All data for each species are contained in a folder named by the four letter abbreviation of the species name (e.g. Bouteloua eriopoda is BOER). Within each separate folder, there are 9 files. The data in these files were derived from the annually mapped quadrats. Below, for each of the 9 species-specific data files, we provide a brief definition for each column.

Here we use XXXX to represent the abbreviation of species names.

1. `XXXX_buf5_dorm1.csv`

Variable name	Variable definition
quad	Name of the quadrat
year	Year of the observation
SP_ID	Identification number for each record
Species	Scientific name of the plant species (genus and species)
area	Area of the individual polygon (cm^2)
x	Location of the polygon centroid in the horizontal direction within the quadrat
y	Location of the polygon centroid in the vertical direction within the quadrat
age	Age of the genet (not used in our current analysis)
survives	Indicator: the genet survives (1) or not (0)
dormancy	Indicator: the genet experiences a dormant stage (1) or not (0)
trackID	Identification number for each unique genet
distEdgeMin	Distance of genet to nearest edge of the quadrat
allEdge	Indicator: the entire genet is located within 5 cm of a quadrat edge (1) or not (0)

2. XXXX_genet_xy.csv

Variable name	Variable definition
quad	Name of the quadrat
year	Year of the observation
trackID	Identification number for each unique genet
area	Area of the individual polygon
x	Location of the polygon centroid in the horizontal direction within the quadrat
y	Location of the polygon centroid in the vertical direction within the quadrat
allEdge	Indicator: the entire genet is located within 5 cm of a quadrat edge (1) or not (0)
totCover	Total cover of a given species
age	Age of the genet (not used in our current analysis)

3. XXXXassign_genets.csv

Variable name	Variable definition
quad	Name of the quadrat
year	Year of the observation
SP_ID	Identification number for each record
x	Location of the polygon centroid in the horizontal direction within the quadrat
y	Location of the polygon centroid in the vertical direction within the quadrat
genID	Identification number for each genet present in the first year each quadrat is mapped

4. XXXXgenets.pdf

This PDF file includes the first and second year's maps for each quadrat. The genID values in the previous file (XXXassign_genets.csv) were assigned by visually comparing the first and second year's maps for each quadrat and assigning each polygon or cluster of polygons a unique identification.

5. growDnoNA.csv

Variable name	Variable definition
quad	Name of the quadrat
year	Year of the observation
trackID	Identification number for each genet
area.t1	Area of a genet in the second year of a transition
area.t0	Area of a genet in the first year of a transition
age	Age of the genet (not used in our current analysis)
allEdge	Indicator: the entire genet is located within 5 cm of a quadrat edge (1) or not (0)
distEdgeMin	Distance of genet to nearest edge of the quadrat

6. quadratCover.csv

Variable name	Variable definition
quad	Name of the quadrat
year	Year of the observation
totCover	Total cover of species in the previous year

7. recArea.csv

Variable name	Variable definition
quad	Name of the quadrat
year	Year of the observation
NRquad	Number of recruits of the focal species observed in the quadrat in a specific year
totParea	Total 'parent' area of the focal species (cover in the previous year)
recArea	Number of recruits per parent area for focal species

8. recSize.csv

Variable name	Variable definition
quad	Name of the quadrat
year	Year of the observation
trackID	Identification number for each newly recruited genet
area	Area for each recruit
survives	Indicator: the recruit survives (1) or not (0)
age	Age of the genet (not used in our current analysis)
distEdgeMin	Distance of genet to nearest edge of the quadrat
allEdge	Indicator: the entire genet is located within 5 cm of a quadrat edge (1) or not (0)

9. survD.csv

Variable name	Variable definition
quad	Name of the quadrat
year	Year of the observation
trackID	Identification number for each newly recruited genet
area	Area of each recruit
survives	Indicator: the recruit survives (1) or not (0)
age	Age of the genet (not used in our current analysis)
distEdgeMin	Distance of genet to nearest edge of the quadrat
allEdge	Indicator: the entire genet is located within 5 cm of a quadrat edge (1) or not (0)