

SUPPORTING INFORMATION

Appendix S1. Number of collared adult female elk.

Table S1. Number of adult female elk monitored from 2005-2015 in eight Greater Yellowstone Ecosystem herds.

Herd	Group	Year										
		2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015
Blacktail	Migrant	0	0	0	0	0	0	25	7	6	4	5
	Resident	0	0	0	0	0	0	1	0	0	1	0
Dome Mountain	Migrant	0	0	12	23	2	0	0	0	0	0	0
	Resident	0	0	0	3	0	0	0	0	0	0	0
Greeley	Migrant	0	0	0	0	0	0	0	0	0	0	5
	Resident	0	0	0	0	0	0	0	0	0	0	10
Madison Valley	Migrant	17	27	2	0	0	0	0	0	0	0	0
	Resident	0	1	0	0	0	0	0	0	0	0	0
Mill Creek	Migrant	0	0	0	0	0	0	0	0	0	0	9
	Resident	0	0	0	0	0	0	0	0	0	0	7
North Madison	Resident	0	0	0	0	0	0	0	0	0	17	7
Paradise Valley	Migrant	0	0	0	0	15	5	0	0	0	0	0
	Resident	0	0	0	1	22	13	0	0	0	0	0
Sage Creek	Migrant	0	0	0	0	0	0	0	16	3	3	2
	Resident	0	0	0	0	0	0	0	9	0	0	0

Appendix S2. Methods for estimating low, average, and heavy snowfall years.

We downloaded snow water equivalent (SWE) data from 19 SNOTEL sites (U.S. Department of Agriculture, Natural Resources Conservation Service) located within the Montana designated surveillance area (DSA) for brucellosis during all years that elk were monitored (2005-2015). At each site in each year, we calculated the cumulative SWE value from 1 October-30 April. Because of the variation in cumulative SWE values among sites, we calculated a SWE anomaly for each site in each year. We calculated the cumulative SWE anomaly by subtracting the mean cumulative SWE value from 2005-2015 for individual sites from the cumulative SWE value for each site in each year. We then identified representative years for low (2010), average (2013), and heavy (2011) snowfall years from among the years of elk monitoring (Fig. S1).

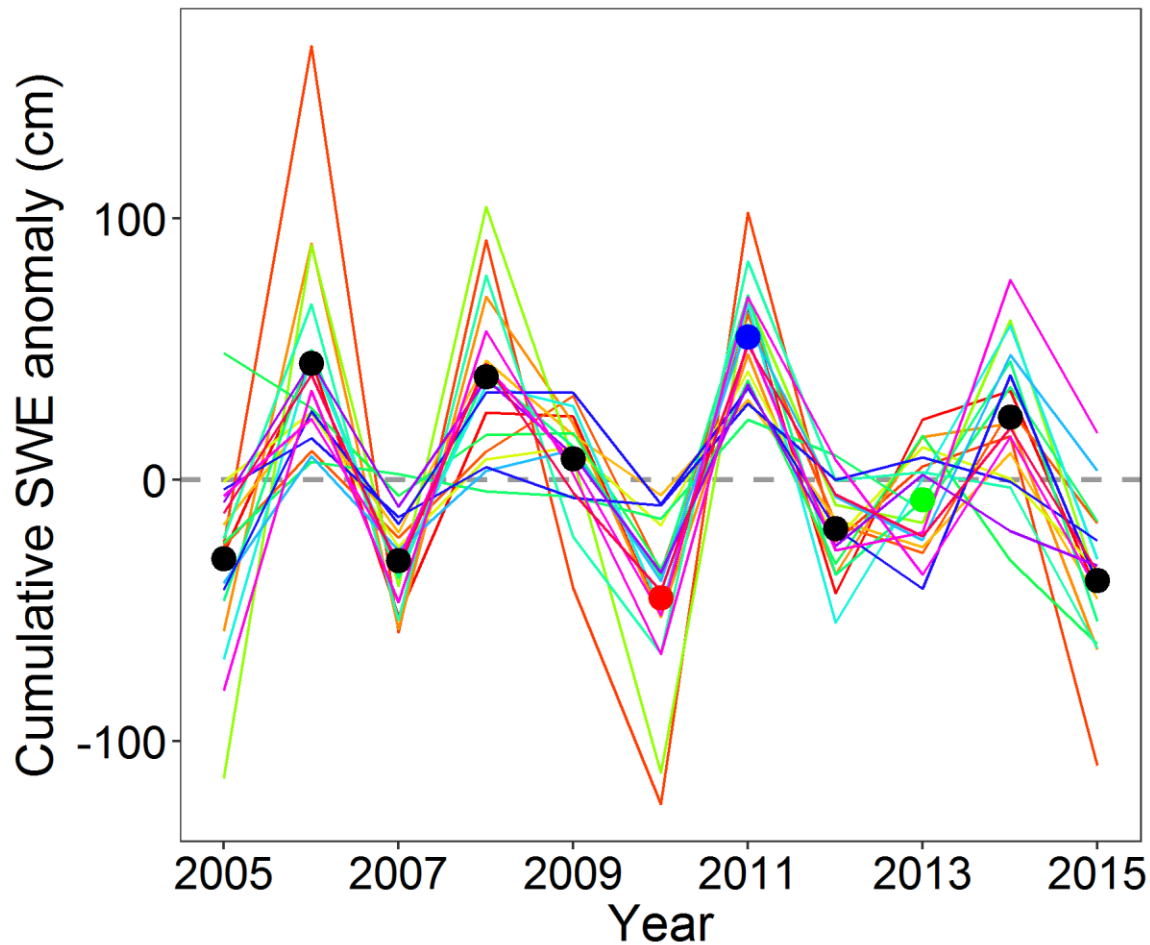


Figure S1. Cumulative snow water equivalent (SWE) anomaly from 1 October-30 April for 19 SNOTEL sites located within the Montana designated surveillance area (DSA) from 2005-2015. Each SNOTEL site is represented by a line. The average cumulative SWE anomaly in each year is shown by filled circles, with low (red circle; 2010), average (green circle; 2013), and heavy (blue circle; 2011) snowfall years identified.

Appendix S3. Elk abundance, brucellosis seroprevalence data, and group density.

Every winter, the Montana Department of Fish, Wildlife, and Parks collects elk survey data on winter range (see Proffitt et al. [2015] for additional details). We used the most recent elk trend counts available (2016 or 2017) and the average calf:female ratios from the 3 most recent available years (this ratio is not estimated every year) to estimate the number of adult female elk $f(g, h)$ from each group g in each herd h as:

$$f(g, h) = \left(1 - \left(\frac{z_h + m}{100 + z_h + m} \right) \right) \times n_h \times q_g \quad (1)$$

where z_h is the estimated number of calves per 100 adult females in herd h , m is the estimated number of males per 100 adult females (assumed to be 10 for all herds), n_h is the elk trend count for herd h , and q_g is the estimated group proportion (i.e., the proportion of migrants or residents, estimated from collared elk-year classifications of migrants and residents; Table S1) for herd h .

The Montana Department of Fish, Wildlife and Parks initiated a multi-year brucellosis surveillance project in 2011. As part of this project, personnel from the department tested hunter-harvested and research-captured adult female elk for exposure to *Brucella abortus*. Where available, we used the proportion of positive results from these tests during 2011-2017 to estimate herd seroprevalence (Table S2). For two herds without data from this project, we used seroprevalence estimates for 2014 estimated from models predicting the trend in seroprevalence over time, which were built using data collected from a combination of hunter-harvested and research-captured adult female elk (Brennan, Cross, Portacci, Scurlock, & Edwards, 2017). Within herds, we assumed that the seroprevalence for migrant and resident groups was the same, because we did not detect any discernable pattern in the seroprevalence of collared migrant and resident elk (Fig. S1).

We estimated the density experienced by migrant and resident groups to explore how density changed during the risk period, and the consequent implications for pathogen transmission. We used our winter range kernels (see Methods) to approximate the area occupied by resident elk throughout the risk period, and estimated the daily density experienced by residents on winter range $D(r, h, t)$ as:

$$D(r, h, t) = \frac{f_{rh} + (f_{mh} \times q_{ct})}{a_{ch}} \quad (2)$$

where f_{rh} is the estimated number of adult female elk from resident group r and herd h , f_{mh} is the estimated number of adult female elk from migrant group m and herd h , q_{ct} is the proportion of migrants inside winter range c at time step t (in days), and a_{ch} is the area (km²) of the herd's winter range kernel (f_{rh} and f_{mh} estimated from eqn 1). To estimate q_{ct} , we used our GPS dataset to calculate the daily average proportion of time migrant groups were inside winter range. We used our K_{xt} sliding window kernels (see eqn 2 in Methods) to approximate the area occupied by migrant elk after they departed from winter range, and estimated the daily density of migrant elk outside of winter range as:

$$D(m, h, t) = \frac{f_{mh} - (f_{mht} \times q_{ct})}{a_{mht} - a_{mht} \cap a_{ch}} \quad (3)$$

where a_{mht} is the area (km²) of the sliding window kernel for migrant group m from herd h at time step t (in days). We then estimated the overall daily density experienced by migrant groups as:

$$D(m, h, t) = \frac{(D(r, h, t) \times (f_{rh} + (f_{mh} \times q_{ct}))) + (D(m, h, o, t) \times (f_{mh} - (f_{mh} \times q_{ct})))}{f_{rh} + f_{mh}} \quad (4)$$

References

- Brennan, A., Cross, P. C., Portacci, K., Scurlock, B. M., & Edwards, W. H. (2017). Shifting brucellosis risk in livestock coincides with spreading seroprevalence in elk. *PLoS ONE*, *12*(6), 1–16. doi: 10.1371/journal.pone.0178780
- Proffitt, K. M., Anderson, N., Lukacs, P., Riordan, M. M., Gude, J. A., & Shamhart, J. (2015). Effects of elk density on elk aggregation patterns and exposure to brucellosis. *Journal of Wildlife Management*, *79*(3), 373–383. doi: 10.1002/jwmg.860

Table S1. Elk trend counts from 2016-2017 for eight Greater Yellowstone Ecosystem elk herds, with the estimated proportion of migrants, the 3-year average calf:female ratio, and the years of data contributing to the average calf:female ratio. Trend counts for the Dome Mountain and Mill Creek herds were conducted in 2017. All other counts were conducted in 2016.

Herd	Population estimate	Proportion of migrants	Calves:100 females	Survey years (calves:100 females)
Madison Valley	3,993	0.98	24.2	2013, 2014, 2016
Blacktail	1,357	0.96	32.7	2010, 2013-2014
Dome Mountain	3,888	0.93	26.0	2015-2017
Sage Creek	2,850	0.63	32.7	2010, 2013-2014
Mill Creek	786	0.56	32.0	2011 ^a
Paradise Valley	1,222	0.40	35.7	2014 ^a
Greeley	1,509	0.33	31.0	2010-2011, 2014
North Madison	2,878	0.00	30.0	2016 ^a

^a No prior survey data available.

Table S2. Estimated brucellosis seroprevalence of adult female elk from eight Greater Yellowstone Ecosystem herds, with 95% confidence intervals (CI), and the number of samples (*n*) contributing to the seroprevalence estimate. For brucellosis surveillance project data, seroprevalence values were estimated from samples from hunter-harvested and research-captured elk during 2011-2017, and confidence intervals were calculated from a binomial distribution. For Brennan et al. (2017) data, confidence intervals were derived from models predicting the trend in seroprevalence over time (see Brennan et al. [2017] for additional details).

Herd	Seroprevalence	95% CI		Source	<i>n</i>
Mill Creek	0.53	0.36	0.70	Brucellosis surveillance project	30
Madison Valley	0.36	0.26	0.47	Brennan et al. 2017 ^a	707
Dome Mountain	0.20	0.13	0.31	Brucellosis surveillance project	74
North Madison	0.17	0.09	0.28	Brucellosis surveillance project	60
Blacktail	0.12	0.07	0.20	Brucellosis surveillance project	100
Paradise Valley	0.06	0.02	0.12	Brennan et al. 2017	245
Sage Creek	0.05	0.02	0.12	Brucellosis surveillance project	92
Greeley	0.02	0.01	0.07	Brucellosis surveillance project	106

^a Brennan, A., Cross, P. C., Portacci, K., Scurlock, B. M., & Edwards, W. H. (2017). Shifting brucellosis risk in livestock coincides with spreading seroprevalence in elk. *PLoS ONE*, 12(6), 1–16. doi: 10.1371/journal.pone.0178780

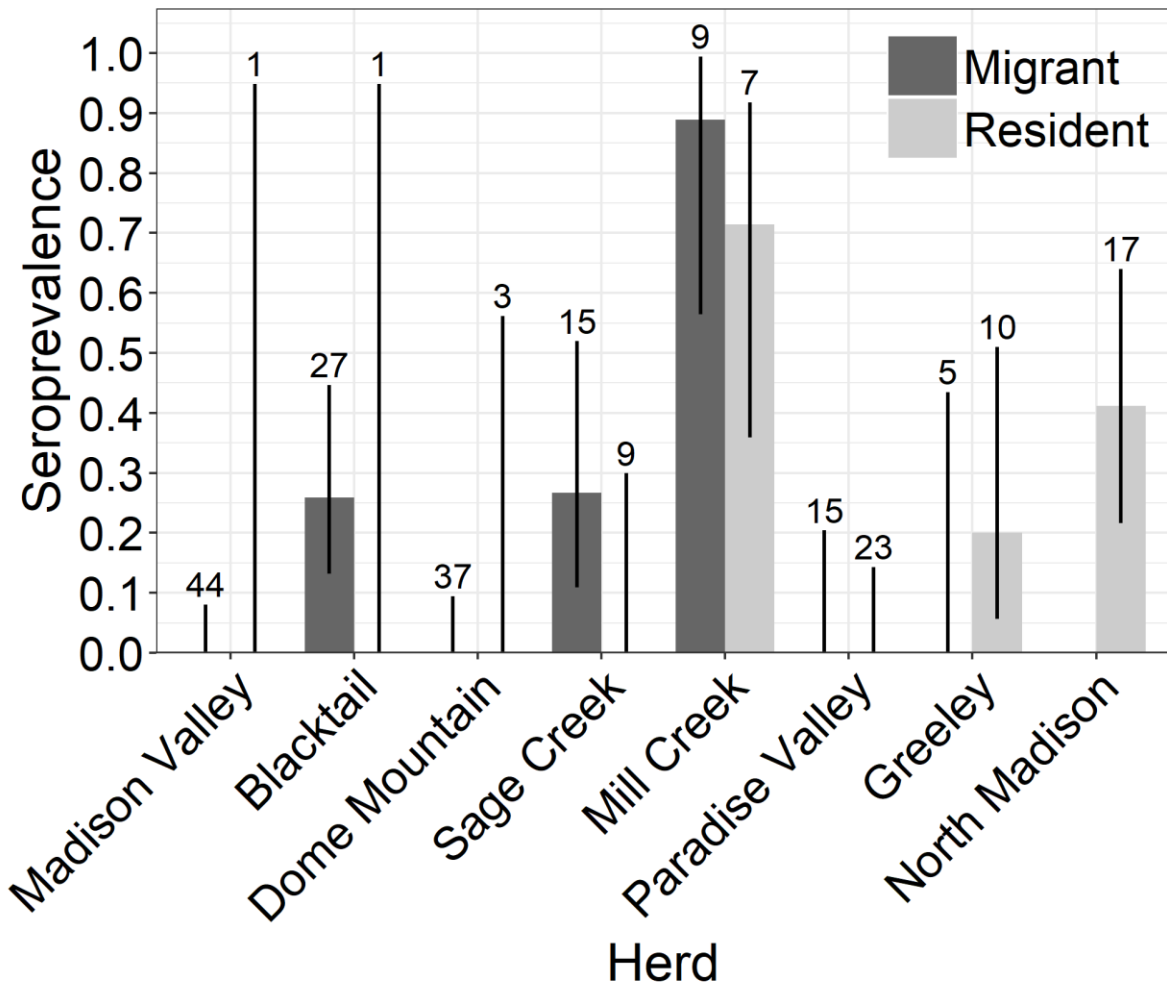


Figure S1. The proportion of positive results from tests for exposure to *Brucella abortus* for collared migrant and resident female elk from eight Greater Yellowstone Ecosystem herds. The number of collared elk in each group is given at the top of the 95% binomial confidence intervals (black lines).

Appendix S4. Areas of grazing land during the risk period.

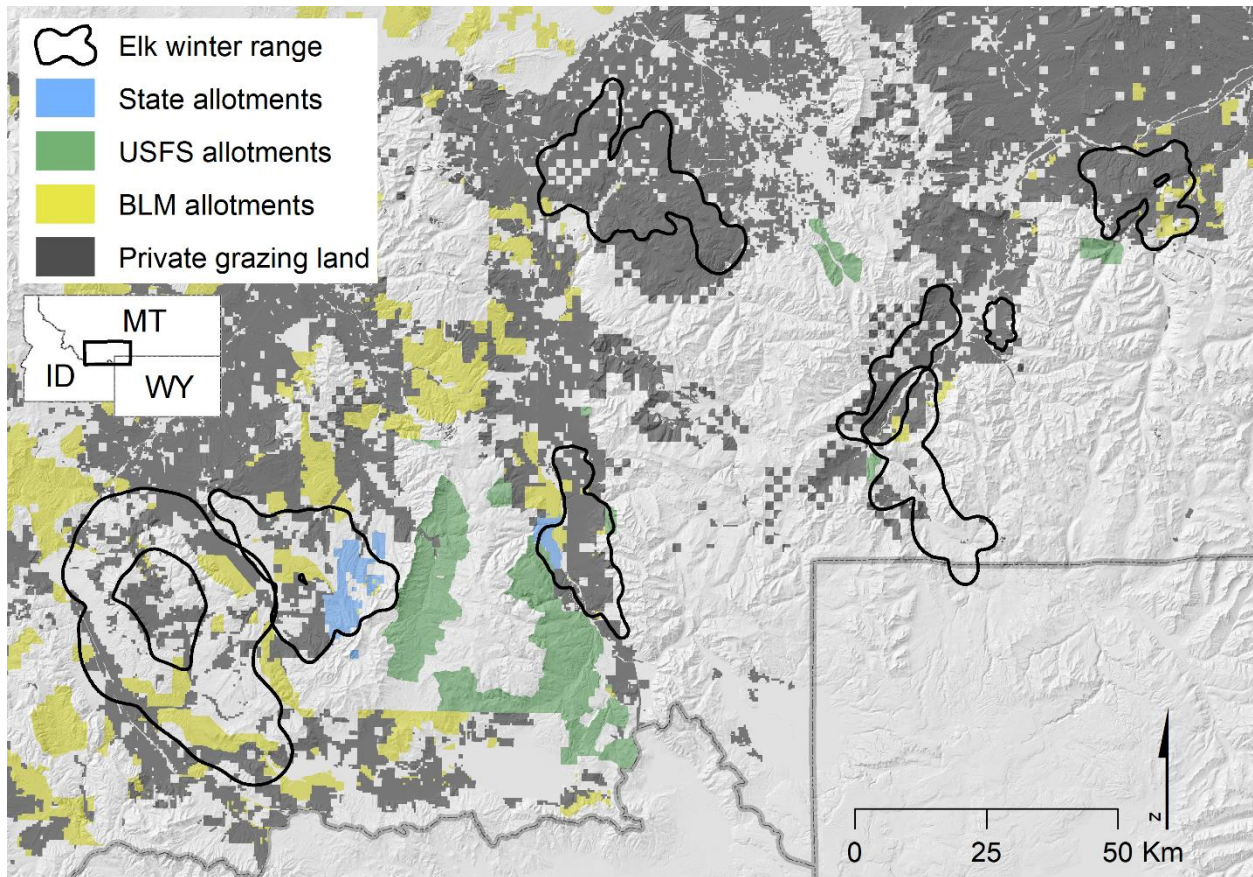


Figure S1. Winter ranges of eight Greater Yellowstone Ecosystem elk herds that wintered in southwest Montana, USA, with areas of grazing land during the risk period. Note that allotments that were not stocked during the risk period are not shown. Shading depicts hillshade of elevation.

Appendix S5. Results from resource selection functions.

Table S1. The average Spearman rank correlation (r_s) between withheld data and ranked bins for 10 repetitions of 5-fold cross validation with 10 bins of equal size for resource selection function models of migrant and resident female elk from eight Greater Yellowstone Ecosystem herds during winter (15 February-31 March), spring (1 April-31 May), and summer (1 June-30 June) seasons.

Herd	Group	Winter		Spring		Summer	
		Mean	Range	Mean	Range	Mean	Range
Blacktail	Migrant	1.00	1.00-1.00	1.00	1.00-1.00	0.99	0.95-1.00
	Resident	0.93	0.89-1.00	0.96	0.92-0.99	0.94	0.86-0.99
Dome Mountain	Migrant	1.00	0.99-1.00	1.00	1.00-1.00	1.00	1.00-1.00
	Resident	0.98	0.95-1.00	0.95	0.88-0.99	0.96	0.93-0.99
Greeley	Migrant	0.99	0.96-1.00	1.00	1.00-1.00	0.97	0.95-1.00
	Resident	0.96	0.93-1.00	1.00	1.00-1.00	0.94	0.90-0.98
Madison Valley	Migrant	1.00	1.00-1.00	1.00	1.00-1.00	1.00	1.00-1.00
	Resident	0.93	0.87-0.99	0.98	0.98-0.99	0.98	0.96-1.00
Mill Creek	Migrant	0.97	0.95-0.99	1.00	0.99-1.00	1.00	0.99-1.00
	Resident	0.99	0.98-1.00	1.00	0.99-1.00	0.87	0.84-0.90
North Madison	Resident	1.00	1.00-1.00	1.00	1.00-1.00	0.98	0.95-0.99
Paradise Valley	Migrant	0.99	0.99-1.00	1.00	1.00-1.00	1.00	0.99-1.00
	Resident	1.00	0.99-1.00	1.00	1.00-1.00	1.00	0.99-1.00
Sage Creek	Migrant	1.00	1.00-1.00	1.00	1.00-1.00	0.94	0.92-0.96
	Resident	0.99	0.96-0.99	1.00	1.00-1.00	1.00	0.99-1.00

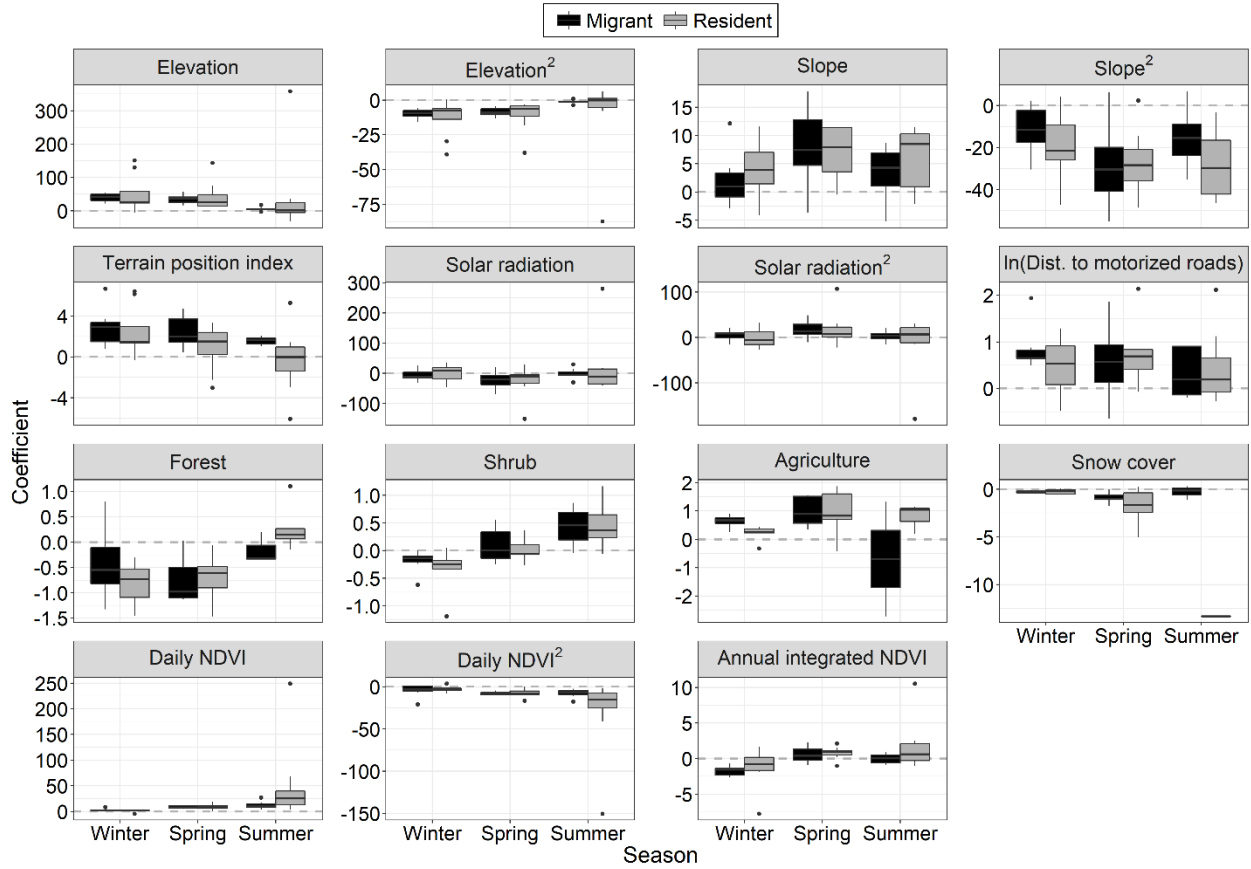


Figure S1. Boxplots of estimated coefficients from resource selection functions for migrant and resident adult female elk from eight Greater Yellowstone Ecosystem herds during winter (15 February-31 March), spring (1 April-31 May), and summer (1 June-30 June) seasons. The grey dashed line in each panel represents an estimated selection coefficient of 0.

Appendix S6. Estimated number of female elk, brucellosis seroprevalence, and abortion risk.

Table S1. Estimated number of adult female elk (2016-2017), brucellosis seroprevalence (2011-2017), and cumulative abortion risk during the risk period for migrants and residents from eight Greater Yellowstone Ecosystem herds.

Herd	Group	Female elk	Seroprevalence	Abortion risk
Madison Valley	Migrant	2,909	0.36	163.39
	Resident	66	0.36	3.71
Dome Mountain	Migrant	2,644	0.20	84.56
	Resident	214	0.20	6.86
North Madison	Resident	2,056	0.17	54.05
Mill Creek	Migrant	311	0.53	26.20
	Resident	242	0.53	20.37
Blacktail	Migrant	917	0.12	17.36
	Resident	34	0.12	0.64
Sage Creek	Migrant	1,248	0.05	10.70
	Resident	749	0.05	6.42
Paradise Valley	Migrant	331	0.06	2.98
	Resident	508	0.06	4.57
Greeley	Migrant	357	0.02	1.06
	Resident	713	0.02	2.12

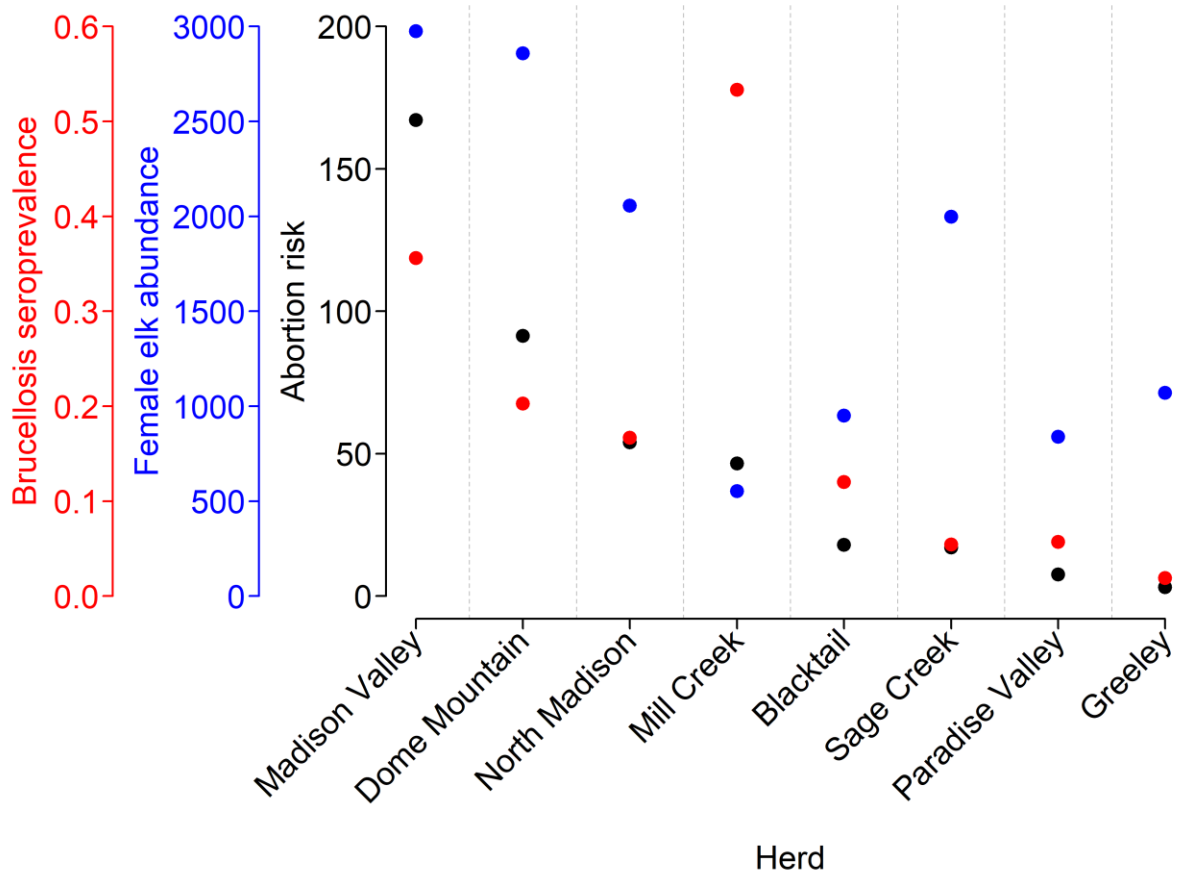


Figure S1. Estimated number of adult female elk (2016-2017), brucellosis seroprevalence (2011-2017), and cumulative abortion risk during the risk period for eight Greater Yellowstone Ecosystem herds.