Appendix E

Methods for Developing the Wildlife Action Network

The development of the Wildlife Action Network drew on a variety of data. Through discussions internally with the Management Team, Core Team, and the Production Advisory Team, several data layers were determined to be most relevant in the development of the network. These data included Species in Greatest Conservation Need (SGCN) population maps based on viable or persistent populations, locations harboring a number of SGCN or "species richness hotspots," threatened and endangered species populations, spatially prioritized Minnesota Biological Survey Sites of Biodiversity Significance, the Minnesota Prairie Conservation Plan cores and corridors (Minnesota Prairie Plan Working Group, 2011), and High Conservation Value Forests. Areas with generally two or more viable SGCN populations or areas with a single threatened or endangered species population were selected for incorporation in the network. In addition to mapped viable aquatic populations and species richness hotspots, streams with an exceptional Index of Biological Integrity (IBI) rating and Lakes of Biological Significance were included. Connectivity between Sites of Biodiversity Significance was provided by Marxan (Ball et al. 2009), a conservation prioritization mapping software that assists in finding the most efficient ways of physically linking conservation target areas, as well as through the inclusion of the Prairie Plan corridors.

Ranked Populations of SGCN

The ultimate goal of the population mapping exercise was to identify and rank viable populations of SGCN or vulnerable populations due to rarity in a region/watershed or within the state. However, since very little information on population viability exists for most species, especially at a given location, we convened workshops where taxa experts ranked populations through review of species occurrences and other GIS data. The data used varied depending on the taxon, but in most cases we used source features from the DNR Natural Heritage Information System converted to points, and observation data (see Table E1 for more information on data sources). Experts generally considered records from 1980 to 2014 to determine if a population was present, although earlier records were sometimes used to help decide if the population had persisted over time. Fish data, in particular, had a large number of records dated prior to 1980 and were commonly used to help determine persistence as well as trends in abundance.

To determine a population rank, the experts considered abundance (number of individuals at a site), persistence (occurrence data spans two or more decades), recruitment (presence of juveniles and/or multiple age classes), presence of suitable habitat based on knowledge of the local area or DNR Native Plant Community data, and experts' local knowledge of the species' population in an area (see ranking guidelines below). These components were used, to varying degrees depending on the available data, to give a population rank of poor, good, or excellent. In rare cases, isolated, but not necessarily viable, populations were also given high ranks in order to ensure these high-risk populations were tracked. This exception was made for 5 species, and were small mapped areas that commonly overlapped with mapped populations of other species and ultimately had little impact on the identification of the Wildlife Action Network or its score (Table E2). Bird populations ranked as poor were not mapped due to time limitations given the large number of species. Viable/persistent SGCN populations were mapped for 156 of the 346 SGCN and included mammals, birds, reptiles,

amphibians, fish, and mussels (Table E3). Invertebrate species other than mussels were not mapped due to insufficient occurrence information. Of the taxa that were mapped, several species within the taxa could not be mapped because they occurred over a wide range with no distinct population centers, or they used habitats that were not readily mappable (e.g., purple martin, a species that centers its populations near artificial nesting compartments). This occurred most often with birds (51 percent mapped) and mammals (67 percent mapped) (Table E3).

Ranking guidelines for SGCN populations

Excellent (strong evidence for viability/persistence):

- The population shows indications (abundance, age class distribution, persistence) of recruitment or immigration, or
- The population represents the only population in the region (ECS section or HUC 4 watershed) or one of three or fewer populations in the state regardless of viability/persistence.
- An additional consideration is that the habitat is known to be of good quality for supporting outstanding viable populations.

Good (evidence for viability/persistence):

- Species has persisted in the area over time.
- Evidence of abundance, recruitment, or persistence either indicates the population is not as viable as a population ranked as excellent, or
- Data and professional judgment are insufficient to rank the populations as excellent.
- An additional consideration can be the quality of the habitat.

Poor (little to no evidence for viability/persistence):

- Species is present but in low numbers.
- Evidence shows lack of persistence, or limited or no reproduction indicates the population is likely not viable.
- An additional consideration is that the habitat quality is known to be poor to the point of limiting population viability.

Mapping workshops lasted a full day and, for several of the taxa, included a second day at a later date (Table E1). Experts systematically worked through SGCN species individually and reviewed occurrence records to identify and rank areas. The experts achieved a consensus for ranking each area.



Taxon	Meeting date	Experts present	Occurrence data sources
Birds	2/28/14	Jan Green, Lee Pfannmueller, Steve Stucker, Tom Will, Ed Zlonis	NHIS Source Features, DNR Observation data, MN Breeding Bird Atlas, Breeding Bird Survey
Birds	3/16/14	Steve Stucker – one on one meeting to complete birds not addressed in first meeting.	NHIS Source Features, DNR Observation data
Mussels	3/28/14	Mike Davis, Mark Hove, Dan Kelner, Bernard Siet- man	DNR Mussel Survey database
Mussels	4/11/14	Mike Davis, Mark Hove, Dan Kelner, Bernard Siet- man	DNR Mussel Survey database
Fish	4/21/14	Luke Borgstrom, Jay Hatch	NHIS Source Features, Fishes of Minnesota (FOM) database, DNR Fish Mapper
Fish	5/23/14	Luke Borgstrom, Jay Hatch	NHIS Source Features, FOM database, DNR Fish Mapper
Herps	5/16/14	Carol Hall, John Moriarty, Krista Larson, Jeff LeClere, Tony Gamble	NHIS Source Features, Observation data compiled by C. Hall
Herps	6/2/14	Carol Hall, John Moriarty, Krista Larson, Jeff LeClere	NHIS Source Features, Observation data compiled by C. Hall
Mammals	5/1/14	Gerda Nordquist	NHIS Source Features, DNR Observation data
Mammals	5/21/14	Gerda Nordquist	NHIS Source Features, DNR Observation data
Dragonflies	9/4/14	Mitchell Haag, Scott King, Ron Lorenz, Kurt Mead, Curt Oien	MN Odonata Survey Project (MOSP) database, Odonata Central database

Таха	Species	Location	Explanation
Bird	Chestnut- collared longspur	Clay County in western Minnesota	Small population represents the only known breeding population in the state, but has been declining over the past 10 to 20 years.
Bird	Common Tern	St. Louis Estuary in northeastern Minnesota.	Represents 1 of 5 known breeding populations that are widely scattered across the north half of Minnesota, but the population requires intensive management to maintain its persistence.
Fish	Flathead Chub	Red River in northwestern Minnesota	Single location (with records from 1890 and 1984) represents the only known records for the species in Minnesota.
Mussel	Elktoe	Pomme de Terre River in west-central Minnesota	Only viable population in the Minnesota River drainage. A good rank was increased to excellent.
Mussel	Spike	Chippewa River in west-central Minnesota	Only viable population in the Minnesota River drainage. A good rank was increased to excellent.

 Table E2. SGCN species given excellent population ranks due to regional or statewide rarity.



	-	Мар	ped?	_
Taxon	Total number of SGCN	Yes	No	% of SGCN mapped
mammals	27	18	9	67
birds	92	47	45	51
amphibians	8	7	1	88
reptiles	15	14	1	93
fishes	43	42	1	98
mussels	30	28	2	93
snails	5	0	5	0
bees	5	0	5	0
butterflies	22	0	22	0
caddisflies	24	0	24	0
dragonflies and damselflies	40	0	40	0
jumping spiders	10	0	10	0
leafhoppers	3	0	3	0
moths	11	0	11	0
tiger beetles	11	0	11	0
Total	346	156	190	45%

Table E3. Number of SGCN with mapped populations by taxa

Mapped areas differed for aquatic and terrestrial species. For aquatic species, we used lake polygons if the population was identified in a lake (Figure E1a). If the population was associated with a stream or river, we used centerlines of streams order 3 and higher clipped by DNR Level 08 catchment basins and buffered by half the average width of the given stream order as identified in Downing et al. (2012). The one exception to this was wood turtle. For this species, stream centerlines were buffered by a quarter mile to capture the adjacent terrestrial habitat used by this species (Hall, C. personal communication 2014). For terrestrial species, several GIS layers were used. First priority was to use Sites of Biodiversity Significance (SOBS) polygons (both Final and Preliminary SOBS layers and, rarely, Survey Priority Areas) if they were available and adequately represented the habitat (Figure E1b). If SOBS polygons could not be used, then a variety of other layers were used depending on what best captured the population and habitat. These included managed area boundaries (e.g., state park), land cover (from GAP or HAPET), Audubon Minnesota Important Bird Area and/or Prairie Conservation Plan core boundaries (used if they were closely aligned with the habitat), manually drawn polygons using aerial photography, and DNR Level 08 catchment basins. The source of the polygon can be found in the "Source" field of the population shapefiles.



b.

Figure E1. Example polygons mapped for a fish species (a) and a bird species (b). Red represents an excellent population rank, orange represents a good population rank, and green represents a poor population rank. In these examples, the fish populations were mapped using lake boundaries and stream segments and the bird populations were mapped using MBS Sites of Biodiversity Significance.

In addition to the above, modeled habitat results available for some bird species were used when it was determined that the model results accurately depicted species presence. Habitat model results were used for northern goshawk from the DNR Nongame Wildlife Program; boreal chickadee and Connecticut warbler, from the University of Minnesota Duluth's Natural Resources Research Institute; and grasshopper sparrow and Le Conte's sparrow, from US Fish and Wildlife Service's Habitat and Population Evaluation Team (HAPET). These model results had different output values, which required different scaling to represent excellent, good, or poor populations. In the goshawk model, habitat was scored on a gradient from 0 to 230, with higher values attributed to a greater potential for goshawk use. We gave an excellent population rank to any habitat with a value of 200 or greater. A good population rank was given to any habitat with a value between 150 and 199 (Figure E2). For boreal chickadee and Connecticut warbler, the original raster files were converted to vector files. For boreal chickadee, values above 60 were given an excellent population rank, values between 50 and 60 were given a good rank, and values below 50 were not included. For Connecticut warbler, values above 80 were given an excellent population rank, values between 60 and 80 were given a good rank, and values below 60 were not included. For grasshopper sparrow and Le Conte's sparrow, original raster values were first multiplied by 1000 and then reclassified. The resulting reclassified raster files were then converted to vector files. For grasshopper sparrow, reclassified values above 70 were given an excellent population rank, values between 50 and 70 were given a good rank, and values below 50 were not included. For Le Conte's sparrow, reclassified values above 200 were given an excellent population rank, values between 100 and 200 were given a good rank, and values below 100 were not included.





Figure E2. Modeled habitat mapped for an example bird species (northern goshawk). Red represents an excellent population rank, and orange represents a good population rank.

In addition to the mapping, careful notes were taken to capture the decisions made and other ideas that emerged from the conversations. For example, we sometimes recorded priority areas for restoration but did not map these as population areas. Following the final mapping workshops, follow-up mapping was completed using the notes and often included additional consultation with DNR Minnesota Biological Survey animal staff.

Population maps were sent out for both internal and external review to various wildlife staff, refuge biologists, land managers, and other taxa experts (see Appendix B). Revisions, including changing ranks of some mapped populations, adding and removing populations, and modifying boundaries of existing maps, were made per comments, suggestions, and additional consultation garnered through this review process and completed in November 2014.

SGCN Richness Hotspot Maps

Since about half of the SGCN populations could not be mapped, a SGCN richness hotspot analysis was also performed to identify additional areas in the Wildlife Action Network with high concentrations of SGCN. To complete this process, observation records of all SGCN, including invertebrates, were used to sum the number of species in 2.5-km-by-2.5 km (~2.4 square miles) blocks across the state. First, we created a grid containing 2.5-km-by-2.5 km blocks in ArcMap and then clipped it to the Minnesota state boundary. The grid block size was a compromise between a smaller area that captured too few points and a larger area that resulted in too much generalization. Next, we intersected all SGCN observation points from NHIS and other sources identified in Table E1 with the grid and then summarized the number of unique species per grid block. We then developed



the following criteria for identifying richness hotspots via clusters of these blocks:

- 1. A single block comprising ten or more species.
- 2. A cluster of at least 4 contiguous blocks each comprising 5 or more species.
- 3. A cluster of at least 8 contiguous blocks each comprising 3 or more species. This cluster must also contain a hotspot already defined in 1 or 2 above.

In the above criteria, "contiguous" includes both adjacent blocks and blocks whose corners touch (Figure E3).



Figure E3. Clusters of grid blocks identified as richness hotspots by the above criteria. The number in each block refers to the number of species that have been observed within the area of each block. All blocks in this example met one of the three criteria listed above, and red circles illustrate examples of each the different criterion for inclusion as a hotspot where (1) represents a single block comprising 10 or more species, (2) represents a cluster of at least 4 contiguous blocks each comprising 5 or more species, and (3) represents a cluster of at least 8 contiguous blocks each comprising 3 or more species. "Contiguous" includes both adjacent blocks and blocks whose corners touch.

SGCN richness clusters that fell outside of the mapped SGCN populations were selected and then the underlying habitat was mapped in a similar manner to selecting habitat polygons for the populations mapping exercise detailed within the previous section, "Ranked Populations of SGCN." If an individual block comprised aquatic species, corresponding lakes and buffered stream centerlines were mapped. If a block comprised terrestrial species, SOBS (final and preliminary) were mapped if available and adequately represented the habitat for the species present. If no SOBS were present or adequate within the area of an individual block, managed area boundaries were mapped next. If no managed area boundaries existed within the area of the block, a polygon was drawn around appropriate habitat using 1-meter resolution 2013 Color infrared and natural color FSA aerial maps. If a block comprised both aquatic and terrestrial species or species that use both, a combination of aquatic and terrestrial habitat polygons were mapped. Note that mapped habitat could extend beyond the boundaries of an individual block as long as some part of it intersected with the boundary of the block (Figure E4).





Figure E4. Example of habitat polygons (light blue) intersecting with a single richness hotspot block (light pink). Note that mapped habitat can extend beyond the boundaries of the block as long as some part of the polygon intersects with the block boundary.

SGCN Composite Population Scores

The population ranks for each species (Ranking Guidelines, p. E2, Appendix E) were assigned multipliers to use in developing a composite map for all taxa. An excellent population was given a score of 2.0; a good population was given a score of 1.0; and a poor population was given a score of 0.1. The 0.1 score for the poor population was chosen to represent that the population was unviable and should contribute very little to the composite map but still be present as a possible area for restoration. Composite maps for each taxon were then created by unioning (i.e., combining) the mapped populations of all SGCN in that taxon. This resulted in a single composite map with many overlapping areas containing a score for each species with a population in that specific location. These scores were then summed, creating a composite score for each overlapping area. Next, to create a composite map of all taxa, these sums were normalized by dividing the sum for each area by the maximum score possible for the given taxa (i.e., the score if an area had an excellent population rank for all species), resulting in five maps of composite population scores (one for each taxon; Figure E5). Since the number of mapped species varied among taxa, individual taxon composite maps were normalized to make the scores comparable between them. The five taxon composite maps were then unioned together, resulting in a single composite map of all mapped taxa. The normalized scores for each taxon were summed together to arrive at a new score for each overlapping area representing all taxa combined (Figure E6).



a) Composite score-birds b) Composite score-reptiles and amphibians b) Composite score-reptiles and amphibians b) Composite score-manuals amphibians b) Composite score-manuals amphibians b) Composite score-manuals c) Composite score-manuals b) Composite score-manuals c) Composite scores c) Li to 5.0% c) Composite scores c) Composite score c) C

Figure E5. Composite population scores by taxon. The color scale represents the distribution of the scores among all polygons ranging from lowest 5 percent of composite scores (green) to the top 50 percent of composite scores (red). The legend breakpoints closely follow a geometrical interval as the data were skewed to the lower end of the distribution for many of the taxa (that is, many areas had few overlapping SGCN populations). This varied by taxa, but the breakpoints were standardized across taxa for clarity. For fish in (d), the area in northeastern Minnesota delineating a portion of Lake Superior represents Minnesota's managed area of the lake.



Figure E6. Composite population scores for all taxa combined. Normalized scores of all taxa were combined with equal weighting among each taxon. The color scale represents the distribution of the scores among all composited polygons ranging from lowest 1.25 percent of composite scores (green) to the top 95 percent of composite scores (red). The top 95 percent score breakpoint represents what was chosen for inclusion in the network, as this generally represents areas with at least one "excellent" SGCN population or at least two "good" SGCN populations. The area in northeastern Minnesota delineating a portion of Lake Superior represents Minnesota's managed area of the lake.

Wildlife Action Network

The Wildlife Action Network was created from several GIS layers. It is important to note that some of the data used in its development are still considered draft, and the Wildlife Action Network will be updated over time as data are refined and new data become available. The following describes the GIS layers used in the Wildlife Action Network:

- a) Top 95 percent of SGCN populations composite (Figure E7a). This piece of the network comprises the areas in the composite populations map for all taxa that placed within the top 95 percent of scores (i.e., everything in red in Figure E6). In omitting the bottom 5 percent of population scores from this piece, we largely captured areas that contained good- or excellent-ranked populations of more than one SGCN, and omitted areas with only one SGCN population or multiple SGCN with poor-ranked populations.
- b) Good or excellent populations of state or federally endangered and threatened species (Figure E7b). Some good or excellent populations of state or federally endangered and threatened species were not represented in the top 95 percent of population scores because they were the only species mapped in a particular area. To ensure that these important populations of rare species were included in the network, all good or excellent mapped populations of state or federally endangered and threatened species were added to the network.
- c) Richness hotspots falling outside the top 95 percent of populations (Figure E7c). We included all SGCN richness hot spots that fell outside of the top 95 percent of population scores. Since the richness hotspots included all SGCN species for which we have observation points and not just those species that we mapped, these areas provide additional information on important SGCN habitat within the network.
- d) Cores and Corridors from Minnesota Prairie Conservation Plan (Figure E7d). These layers from the Minnesota Prairie Conservation Plan (MN 2011) include the January 2015 revised cores and the original corridors. The cores represent high concentrations of native prairie and surrogate grassland. The corridors represent planned areas of grassland restoration.
- e) Marxan outputs from the Scientific and Natural Area strategic plan (Figure E7e). Development of the Scientific and Natural Area (SNA) Strategic Land Protection Plan (SNA 2014) utilized Marxan conservation planning software to spatially prioritize and identify connections between the high and outstanding ranked MBS Sites of Biodiversity Significance. To create the output used in the Wildlife Action Network, we selected all areas with a Marxan rank of 3, 4 or 5 from the original Marxan outputs.
- f) New Marxan runs of additional final and preliminary sites of biodiversity significance in remaining ecological subsections not analyzed for the SNA strategic plan (Figure E7f). The SNA strategic plan used final Sites of Biodiversity data for the Marxan analysis in 2014. At the time, the status of Sites of Biodiversity Significance was preliminary or unmapped in a significant portion of northern Minnesota. Since the SNA Marxan analysis was completed, additional data have become finalized, and new areas have preliminary data. After consulting with MBS plant ecologist staff on which preliminary data were less likely to change significantly in terms of boundaries and rankings, additional Marxan runs were completed in the Agassiz Lowlands, Border Lakes, Chippewa Plains, Pine Moraines, St. Louis Moraines, and Tamarack Lowlands subsections. Data were limited to only the south half of the Agassiz Lowlands.



g) Sites of Biodiversity Significance that intersect with Marxan outputs and high and outstanding sites where Marxan runs were not completed (Littlefork-Vermillion Uplands and the north half of the Agassiz Lowlands subsections) (Figure E7g). These include all final and preliminary sites of Biodiversity Significance (SOBS) that intersect with the Marxan files in 7e and 7f. All ranks are included (i.e. Outstanding, High, Moderate, and Below). These mostly do not add anything new to the network from what is already represented by the Marxan outputs, but are included because they represent ground-truthed, mapped habitat. The Marxan layers represent modeled prioritized areas and include areas not mapped as SOBS. These areas can be considered as priorities for increasing buffers and connectivity of SOBS.

In addition, some preliminary polygons of Sites of Biodiversity Significance were mapped in the Littlefork-Vermillion Uplands and the north half of the Agassiz Lowlands subsections, but these areas were not complete enough to effectively do a Marxan spatial prioritization. High and outstanding ranked polygons, where MBS plant ecologist staff were reasonably confident of their boundaries and rankings, were included. These areas will be prioritized using Marxan when mapping of Sites of Biodiversity is completed.

- h) High conservation value forests (Figure E7h). We included all high conservation value forests as identified by the DNR as part of forest certification with the Forest Stewardship Council. These forests potentially offer important habitat for many SGCN and a diversity of forest wildlife.
- i) Lakes of biological significance (Figure E7i). We included the final 2015 draft of Lakes of Biological Significance. These lakes offer important habitat for SGCN and a variety of wetland and aquatic wildlife.
- i) Streams with an exceptional index of biological integrity score (Figure E7). We extracted all streams that met the draft index of biological integrity (IBI) "exceptional" score for fish (Table E4) or a non-mussel invertebrate IBI score of 80 or higher using the normalized Watershed Health Assessment Framework (WHAF) IBI values. We then added stream reaches downstream to the next confluence, or upstream to the source or next confluence, if the stream reach met the general use threshold or if no IBI data were available and if the stream was not ditched and if no other tributaries with low IBI scores (below general use threshold) flowed into the selected stream reach. Streams were then buffered based on average stream width (diameter = ½ width) by stream order (from Downing et al. 2012). Our assumption is that these streams offer important habitat or ecological functionality for aquatic SGCN and other wildlife.

These ten layers were then overlayed to create the complete Wildlife Action Network (Fig. E8).

a) Top 95% of SGCN populations composite



c) Richness hotspots falling outside the top 95 percent of populations



b) Populations of endangered and threatened species



e) Marxan outputs from the Scientific and Natural Area Strategic Plan

g) Sites of Biodiversity Significance that intersect with Marxan prioritization

f) New Marxan prioritization of Sites of Biodiversity Significance

h) High Conservation Value Forests

i) Lakes of Biological Significance

j) Streams with exceptional IBI scores

Figures E7a-j. Layers comprising the Wildlife Action Network. In each map, the blue represents areas that were included as part of the Wildlife Action Network. See text above for a description for each of these layers. The area in northeastern Minnesota delineating a portion of Lake Superior represents Minnesota's managed area of the lake.

 Table E4.
 Fish IBI general use and exceptional thresholds by stream class.

Stream class	Class description	General use threshold	Exceptional threshold
1	southern rivers	49	71
2	southern streams	50	66
3	southern headwaters	55	74
4	northern rivers	38	67
5	northern streams	47	61
6	northern headwaters	42	68
7	low gradient	42	70
10	southern coldwater	50	82
11	northern coldwater	35	60

Figure E8. Wildlife Action Network (blue). The area in northeastern Minnesota delineating a portion of Lake Superior represents Minnesota's managed area of the lake.

Scoring the Wildlife Action Network

To help prioritize the information provided in the conservation network, we carried out a GIS scoring exercise. This exercise was limited to five layers that were entirely or almost entirely statewide in extent and had a score that was either a continuous variable or an ordinal categorical variable. The five layers were also chosen for their complementarity. The composite SGCN population scores and the SGCN richness grid represent aquatic and terrestrial SGCN populations and occurrences. Marxan scores represent mainly terrestrial areas of biological significance, while the Stream Index of Biological Integrity and the Lakes of Biological Significance represent aquatic components of biological significance for those respective systems. While the SGCN population scores and SGCN richness grids are likely highly correlated, it was decided to use both as scoring variables since the SGCN richness grids provide information on SGCN that did not have mapped populations. With the exception of the composite SGCN population scores, the raw values of continuous variables were rescaled between 0 and 1. The highly skewed distribution of the composite SGCN population scores required first categorizing the data using Jenks natural breaks (Jenks 1977) in ArcMap and then scoring based on five categories. Other categorical variables had three categories and were linearly scaled starting at 0.4. This starting point was used since these data already represent a prioritization, and other areas not represented in this prioritization (e.g., Sites of Biodiversity Significance mapped as "below" or not mapped at all) likely have a distribution of levels with a "quality" below these prioritized layers.

- a) Composite SGCN Population Scores (Figure E9a). The composite population map including all levels of composite scores (not just the top 95 percent) was rasterized with a cell size of 90m and then multiplied by 10 to create an integer raster with an attribute table. The count of cells was added cumulatively for each value, resulting in a sum field capturing the amount of area (in raster cells) occupied for a particular value. This sum field was then reclassified by 5 natural breaks (Jenks) and then converted back to a vector shapefile. Within this new shapefile, the lowest break was scored as a 0.2, the second lowest break was scored as a 0.4, the middle break was scored as a 0.6, the second highest break was scored as a 0.8, and the highest break (i.e., the areas with the highest summed values) were scored as a 1.0.
- **b) SGCN richness grid used in the hotspot analysis (Figure E9b).** The score for each block in the grid was divided by the maximum number of species found among all blocks, such that the block with the maximum number of species was given a score of 1.
- c) Marxan scores of prioritized Sites of Biodiversity Significance (Figure E9c). An area with a rank of 5 was given a score of 0.8; with a rank of 4, a score of 0.6; with a rank of 3, a score of 0.4; with a rank of 2, a score of 0.2; and with a rank of 1, a score of 0. For the Littlefork-Vermillion Highlands subsection in which the Marxan analysis was not run for reasons given in section g on page E12, preliminary and survey priority Sites of Biodiversity Significance were scored as follows: "outstanding" sites were given a score of 0.8, and "high" sites were given a score of 0.6. "Moderate" sites and below were not included in the scoring scheme.
- d) Stream Index of Biological Integrity (Figure E9d). All stream orders 3 and above were buffered using the stream width guidelines from Downing et al. (2012) and intersected with the DNR Level 08 catchments basins. The maximum IBI score for the stream (out of the fish, non-mussel invertebrate, and the corresponding extrapolated IBI scores from the WHAF) was divided by the maximum score among all the stream IBIs, such that the stream with the highest IBI score was given a score of 1.

e) Lakes of Biological Significance (Figure E9e). A lake identified as "outstanding" was given a score of 0.8; a lake identified as "high," a score of 0.6; and a lake identified as "moderate," a score of 0.4

c) Marxan scores of prioritized Sites of Biodiversity Significance

d) Stream Index of Biological Integrity

Figure E9. Layers scored for prioritization and are a) Composite SGCN Population Scores, b) SGCN richness grid, c) Marxan scores of prioritized Sites of Biodiversity Significance, d) Stream Index of Biological Integrity, e) Lakes of Biological Significance. See text for how each layer was scored. The break points in the legends for each of the layers are different because each layer varies in the distribution of the data. The area in northeastern Minnesota delineating a portion of Lake Superior represents Minnesota's managed area of the lake.

After the above layers were given their prioritization scores, each layer was converted to a raster file with a cell size of 90 by 90m. (Note: for stream orders 3–7, the buffer was increased to 90m to ensure that the raster cell captured the score.) Within each raster layer, each cell contained an individual value representing the score per the above scheme. These raster files were then added together using the raster calculator in ArcMap, resulting in a single raster file with each cell containing the sum of the scores of the five individual raster files. The resulting layer of combined scores was then clipped to the Wildlife Action Network boundary and reclassified based on the distribution of the data. Reclassification reflected the skewed nature of the distribution of data points and was classified into highest = the top 50 percent , high = 25–50 percent , medium = 15–25 percent , low = 5–15 percent, and lowest = the bottom 5 percent of the distribution of scores. This reclassified raster was then converted back into a vector shapefile showing the score cutoffs (Figure E10).

Figure E10. The Wildlife Action Network Scored. Scores are based on five scalable metrics: SGCN population viability scores, SGCN richness, spatially prioritized Sites of Biodiversity Significance, ranks of Lakes of Biological Significance, and Stream Indices of Biological Integrity (IBI). Lower scores (green) in a given area indicate the metric scores for any of these five components were either relatively low or zero, while high scores (red) indicate that multiple metrics of high scores overlap. For example, a red area could indicate several good or excellent SGCN populations, high SGCN richness (including species that did not have population maps available) and were either a high scored Site of Biodiversity Significance, lake of Biological significance, or stream IBI. The area in northeastern Minnesota delineating a portion of Lake Superior represents Minnesota's managed area of the lake.

Conservation Focus Areas

The scored Wildlife Action Network (Figure E10) was then used as a guide for regional DNR Nongame Wildlife staff and others to identify a set of potential Conservation Focus Areas, concentrating on areas with conservation needs, issues, and opportunities. Areas in red in Figure E10 potentially have the most importance to SGCN populations and a diversity of wildlife, and thus they represent top conservation priorities. However, this prioritization map was just one piece of information considered when creating Conservation Focus Areas. Conservation needs and opportunities, investment required to address the needs, and return on investment in terms of species or habitats benefited were all considerations for identifying Conservation Focus Areas. For example, if an area is red on the prioritization map but already being actively managed and monitored for wildlife, including SGCN, the area is obviously important, but it may not represent a focus for the Wildlife Action Plan over the next 10 years. Following initial input from MN DNR Nongame Wildlife Program staff, additional input on the draft Conservation Focus Areas was then solicited in day-long workshops with DNR regional staff from several DNR divisions. Following these meetings, staff from the Wildlife Action Plan management team further prioritized the draft proposed Conservation Focus Areas by evaluating them primarily based on conservation needs and opportunities, as well as investment required to address the needs, and return on investment in terms of species or habitats benefited.

Given the statewide scope of the plan and limited information to quantitatively assess each Conservation Focus Area for its needs and opportunities, decision guidelines were set such that any area that was determined to have relatively low needs or opportunities was removed from the potential list. A Conservation Focus Area was also removed if it was decided that the investment was too high, the return on investment was relatively low, or the area was primarily a single species focus. A candidate area may have received a low score if, for example, a large financial or staff investment is required, conservation actions are already adequately addressed by other partners, or an area focuses on a single species, thus limiting the return on investment. In some cases, areas with primarily a single species focus will be treated through fine-filter objectives (e.g., wood turtle, Blanding's turtle). This evaluation resulted in the final 36 Conservation Focus Areas, of which at least 6 will be identified for work over the next 10 years.

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Data sources referenced

DNR Fish Mapper: http://www.dnr.state.mn.us/maps/fom/mapper.html?layers=lakes+streams+wshd lev01py3+occurrences

DNR Level 08 catchment basins: https://gisdata.mn.gov/dataset/geos-dnr-watersheds

DNR Mussel Survey Database: no link available.

DNR Native Plant Community: http://www.dnr.state.mn.us/npc/index.html and https://gisdata.mn.gov/ dataset/biota-dnr-native-plant-comm

DNR Natural Heritage Information System (NHIS): http://www.dnr.state.mn.us/nhnrp/nhis.html

DNR Observation Data: no link available.

Fishes of Minnesota (FOM) Database: no link available.

Habitat and Population Evaluation Team (HAPET): http://www.fws.gov/midwest/hapet/

High Conservation Value Forests: http://www.dnr.state.mn.us/forestry/certification/hcvf.html

HUC 4 watersheds: https://gisdata.mn.gov/dataset/geos-dnr-watersheds

Important Bird Area: http://mn.audubon.org/saving-important-bird-areas-5

Index of Biological Integrity (IBI): http://www.pca.state.mn.us/index.php/water/water-monitoring-and-reporting/biological-monitoring/index-of-biological-integrity.html

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Minnesota Breeding Bird Atlas Project: http://mnbba.org/

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