from 1999–2014. Because bighorn sheep are polygynous (Geist 1971), population growth rates are determined by the number of reproducing females. Thus, we restricted the model to females (Morris and Doak 2002). The model was based on 4 approximate life stages: 2 juvenile and 2 adult stage classes (Cahn 2011 and Johnson et al. 2010). We incorporated a ceiling model of density dependence only in the survival of the youngest class and used 100 bighorn sheep for carrying capacity (Cahn 2011). To incorporate environmental variation, we generated random values of vital rates by parametric bootstrapping. We also incorporated demographic stochasticity in survival and reproduction (Mills and Smouse, 1994). For each model we ran 1,000 iterations and calculated probabilities for the following outcomes: 1) 5 ewes as a quasi-extinction threshold, 2) 15 ewes as the number of animals below which demographic stochasticity and genetic stochasticity may contribute to an extinction vortex (Morris and Doak 2002), 3) 25 ewes as the Recovery Plan target for each population, and 4) 25 ewes for more than 7 years to represent realization of delisting goals.

We modeled harvests from source populations over a 10 year period removing 10-15 ewes every third year (Table 2). While long-term operational guidelines allow for removals every other year (see below), we prefer to harvest animals for translocation every 3 years to prevent potential demographic effects that may result from perturbations to social structure. This removal strategy predicts that 170 females will be removed from 4 populations over the next 10 years (Table 2).

Table 2. Projected female population size (N) for all age classes with removals for translocation stock as indicated by year.

		Baxter	**Langley**	**Sawmill**	**Wheeler**	**Totals**
2015	remove	10	15	0	0	**25**
	$\hat{N}$	58	60	53	61	
2016	remove	0	0	15	10	**25**
	$\hat{N}$	50	51	57	63	
2017	remove	0	0	0	0	**0**
	$\hat{N}$	51	54	46	55	
2018	remove	15	15	0	0	**30**
		53	58	47	56	
2019	remove	0	0	0	15	**15**
	$\hat{N}$	40	47	51	57	
2020	remove	0	0	15	0	**15**
	$\hat{N}$	41	49	55	44	
2021	remove	10	15	0	0	**25**
	$\hat{N}$	43	52	43	45	
2022	remove	0	0	0	10	**10**
	$\hat{N}$	35	41	45	37	
2023	remove	0	0	0	0	**0**
	$\hat{N}$	36	42	47	38	
2024	remove	0	10	15	0	**25**
	$\hat{N}$	37	45	50	39	
	Totals	**35**	**55**	**45**	**35**	**170**

Table 3 shows the projected effects of removals on the source populations over a 5-year, 10-year and 20-year time span. Over the 20 years in which population size was projected by the demographic model, removals every third year for 10 years decreased the probability of reaching recovery goals by 25-30% in each population (Table 3). The probability of source populations declining to less than 15 individuals, a threshold below which populations are more susceptible to stochasticity, increases by 20-27% (Table 3). After removal of 170 females (Table 2), up to 100 of which are needed to complete phase 1 translocations and meet recovery goals, source populations are predicted to recover and reach delisting goals with an additional 10-20 years of population growth (data not shown). The removals modeled here are more than we anticipate needing to implement phase 1 translocations, which we will likely accomplish within 5-10 years. We will monitor the demographic effects of removals for translocation and other stochastic factors like weather and predation to employ adaptive management for source herds; this will ensure that source populations do not experience undue risk of decline.

The modeled variability in survival rates incorporated predation to the extent predation occurred during the data-collection period (1999-2014). During this period, mountain lions were responsible for 90% of the known predator kills of bighorn ewes (28 of 31). During 2007 and 2008, 11 ewes were killed by mountain lions in the Mt. Baxter and Sawmill Canyon herds, and in 2008 the annual survival rate of collared ewes at Mt. Baxter declined dramatically (Stephenson et al. 2012). This predation prevented growth of the Mount Baxter herd for several years (Stephenson et al. 2012). Consequently, predator management focused on removing specific mountain lions documented to have killed Sierra bighorn.

Table 3. Projected probabilities of attaining various population sizes in existing populations intended to serve as sources of translocation stock. Probabilities are calculated using a stochastic density dependent model projected for 20 years for female Sierra Nevada bighorn sheep. Removal of individuals for translocation represents sustainable harvests during the next 10 years based on actual demographic rates for each population. Population projections are based on demographic data collected 1999-2014 in the Sierra Nevada mountains.

Source Population and Translocation Details	Yr	Pr (N<5)	Pr (N>15)	Pr(N>25)	Pr (N>25 for >7 consecutive yr)
Wheeler Ridge					
no removals	5	0	0.998	0.969	NA
	10	0	0.989	0.958	0.944
	20	0.004	0.966	0.923	0.975
with removals	5	0.048	0.853	0.695	0
	10	0.126	0.712	0.571	0.647
	20	0.153	0.756	0.633	0.693
Mt. Baxter					
no removals	5	0.001	0.988	0.937	NA
	10	0.002	0.976	0.913	0.896
	20	0.011	0.945	0.896	0.942
with removals (see Table 2)	5	0.061	0.842	0.686	0
	10	0.174	0.684	0.54	0.479
	20	0.204	0.708	0.599	0.592
Sawmill Canyon					
no removals	5	0.01	0.95	0.889	NA
	10	0.027	0.907	0.826	0.812
	20	0.07	0.875	0.8	0.898
with removals (see Table 2)	5	0.049	0.891	0.807	0
	10	0.297	0.577	0.487	0.598
	20	0.336	0.608	0.532	0.641
Mt. Langley					
no removals	5	0	0.996	0.986	NA
	10	0	0.995	0.974	0.974
	20	0	0.994	0.979	0.994
with removals (see Table 2)	5	0.032	0.925	0.811	0
	10	0.206	0.666	0.538	0.589
	20	0.216	0.738	0.669	0.652

Removing mountain lions reduced predation rates of Sierra bighorn. If in the future mountain lion predation on Sierra bighorn increases and is not controlled in a similar manner, demographic rates for source populations may decline. If such declines occur, the populations at Mt. Baxter and Sawmill Canyon may not support removals for translocation. For each source population from which we are no longer able to harvest, source stock for translocations decreases by 25%. These circumstances could prolong the time needed to reach delisting goals because lower rates of population growth and fewer source herds would produce fewer surplus animals for reintroductions and augmentations. To enable a response to increased predation that may threaten sources of translocation stock, we are developing a predator management plan.

Sensitive Species

The translocations proposed in Table 1 will occur on lands managed by the Inyo National Forest, Yosemite National Park, and Sequoia and Kings Canyon National Parks (SEKI). SEKI evaluated the impacts of helicopter net-gun captures and translocations (USDI NPS, 2011) and concluded that there would be short-term moderate adverse effects on wildlife, due primarily to disturbance from helicopter use. The analyses also determined that there would be long-term beneficial effects on wildlife by restoring a species into previously occupied habitat. Within Yosemite National Park, rare plants are likely to occur within portions of the area where translocations are proposed, particularly on metamorphic features. One rare species, Claytonia megarhiza, may occur on generally north-facing scree slopes between and bordering rock outcrops in sites very likely to be preferred bedding sites for bighorn and where trails are likely to form from regular use by bighorn. Reintroduction of Sierra bighorn to areas supporting rare plants like Claytonia megarhiza would likely impact individual plants, but the presence of Sierra bighorn would be unlikely to have population-level effects (P. Moore, personal communications).

The U.S. Forest Service evaluated the potential impacts of translocations on Forest Service Pacific Southwest Region sensitive aquatic, plant, and wildlife species (Murphy and Sims 2011 and Weis 2011). This analysis identified potential habitat for 2 sensitive wildlife species, Sierra Nevada red fox (*Vulpes vulpes necator*) and wolverine (*Gulo gulo*) (Murphy and Sims 2011). The U.S. Forest Service determined that translocation activities would have negligible effects at the species level because of the short duration of potential impacts from noise and the presence of a helicopter (Murphy and Sims 2011). The U.S. Forest Service also determined that translocations of Sierra bighorn may impact individuals but would not lead toward federal listing or a loss of viability for the following special status plant species: *Arabis tiehmii, Astragalus ravenii, Botrychium lineare, Botrychium lunaria, Botrychium minganense, Carex tiogana, Cordylanthus eremicus var. olanchense, Draba asterophora var. asterophora, Eriogonum wrightii var. olanchense, Lupinus padre-crowleyi, Monardella beneolens, Streptanthus gracilis, Trifolium dedeckerae,* and *Draba sharsmithii*. Specifically, the U.S. Forest Service concluded that the timing of the helicopter capture flights, the limited number of landings, the short duration of the activities, the small number of animals to be translocated, and the normal use patterns of bighorn would result in minimal potential impacts (Weis 2011).

Likelihood of Success of Translocation

Translocation of bighorn sheep is the primary means of reoccupying historic habitat. Many reintroductions in the western U.S. have consisted of groups of 12 to 40 animals (Singer et al. 2001). The minimum number suggested for reintroduction is 20 (Wilson and Douglas, 1982). Limited numbers of Sierra bighorn are available for translocations. For example, during the last large translocation program between 1979 and 1988 approximately 90 Sierra bighorn were translocated in groups of 8-25 animals to reoccupy historic habitat in the Mt. Langley, Wheeler Ridge, and Mt. Warren herd units (Bleich et al. 1990a and Stephenson et al. 2012). It will be important to utilize translocation stock in a way that maximizes recovery in the shortest period while minimizing risk to existing herds of Sierra bighorn.

Population Viability Analysis: Recipient Populations

We performed population viability analyses to determine the probability of successful reintroduction with varying augmentation regimes. Similar to the models presented for the source populations, the recipient models are based on females only (see above Population Viability Analysis: Source Populations for methods). For recipient populations we modeled 4 different cases: 1) a single translocation consisting of 10 pregnant ewes and 5 rams (rams not included in model), 2) the initial reintroduction of 10 ewes and additional augmentation of 5 pregnant ewes at year 3, 3) the initial reintroduction of 10 ewes and additional augmentation of 10 pregnant ewes at year 3, and 4) the initial reintroduction of 10 ewes and two additional augmentations of 5 pregnant ewes at year 3 and year 5. Two demographic rates were modeled representing the best and worst case scenarios based on observed demographic patterns of Sierra bighorn: positive population growth ($\lambda = 1.018$) using demographic rates from Mt. Langley and negative growth ($\lambda = 0.991$) using demographic rates from the Mono Basin (Mt. Warren and Mt. Gibbs). Lambda for reintroduced (i.e., recipient) populations was calculated using the vital rates from these populations, and population estimates were projected for 20 years.

In Table 4 the results show that with positive population growth and a single translocation of 10 ewes the probability of achieving delisting goals in 20 years is 0.37. Augmentation of 10 additional ewes in a single translocation or 2 augmentations of 5 ewes each increases the probability of reaching delisting goals in 20 years to 0.76 or 0.71, respectively (Table 4). If reintroduced populations were to experience negative growth, an augmentation of 10 ewes would increase the probability of achieving delisting goals; however, the probability of reaching delisting goals in 20 years is only 0.17. This scenario, of negative population growth, presents a dilemma. If the long-term trends are truly negative, the population would be a sink and require periodic influxes to remain viable. Under this scenario, larger-scale (Sierra wide) metapopulation dynamics, not modeled here, would be required to support long-term population viability (Rung et al. 2006).

Based on these population viability analyses, we have determined that the most successful strategy for reintroducing Sierra bighorn is to reintroduce 10 ewes as an initial population followed by 10 additional ewes in one or two subsequent augmentations. The first augmentation will occur within two years following the initial reintroduction (see below Long-Term Operational Guidelines). While a single augmentation of 10 ewes produces a population with a slightly higher probability of reaching delisting goals than 2 augmentations of 5 ewes each, there is less risk associated with augmenting new populations twice with smaller ewe groups. This strategy avoids placing large numbers of animals in a novel environment in one winter when stochastic weather events may cause significant mortality. Fortunately, we have not observed significant translocation associated mortality in the 41 ewes that were translocated since listing in 1999. The annual survival rate of these ewes for the two years after translocation is greater than 95% which is slightly higher than the annual survival rate of non-translocated ewes. The strategy of two smaller augmentations also provides behavioral advantages allowing ewes to learn migratory routes and patterns of habitat use from which newly translocated animals may benefit.

Table 4. Estimated probabilities of attaining various levels of females in reintroduced populations. Population projections are based on demographic data collected 1999-2011 in the Sierra Nevada mountains. Positive growth is based on demographics from the Mt. Langley population and negative growth is based on the Mono Basin populations. Probabilities listed represent: 1) 5 ewes as a quasi-extinction threshold, 2) 15 ewes as the number of animals below which demographic stochasticity and genetic stochasticity may contribute to an extinction vortex (Morris and Doak 2002), 3) 25 ewes as the Recovery Plan target for each population, and 4) 25 ewes for more than 7 years to represent realization of delisting goals.

Demographic Rates and Translocation Details	**Yr**	**Pr (N<5)**	**Pr (N>15)**	**Pr(N>25)**	**Pr (N>25 for >7 consecutive yr)**
Positive Growth (λ =1.018)					
10 ewes start, no augmentation	5	0.025	0.461	0.034	NA
	10	0.055	0.617	0.289	0.004
	20	0.091	0.767	0.581	0.369
10 ewes start, +5 year 3	5	0.006	0.758	0.234	NA
	10	0.016	0.794	0.51	0.084
	20	0.027	0.866	0.713	0.589
10 ewes start, +10 year 3	5	0	0.915	0.54	NA
	10	0.005	0.929	0.726	0.332
	20	0.017	0.937	0.853	0.761
10 ewes start, +5 year 3, +5 year 5	5	0.003	0.914	0.484	NA
	10	0.008	0.882	0.667	0.288
	20	0.023	0.904	0.796	0.714
Negative Growth (λ =0.991)					
10 ewes start, no augmentation	5	0.042	0.162	0.001	NA
	10	0.155	0.178	0.02	0
	20	0.349	0.194	0.053	0.02
10 ewes start, +5 year 3	5	0.013	0.484	0.039	NA
	10	0.064	0.427	0.101	0.008
	20	0.205	0.361	0.14	0.092
10 ewes start, +10 year 3	5	0.004	0.776	0.217	NA
	10	0.027	0.63	0.271	0.068
	20	0.136	0.465	0.224	0.216
10 ewes start, +5 year 3, +5 year 5	5	0.004	0.765	0.173	NA
	10	0.025	0.598	0.203	0.057
	20	0.139	0.434	0.197	0.169

Genetic Variability

Sierra bighorn are recognized for their genetic uniqueness as a subspecies; therefore, recovery efforts for this taxon are ultimately about conserving and enhancing this unique gene pool. Genetic drift erodes gene pool diversity over time when, by chance, alleles drift to lower frequencies and then disappear. The populations most vulnerable to erosion of gene pool diversity by genetic drift are those that are smaller and with higher isolation (less gene flow). Recent microsatellite data were compiled for Sierra bighorn herds that have been sampled, as well as for a variety of populations of desert bighorn sheep for comparison (Table 5). For the average number of alleles per locus (A), Sierra bighorn have the lowest genetic diversity of the populations sampled. When the frequency distribution of those alleles is also considered, Sierra bighorn are joined at the bottom by the Pilares and Red Rock captive herds relative to effective number of alleles (A_E) and expected heterozygosity (H_E -- heterozygosity expected at Hardy Weinberg equilibrium; Table 5). These microsatellite analyses and bottleneck tests (J.D. Wehausen, unpublished data) of Sierra bighorn indicate that a considerable amount of genetic diversity has been lost. Further, Johnson et al. 2011 found a heterozygosity-fitness correlation suggesting that

Table 5. Population genetic statistics for Sierra bighorn and desert bighorn populations. N = sample size, H_O = average observed heterozygosity, H_O Range = range of individual observed heterozygosities, CV = the coefficient of variation of individual heterozygosities, H_E = expected heterozygosity (at Hardy Weinberg equilibrium; Nei 1987), A = average number of alleles per locus, A_E = effective number of alleles (number of alleles at equal frequency that would produce the observed homozygosity), Fixed = the number of invariant loci.

Herd/loci	ST	N	H_O Range	H_O	CV	H_E	A	A_E	Fixed
17 loci									
Sierra Nevada									
Gibbs	CA	12	0.059-0.588	0.363	41.3	0.316	1.9	1.6	4
Langley	CA	21	0.235-0.706	0.443	25.5	0.422	2.4	1.9	1
Wheeler Ridge	CA	52	0.235-0.765	0.480	24.9	0.467	2.6	2.0	1
Warren	CA	22	0.235-0.765	0.479	24.7	0.436	2.5	2.0	1
Baxter/Sawmill	CA	26	0.294-0.706	0.489	24.5	0.484	2.6	2.1	1
Williamson	CA	20	0.412-0.765	0.556	17.9	0.476	2.6	2.1	1
Desert									
Pilares (captive)	MX	10	0.235-0.529	0.412	27.1	0.436	2.9	2.0	1
Red Rock (captive)	NM	27	0.235-0.824	0.616	24.9	0.482	3.5	2.1	0
Upper San Juan River Cyn.	UT	12	0.529-0.823	0.651	16.9	0.578	3.1	2.5	0
Different 17 loci									
Sierra Nevada									
Gibbs	CA	12	0.176-0.588	0.353	46.1	0.303	1.9	1.5	4
Langley	CA	21	0.235-0.647	0.451	25.9	0.439	2.4	1.9	1
Warren	CA	22	0.235-0.765	0.500	25.3	0.445	2.5	2.0	1
Wheeler Ridge	CA	52	0.235-0.765	0.490	24.4	0.472	2.6	2.0	1
Baxter/Sawmill	CA	26	0.294-0.765	0.491	23.5	0.474	2.6	2.1	1
Desert									
Pilares (captive)	MX	10	0.235-0.588	0.453	27.9	0.469	3.1	2.2	1
Red Rock (captive)	NM	27	0.353-0.823	0.521	25.5	0.493	3.7	2.2	0
Spring Range, Brownstone Bas.	NV	17	0.412-0.824	0.578	23.5	0.608	4.3	2.8	0
Spring Range, Little Devil Pk.	NV	19	0.353-0.941	0.622	22.2	0.580	4.3	2.7	0
River Mts.	NV	46	0.353-0.882	0.639	23.1	0.635	4.8	3.0	0
Castle Mts.	CA	19	0.471-0.882	0.656	18.9	0.614	4.4	3.0	0
Highland Range	NV	20	0.412-0.941	0.685	18.3	0.659	4.5	3.1	0
Eldorado Mts., Goldstrike Cyn.	NV	20	0.529-0.882	0.674	18.2	0.638	4.6	3.0	0
McCullough Range	NV	23	0.471-0.882	0.683	18.1	0.661	4.6	3.1	0
Muddy Mts.	NV	34	0.353-0.824	0.623	16.9	0.591	4.4	2.8	0
Black Mts.	AZ	38	0.471-0.824	0.636	16.3	0.641	4.4	3.0	0
Upper San Juan River	UT	12	0.471-0.823	0.670	14.1	0.588	3.2	2.6	0
Newberry Mts.	NV	15	0.529-0.882	0.718	13.8	0.663	4.7	3.2	0
Eldorado Mts., Black Cyn.	NV	20	0.529-0.765	0.653	10.2	0.659	4.6	3.2	0

genetic diversity has declined far enough that Sierra bighorn at the lower end of the heterozygosity spectrum may be less fit. This presents the challenge of whether it might be possible to increase heterozygosity levels in small and reintroduced populations to enhance their population fitness and success.

Management actions have the greatest influence on genetic diversity when populations are small and founder effects can be manipulated. Bringing in animals from outside populations, such as desert or Rocky Mountain bighorn, is not recommended because one of the stated goals of the Recovery Plan is to preserve the genetic uniqueness of Sierra bighorn (Recovery Action 4, USFWS 2007). Also there is risk of outbreeding depression for sheep that appear to be adapted to very different habitats.

Careful genetic planning for translocations can maximize genetic diversity within small herds by efficiently utilizing the limited sources of Sierra bighorn translocation stock. Helicopter net-gunning allows selective captures of individual sheep, and modern methods of genetic analysis allow relative levels of heterozygosity to be measured for individual bighorn. With the microsatellite loci currently available, our estimates of heterozygosity may have up to 20% error; thus, ideally we would select individuals with observed heterozygosity greater or equal to 0.7 to ensure above average heterozygosity. Because translocation stock is limited, we will select individuals with observed heterozygosity greater than 0.6 to bias genetic diversity in an upward direction.

This analysis is separated into 2 topics: translocations for reintroductions and augmentation of existing herds for genetic rescue.

Reintroductions

Laurel Creek, the Cathedral Range, Coyote Ridge, and the Black Divide are areas where Sierra bighorn may be reintroduced to unoccupied habitat (Table 1). Each of these herd units will likely be peripheral populations with limited sources of gene flow. This and the potential for faster growth because of higher fitness of females are reasons to initiate herds with the highest genetic diversity in these areas. The ability to selectively capture individuals with known levels of heterozygosity opens the door to potentially initiate herds with higher genetic diversity than existing herds. Various authors have recommended that large numbers of bighorn sheep be used in reintroductions to maximize the sampling of genetic diversity in the new herd and reduce founder effects (Fitzsimmons et al. 1997, Griffiths et al. 1982, and Wolf et al. 1996). However, Sierra bighorn translocation stock is both limited by the number of animals available and the genetic diversity of those animals. With a selective approach it may be possible to initiate herds with fewer animals in such a way that increases genetic diversity by maximizing the number and distribution of alleles in the founding gene pool.

There are currently 4 herd units, Mt. Langley, Mt. Baxter, Sawmill Canyon, and Wheeler Ridge that are of sufficient size to provide animals for translocation. Genetically these sources of translocation stock can be considered 3 populations because the Mt. Baxter and Sawmill Canyon herd have contiguous habitat within which rams frequently move; consequently, these two herds represent 1 gene pool. The Mt. Langley and Wheeler Ridge herd units stem from reintroductions in 1979-88 from the Mt. Baxter/Sawmill Canyon gene pool (Map 2). Variation in observed heterozygosity in each herd is high (Table 6) and an ANOVA of those heterozygosity values found no difference among samples from these 3 gene pools (F = 0.787; *P* = 0.458). These data suggest that individuals from all 3 gene pools could be used for translocation stock. However, expected heterozygosity indicates that at Hardy Weinberg equilibrium the herds (Wheeler Ridge, Mt. Langley, and Mt. Warren) created through translocations from the Baxter/Sawmill gene pool all will have less genetic variation than the source gene pool (Table 6). This is also evident in the effective number of alleles (Table 6) where the sampling of the Baxter/Sawmill gene pool identified more alleles than in the reintroduced herds. For the potential sources of translocation stock, Mt. Langley is the most extreme, missing 4 alleles out of 53 total alleles (7.5%) present in analyzed loci. In contrast, Wheeler Ridge is missing only 1 allele (1.9%) in the current sampling. If 1 of these reintroduced herds were used unselectively to create new herds, there is the risk of further reducing genetic diversity. Consequently, 19 variable microsatellite loci were used to investigate the genetic consequences of potential reintroduction approaches. To explore different genetic management options and their relationship with observed and expected heterozygosities, we simulated the genetics for two scenarios of the founding population: 1) individuals were selected for high observed heterozygosity values and 2) individuals were selected at random from each of the 3 gene pools of translocation stock. Results for both of these samplings are presented in Table 6 along with statistics for each of the 3 translocation source gene pools.

When a biased population is created with individuals selected for high heterozygosity, the result is a population with a large heterozygosity excess relative to H_E (Table 6). However, the numbers of alleles in the Sierra bighorn population limit what the heterozygosity level will be at Hardy Weinberg equilibrium, which is reflected in the H_E values. To the extent that more heterozygous individuals may have a higher fitness, this might be advantageous in maximizing early population growth. Faster initial population growth is desirable for both demographic and genetic reasons. However, it needs to be recognized that the population will not maintain that initial level of heterozygosity when equilibrium is reached (compare H_O to H_E, Table 6). Nevertheless, this approach does produce a founding population with a higher H_E than any of the source populations (Table 6).

Table 6. Founding populations of 11 and 18 Sierra bighorn were selected, constituting individuals with the highest heterozygosity levels for the 19 loci measured. In contrast, 6 Sierra bighorn from each of the 3 gene pools were randomly selected without replacement from the pool of currently sampled animals to make a total of 18 Sierra bighorn. This random sampling was carried out 10 times and population genetic measures were obtained for each sampling.

Herd or Subsample	**N**	**H_O Range**	**H_O**	**H_E**	**A**	**A_E**
Sierra Nevada Source Herd						
Langley	21	0.210-0.737	0.471	0.457	2.5	2.0
Baxter/Sawmill	26	0.263-0.737	0.504	0.508	2.7	2.1
Wheeler	52	0.263-0.789	0.511	0.495	2.7	2.1
Averages			0.495	0.487		
Subsamples						
11 highest heterozygosities	11	0.684-0.789	0.718	0.536	2.7	2.3
18 highest heterozygosities	18	0.623-0.789	0.684	0.537	2.7	2.3
Random draws (18 sheep from diff. herds)	10	Averages:	0.496	0.497	2.65	2.1
		Lowest	0.436	0.487	2.6	2.0
		Highest	0.529	0.520	2.7	2.2

At the other end of the spectrum, random sampling from the 3 gene pools provide a glimpse at what the genetic structure of a founding population might look like with no selectivity. As might be expected, the average H_O is very close to the average of the 3 gene pools sampled. However, this is not the case for H_E. Instead, the lowest value obtained equals the average of the 3 gene pools sampled, and the highest exceeds any of those of the source gene pools (Table 6). This reflects the advantage of mixing samples from 3 different gene pools that have drifted apart, resulting in different allele frequencies that complement each other when combined. Thus, a strategy of sampling equally from these 3 gene pools produces populations biased toward greater genetic diversity. Even so, the average H_E from these 10 random samples is lower than that of the Baxter/Sawmill gene pool.

Given the already-compromised genetic diversity in Sierra bighorn, a goal for reintroductions is to create herds with H_E values at least as high as the Baxter/Sawmill gene pool. Between the 2 extreme approaches to reintroductions presented in Table 6 lie many possible strategies. Greater selectivity in the individuals used to initiate a population should allow for fewer animals to be used to represent variation in the gene pool, but the downside of a smaller founding population is that matings between close relatives are more likely to occur, and such inbreeding can negate the advantages of the initial selectivity. Another possible strategy would involve randomly selecting the females for reintroductions, but being very selective in the heterozygosity levels of rams for the first generation. This strategy was explored by simulating breeding between a single dominant high heterozygosity male and 10 ewes randomly selected from a single source population. The H_O of the 10 lambs produced from this simulated mating was calculated, and the simulation was repeated 1,000 to times to generate average H_O. Table 7 shows that in general, the H_O of F1 lambs are higher when higher heterozygosity rams do the breeding. However, selecting the highest heterozygosity ram does not necessarily produce the highest heterozygosity lambs. In several simulations, the F1 lambs have more genetic diversity than would be expected when mating occurs with a ram of lower genetic diversity from a different source population than the ewes (compare the heterozygosity of lambs produced by Wheeler ram S233 and Baxter/Sawmill ewes and that produced by Sawmill rams S202 and S259 breeding ewes from the same population). Table 7 also shows that any of the 3 genetic source populations have sufficient genetic diversity to allow random selection of ewes for reintroductions as long as rams are selected from different source populations.

Table 7. Averaged observed heterozygosity of lambs produced by 1,000 iterations of simulated breeding between a selected high heterozygosity ram and 10 randomly selected ewes from a single source population.

		Selected Ram						
		Sawmill	Sawmill	Sawmill	Wheeler	Baxter	Bubbs	Langley
		S202	S259	S200	S233	S196	S193	S210
		0.75	0.6875	0.625	0.625	0.625	0.5	0.5
Source Ewes	Bax/Saw(0.530)	0.518	0.545	0.583	0.582	0.54	0.527	0.487
	Wheeler (0.514)	0.546	0.562	0.557	0.566	0.534	0.48	0.487
	Langley (0.475)	0.485	0.563	0.634	0.569	0.55	0.486	0.42

A further issue is the potential effect on each source population gene pool of selectively removing individuals with the highest heterozygosity. Based on the combination of factors discussed above including capture logistics, the focus for initial reintroductions will be that of randomly selecting largely uncollared females and selecting males of known genotypes with high heterozyosity from various herds. We will attempt to further select rams such that the founding population of rams has a staggered age structure. This should reduce the probably that a ram will breed his daughters. If multiple populations are initiated within a short time period, rams of high heterozygosity may be used sequentially in multiple herds to further prevent rams from breeding their daughters. Whenever possible, subsequent augmentations will utilize translocation stock from herds other than those used in the initial reintroduction and select individuals with alleles absent or present at low frequencies in the founding population.

Augmentations

It is at small population sizes that we can have the greatest influence on genetic population structure by adding high heterozygosity individuals. The first question relative to this type of genetic rescue is what populations might need it and why. To address that question, microsatellite data collected through 2011 were compiled for Sierra bighorn herds that have been sampled (Table 5). Within Sierra bighorn, the Mt. Gibbs herd unit stands out in showing clear signs of low genetic diversity, which is consistent with its demographic history and substantial isolation. According to the data in Table 5, this is the 1 herd that currently shows a clear need for genetic management. Additional herds at Mt. Warren and Convict Creek are small and have the potential for declines in genetic diversity. Augmentations to these herds are planned for multiple purposes (Table 1), and their genetic diversity will be considered prior to implementing translocations.

There are two strategies for enhancing genetics of small populations. The first strategy is to translocate a small number of rams of high heterozygosity. This could radically change the reproductive output of resident ewes. However, there is great uncertainty whether those rams would be reproductively successful or even remain with that herd. Past translocations of rams indicate there is a high probability that newly translocated rams will make large exploratory movements or return to their home herd increasing the risk of contact with domestic sheep and disease transmission. Also the resident rams, with prior knowledge of habitat and individuals in a population might socially outrank introduced rams for some years which would prevent the introduced rams from increasing genetic diversity until they establish themselves in the herd. The second strategy for genetic management would be to translocate pregnant ewes of high heterozygosity. Because Sierra bighorn are polygynous, the introduction of additional ewes into a small existing herd would be the most effective approach to increase genetic diversity. If inbreeding is limiting the current herd, such an augmentation should trigger an increase in reproductive output and a population increase. Ram lambs born to the translocated ewes will likely add further genetic diversity when they reach breeding age. This second approach is consistent with the recommendations of Hedrick and Fredrickson (2010) and is the preferred approach particularly in areas where there is risk of contact with domestic sheep and goats.

Evidence for the success of the genetic rescue approaches discussed above comes from the Mt. Gibbs herd where, in 2012, the two old collared rams in this herd died. In the same year, population counts and genetic analyses indicate 2 rams immigrated to the herd. In the last 2 years the 7-8 resident ewes experienced much higher lambing rates producing an unprecedented 5 lambs in 2013 and 6 lambs in 2014. A natural genetic rescue appears to have occurred at Mt. Gibbs.

Habitat Suitability

Johnson et al. 2006 used resource selection functions (RSFs) to identify potential summer and winter habitat for female Sierra bighorn using GPS locations collected during 2002-2004. Data collected during this period largely represents habitat use in the Southern and Central Recovery Units. Subsequent to this analysis, GPS collars were deployed on females utilizing habitat west of the crest in the Bubbs Creek and Big Arroyo herd units and in herd units in the Northern Recovery Unit at Mt. Gibbs and Mt. Warren. We have gained substantial information about winter strategies from these deployments.

Altitudinal migration from summer alpine habitat to lower elevation winter ranges maximizes nutrient intake (Wehausen 1992 and Wehausen 1996). At the time the Recovery Plan was written, low elevation winter ranges were thought to be required for robust herds of Sierra bighorn, and the association between number of reproductive females, a measure of herd success, and size of low elevation winter range observed by Johnson et al. 2006 appears to confirm this hypothesis. Recent GPS locations indicate that Sierra bighorn can persist or even thrive with alternative winter strategies using high elevation wind swept ridges and mid-elevation south facing slopes, which are often snow free. Along the Sierra crest, Sierra bighorn winter on high elevation wind-swept ridges above 11,000 ft in the Mt. Gibbs herd. These bighorn regularly have the best body condition in the Sierra and the highest survival. A similar winter strategy and survival rate has been observed at Convict Creek, which is also along the crest; however, we currently lack data in that herd unit to make conclusions about body condition. At Bubbs Creek and Mt. Warren, Sierra bighorn appear to utilize mid-elevation winter ranges on south facing slopes between 6,500 and 8,000 ft and between 8,000 and 11,000 ft, respectively. In addition, habitat use west of the crest is remarkably different than that seen east of the crest. For example, Bubbs Creek females spend significant time in areas of dense shrubs such as manzanita (*Arctostaphylos spp*.), chinquapin (*Castanopsis sp.*), and whitethorn (*Ceanothus spp.*), particularly in winter.

Here we present updated RSFs for both summer and winter habitat based on GPS locations of female Sierra bighorn collected 2002-2013. These locations encompass a larger area than those used in previous RSFs (Johnson et al. 2006) and show more variability in habitat use. These updated RSFs now include additional habitat predictor variables from satellite imagery to represent forage (normalized differential vegetation index) and snow cover (fractional snow cover) in addition to traditional variables that represent terrain and vegetation types: elevation, elevation^2, slope, hillshade, escape terrain, distance to escape terrain, distance to meadow, aspect, ruggedness, and forested/non-forested. Using predictive maps of summer and winter habitat generated from these RSFs, we examine the quantity and quality of predicted summer and winter habitat across the Sierra within each recovery unit. Connectivity between winter range, lambing habitat, and summer range is discussed for each new herd unit identified for reintroductions. Connectivity within a recovery unit and between recovery units is analyzed in the context of both phase 1 and phase 2 translocations and disease concerns, although connectivity between recovery units will most likely occur when populations of Sierra bighorn are much larger in size than at present.

Summer and winter habitat

The new summer and winter RSFs confirmed the presence of suitable habitat in all herd units identified in the Recovery Plan (USFWS 2007). The summer RSF also identified three large expanses of predicted summer range that were not recognized in the Recovery Plan: 1) the Cathedral Range of Yosemite National Park 2) the Black Divide in Kings Canyon National Park, and 3) the northern end of the Great Western Divide north of the Big Arroyo herd unit in Sequoia National Park (Map 5). Winter habitat predicted by an RSF and a factional snow cover layer masking areas with >50% probability of snow cover were used to determine the amount of winter habitat available in these areas.

In the Northern Recovery Unit, the winter habitat model predicted mid-elevation winter range on the generally south facing slopes which begin at approximately 7,500 ft above Washburn and Merced Lakes (Map 6). This winter RSF also identified high elevation wind swept ridges utilized as winter range by the

Mt. Gibbs herd and mid-elevation winter range used by the Mt. Warren herd on the north side of Lundy Canyon (Map 6). These results suggest that the winter model is sensitive enough to predict small patches of winter range important for Sierra bighorn; thus, it is likely that patches of mid-elevation habitat above Washburn and Merced Lakes are suitable for Sierra bighorn. In the Black Divide, the winter RSF predicted a single large patch of winter range that rises up the south facing slopes of the Black Divide above the middle fork of the Kings River at 6,000 ft (Map 7). The size and elevation of this predicted winter range is very similar to that observed on the south facing slopes above Bubbs Creek used by bighorn in that herd unit south of the Black Divide (Map 8). The northern end of the Great Western Divide, while providing extensive summer range (Map 5), does not appear to have winter habitat similar to that available in the Big Arroyo and Laurel Creek herd units to the south (Map 8). The majority of predicted winter range in the Kern Recovery Unit is on east facing slopes above the Kern River (Map 8). The winter RSF predicts this to begin at the northern end of the Chagoopa Plateau at approximately 8,000 ft and continue south to the southern end of the Laurel Creek herd unit at approximately 6,500 ft (Map 8). Given the lack of winter range at the northern end of the Great Western Divide we have not considered this area for future reintroductions. The Cathedral Range and Black Divide both offer significant summer and winter habitat, thus we consider connectivity between winter range, lambing habitat, and summer range for these two proposed herd units below.

Connectivity within herd units

We evaluated connectivity within herd units that were not identified in the Recovery Plan, the Cathedral Range and the Black Divide. The Lyell Fork of the Merced River and Hutchings Creek provide connectivity between the alpine summer habitat in the Cathedral Range and the potential winter range above Washburn Lake (Map 6 and Map 9). While the bottom of the Lyell Fork drainage is forested, the south facing slopes above the valley floor offer open terrain that will likely be used as a migratory corridor between summer and winter ranges. These slopes are less vegetated than the slopes above Washburn and Merced Lakes, thus use will likely be brief each season. Lambing will likely occur on the slopes directly above winter range where forage is more abundant. While the migration corridor in this herd unit is slightly longer than that used by other reintroduced herds east of the crest, connectivity between summer and winter ranges is unobstructed. In contrast, summer alpine habitat in the Black Divide is immediately adjacent to mid-elevation winter habitat above the middle fork of the Kings River (Map 7 and Map 10). In the Black Divide, there is a continuous gradient of habitat between winter range, lambing habitat, and alpine summer range. The degree of connectivity and migratory distances in the Black Divide are similar to that observed for the most abundant herds of Sierra bighorn east of the Sierra crest. The availability of summer, winter, and lambing habitats and the connectivity between these habitats suggest that both the Cathedral Range and the Black Divide would support populations of Sierra bighorn.

Recovery unit connectivity

The naturally fragmented distribution of bighorn sheep has led to the application of a broad landscape approach to their population ecology. This approach groups geographically distinct herds into metapopulations, referred to in the Recovery Plan as recovery units, which are networks of interacting herds (Schwartz *et al*. 1986, Bleich *et al*. 1990b and 1996, and Torres *et al*. 1996). Thus, this approach considers long-term viability not of individual herds, *per se*, but rather of entire metapopulations; consequently, both genetic and demographic factors are considered. Inbreeding and genetic drift (random changes in gene frequencies) accompany decreasing population sizes and, over time, can lead to decreases in genetic diversity that may have negative demographic effects through inbreeding depression (reduction in fitness due to mating among relatives) (Soulé 1980) and loss of adaptability.

The other important long-term process in metapopulation dynamics is the balance between rates of natural extinction and colonization among constituent populations. Colonization rates must exceed extinction rates for a metapopulation to persist (Hanski 1991). Metapopulation structure has profound implications for the conservation of Sierra Nevada bighorn sheep. Conservation objectives for Sierra bighorn must simultaneously address all levels of population organization to achieve recovery goals. Recovery units, herd units, and separate demes within herd units are all relevant to overall recovery of Sierra bighorn. Here we address how the translocations proposed in this plan relate to metapopulation structure in terms of connectivity within and between recovery units.

Connectivity within recovery units

The Recovery Plan considered metapopulation dynamics in the conservation of Sierra bighorn by defining 4 recovery units that might independently function as metapopulations until Sierra bighorn populations are large enough for metapopulation dynamics to occur throughout the Sierra. The summer RSF predicts high quality habitat connecting all herd units in the Southern Recovery Unit (Map 5). Genetic analyses and GPS locations (data not shown) indicate that gene flow readily occurs among the Mt. Williamson, Bubbs Creek, Mt. Baxter, and Sawmill Canyon herds in the Southern Recovery Unit. We propose augmentations to create new demes at the northern end of the Mt. Williamson herd unit (Symmes and Pinyon Creeks), the southern end of the Mt. Langley herd unit (Cottonwood Creek), and the northern end of the Olancha Peak herd unit (Cartago and Ash Creeks) to further connect existing herds within the Southern Recovery Unit (Map 4). Population surveys and observations of bighorn suggest that there is gene flow between the Wheeler Ridge and Convict Creek herds in the Central Recovery Unit. Genetic analyses are being performed and GPS collars are being deployed to confirm this in future years. The sporadic appearance of immigrants and a ram from Mt. Warren traveling through the Mt. Gibbs herd unit (Stephenson et al. 2012) suggest that there is habitat of sufficient quality to connect these two herd units; the summer and winter RSFs confirm connectivity between these herds at Lee Vining Canyon (Map 9 and Map 6). The summer RSF also shows connectivity between the Cathedral Range and Mt. Gibbs herd units through alpine habitat surrounding Donohue Pass (Map 9). Proposed augmentations to create new demes at Lee Vining Canyon in the Mt. Warren herd unit and at Alger Creek in the Mt. Gibbs herd unit (Map 3) will ensure connectivity in the Northern Recovery Unit.

Connectivity between recovery units

At present there is very limited evidence of connectivity among any of the 4 recovery units in the Sierra; however, as existing populations grow, we anticipate occasional gene flow between the Kern Recovery Unit and the Southern Recovery Unit. Connectivity among the Southern, Central, and Northern Recovery Units will be enhanced by the creation of two new herd units, the Black Divide and Cathedral Range, as well as augmentations to existing herds units, specifically phase 2 translocations. As the potential for connectivity increases between recovery units, the consequences of disease transmission between populations of Sierra bighorn increase dramatically. Fortunately, Sierra bighorn have not experienced demographic declines associated with disease from domestic sheep and goats since the 1970's; however there are domestic sheep in close proximity to herds of Sierra bighorn in all 3 recovery units east of the Sierra crest. Mitigation measures need to be in place for high risk domestic sheep on private land and government allotments prior to implementation of translocations that will significantly increase connectivity between recovery units.

The Kern Recovery Unit is 7-10 miles to the west of the Mt. Langley herd, one of the most populous herds in the Sierra, and there are islands of alpine summer habitat east of the Kern River that could connect these two herds (Map 11). An alternative path for gene flow between the Southern and Kern

Recovery Units is through the predicted summer habitat north of the Big Arroyo herd unit (Map 11). Summer habitat in the northern Great Western Divide and in the Kings-Kern Divide is contiguous with summer habitat in the Mt. Williamson herd (Map 11). In the first summer after reintroduction to the Big Arroyo herd unit, ewes moved north out of the Big Arroyo herd unit to Kern Point suggesting that this may be a viable corridor for gene flow as populations increase.

A new herd unit in the Black Divide would provide additional connectivity between the Wheeler Ridge herd unit in the Central Recovery Unit and the Southern Recovery Unit (Map 10). There is sufficient connectivity between summer range in the Black Divide and the summer ranges of the Coyote Ridge and Taboose Creek herd units that gene flow could occur (Map 10). Translocations to these three herd units and an augmentation to create a new deme in the Mt. Tom region of Wheeler Ridge (Maps 3 and 4) will likely ensure these connections. At present, there is substantial risk of disease through contact with domestic sheep in the Central Recovery Unit. The risk of disease transmission needs to be reduced before phase 2 translocations (Mt. Tom, Coyote Ridge, and Black Divide, Table 1) proceed.

Reintroduction of Sierra bighorn to the Cathedral Range and augmentation to create a new deme north of McGee Creek in the Convict Creek herd will increase the probability of connectivity between the Central and Northern Recovery Units (Map 3). It will be important to consider the growth rate of the Cathedral Range herd, its connectivity to the Mt. Gibbs herd, and the threat of disease in the Northern and Central Recovery Units before enhancing connectivity between recovery units by creating a new deme north of McGee Creek.

Threatening Factors

Disease

Respiratory disease is widely recognized as one of the greatest threats to the persistence of bighorn sheep throughout the western United States (Wehausen et al. 2011). The Recovery Plan for Sierra bighorn identifies respiratory disease from domestic sheep as one of the primary threats to recovery and stipulates that contact with domestic sheep must be prevented in order to meet recovery goals (Recovery Criterion A2; USFWS 2007). When the Recovery Plan was finalized in 2007 there remained more than 31 domestic sheep allotments totaling more than 350,000 acres on public land within 20 km of habitat occupied by Sierra bighorn. Most of the allotments recommended for closure in the Recovery Plan were vacated by 2011.

Translocation of bighorn sheep has the potential to spread disease through multiple mechanisms. First, if animals in source populations are infected, translocation would move those pathogens to new or existing herds. Second, previous recovery program translocations have demonstrated that Sierra bighorn are likely to make large exploratory movements in the months following translocation as they learn their new surroundings. This increases the probability of encountering domestic sheep or goats and returning to the bighorn herd with disease causing pathogens. Third, as more habitat is occupied by translocation efforts, bighorn sheep populations will become more connected. This increases the likelihood that a disease outbreak in one herd will spread to a neighboring herd through natural movements of Sierra bighorn.

The first mechanism of disease transmission by translocation, infection of the source population, is addressed by disease surveillance. Herds of Sierra bighorn that are used as sources of translocation stock are sampled for disease during October captures prior to implementation of translocations in March. Surveillance of respiratory pathogens is of primary interest and includes analyses for *Pasteurella* *spp.* and *Mycoplasma ovipneumoniae*. If disease is suspected in a population, translocation activities will be postponed. We currently have extensive health histories for all herds of Sierra bighorn that date back to 2001.

The second mechanism of disease transmission results from exploratory movements of translocated animals, which causes a transient increase in the risk of disease transmission. This mechanism of disease transmission is addressed by determining the level of risk present in the area where bighorn will be moved, selecting the sex of bighorn to be moved according to the level of risk, and timing the translocation to minimize encounters with domestic animals. In areas where the risk of encountering domestic sheep or goats is high, translocations will not be conducted until mitigation measures are in place to reduce the risk of contact. In areas where the risk of contact is moderate, no males will be translocated. In these cases, pregnant females, who are much less likely to make exploratory movements immediately following translocation, will be moved. In areas where the risk of contact with domestic sheep or goats is low, bighorn of both sexes can be translocated.

Baumer et al. (2009) outline a process that identifies criteria to assess the threat of disease transmission from domestic sheep grazing near Sierra bighorn habitat. Risk of contact between Sierra bighorn and domestic sheep was modeled using GPS locations of Sierra rams to combine habitat suitability and distance of core herd home ranges to domestic sheep. The mean inverse weighted distance (MIWD) characterizes the cost of movement across the landscape in terms of where Sierra bighorn will travel given their habitat preferences. Croft et al. (2010) further established, based on the movement of rams in the recovery area from 2001 to 2006, that a MIWD of 0.833 represents a threshold above which the risk of contact between the 2 species is unacceptable.

The model described in Croft et al. (2010) was rerun using GPS location data collected from 2002 to 2014. The preliminary results of the new model run indicate that the previous MIWD value of 0.833 has changed to 0.820. The boundary reflecting this new value is shown in Map 12 along with locations of domestic sheep and goats in the recovery area. Croft et al. (2010) also outlined how federal agencies should manage federal lands based on a threshold of unacceptable risk (i.e., 0.833). In the near future, we will be working with the USFWS and the relevant federal land managers to discuss the results of the new model run and resultant new threshold of unacceptable risk and revise the Croft et al. (2010) document as necessary.

Each of the high risk occurrences of domestic sheep or goats are listed in Table 8. There is at least one major area of risk in each of the 3 most populous recovery units, Northern, Central, and Southern. There are 9 allotments on public lands and 8 private holdings that are leased to domestic sheep operators or contain small hobby farms that lie within the MIWD threshold. Hobby farms on private lands near occupied bighorn habitat now pose a significant threat to the recovery of Sierra bighorn. Education and assistance to create effective spatial and temporal separation will be required to mitigate this risk. This analysis identifies 5 potential translocations to recipient populations where there is significant risk of contact with domestic sheep (both augmentations planned for the Convict Creek herd with one being north of McGee Creek, both augmentations planned for the Mt. Warren herd with one being to Lee Vining Canyon, and the augmentation at Cottonwood Creek in the Mt. Langley herd, Table 1). We are currently working with private land owners and public land management agencies across the Sierra to reduce the threat that domestic sheep and goats present to Sierra bighorn recovery.

Table 8. Domestic sheep grazing allotments and private holdings with risk of contact with bighorn sheep. Grazed allotments with a mean MIWD value greater than 0.82 are high risk and highlighted in dark grey. Allotments which cross the 0.82 line (Map 12) but lie largely outside of the 0.82 line are identified in light grey.

FID	NAME	TYPE	ALLOT. TYPE	STATUS	MAX MIWD	MEAN MIWD	RU
	Carroll Crk	Sheep/goat	Private		0.996468	0.992686	S
26	Dunderberg S&G	Temp. Closed	Toiyabe NF	VACANT	1	0.979178	N
30	Mattly	Sheep	Mono Co.		0.986134	0.97265	N
25	Dunderberg S&G	Temp. Closed	Toiyabe NF	VACANT	0.999564	0.956428	N
48	Rock Creek	Sheep	Inyo NF	VACANT	0.97869	0.956021	C
	Swall Mdws	Sheep/goat	Private		0.954888	0.954439	C
	Mono City	Sheep/goat	Private		0.957435	0.954145	N
40	Alger Lake	Sheep	Inyo NF	CLOSED	0.986619	0.950643	N
63	Mono Settlement	Sheep	BLM	OPEN	0.961774	0.943919	N
33	Bloody Canyon	Sheep	Inyo NF	CLOSED	0.985288	0.942089	N
46	McGee	Sheep	Inyo NF	VACANT	0.979076	0.939348	C
50	Rock Creek	Sheep	Inyo NF	VACANT	0.965036	0.937903	C
34	Horse Meadow	Sheep	Inyo NF	CLOSED	0.961926	0.934638	N
68	Little Round Valley	Sheep	BLM	OPEN	0.953174	0.9327	C
31	Conway	Sheep	Mono Co.		0.953602	0.93063	N
32	Horse Meadow	Sheep	Inyo NF	CLOSED	0.933601	0.927687	N
24	Dunderberg S&G	Temp. Closed	Toiyabe NF	VACANT	0.928527	0.925973	N
	McGee Petting Zoo	Sheep/goat	Private		0.924684	0.922389	C
51	Rock Creek	Sheep	Inyo NF	VACANT	0.941503	0.919614	C
28	Green Creek S&G	Sheep & Goat	Toiyabe NF	VACANT	0.947889	0.917248	N
69	Little Round Valley	Sheep	BLM	OPEN	0.927809	0.907115	C
45	Tobacco Flat	Cattle/Sheep	Inyo NF	VACANT	0.93349	0.904413	C
	Round Valley	Sheep/goat	Private		0.906033	0.904231	C
8	Tamarack S&G	Sheep & Goat	Toiyabe NF	VACANT	0.944977	0.89987	N
70	Little Round Valley	Sheep	BLM	OPEN	0.908554	0.89898	C
27	Cameron Canyon S&G	Sheep & Goat	Toiyabe NF	VACANT	0.936231	0.898301	N
49	Rock Creek	Sheep	Inyo NF	VACANT	0.887101	0.886877	C
29	Little Round Valley	Sheep	LADWP		0.905845	0.885692	C
47	Rock Creek	Sheep	Inyo NF	OPEN	0.92533	0.882414	C
60	Dog Creek	Sheep	BLM	VACANT	0.95334	0.877902	N
43	Casa Diablo	Sheep	Inyo NF	OPEN	0.858694	0.852356	C
7	Summers Meadow S&G	Sheep & Goat	Toiyabe NF	OPEN	0.87147	0.840719	N
58	Green Creek	Sheep	BLM	VACANT	0.898748	0.839207	N
37	June Lake	Sheep	Inyo NF	OPEN	0.887168	0.826329	N
66	Casa Diablo	Sheep	BLM	OPEN	0.873767	0.824734	C
59	Little Mormon	Sheep	BLM	OPEN	0.881149	0.815214	N
14	Rickey S&G	Sheep & Goat	Toiyabe NF	OPEN	0.834316	0.812658	N
61	Rancheria Gulch	Sheep	BLM	OPEN	0.961546	0.805488	N
42	Casa Diablo	Sheep	Inyo NF	OPEN	0.793968	0.783846	C
62	Mormon Ranch	Sheep	BLM	OPEN	0.798031	0.765552	N
41	Sherwin/Deadman	Sheep	Inyo NF	OPEN	0.839419	0.745292	N/C
67	Volcanic Tablelands	Sheep	BLM	OPEN	0.887561	0.740857	C
56	Travertine Hills	Sheep	BLM	OPEN	0.802635	0.735487	N
44	Casa Diablo	Sheep	Inyo NF	OPEN	0.869197	0.725938	C
36	Mono Mills	Sheep	Inyo NF	OPEN	0.821502	0.70356	N
13	Rickey S&G	Sheep & Goat	Toiyabe NF	OPEN	0.732595	0.700023	N

The third mechanism for disease transmission, increasing connectivity, is being addressed by structuring the translocation program into 2 phases. Phase 1 translocations, while increasing occupied habitat, are designed to, in the short-term, maintain separation between recovery units. Phase 2 translocations will greatly increase connectivity between herd units and recovery units; thus, these translocations will not begin until renewed efforts to decrease the risk of contact with domestic sheep and goats are successful. Furthermore, removals from source populations to support this translocation program will keep the largest populations of Sierra bighorn near 40 total ewes, thereby reducing connectivity for the duration of translocation efforts. In addition to the steps described above to reduce the risk of a wide-spread disease outbreak, the remote populations proposed in the Kern Recovery Unit, the Cathedral Range, and the Black Divide will act as important refugia from disease as long as they remain relatively small and isolated.

The operational section of this translocation plan and future annual operational plans will describe how the risk of contact of bighorn and domestic sheep is managed with regard to immediate translocation efforts. These annual plans will also provide updates on the implementation of mitigation measures to maintain spatial and temporal separation of bighorn and domestic sheep. Continued efforts to reduce the overall risk of disease transmission, including education of private landowners, are needed to ensure that future translocations can move forward and recovery criteria are met. To focus these efforts CDFW is producing a Disease Management Plan. The updated risk assessment presented here is a step toward renewed efforts to reduce the risk of contact between Sierra bighorn and domestic sheep and goats.

Predation

Bobcats, coyotes, and golden eagles are important predators of bighorn lambs. Mountain lions are the primary predator of adult Sierra bighorn (Stephenson et al. 2012). Mountain lion predation on bighorn is more likely to occur in areas where bighorn and mule deer (*Odocoileus hemionus*) winter range overlap or are adjacent because mule deer, typically much more abundant, are the primary prey for mountain lions (Cooley et al. 2008, Johnson et al. 2012). Apparent competition can occur with a generalist predator like the mountain lion when the presence of a primary prey species, like deer, results in a disproportionately high level of predator activity on a sympatric and rarer secondary prey species such as Sierra bighorn. The primary risk of mountain lion predation on Sierra bighorn will be highest during the winter when bighorn and deer winter ranges overlap (Maps 13 and 14). During the summer, mule deer occupy ranges at lower elevations than bighorn, which are typically above tree line in alpine habitat, and there is very little overlap between the species.

The Recovery Plan identifies mountain lions as one of the primary threats to recovery and recommends predator management to reduce mountain lion caused mortality of Sierra bighorn (Recovery Action 2.1, USFWS 2007). Mountain lion predation can impact the success of translocations in 3 different contexts: by limiting the availability of translocation stock in source herds, by decreasing the survival of translocated individuals in their new habitat, and by necessitating the use of limited translocation stock to augment small herds experiencing lion predation rather than creating new herds. These potential impacts are evaluated in this section; however, anticipated predation levels for newly translocated animals will be discussed only generally in this section and in greater detail in the annual Operational Section where the most current information can be provided.

Source populations

The Mount Langley, Mount Baxter, Sawmill Canyon, and Wheeler Ridge herds will serve as source populations for future reintroductions and augmentations; thus, manageable causes of mortality should be reduced, consistent with Recovery Plan guidelines (Recovery Action 2.1, USFWS 2007). In a nutritionally-limited population in which predation replaces other forms of mortality such as starvation, mountain lion predation can be compensatory, leading to no net loss in numbers. In populations that are not nutritionally limited, predation can be additive, resulting in additional mortalities. Because translocations remove animals from source populations, thereby reducing competition for forage, predation losses are not likely to be compensatory in those herds. Instead, those losses will be additive and limit availability of bighorn for translocations.

The 4 source herds for translocations have experienced mountain lion predation in the past (Stephenson et al. 2012, Davis et al. 2012). Bighorn in the Wheeler Ridge herd winter in habitat that overlaps with winter habitat for the large herd of mule deer at Round Valley (Map 13). The Sawmill Canyon and Mt. Baxter herds of Sierra bighorn share winter range with the Goodale deer herd (Map 13). All 3 of these herds of Sierra bighorn have experienced high levels of mountain lion predation at various times (Stephenson et al. 2012). The Mt. Langley herd of Sierra bighorn has experienced moderate levels of mountain lion predation and overlaps the southern extent of the Goodale deer winter range (Map 13). If mountain lion predation substantially inhibits population growth and thereby limits removals of translocation stock from these source herds, mountain lion management will be needed during implementation of this translocation program.

Recipient populations

As observed for Sierra bighorn source populations (above), densities of mule deer are good predictors of mountain lion abundance and predation on Sierra bighorn. Here we use known mule deer winter ranges to estimate the probability of predation on translocated Sierra bighorn (Map 14). Herds that use or will use low elevation winter range east of the crest have the highest probability of overlap with wintering mule deer populations and thus mountain lion predation (Map 14). Translocations where predation risk is moderate to high include Olancha Peak and the augmentation to Cartago and Ash Creeks in that herd unit, the Cottonwood Creek area at Mt. Langley, the Symmes Creek augmentation at Mt. Williamson, Taboose Creek, Coyote Ridge, and an augmentation to the Mt. Tom area of Wheeler Ridge (Table 1 and Map 14). While not immediately adjacent to large deer populations, in past years, we have recorded significant mountain lion predation on Sierra bighorn in the Mt. Warren herd unit both in Lee Vining Canyon and in Lundy Canyon (Map 14). Therefore, all augmentations to this herd are listed as having risk of predation in Table 1.

Recovery Action 2.1 calls for the cessation of predation management after populations exceed 25 ewes, and the re-instatement of such management if they decline to fewer than 20 females due to predation losses (USFWS 2007). Sources of translocation stock were treated as a potential exception to that rule, i.e. predation management might continue after source herds reach 25 ewes. This is particularly appropriate given that this plan recommends management to prevent source herds from declining below 30 ewes. Currently, Mt. Warren is the only population that was larger but has declined below the threshold of 20 females, and in early spring of 2013 significant lion mortality was detected in that herd. All other herds with fewer than 20 females (the newly reintroduced herds at Olancha and Big Arroyo, the natural colonizations at Bubbs and Convict Creek, and the small at Mt. Gibbs) are stable or increasing in size; however, we plan to develop a predator management plan to address the needs of these small herds as they arise and also to protect the 4 source herds of translocation stock should substantial predation occur.

Long-Term Operational Guidelines

(Adapted from Few et al. 2013)

1. Removals for translocations will not be considered unless the source populations exceed 40 adult and yearling ewes.
2. Removals for translocations will not reduce source herds to fewer than 30 adult and yearling ewes.
3. The goal for reintroductions is to release a minimum of 10 ewes during the initial release.
4. Augmentations will follow after reintroductions within 2 years.
5. Augmentations of small existing herds will consider genetics of translocated individuals to allow for genetic rescue if necessary.
6. Sierra Bighorn in source populations will not be captured on low-elevation winter range within a particular subpopulation in consecutive years. Captures at high elevation are acceptable in consecutive years within a subpopulation. Translocations will be implemented using an adaptive management approach and will be postponed if exceptionally difficult winter or drought conditions exist.
7. All translocated individuals will be released with VHF collars at a minimum. More typically we expect to fit most animals with GPS collars as well.
8. Herds containing newly-translocated individuals will be closely monitored and surveyed annually.
9. A predation action plan will be developed to enable a response to increased predation that will minimize such effects on bighorn population growth where needed.
10. Adaptive management will be applied to all translocations of Sierra bighorn with population viability analyses, genetic simulations, and habitat models contributing to the science based conservation of this rare subspecies.

II. Operational Planning: 2015 Translocations

Four translocations are planned for March 2015: reintroductions to Laurel Creek and the Cathedral Range and augmentations at Mt. Gibbs and Olancha Peak. The sex and numbers of animals, the source herds from which the animals will be removed, and the specific release sites can be found in Table 9. For translocations where the source herd is listed as various locations in Table 9, high heterozygosity individuals will be selected to maximize genetic diversity in the recipient populations. Habitat suitability, disease threat, genetics, and predation potential are discussed below for each translocation within the context of the recovery unit.

Table 9. Translocations planned for 2015

Recovery Unit	Herd Unit	Sex	Number	Source Herd	Release Location
Kern	Laurel Creek	F	10	Mt. Baxter	Outlet of Laurel Ck (Map 16)
		M	3-5	Various locations	Outlet of Laurel Ck (Map 16)
Northern	Cathedral Range	F	10	Mt. Langley	Washburn Lake (Map 9)
		M	3-5	Various locations	Washburn Lake (Map 9)
	Mt. Gibbs	F	5	Mt. Langley/Mt. Baxter	Alger Lake
Southern	Olancha Peak	M	2	Various locations	Falls Creek

Kern Recovery Unit

The Laurel Creek herd unit, where a reintroduction of 10 ewes and 3-5 rams is planned for March 2015, is immediately south of and adjacent to the Big Arroyo herd unit. The Laurel Creek herd unit is one of two herd units in this recovery unit (Map 1) essential to meet Downlisting Criterion A1 and Delisting Criterion B2 (USFWS 2007). This herd unit was selected for inclusion in recovery criterion based on the historic occurrence of Sierra bighorn in the Mineral King area and the Kaweah Peaks (Map 15 and Wehausen and Jones 2014), which is partially included in this herd unit and the Big Arroyo herd unit to the north. Further evidence that this region supported a large population of Sierra bighorn comes from reports of a large scabies die-off in the 1870’s (Jones 1950).

In March 2014 Sierra bighorn (10 ewes and 4 rams) were reintroduced to the Big Arroyo herd unit in the Kern Recovery Unit. These bighorn were released at the northwest corner of the confluence of Big Arroyo Creek and the Kern River at the southern end of the Big Arroyo herd unit (Map 16). In the summer and fall of 2014, 3 ewes and 1 ram from the Big Arroyo reintroduction traveled to and remained in the Laurel Creek herd unit with 2 of the ewes staying for 3 months (Map 16). Selection of alpine habitat in Laurel Creek by Sierra bighorn indicates preference for the alpine in this herd unit. Furthermore, the summer habitat model (Map 16) predicts there is much more habitat of this quality or higher in the Laurel Creek herd unit. This suggests that there is sufficient alpine forage to support additional animals. These exploratory forays also indicate that gene flow will likely occur between the Laurel Creek herd and the Big Arroyo herd allowing these two herds to function as a metapopulation if not as a single herd.

Increasing numbers of Sierra bighorn in the Kern Recovery Unit is an important step at this stage of recovery for Sierra bighorn. As populations east of the Sierra crest grow and become more connected, the risk of a disease outbreak spreading between populations increases. With more than 600 bighorn in the Sierra and multiple locations of domestic sheep or goats in close proximity to Sierra bighorn east of the crest (Table 8 and Map 12), it is an important and timely step in the recovery process to create populations that are geographically isolated from disease carrying domestic sheep and goats. Both herds in the Kern Recovery Unit serve this purpose because they are located within Sequoia National Park boundaries and adjacent to the Sequoia National Forest, both of which do not permit domestic sheep or goat grazing. The reintroduction at Laurel Creek should facilitate population growth in the Kern Recovery Unit, which is an important step in building a reserve of Sierra bighorn isolated from the risk of disease in the short-term.

Winter habitat models predict winter range along east facing slopes above the Kern River and south facing slopes in the lower reaches of the Laurel and Rattlesnake Creek drainages (Map 8). These slopes are all above 6,500 ft which is higher than the typical low elevation winter ranges used by the largest herds of Sierra bighorn east of the crest. In the heaviest winters these mid-elevation winter ranges will not remain consistently snow free. It is possible that, historically, populations of Sierra bighorn in this area wintered on the west slopes of the Sierra Nevada (Wehausen and Jones 2014) prior to fire suppression efforts in the last century which have now created heavily forested western slopes unsuitable to bighorn. With recent GPS location data for Sierra bighorn, we have learned that winter patterns of habitat use are highly variable both between populations and for a single individual. West of the crest Sierra bighorn in the Bubbs Creek herd use similar mid-elevation winter ranges and have persisted without management intervention since they were discovered there in 2002 (Map 8). Unlike alpine areas along the Sierra crest where wind scours snow off ridge lines that are used by bighorn, snow-free alpine winter ranges do not occur in the Great Western Divide. The uncertainly of winter habitat quality dictates a slow reintroduction of animals to the Kern Recovery Unit to allow time for animals to develop appropriate winter migratory behaviors. The reintroduction to the Big Arroyo herd unit occurred in March 2014, and a subsequent augmentation is scheduled for 2016. Future augmentations to Laurel Creek will follow a similar timeline and allow for adaptive management.

The Kern River drainage is mule deer habitat, and mule deer have been observed there in the summer months (Davis et al. 2012 and A. Few, unpublished observations); however, mule deer were not observed in large numbers like they were in other areas in the western Sierra Nevada (Davis et al. 2012). The upper Kern River drainage is also unlikely to serve as winter range for mule deer because of the elevation and snow depth. Predator surveys of the Kern River drainage produced only one observation of lion sign in the area (Davis et al. 2012). This is in contrast to what was observed in other mule deer habitat west of the crest in the Mineral King region (Davis et al. 2012) and east of the crest at Wheeler Ridge, Sawmill Canyon, and Mt. Baxter herd units (Stephenson et al. 2012). While additional monitoring is necessary to conclude that predation by mountain lions will be minimal, it is unlikely that predation will be a significant source of adult mortality at Laurel Creek.

Northern Recovery Unit

The Northern Recovery Unit, as described in the Recovery Plan (USFWS 2007), includes the Mt. Gibbs, Mt. Warren, Green Creek, and Twin Lakes herd units. To meet Downlisting Criterion A1 and Delisting Criterion B2, the Northern Recovery Unit needs at least 2 occupied herd units with a total of at least 50 females. To reduce conflict with domestic sheep grazing in the Bridgeport region, the Recovery Plan recommended the Green Creek and Twin Lakes herd units not be considered for translocations (USFWS 2007). Summer surveys in 2014 counted 24 female bighorn in the Mt. Gibbs and Mt. Warren herd units. Translocations to both herds are necessary to increase population growth and ensure the viability of these small populations. Due to domestic sheep grazing in close proximity to the Mt. Warren herd, we do not recommend augmenting the Mt. Warren herd until that risk of contact with sheep is mitigated. To meet recovery goals, the Northern Recovery Unit likely needs an additional herd. Yosemite's Cathedral Range is an excellent location for a new herd unit because it has numerous historical detections (Map 17 and Wehausen and Jones 2014), superb summer habitat providing abundant nutrition, potential for connectivity with the Mt. Gibbs herd, and initial separation from domestic sheep which pose the threat of disease.

Cathedral Range reintroduction

We plan to reintroduce 10 ewes and 3-5 rams to the Cathedral Range herd unit in March 2015. Contiguous bighorn sheep summer habitat in the Cathedral Range herd unit (Map 9) lies within Yosemite National Park with a portion of habitat on the Sierra National Forest. Within Yosemite National Park and the Wilderness on the Sierra National Forest, there are no domestic sheep grazing allotments. Thus, there is little danger of these bighorn contacting domestic sheep. While it remains small, this herd will serve as a refuge from disease similar to the 2 herd units in the Kern Recovery Unit. The summer habitat model identified a corridor of alpine habitat at Donohue Pass connecting the Cathedral Range and the Mt. Gibbs herd units (Map 9). Once a large population is established in the Cathedral Range, rams will likely move between these two herds allowing gene flow, crucial to preventing inbreeding depression, in this recovery unit. The potential for future connectivity also brings the risk of disease. This highlights the importance of renewed efforts to reduce the risk of contact with domestic sheep and goats in the Northern Recovery Unit.

The summer habitat model predicts large expanses of summer range among the alpine peaks of the Cathedral Range (Map 9) where many historical detections have occurred (Map 17). We expect this to be some of the best quality summer habitat available in the Sierra. The abundance and species composition of summer forage appears to be similar to that found in the Mt. Gibbs herd unit which produces the largest bighorn with the best body condition in the Sierra. Adult bighorn in the Mt. Gibbs herd also have the highest survival of any herd of Sierra bighorn despite having winter habitat that consists of windswept ridges above 11,000 ft. Exceptional body condition and survival rates along with the patterns of habitat use of the Mt. Gibbs herd suggest that high quality summer forage found in this area may produce fat reserves sufficient to allow Sierra bighorn to overwinter with limited forage.

The winter habitat model predicts mid-elevation winter range in the Cathedral Range herd unit on south-facing slopes that rise above Washburn and Merced Lakes between 7,500 and 9,500 ft (Map 6). The quantity of winter habitat, particularly in alpine areas, is uncertain due to higher snow cover west of the crest. On the north side of the Merced River west of Washburn Lake and above Merced Lake, slopes contain large expanses of granite slabs. East of Washburn Lake, the cliffs are more broken containing vegetated gullies and flat ledges connecting granite outcrops. A variety of vegetation is found on these ledges and gullies. Vegetation surveys found 252 different species here (R. Klinger, unpublished data). Above 8,800 ft, herbaceous species, specifically graminoids, were abundant and would likely provide good forage during lambing season when sheep move to steep, higher elevation terrain. Plant species include *Juncus parryi, Carex excerta, Carex rossii, Sedum sp., Potentilla sp., Penstemon newberryi, Eriogonum sp.*, and *Achillea sp*. Below 8,800 ft, shrub cover is more abundant and herbaceous vegetation is restricted to small patches. Here, *Artemsia ludoviciana, Holodiscus sp., Leptodacylon sp.,* Scrub Oak (*Quercus spp.*), and Manzanita (*Arctostaphlos spp.*) are abundant. These slopes when snow free will likely provide adequate winter forage. Given the elevation and vegetation of the upper cliffs, ewes would be expected to bear lambs in this habitat.

The presence of mule deer and mountain lions in the Washburn Lake area will likely determine the extent to which bighorn experience mountain lion predation, which can inhibit growth of small recovering herds. There is a population of deer in the Washburn Lake area in summer. We suspect that most of these deer move west to lower elevations during winter. Other potential predators observed in the area include golden eagles and coyotes which may prey upon juvenile age classes.

Mt. Gibbs augmentation

Since the mid-1990s, the population at Mt. Gibbs has grown from a reproductive base of just 1 ewe to 8 ewes, but in recent years it has not increased further because of low reproductive rates. One hypothesis is that this population has reached the carrying capacity that its habitat can support. This appears to be unsupported given the particularly fat condition of Sierra bighorn in this herd that has been measured by ultrasound, which suggests that these bighorn have sufficient nutrient intake. However, we cannot explain why lamb recruitment has been poor. An alternative to the carrying capacity hypothesis is that inbreeding is limiting growth of this population through inadequate reproduction (Johnson et al. 2011). Genetic analyses indicate that this herd has the lowest observed heterozygosity and effective number of alleles of all herds of Sierra bighorn (Table 5). Several management interventions in the form of augmentations might test this hypothesis. A further hypothesis is that predation limits lamb recruitment, but we have no cause-specific mortality data for lambs.

In 2013 we considered two strategies for augmenting the Mt. Gibbs population. The first strategy was to translocate 1-3 rams of high heterozygosity into this herd. This could radically change the reproductive output of the resident ewes if inbreeding was limiting reproduction. However, there is great uncertainty whether those rams would be reproductively successful or even remain with that herd. The second strategy for genetic management was to initially to translocate 2-3 pregnant ewes of high heterozygosity into this herd with the plan to add more in subsequent years. Because there is a much higher risk of newly translocated rams making large exploratory forays near domestic sheep and goats than newly translocated pregnant ewes, we implemented the second strategy in March 2013 by translocating 3 high heterozygosity ewes from Mt. Langley.

Population surveys since 2012 and genetic analyses suggest the presence of 2 immigrant rams. Coincident with the arrival of these rams and the death of the two oldest rams, native ewes in the Mt. Gibbs herd have shown increased lamb production. What appears to have happened at Mt. Gibbs is a natural genetic rescue through the immigration of two rams. This is a problematic situation relative to our attempt to use high heterozygosity ewes for genetic rescue because we now have considerably more low heterozygosity ewes producing lambs. Reproduction by the resident ewes will likely dominate the future gene pool unless there are selective differences between offspring of the 2 ewe groups. It is at small population sizes that we can have the greatest influence on genetic population structure. Consequently, we plan to translocate 5 high heterozygosity ewes in 2015 to Alger Creek on the south side of Mt. Wood with the goal of creating a new deme in the Mt. Gibbs herd unit. Expanding habitat use and increasing genetic diversity in the Mt. Gibbs herd unit will allow population growth rates to increase and move the Northern Recovery Unit toward Downlisting Criterion A1 and Delisting Criterion B2.

Observations of Sierra bighorn suggest that the Alger Creek area in the Mt. Gibbs herd unit is suitable habitat. Rams have been wintering on Mt. Wood for many years, and ewes did so for one winter before returning to Mt. Gibbs. The winter habitat model predicts patches of mid-elevation winter range on the south facing slopes of Mt. Wood near Alger Lakes and on the south east facing slopes of Mt. Wood above Alger Creek just east of the herd unit boundary (Map 6). Summer habitat in this area is abundant (Map 9) and will likely produce animals with similar body condition to those at Mt. Gibbs.

Southern Recovery Unit

Olancha Peak augmentation

In March 2013, 10 ewes from the Sawmill Canyon herd and 4 rams selected for high levels of genetic diversity from the Sawmill Canyon and Mt. Langley herds were reintroduced to historic habitat at Olancha Peak. In March 2014, this fledging herd was augmented with 4 additional ewes from Sawmill Canyon. In summer of 2013, one ram returned to his home herd at Mt. Langley, and in October 2014, a ram died from unknown causes. Thus, 2 mature rams remain in the Olancha Peak herd. To further increase genetic diversity and reduce the probability of rams breeding their daughters, we plan to augment the herd with 2 high heterozygosity rams in March 2015. We plan to select these 2 rams from source herds other than those used previously to maximize genetic mixing and diversity. The potential impacts of disease, predation, and habitat were analyzed prior to the 2013 reintroduction (Few et al. 2013) and will not be repeated here.

Logistics

The Recovery Program at CDFW has carried out small augmentations since listing in 1999. The logistics of these small augmentations are simple with most animals being released from trucks on roads at the base of bighorn winter ranges. The logistics of reintroductions are more complex than small augmentations. Ideally, all animals will be released simultaneously into their new habitat. This maximizes the probability that ewes will remain in a large group requiring less vigilance behavior from each individual. Release of rams and ewes together increases the likelihood that rams will remain in the new habitat and not return home. For reintroductions to remote areas with no road access, a second transport helicopter is required to sling bighorn in aluminum transport boxes to release sites. Ideally, animals will be captured from source populations and slung to the release site in the same day to minimize stress to the animals. Since 2013, we have reintroduced Sierra bighorn to 2 unoccupied herd units, Olancha Peak and Big Arroyo. We have not been able to achieve all of the ideals described above on either reintroduction. In both reintroductions all ewes were released with 1 or 2 rams and another 2-3 rams were released in subsequent days. Selecting high heterozygosity rams for capture requires more helicopter flight hours, and shorter days in late March limit the number of hours helicopters may operate.

We anticipate similar logistical constraints in the reintroductions planned for 2015 to Laurel Creek and the Cathedral Range herd units. Weather in the mountains of the eastern Sierra is highly variable in the spring. Often extreme winds prevent helicopters from operating at the elevations required to capture and transport Sierra bighorn. To accommodate these uncertainties we include a discussion of logistics here where various contingencies are presented. We may reintroduce Sierra bighorn in 2-3 separate groups of animals. No individuals will be released alone. To increase the group size being released, we may hold animals for 1 night near the capture site and transport them for release the following day. It is also possible that rams will be released more than 1 day after ewe releases. While all of these contingency plans are less than ideal, we do not anticipate major impacts to the individuals being reintroduced. Ram and ewe groups are typically segregated at this time of year; thus, separate releases should not impact individual success. If animals are to be held overnight, they will be placed in transport boxes unrestrained. We will hold rams individually, and ewes in smaller groups of 2-3. Natural forage, such as needle grass, may be provided for consumption in transport boxes depending on holding times. Ice blocks will be provided for water. In the event that animals are held overnight, transport to the release site will occur as soon as possible the next morning.

Genetic Considerations
Sierra bighorn ewes for the Laurel Creek reintroduction will come from the Mt. Baxter herd (Table 9). This will ensure genetic diversity within the Kern Recovery unit because ewes in the Big Arroyo herd unit came from the Wheeler Ridge herd. Creating new populations with animals from different source herds maximizes genetic diversity because of different allele frequencies in different populations (see genetics section above). Ewes for the Cathedral Range reintroduction will come from the Mt. Langley herd. Similar to reintroductions at Big Arroyo and Olancha Peak, 3-5 individual rams will be selected from various herd units for each reintroduction. We will select rams with observed heterozygosity values greater than or equal to 0.6. The purpose of the ewe augmentation to Alger Creek is to further enhance genetic variability at Mt. Gibbs. Ewes will be selected, similar to rams, with observed heterozygosity greater than or equal to 0.6. We plan to select these ewes from the Mt. Langley herd; however, logistical constraints may require selection of ewes from various herd units. In previous augmentations, we observed that translocated ewes from the same herd remain together. To facilitate this positive social behavior in the augmentation to Alger Creek, we would like as many ewes as possible to come from the same source herd.

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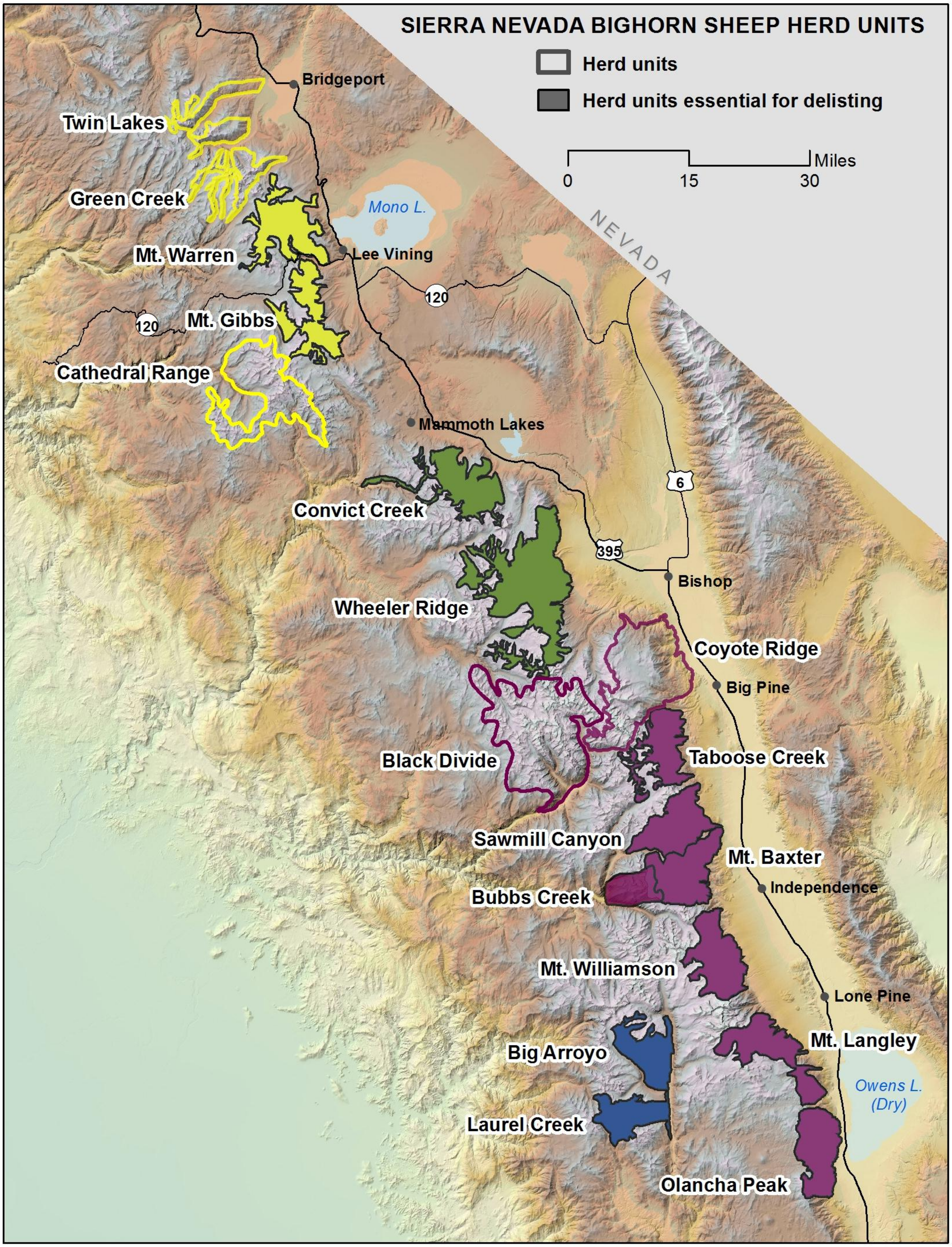
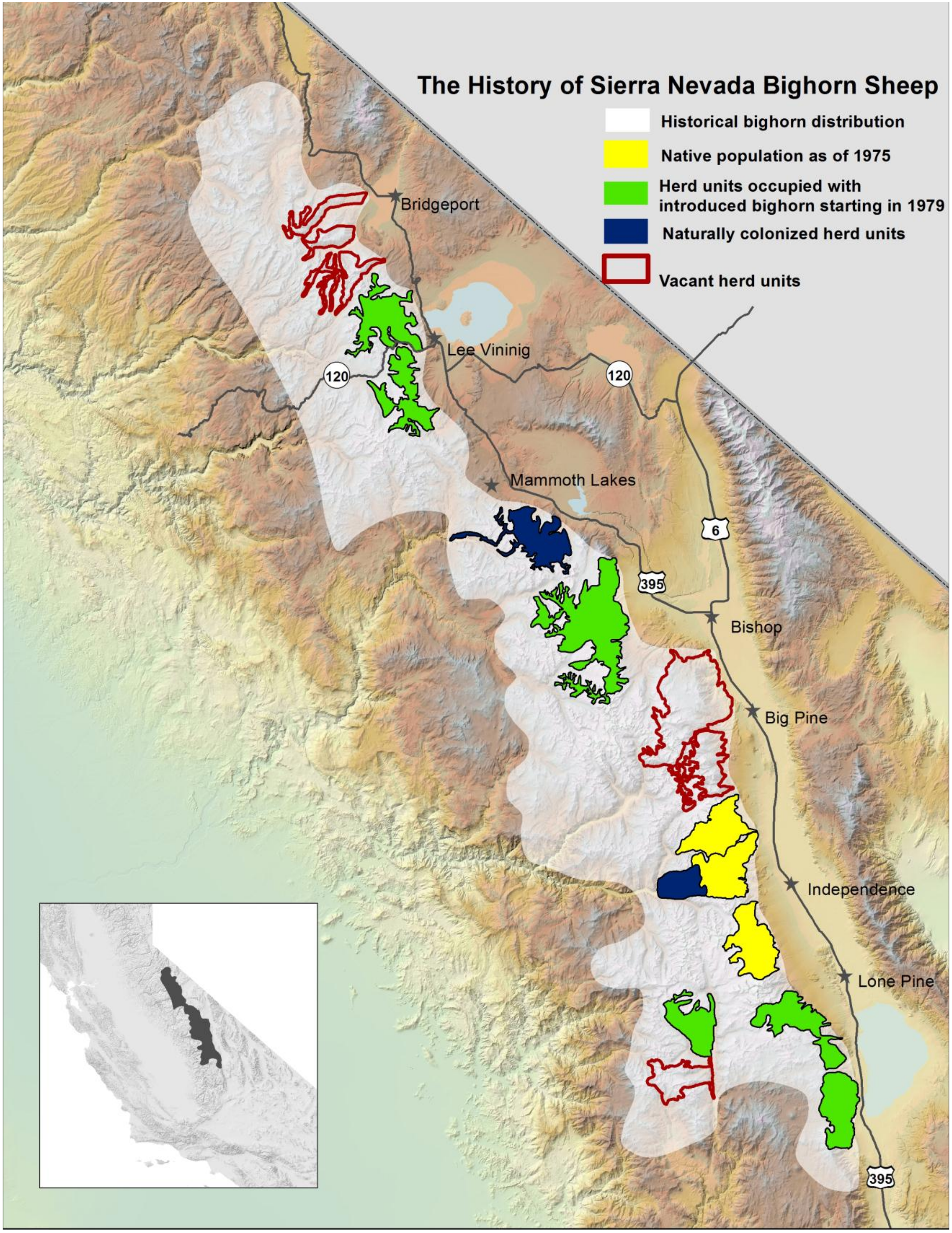
Map 1

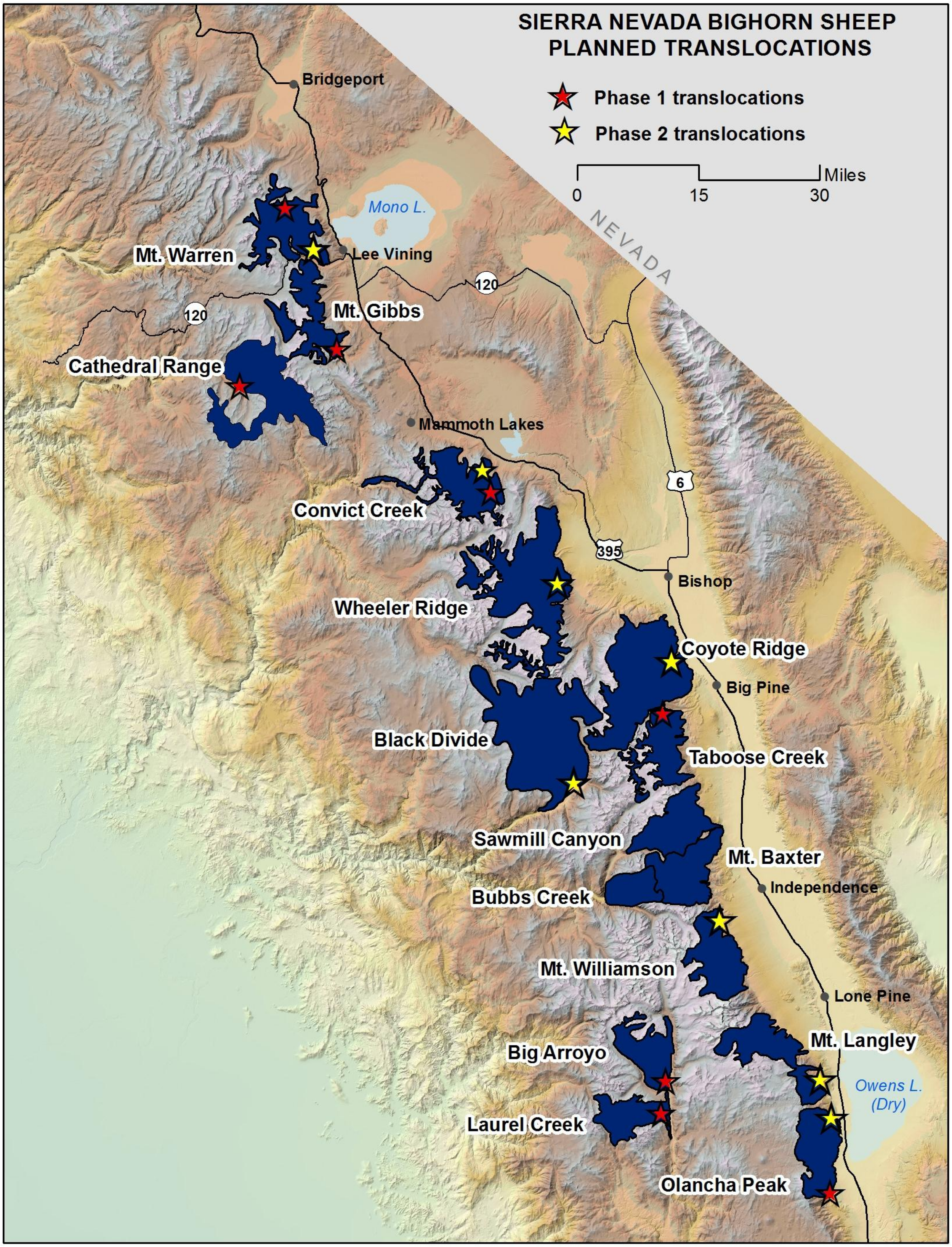

SIERRA NEVADA BIGHORN SHEEP HERD UNITS
☐ Herd units
■ Herd units essential for delisting
0
15
30
Miles
NEVADA
Bridgeport
Twin Lakes
Green Creek
Mono L.
Mt. Warren
Lee Vining
120
Mt. Gibbs
120
Cathedral Range
Mammoth Lakes
6
Convict Creek
395
Bishop
Wheeler Ridge
Coyote Ridge
Big Pine
Black Divide
Taboose Creek
Sawmill Canyon
Mt. Baxter
Bubbs Creek
Independence
Mt. Williamson
Lone Pine
Mt. Langley
Big Arroyo
Owens L. (Dry)
Laurel Creek
Olancha Peak

Map 2

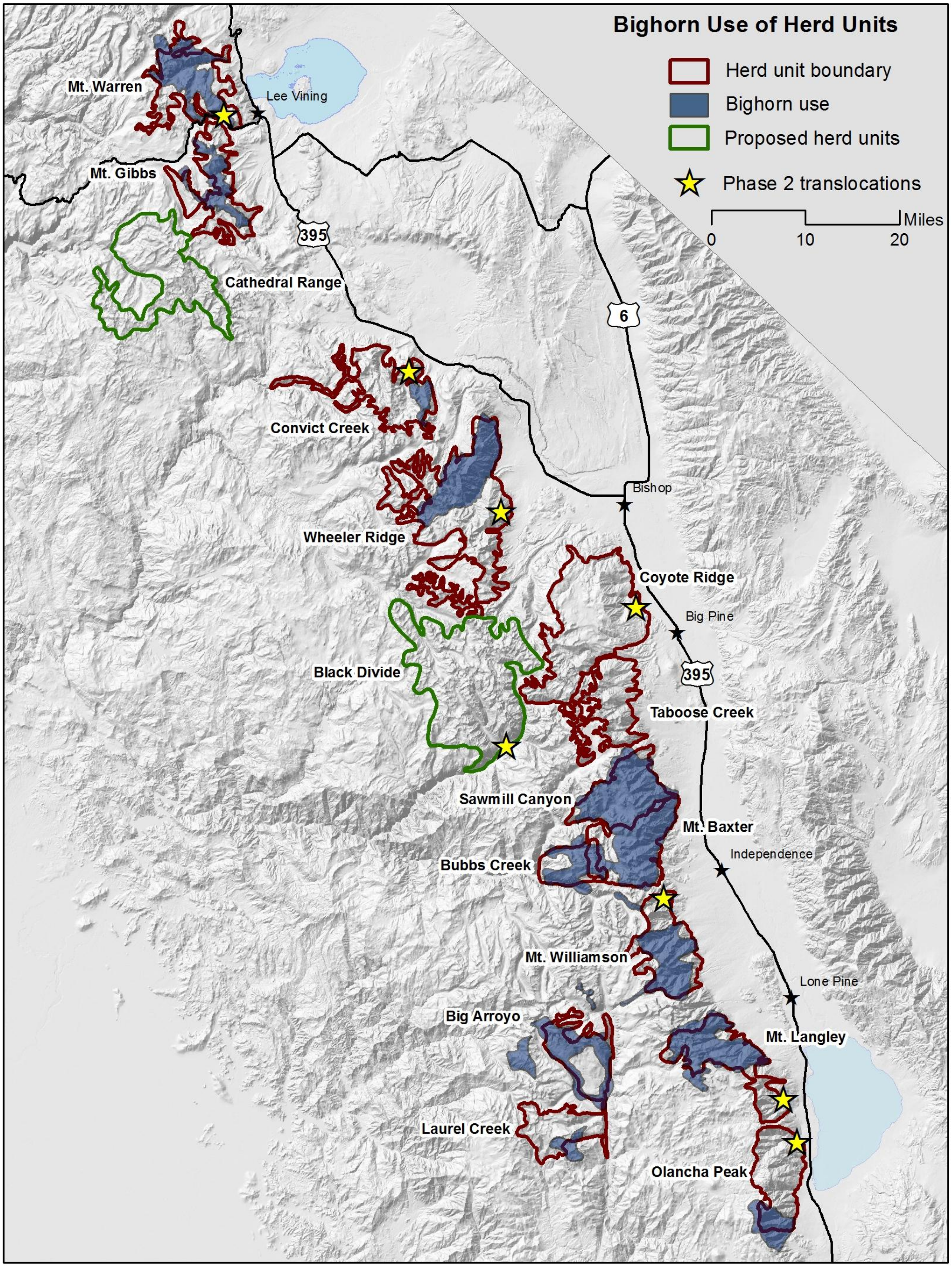


The History of Sierra Nevada Bighorn Sheep
Historical bighorn distribution
Native population as of 1975
Herd units occupied with introduced bighorn starting in 1979
Naturally colonized herd units
Vacant herd units
Bridgeport
Lee Vininig
120
120
Mammoth Lakes
6
395
Bishop
Big Pine
Independence
Lone Pine
395

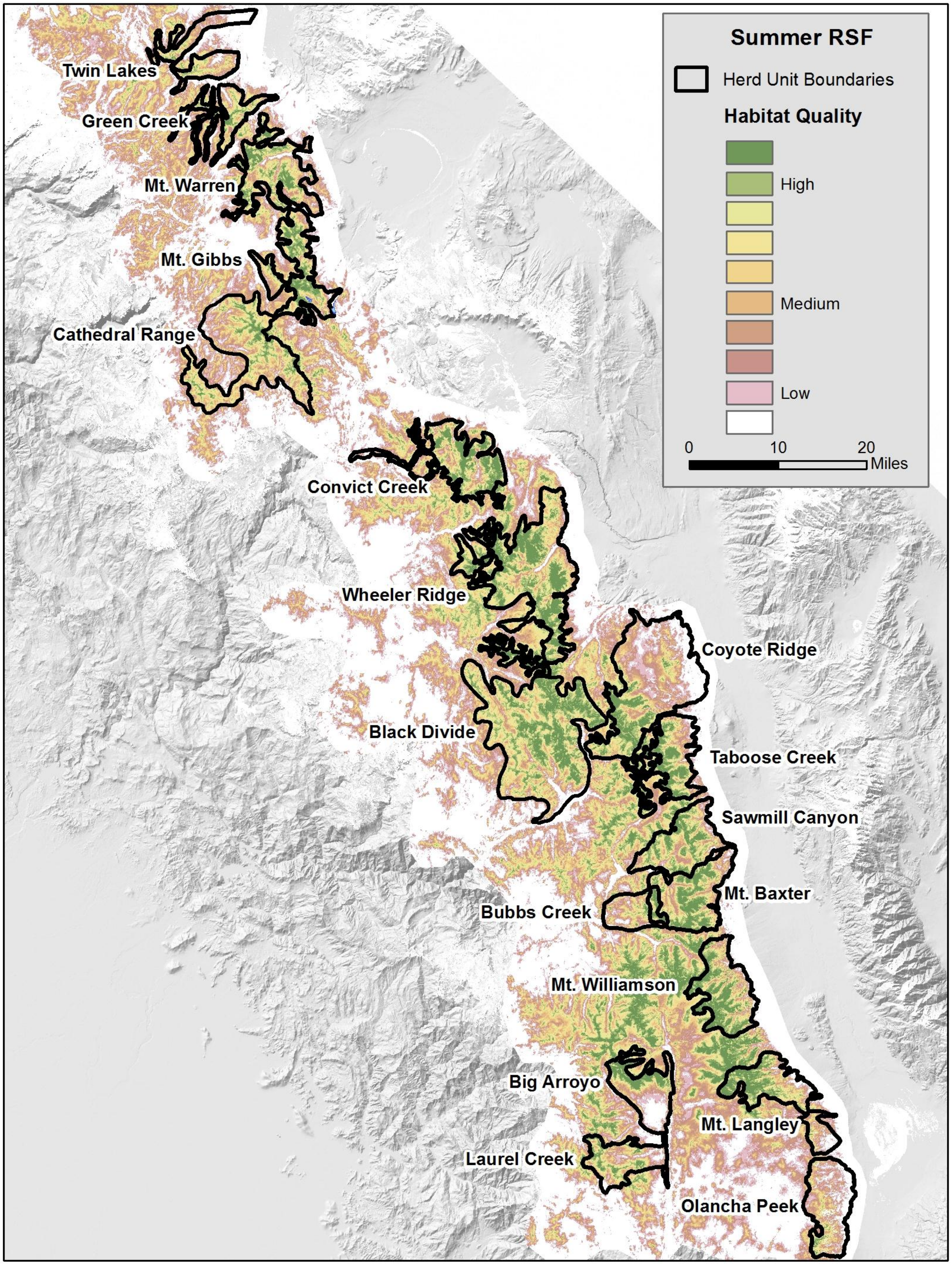
Map 3


SIERRA NEVADA BIGHORN SHEEP
PLANNED TRANSLOCATIONS
Phase 1 translocations
Phase 2 translocations
0
15
30
Miles
NEVADA
Bridgeport
Mono L.
Lee Vining
Mt. Warren
120
120
Mt. Gibbs
Cathedral Range
Mammoth Lakes
6
Convict Creek
395
Bishop
Wheeler Ridge
Coyote Ridge
Big Pine
Black Divide
Taboose Creek
Sawmill Canyon
Mt. Baxter
Independence
Bubbs Creek
Mt. Williamson
Lone Pine
Mt. Langley
Big Arroyo
Owens L.
(Dry)
Laurel Creek
Olancha Peak

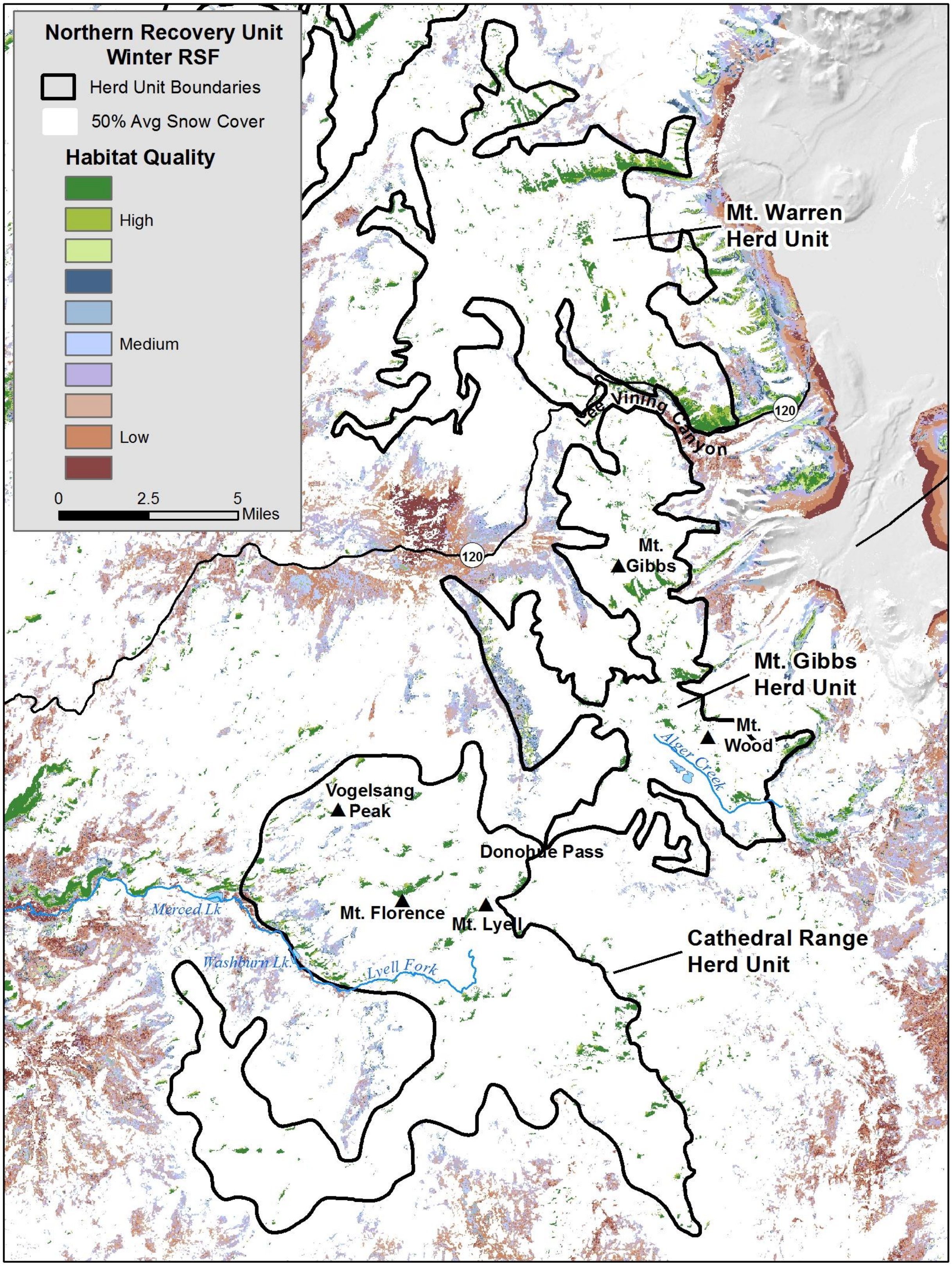
Map 4


Bighorn Use of Herd Units
Herd unit boundary
Bighorn use
Proposed herd units
Phase 2 translocations
0
10
20
Miles
Mt. Warren
Lee Vining
Mt. Gibbs
395
Cathedral Range
6
Convict Creek
Wheeler Ridge
Bishop
Coyote Ridge
Big Pine
395
Black Divide
Taboose Creek
Sawmill Canyon
Mt. Baxter
Independence
Bubbs Creek
Mt. Williamson
Lone Pine
Big Arroyo
Mt. Langley
Laurel Creek
Olancha Peak

Map 5

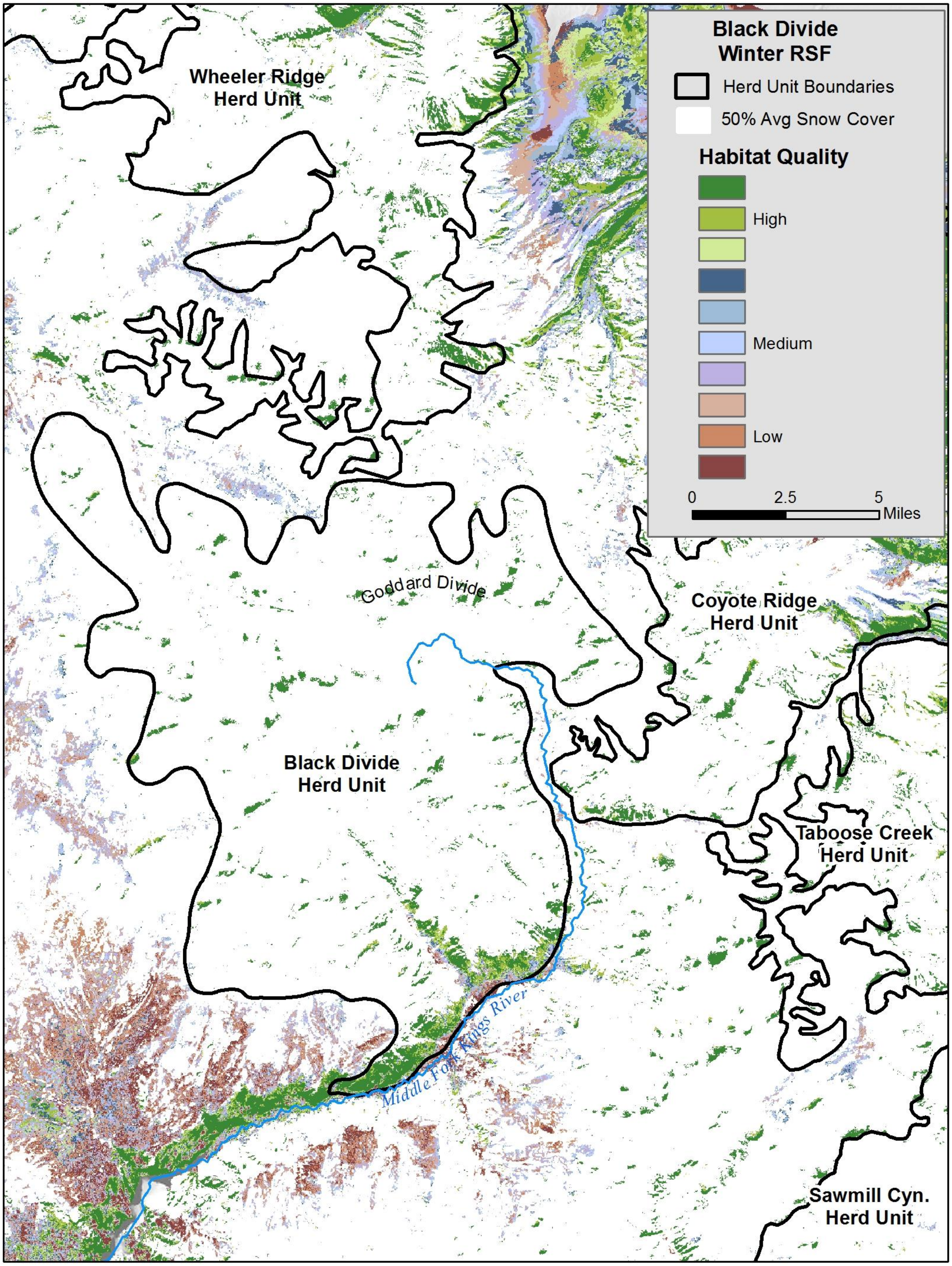

Summer RSF
Herd Unit Boundaries
Habitat Quality
High
Medium
Low
0
10
20
Miles
Twin Lakes
Green Creek
Mt. Warren
Mt. Gibbs
Cathedral Range
Convict Creek
Wheeler Ridge
Coyote Ridge
Black Divide
Taboose Creek
Sawmill Canyon
Mt. Baxter
Bubbs Creek
Mt. Williamson
Big Arroyo
Mt. Langley
Laurel Creek
Olancha Peek

Map 6

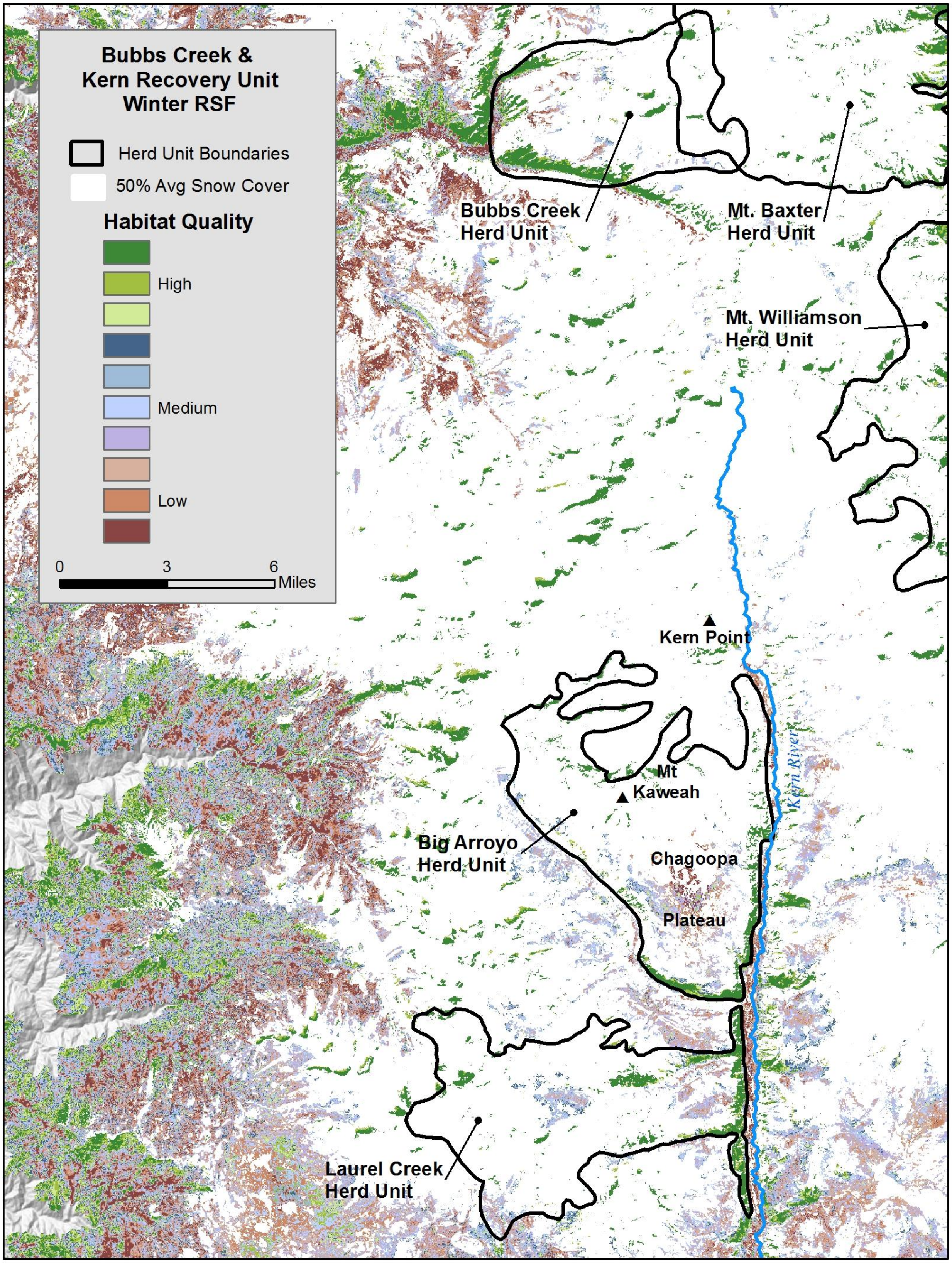


Northern Recovery Unit Winter RSF
Herd Unit Boundaries
50% Avg Snow Cover
Habitat Quality
High
Medium
Low
0
2.5
5
Miles
Mt. Warren Herd Unit
Lee Vining Canyon
120
120
Mt. Gibbs
Mt. Gibbs Herd Unit
Mt. Wood
Alger Creek
Vogelsang Peak
Donohue Pass
Mt. Florence
Mt. Lyell
Merced Lk
Washburn Lk.
Lyell Fork
Cathedral Range Herd Unit

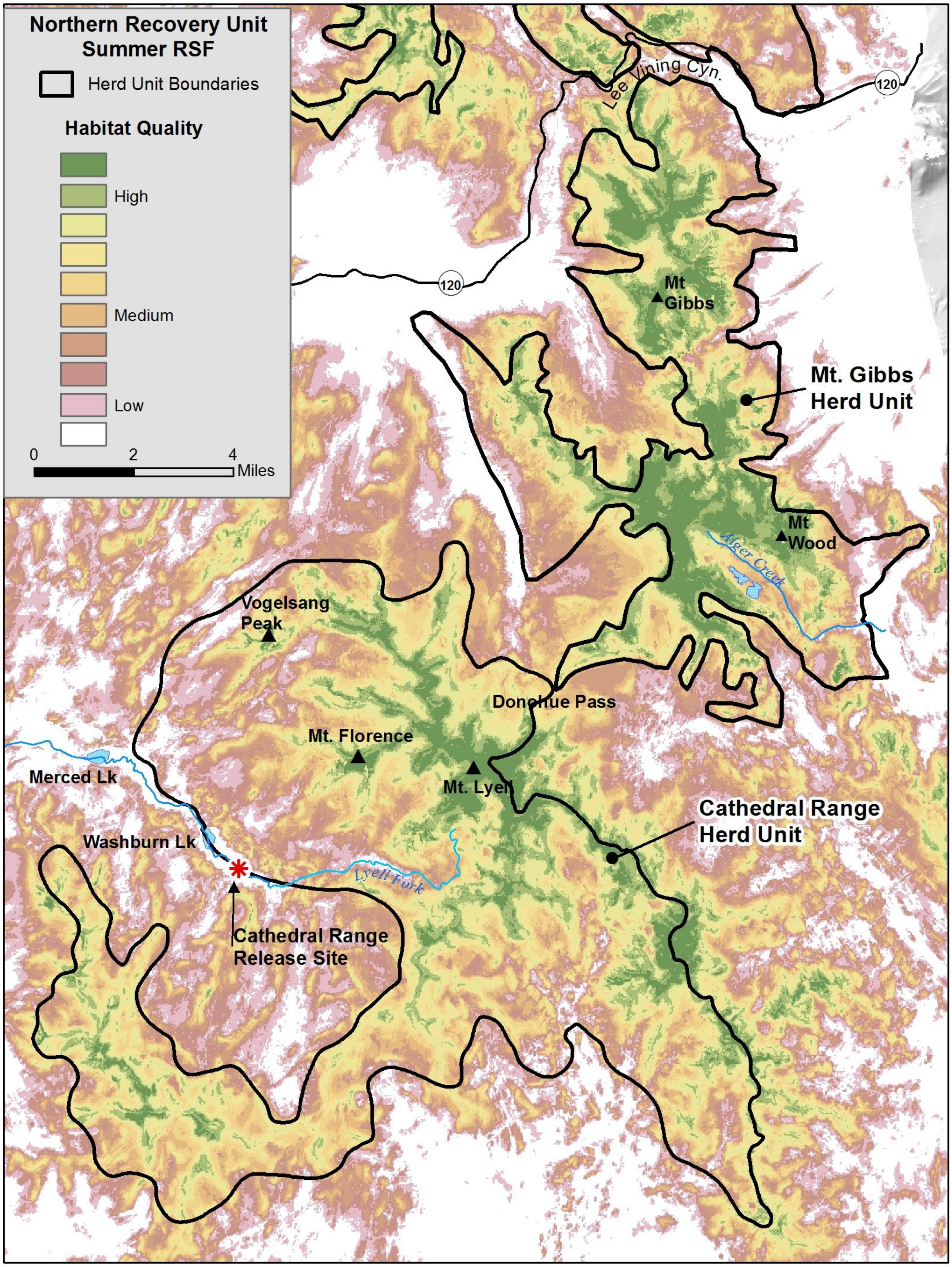
Map 7


Black Divide
Winter RSF
Herd Unit Boundaries
50% Avg Snow Cover
Habitat Quality
High
Medium
Low
0
2.5
5
Miles
Wheeler Ridge
Herd Unit
Goddard Divide
Coyote Ridge
Herd Unit
Black Divide
Herd Unit
Taboose Creek
Herd Unit
Middle Fork Kings River
Sawmill Cyn.
Herd Unit

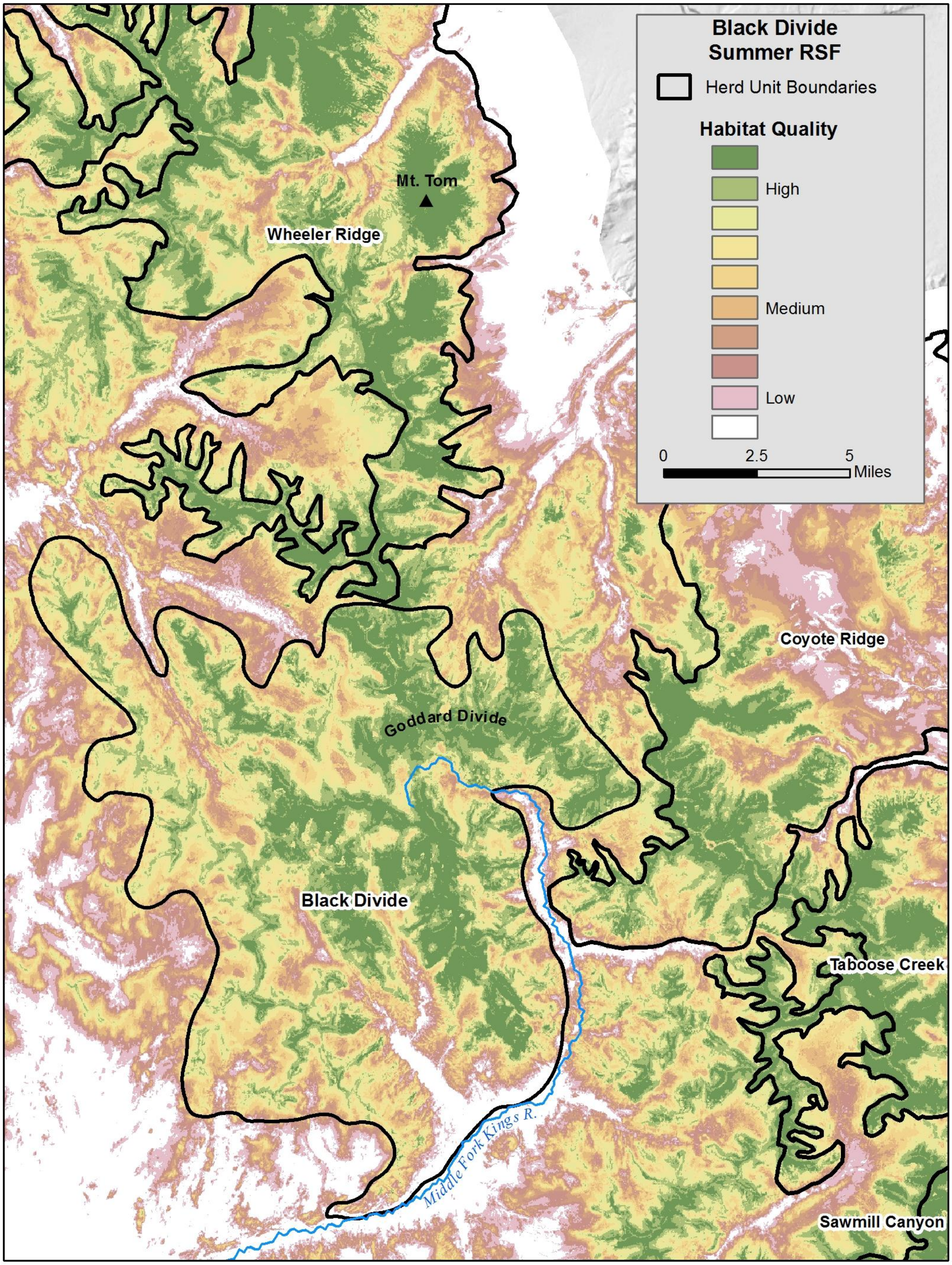
Map 8


Bubbs Creek & Kern Recovery Unit Winter RSF
Herd Unit Boundaries
50% Avg Snow Cover
Habitat Quality
High
Medium
Low
0
3
6
Miles
Bubbs Creek Herd Unit
Mt. Baxter Herd Unit
Mt. Williamson Herd Unit
Kern Point
Kern River
Mt Kaweah
Big Arroyo Herd Unit
Chagoopa
Plateau
Laurel Creek Herd Unit

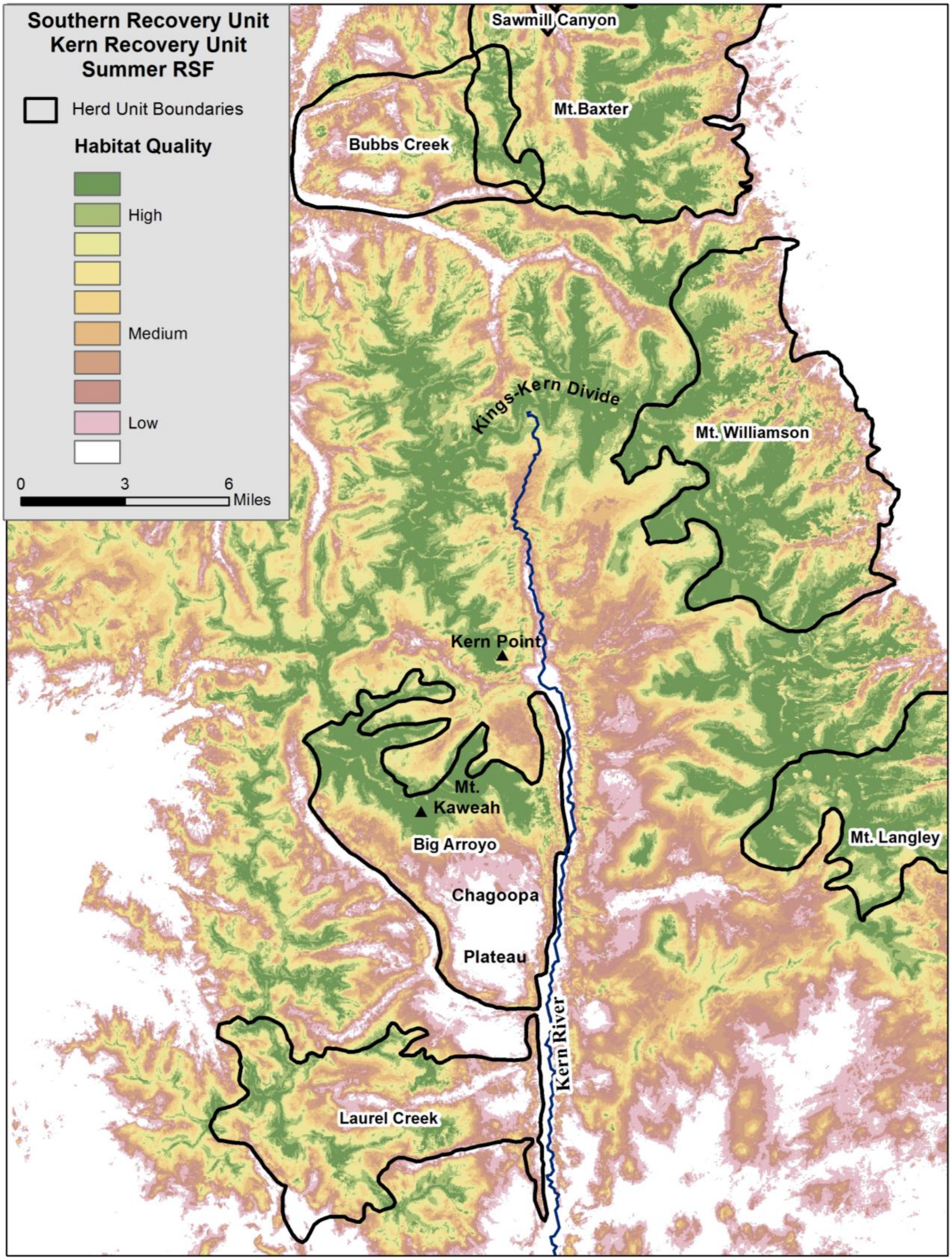
Map 9


Northern Recovery Unit
Summer RSF
Herd Unit Boundaries
Habitat Quality
High
Medium
Low
0
2
4
Miles
Lee Vining Cyn.
120
120
Mt
Gibbs
Mt. Gibbs
Herd Unit
Mt
Wood
Alger Creek
Vogelsang
Peak
Donohue Pass
Mt. Florence
Mt. Lyell
Merced Lk
Washburn Lk
Lyell Fork
Cathedral Range
Herd Unit
Cathedral Range
Release Site

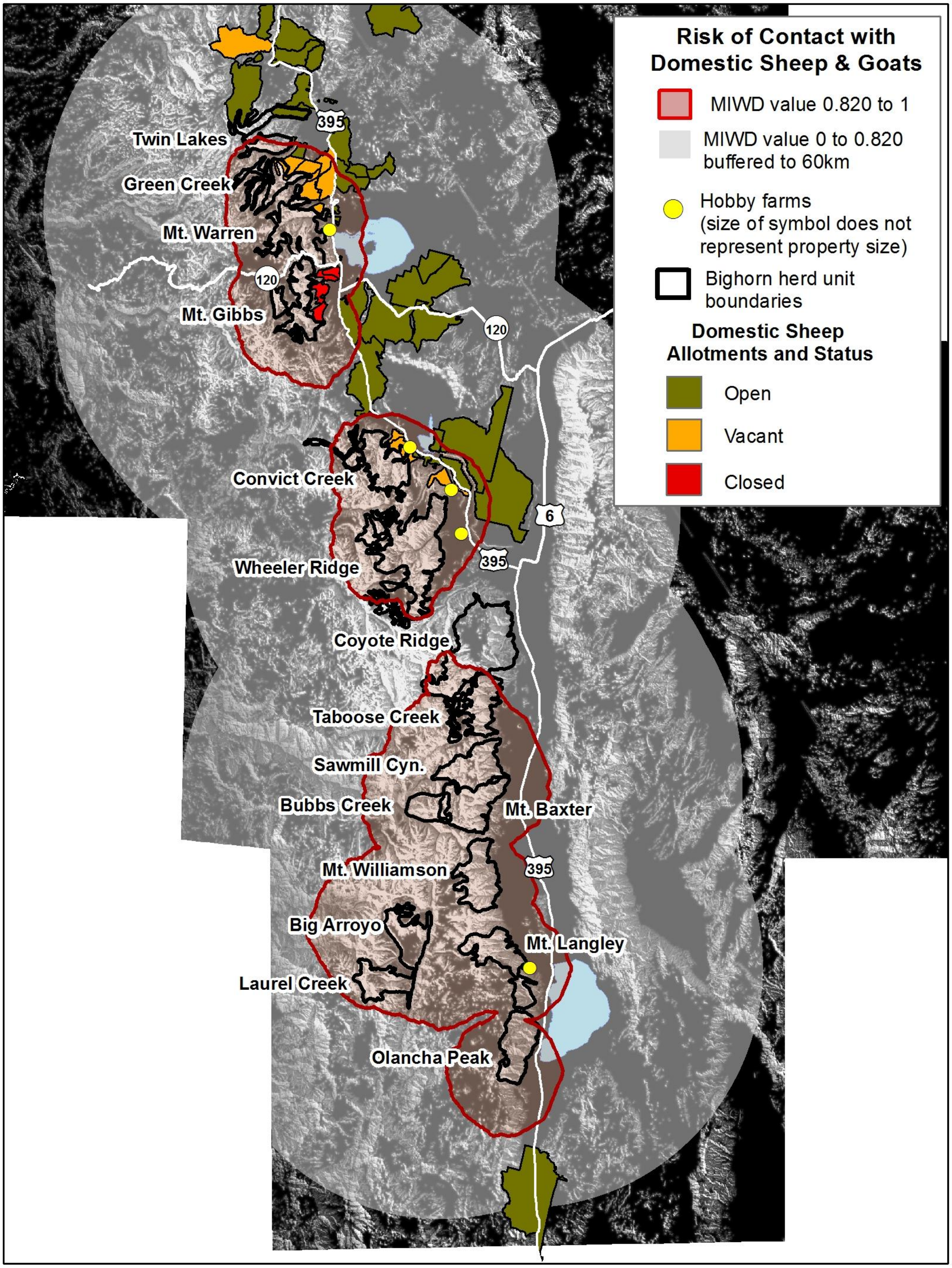
Map 10


Black Divide
Summer RSF
Herd Unit Boundaries
Habitat Quality
High
Medium
Low
0
2.5
5
Miles
Mt. Tom
Wheeler Ridge
Coyote Ridge
Goddard Divide
Black Divide
Taboose Creek
Sawmill Canyon
Middle Fork Kings R.

Map 11

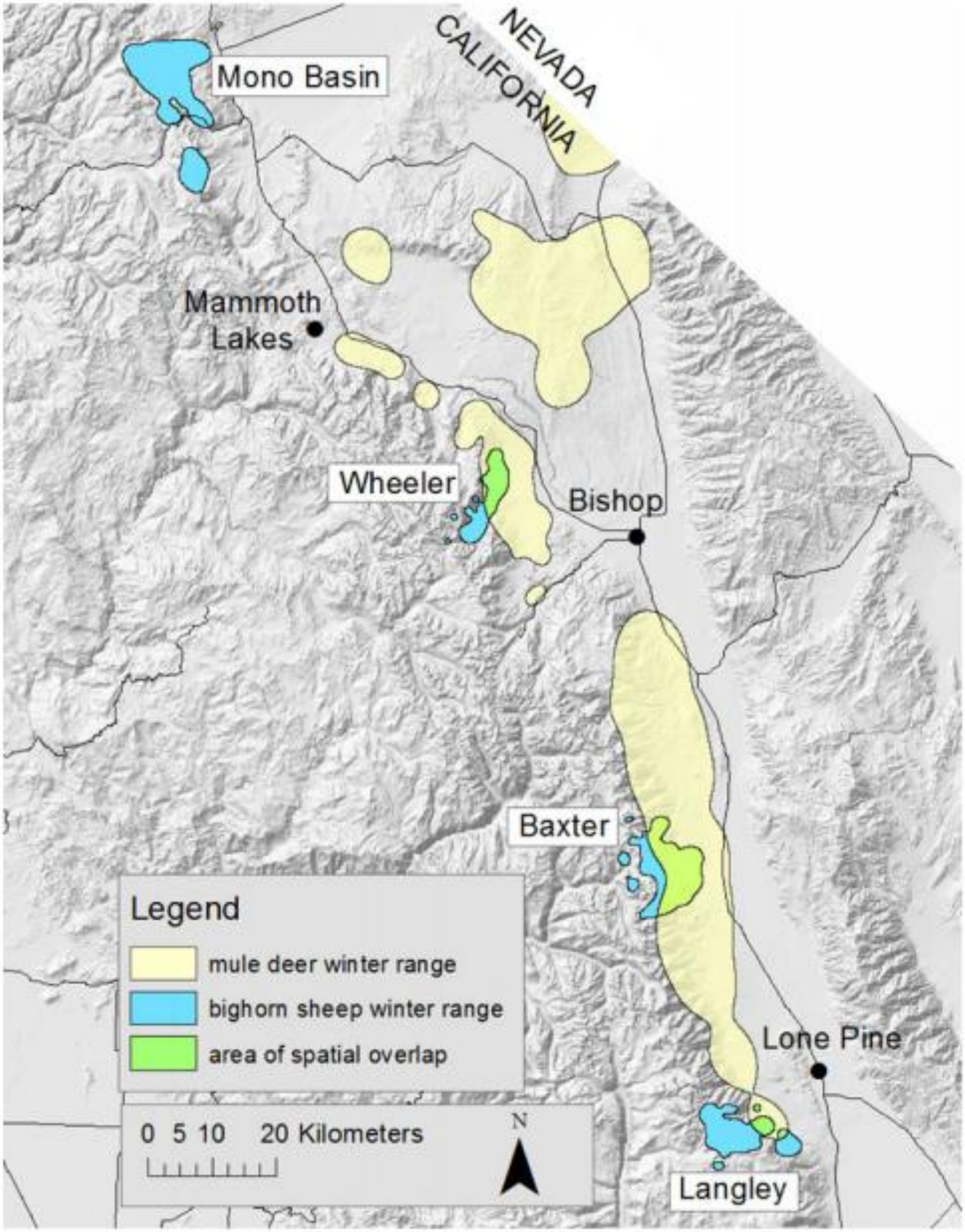

Southern Recovery Unit
Kern Recovery Unit
Summer RSF
Herd Unit Boundaries
Habitat Quality
High
Medium
Low
0
3
6
Miles
Sawmill Canyon
Mt.Baxter
Bubbs Creek
Kings-Kern Divide
Mt. Williamson
Kern Point
Mt. Kaweah
Big Arroyo
Chagoopa Plateau
Mt. Langley
Kern River
Laurel Creek

Map 12

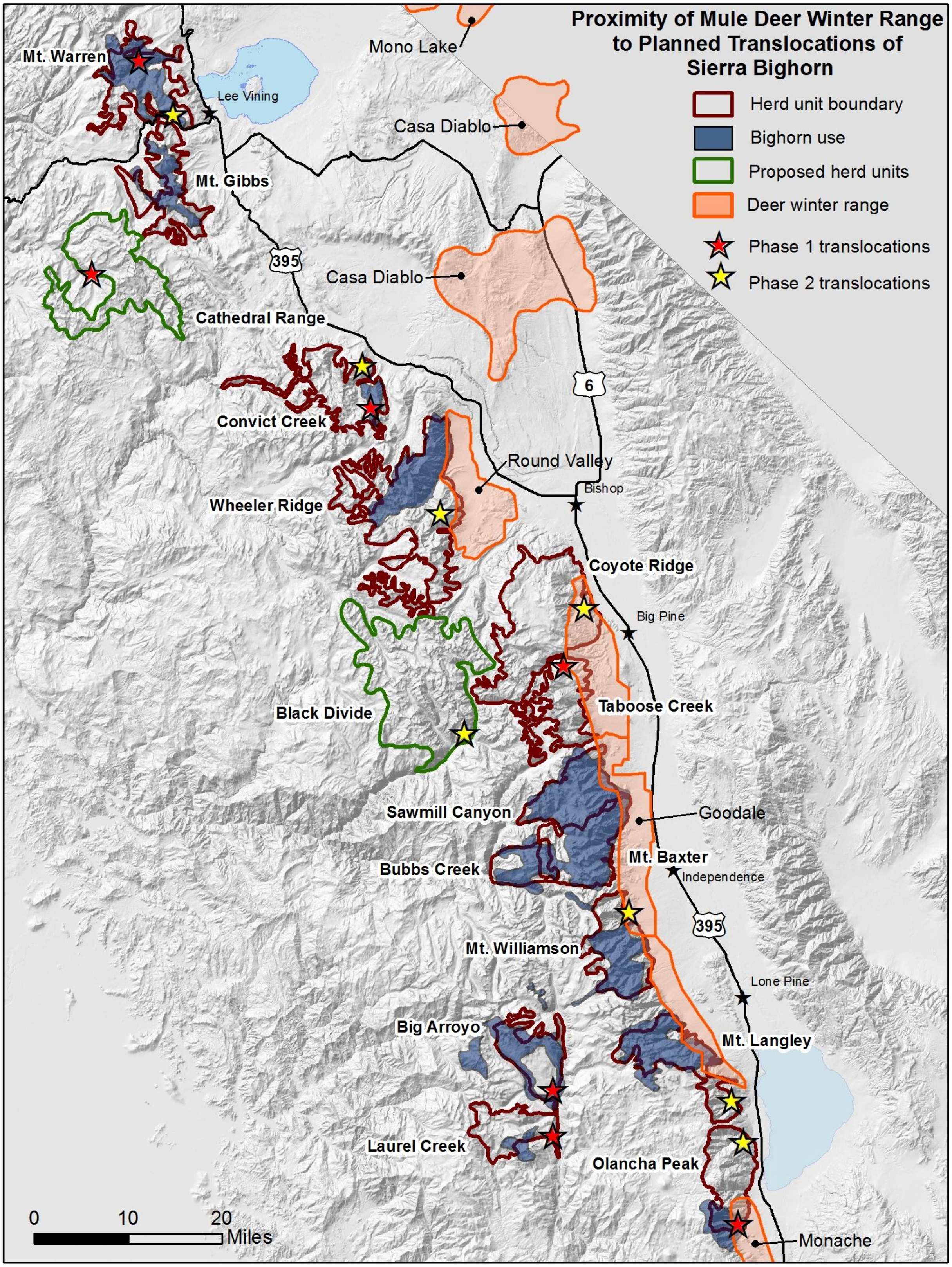


Risk of Contact with Domestic Sheep & Goats
MIWD value 0.820 to 1
MIWD value 0 to 0.820 buffered to 60km
Hobby farms (size of symbol does not represent property size)
Bighorn herd unit boundaries
Domestic Sheep Allotments and Status
Open
Vacant
Closed
Twin Lakes
Green Creek
Mt. Warren
Mt. Gibbs
Convict Creek
Wheeler Ridge
Coyote Ridge
Taboose Creek
Sawmill Cyn.
Bubbs Creek
Mt. Baxter
Mt. Williamson
Big Arroyo
Laurel Creek
Mt. Langley
Olancha Peak
395
120
6

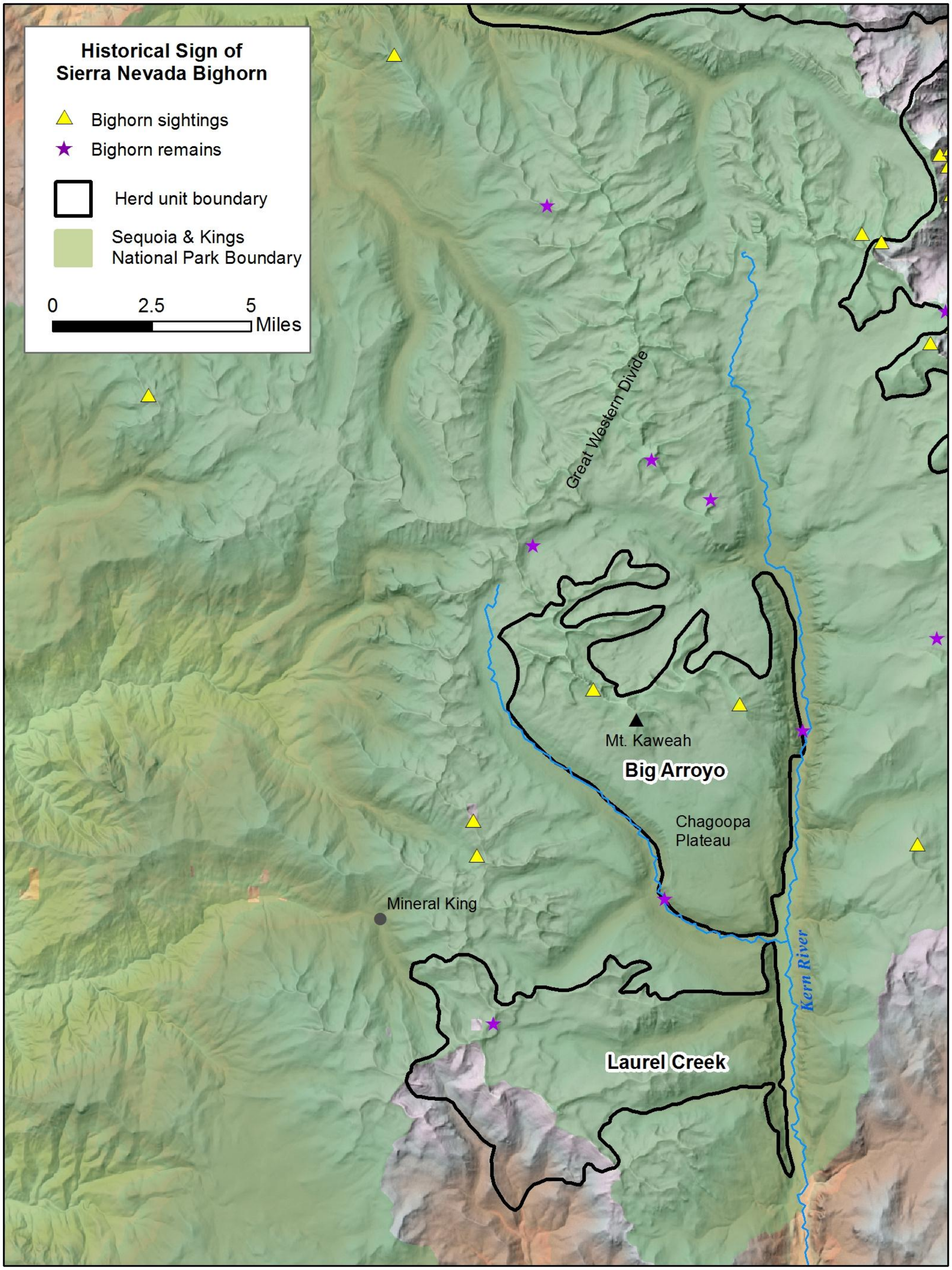
Map 13. Sierra bighorn winter ranges for source populations of translocation stock and their respective areas of overlap with mule deer (adapted from Johnson et al. 2013).



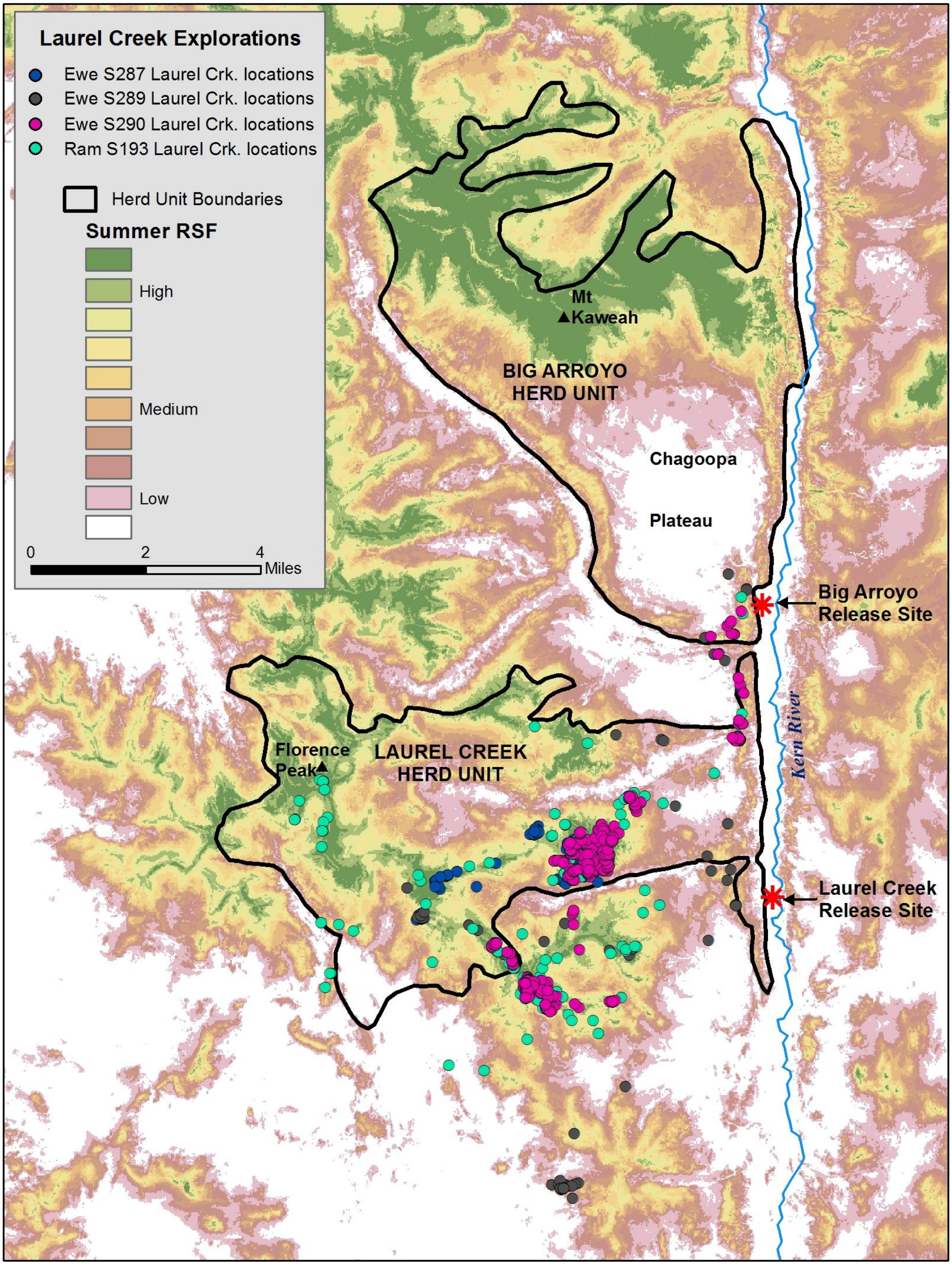
Map 14


Proximity of Mule Deer Winter Range to Planned Translocations of Sierra Bighorn
Herd unit boundary
Bighorn use
Proposed herd units
Deer winter range
Phase 1 translocations
Phase 2 translocations
Mono Lake
Mt. Warren
Lee Vining
Casa Diablo
Mt. Gibbs
395
Casa Diablo
Cathedral Range
6
Convict Creek
Round Valley
Bishop
Wheeler Ridge
Coyote Ridge
Big Pine
Taboose Creek
Black Divide
Sawmill Canyon
Goodale
Bubbs Creek
Mt. Baxter
Independence
395
Mt. Williamson
Lone Pine
Big Arroyo
Mt. Langley
Laurel Creek
Olancha Peak
Monache
0
10
20
Miles

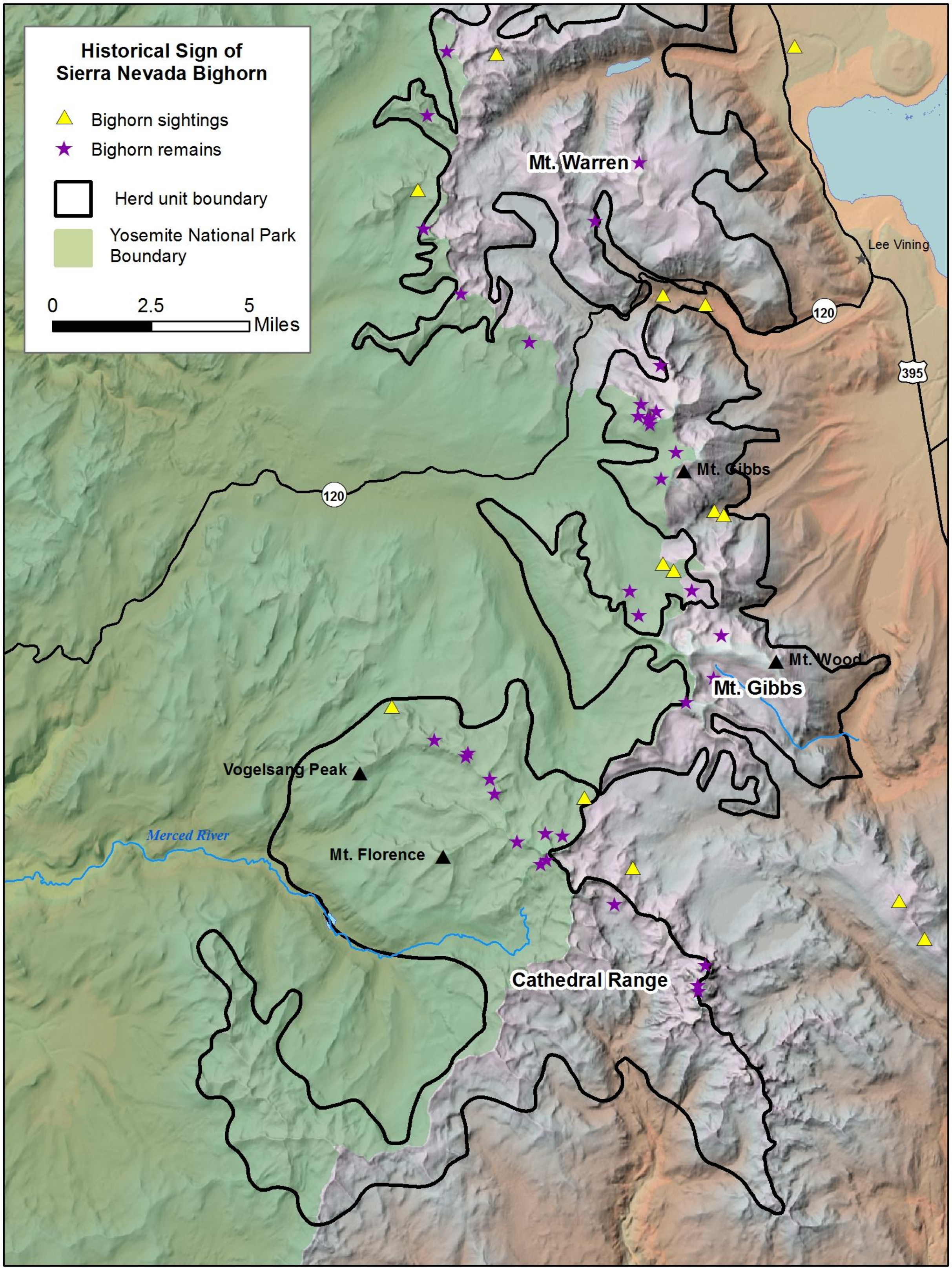
Map 15


Historical Sign of Sierra Nevada Bighorn
△ Bighorn sightings
★ Bighorn remains
☐ Herd unit boundary
🟩 Sequoia & Kings National Park Boundary
0
2.5
5
Miles
Great Western Divide
Mt. Kaweah
Big Arroyo
Chagoopa Plateau
Mineral King
Kern River
Laurel Creek

Map 16


Laurel Creek Explorations
Ewe S287 Laurel Crk. locations
Ewe S289 Laurel Crk. locations
Ewe S290 Laurel Crk. locations
Ram S193 Laurel Crk. locations
Herd Unit Boundaries
Summer RSF
High
Medium
Low
0
2
4
Miles
Mt Kaweah
BIG ARROYO HERD UNIT
Chagoopa
Plateau
Big Arroyo Release Site
Kern River
Florence Peak
LAUREL CREEK HERD UNIT
Laurel Creek Release Site

Map 17


Historical Sign of
Sierra Nevada Bighorn
Bighorn sightings
Bighorn remains
Herd unit boundary
Yosemite National Park Boundary
0
2.5
5
Miles
Mt. Warren
Lee Vining
120
395
Mt. Gibbs
120
Mt. Wood
Mt. Gibbs
Vogelsang Peak
Merced River
Mt. Florence
Cathedral Range