

# Supplementary Information for Giglio et al. 2018. Pedigree-based genetic management improves bison conservation. Journal of Wildlife Management

Table S1. Simulated loss of genetic diversity and accumulation of inbreeding for the Fort Niobrara Wildlife Refuge FTN, Nebraska, USA bison herd under 3 different culling strategies: Random (yearlings are culled at random), all-allele conservation ([AAC] keeps yearlings with rare alleles in the herd; with rare alleles defined as those falling below a frequency of either 2% or 5% in the herd), and mean kinship ([MK], culls yearlings that have a higher mean kinship). We initialized simulations with microsatellite loci (55 target loci, used to prioritize yearlings for cull, and 55 non-target loci, used to monitor genetic variation at loci not considered when choosing yearlings for cull) from the FTN bison herd (2004). We summarized measures of genetic variation (allelic richness [ $A$ ], observed heterozygosity [ $H$ ], gene diversity [ $GD$ ], and coefficient of inbreeding [ $F$ ]) at 100, 200, and 500-year time steps over 1,000 iterations of each simulated culling strategy. For each culling strategy, we report the mean and coefficient of variation (CV; in parentheses).

Culling strategy	Measures of genetic variation	Founding population	100 years	200 years	500 years
Random	Target $A$	4.418	3.688 (0.022)	3.250 (0.031)	2.459 (0.052)
	Non-target $A$	4.373	3.626 (0.055)	3.186 (0.051)	2.413 (0.059)
	Target $H$	0.585	0.541 (0.026)	0.494 (0.039)	0.381 (0.076)
	Non-target $H$	0.586	0.529 (0.045)	0.484 (0.056)	0.372 (0.087)
	$GD$	0.998	0.903 (0.008)	0.825 (0.016)	0.635 (0.041)
	$F$	0.000	0.089 (0.083)	0.168 (0.076)	0.360 (0.071)
AAC 0.02	Target $A$	4.418	3.920 (0.027)	3.626 (0.039)	2.894 (0.057)
	Non-target $A$	4.455	3.779 (0.019)	3.322 (0.030)	2.468 (0.047)
	Target $H$	0.585	0.553 (0.024)	0.517 (0.036)	0.421 (0.061)
	Non-target $H$	0.604	0.549 (0.026)	0.502 (0.039)	0.381 (0.076)
	$GD$	0.998	0.904 (0.007)	0.827 (0.012)	0.631 (0.029)
	$F$	0.000	0.087 (0.071)	0.166 (0.058)	0.363 (0.050)
AAC 0.05	Target $A$	4.418	3.815 (0.018)	3.524 (0.028)	2.971 (0.066)
	Non-target $A$	4.236	3.731 (0.018)	3.319 (0.030)	2.503 (0.048)
	Target $H$	0.585	0.554 (0.025)	0.522 (0.036)	0.447 (0.070)
	Non-target $H$	0.597	0.545 (0.027)	0.500 (0.040)	0.388 (0.072)
	$GD$	0.998	0.906 (0.007)	0.831 (0.012)	0.644 (0.031)
	$F$	0.000	0.086 (0.071)	0.162 (0.062)	0.351 (0.056)
MK	Target $A$	4.418	3.824 (0.017)	3.480 (0.023)	2.787 (0.035)
	Non-target $A$	4.327	3.684 (0.025)	3.351 (0.025)	2.707 (0.035)
	Target $H$	0.585	0.557 (0.022)	0.524 (0.030)	0.437 (0.051)
	Non-target $H$	0.578	0.543 (0.023)	0.512 (0.033)	0.426 (0.054)
	$GD$	0.998	0.931 (0.003)	0.876 (0.005)	0.732 (0.009)
	$F$	0.000	0.061 (0.053)	0.116 (0.035)	0.262 (0.025)

Table S2. We simulated the loss of genetic diversity and accumulation of inbreeding for the National Bison Range [NBR], Montana, USA bison herd under 3 different culling strategies: Random (yearlings are culled at random), all-allele conservation ([AAC] keeps yearlings with rare alleles in the herd; with rare alleles defined as those falling below a frequency of either 2% or 5% in the herd), and mean kinship ([MK], culls yearlings that have a higher mean kinship). We initialized simulations with microsatellite loci (55 target loci, used to prioritize yearlings for cull, and 55 non-target loci, used to monitor genetic variation at loci not considered when choosing yearlings for cull) from the NBR bison herd (2013). We summarized measures of genetic variation (allelic richness [ $A$ ], observed heterozygosity [ $H$ ], gene diversity [ $GD$ ], and coefficient of inbreeding [ $F$ ]) at 100, 200, and 500-year time steps over 1,000 iterations of each simulated culling strategy. For each culling strategy, we report the mean and coefficient of variation (CV; in parentheses).

Culling strategy	Measures of genetic variation	Founding population	100 years	200 years	500 years
Random	Target $A$	4.982	3.566 (0.039)	2.969 (0.046)	2.184 (0.057)
	Non-target $A$	5.127	3.683 (0.033)	3.002 (0.044)	2.166 (0.058)
	Target $H$	0.437	0.420 (0.049)	0.384 (0.060)	0.295 (0.094)
	Non-target $H$	0.450	0.414 (0.037)	0.378 (0.053)	0.291 (0.094)
	$GD$	0.999	0.909 (0.008)	0.830 (0.015)	0.638 (0.040)
	$F$	0.000	0.083 (0.087)	0.163 (0.076)	0.357 (0.071)
AAC 0.02	Target $A$	4.982	4.067 (0.034)	3.646 (0.047)	2.802 (0.065)
	Non-target $A$	4.582	3.494 (0.025)	2.979 (0.031)	2.217 (0.043)
	Target $H$	0.437	0.454 (0.045)	0.433 (0.053)	0.365 (0.077)
	Non-target $H$	0.483	0.448 (0.029)	0.410 (0.042)	0.313 (0.077)
	$GD$	0.999	0.913 (0.005)	0.836 (0.009)	0.637 (0.021)
	$F$	0.000	0.079 (0.064)	0.157 (0.047)	0.357 (0.037)
AAC 0.05	Target $A$	4.982	3.636 (0.033)	3.189 (0.036)	2.689 (0.067)
	Non-target $A$	5.127	3.701 (0.031)	3.021 (0.039)	2.177 (0.051)
	Target $H$	0.437	0.430 (0.048)	0.409 (0.056)	0.362 (0.087)
	Non-target $H$	0.450	0.415 (0.037)	0.380 (0.051)	0.293 (0.087)
	$GD$	0.999	0.910 (0.006)	0.833 (0.011)	0.644 (0.028)
	$F$	0.000	0.082 (0.072)	0.160 (0.057)	0.351 (0.050)
MK	Target $A$	4.982	3.830 (0.029)	3.286 (0.036)	2.498 (0.043)
	Non-target $A$	5.127	3.941 (0.026)	3.316 (0.033)	2.468 (0.040)
	Target $H$	0.437	0.439 (0.039)	0.414 (0.049)	0.345 (0.070)
	Non-target $H$	0.450	0.427 (0.030)	0.401 (0.041)	0.334 (0.064)
	$GD$	0.999	0.935 (0.003)	0.880 (0.004)	0.735 (0.008)
	$F$	0.000	0.057 (0.055)	0.112 (0.035)	0.259 (0.024)

Figure S1. The number of years that individual males were dominant based on pedigree data from the Fort Niobrara Wildlife Refuge [FTN], Nebraska, USA bison herd (2004–2010). The majority of males were dominant for only 1 year.

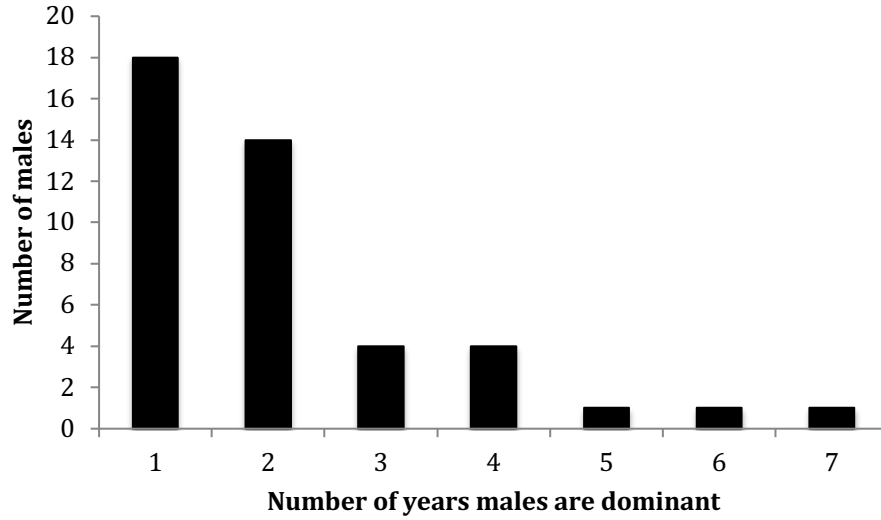


Figure S2. Simulated loss of genetic diversity and accumulation of inbreeding for the Fort Niobrara Wildlife Refuge FTN, Nebraska, USA bison herd under 3 different culling strategies: Random (yearlings are culled at random), all-allele conservation ([AAC] keeps yearlings with rare alleles in the herd; with rare alleles defined as those falling below a frequency of either 2% or 5% in the herd), and mean kinship ([MK], culls yearlings that have a higher mean kinship). We initialized simulations with microsatellite loci (55 target loci, used to prioritize yearlings for cull, and 55 non-target loci, used to monitor genetic variation at loci not considered when choosing yearlings for cull) from the FTN bison herd (2004). We ran this set of simulations with an alternative mating parameter that selected dominant males for a tenure of 2 consecutive years. More genetic variation was lost for all strategies compared to when dominant males were selected independently each year. The MK strategy performed best at retaining genetic variation and reducing the accumulation of inbreeding for all summary statistics.

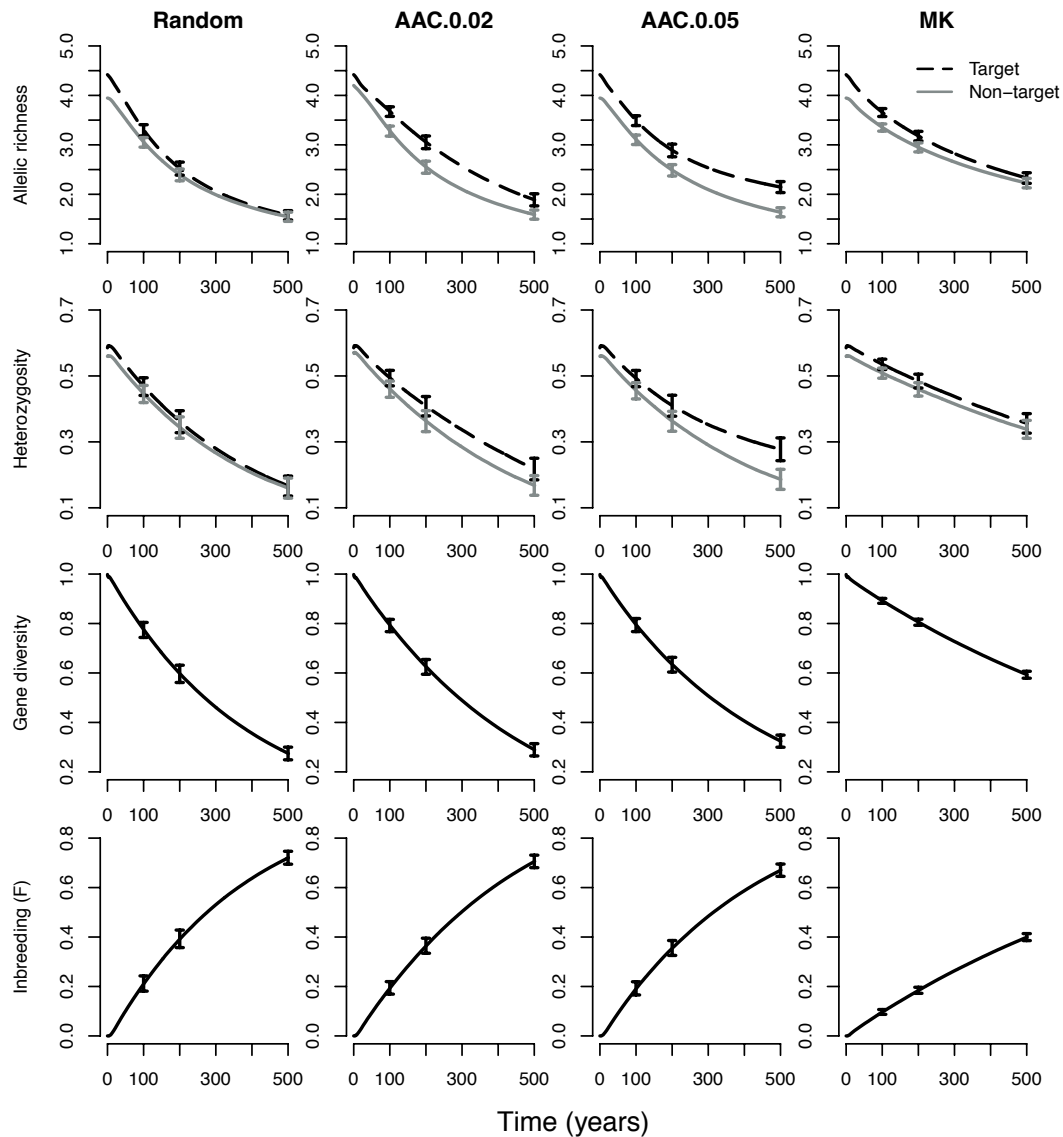


Figure S3. Simulated loss of genetic diversity and accumulation of inbreeding for the National Bison Range [NBR], Montana, USA bison herd under 3 different culling strategies: Random (yearlings are culled at random), all-allele conservation ([AAC] keeps yearlings with rare alleles in the herd; with rare alleles defined as those falling below a frequency of either 2% or 5% in the herd), and mean kinship ([MK], culls yearlings that have a higher mean kinship). We initialized simulations with microsatellite loci (55 target loci, used to prioritize yearlings for cull, and 55 non-target loci, used to monitor genetic variation at loci not considered when choosing yearlings for cull) from the NBR bison herd (2013). We ran this set of simulations with an alternative mating parameter that selected dominant males for a tenure of 2 consecutive years. More genetic variation was lost for all strategies compared to when dominant males were selected independently each year. The MK strategy performed best at retaining genetic variation as well as reducing the accumulation of inbreeding for all summary statistics.

