# Inbreeding and fitness

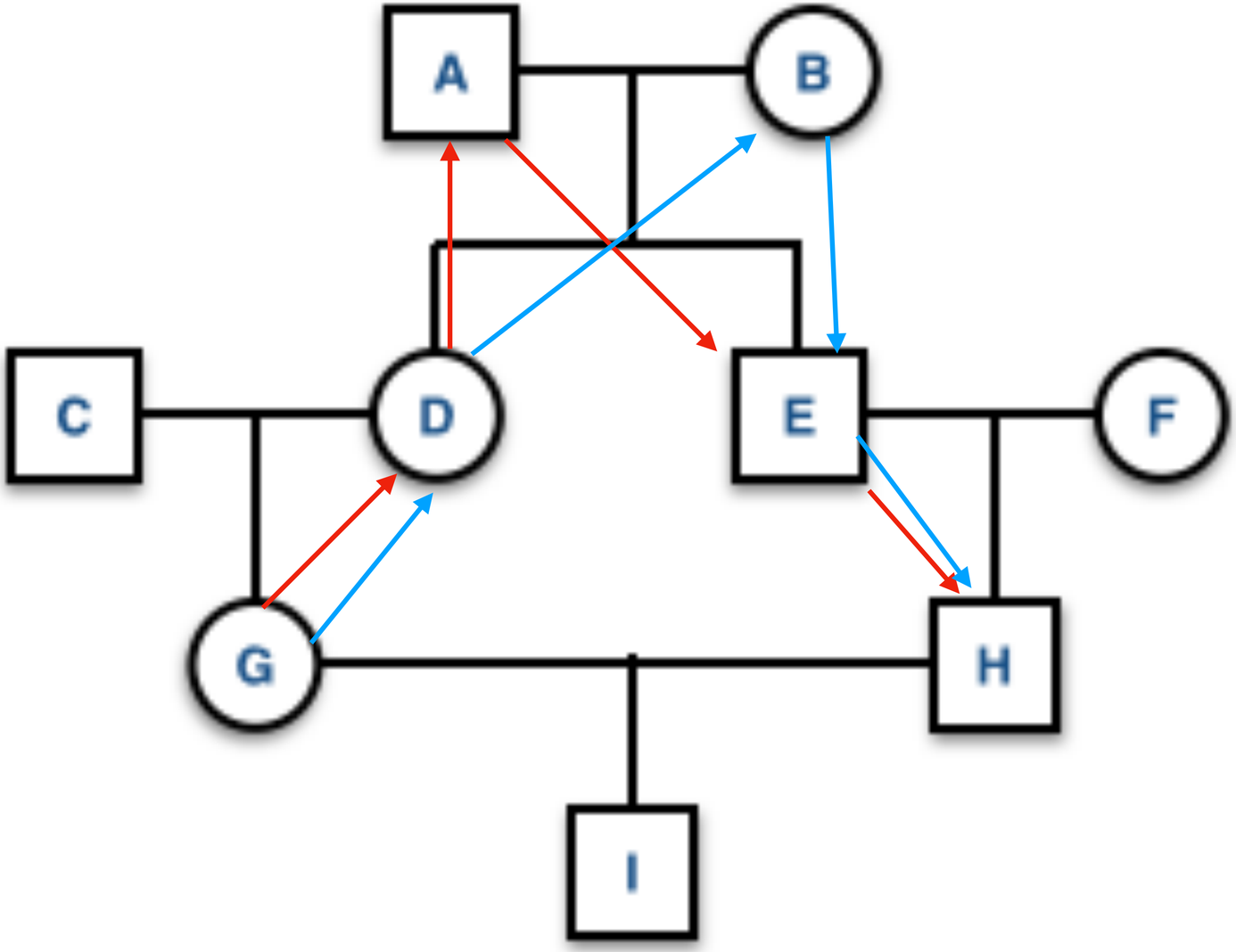
Anubhab Khan

# Probability that two alleles at a locus are identical by descent

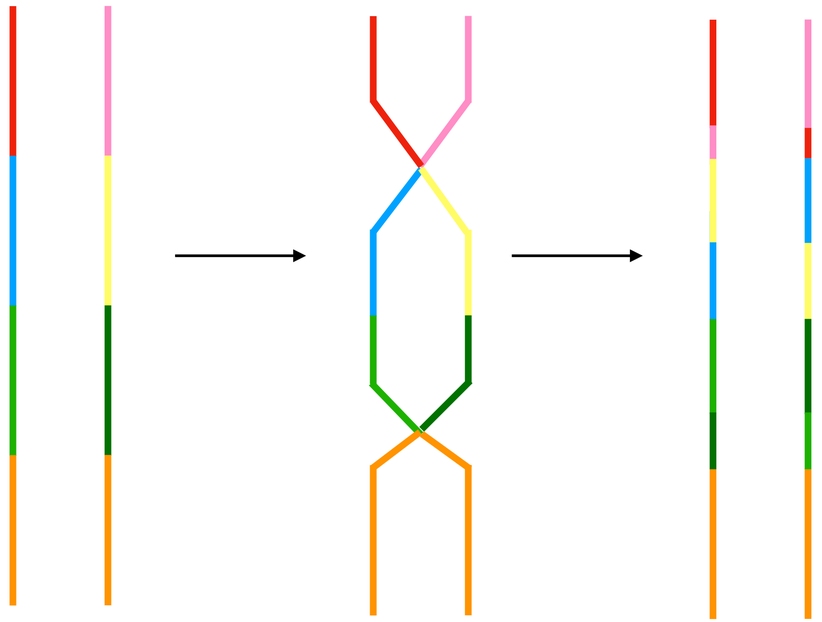
# Why does this happen?

# How do we measure inbreeding?

# Pedigree

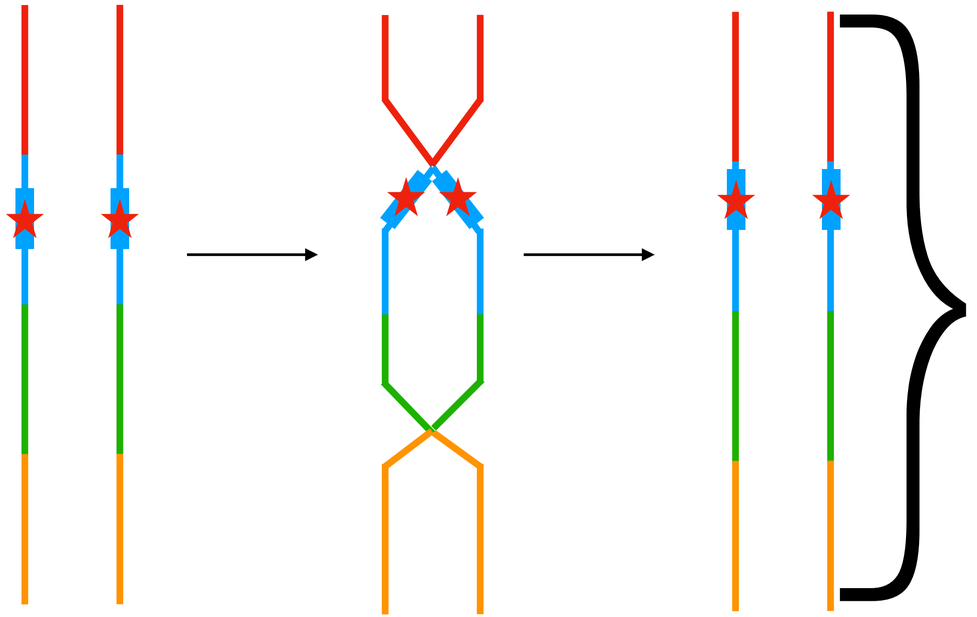


# Runs of Homozygosity

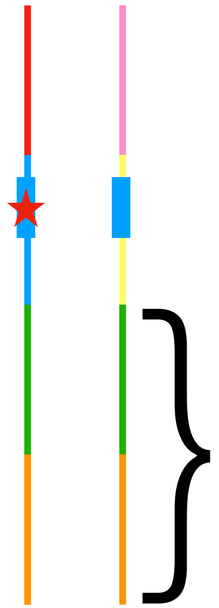


A stretch of the genome where consecutive loci are identical by descent

# Runs of Homozygosity



Run of
Homozygosity



Run of Homozygosity

# How does inbreeding impact the fitness of a population?

# Case: Isle Royale Wolves

# Isle Royale is isolated


Google images

# Isle Royale is isolated

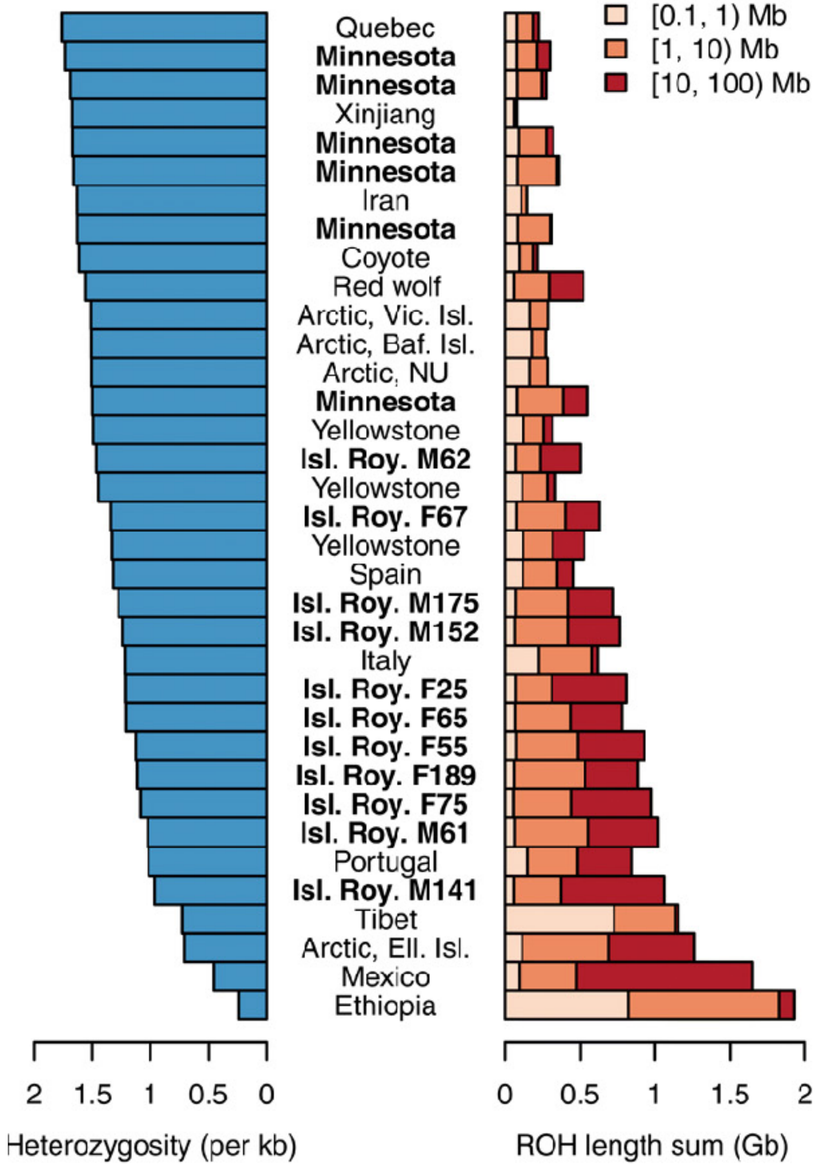
Google images

# Isle Royale has population of wolves

Google images

# What is the impact of isolation on the wolves?

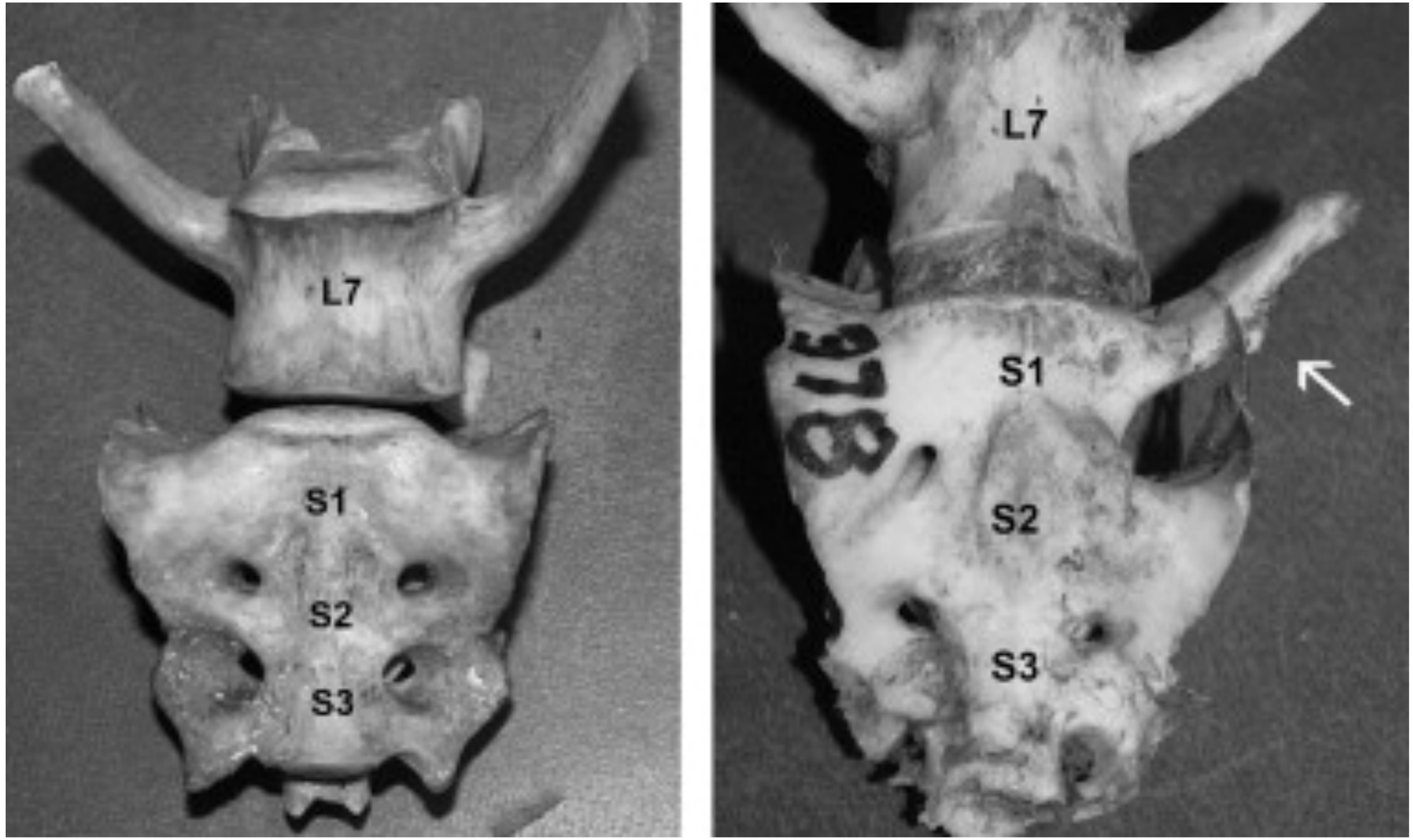
# High inbreeding in Isle Royale wolves




Robinson, J.A., Räikkönen, J., Vucetich, L.M., Vucetich, J.A., Peterson, R.O., Lohmueller, K.E. and Wayne, R.K., 2019. Genomic signatures of extensive inbreeding in Isle Royale wolves, a population on the threshold of extinction. *Science Advances*, *5*(5), p.eaau0757.

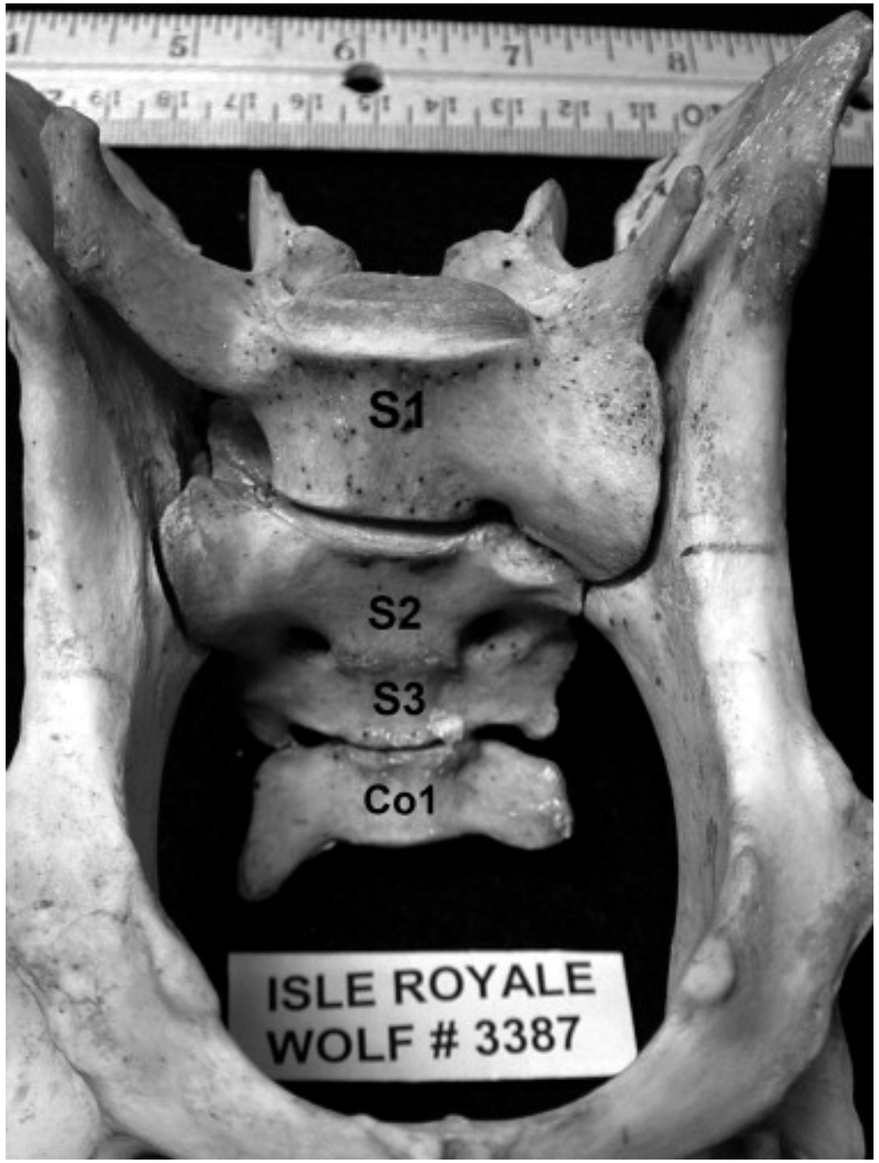
# Are the Wolves going to be fine?

# Bone deformities in Isle Royal Wolves




Räikkönen, J., Vucetich, J.A., Peterson, R.O. and Nelson, M.P., 2009. Congenital bone deformities and the inbred wolves (Canis lupus) of Isle Royale. *Biological Conservation*, *142*(5), pp.1025-1031.

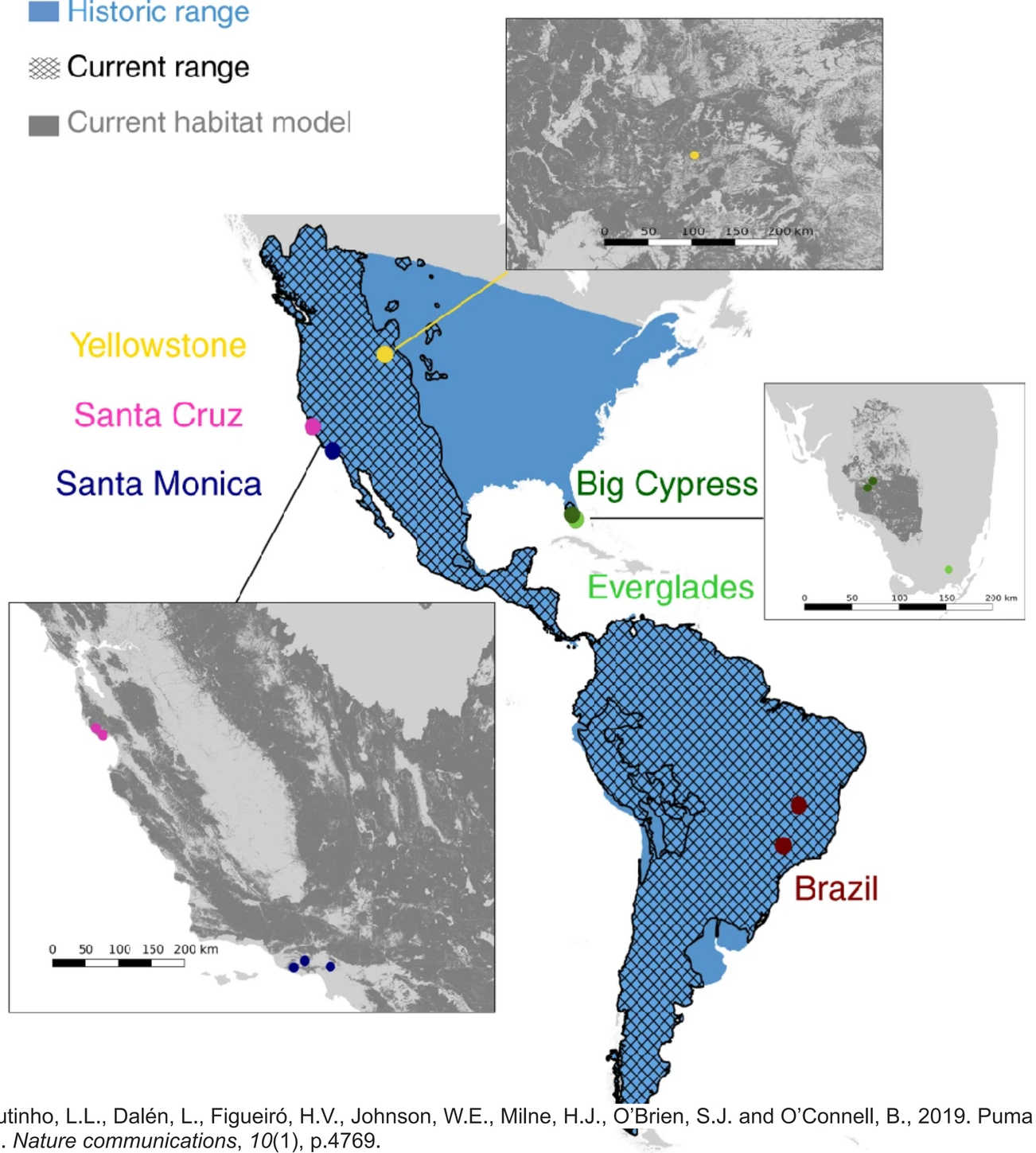
Räikkönen, J., Vucetich, J.A., Peterson, R.O. and Nelson, M.P., 2009. Congenital bone deformities and the inbred wolves (Canis lupus) of Isle Royale. *Biological Conservation*, *142*(5), pp.1025-1031.




Räikkönen, J., Vucetich, J.A., Peterson, R.O. and Nelson, M.P., 2009. Congenital bone deformities and the inbred wolves (Canis lupus) of Isle Royale. *Biological Conservation*, *142*(5), pp.1025-1031.

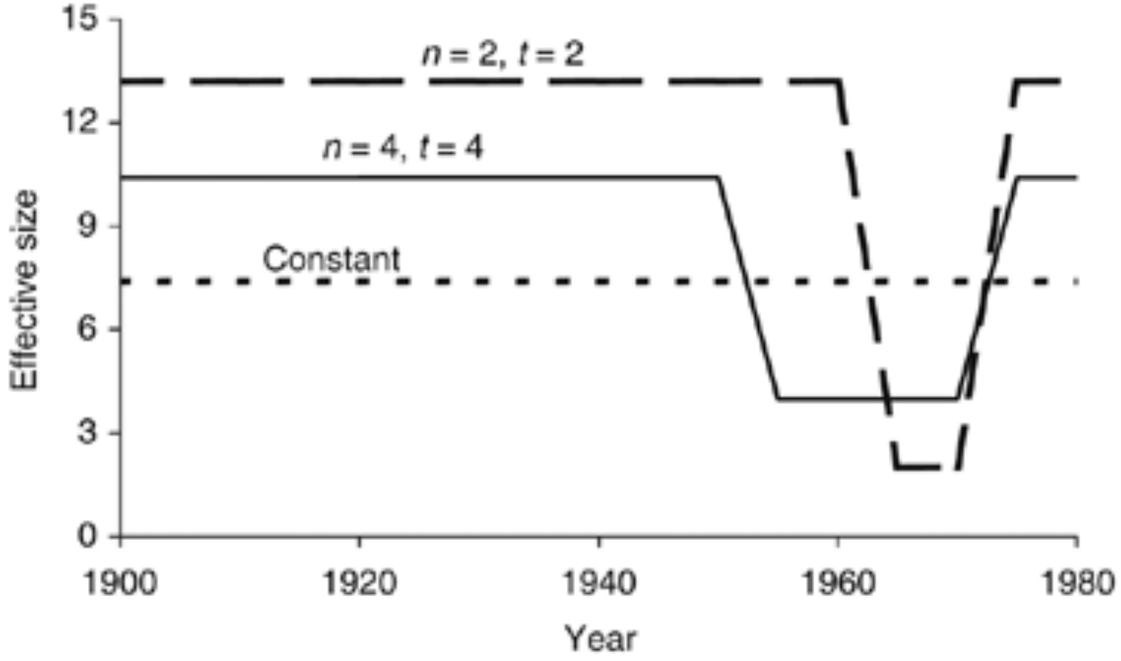
# Case: Florida Panthers

# Florida Panther/Puma/Cougar




Saremi, N.F., Supple, M.A., Byrne, A., Cahill, J.A., Coutinho, L.L., Dalén, L., Figueiró, H.V., Johnson, W.E., Milne, H.J., O'Brien, S.J. and O'Connell, B., 2019. Puma genomes from North and South America provide insights into the genomic consequences of inbreeding. *Nature communications*, *10*(1), p.4769.

# Potential demographic history of Florida panthers



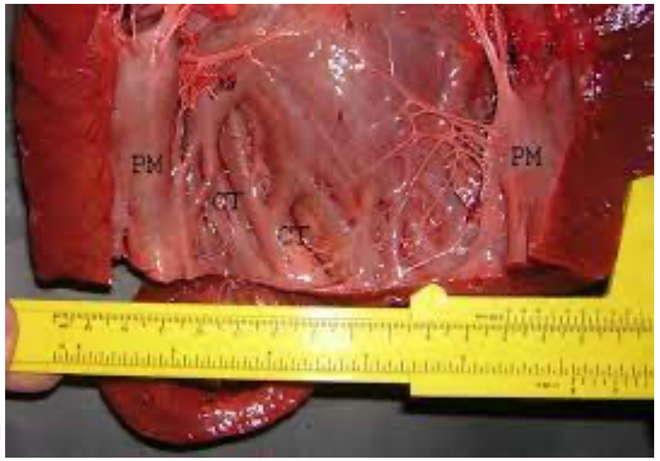

Culver, M., Hedrick, P.W., Murphy, K., O'Brien, S. and Hornocker, M.G., 2008. Estimation of the bottleneck size in Florida panthers. *Animal Conservation*, *11*(2), pp.104-110.

# Were the Florida panthers fine?

# Diseases in Florida panthers

Abnormal panther sperm

Normal panther sperm



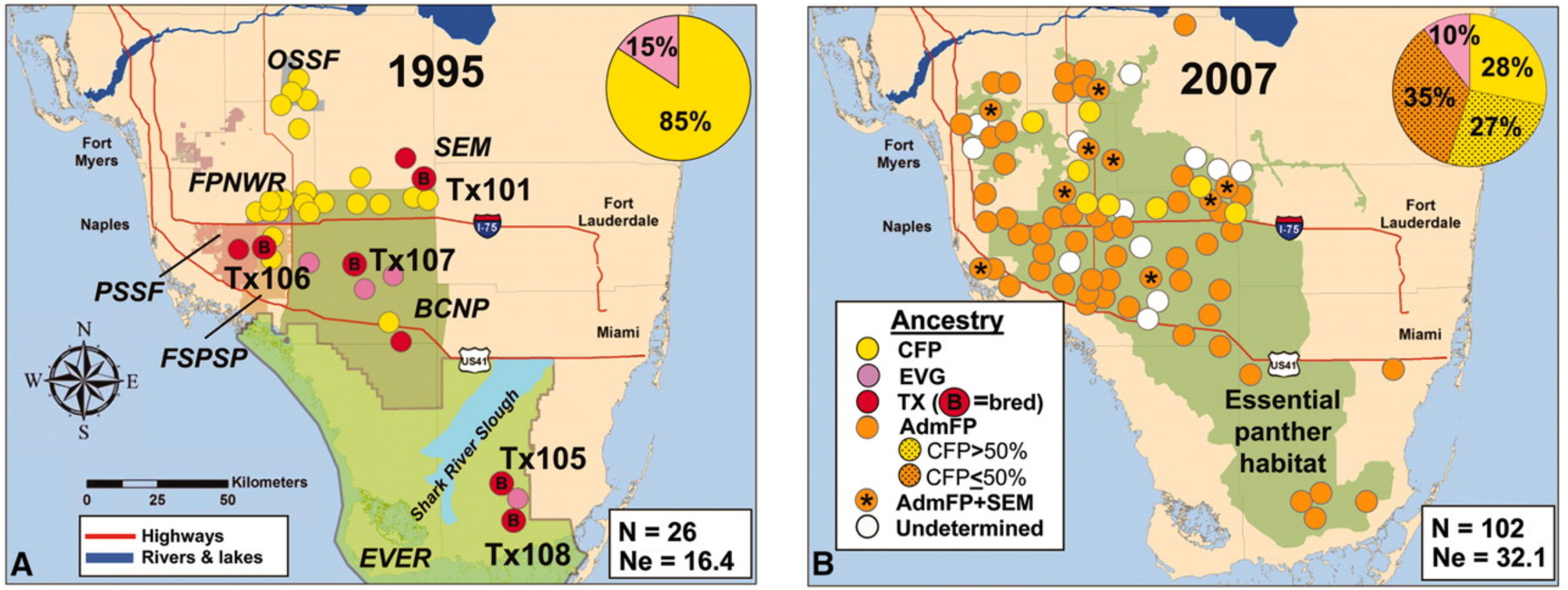


*Discover Biology*, 5/e Figure 18.5 part 2

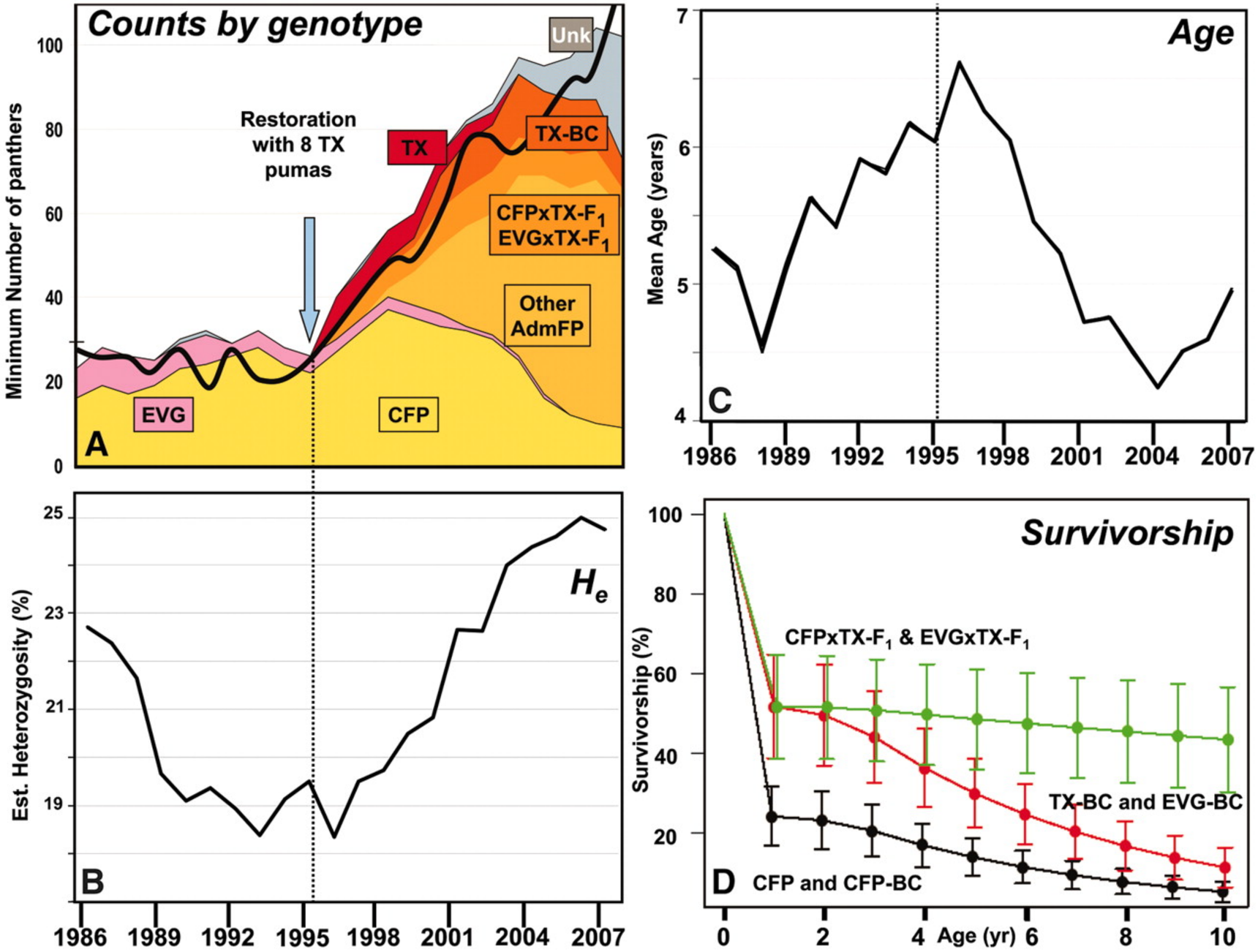

Roelke, M.E., Martenson, J.S. and O'Brien, S.J., 1993. The consequences of demographic reduction and genetic depletion in the endangered Florida panther. *Current Biology*, *3*(6), pp.340-350.

# Genetic Rescue

# Translocation of Florida panthers




Johnson, W.E., Onorato, D.P., Roelke, M.E., Land, E.D., Cunningham, M., Belden, R.C., McBride, R., Jansen, D., Lotz, M., Shindle, D. and Howard, J., 2010. Genetic restoration of the Florida panther. *Science*, *329*(5999), pp.1641-1645.

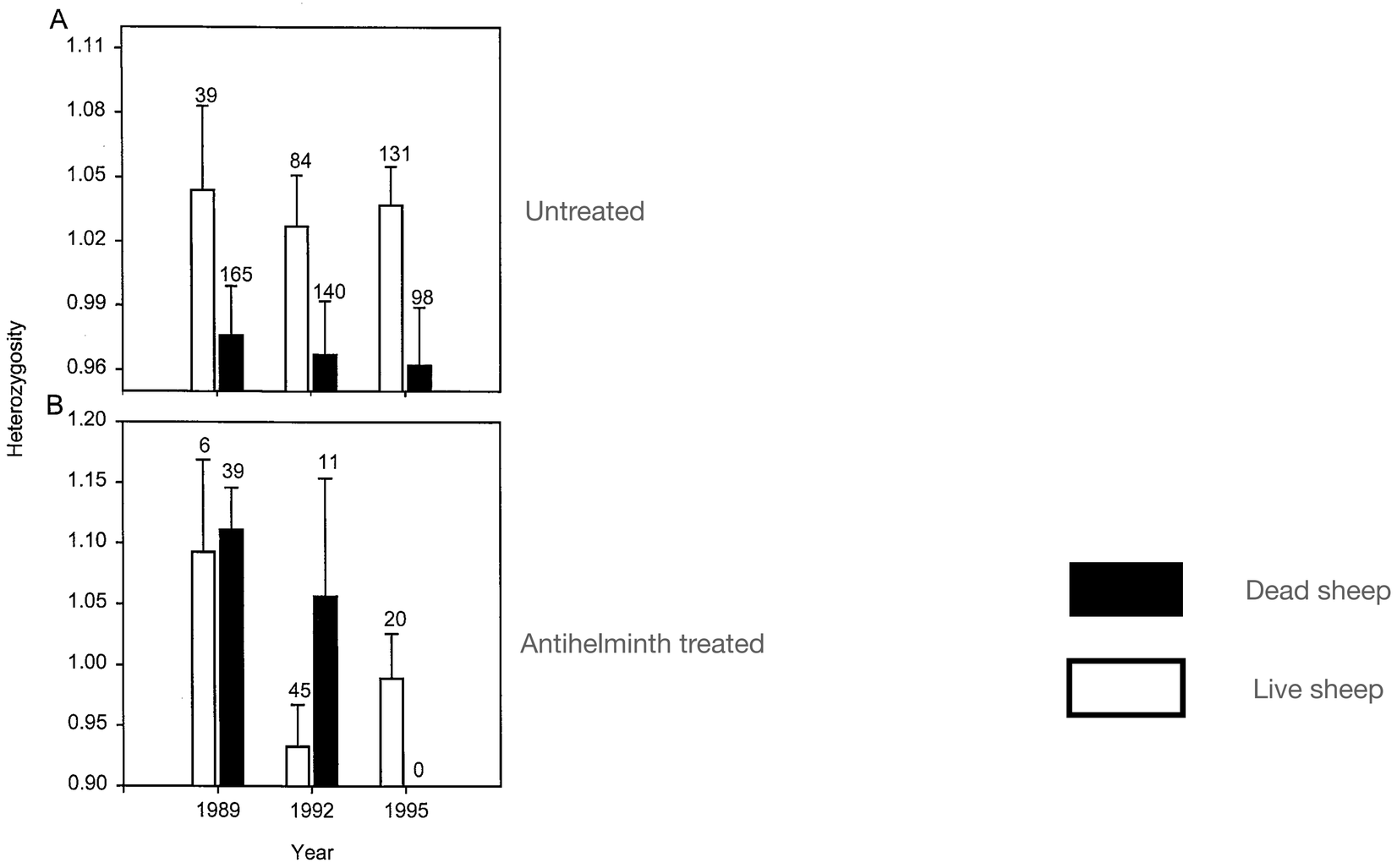



Johnson, W.E., Onorato, D.P., Roelke, M.E., Land, E.D., Cunningham, M., Belden, R.C., McBride, R., Jansen, D., Lotz, M., Shindle, D. and Howard, J., 2010. Genetic restoration of the Florida panther. *Science*, *329*(5999), pp.1641-1645.

# Environmental Rescue

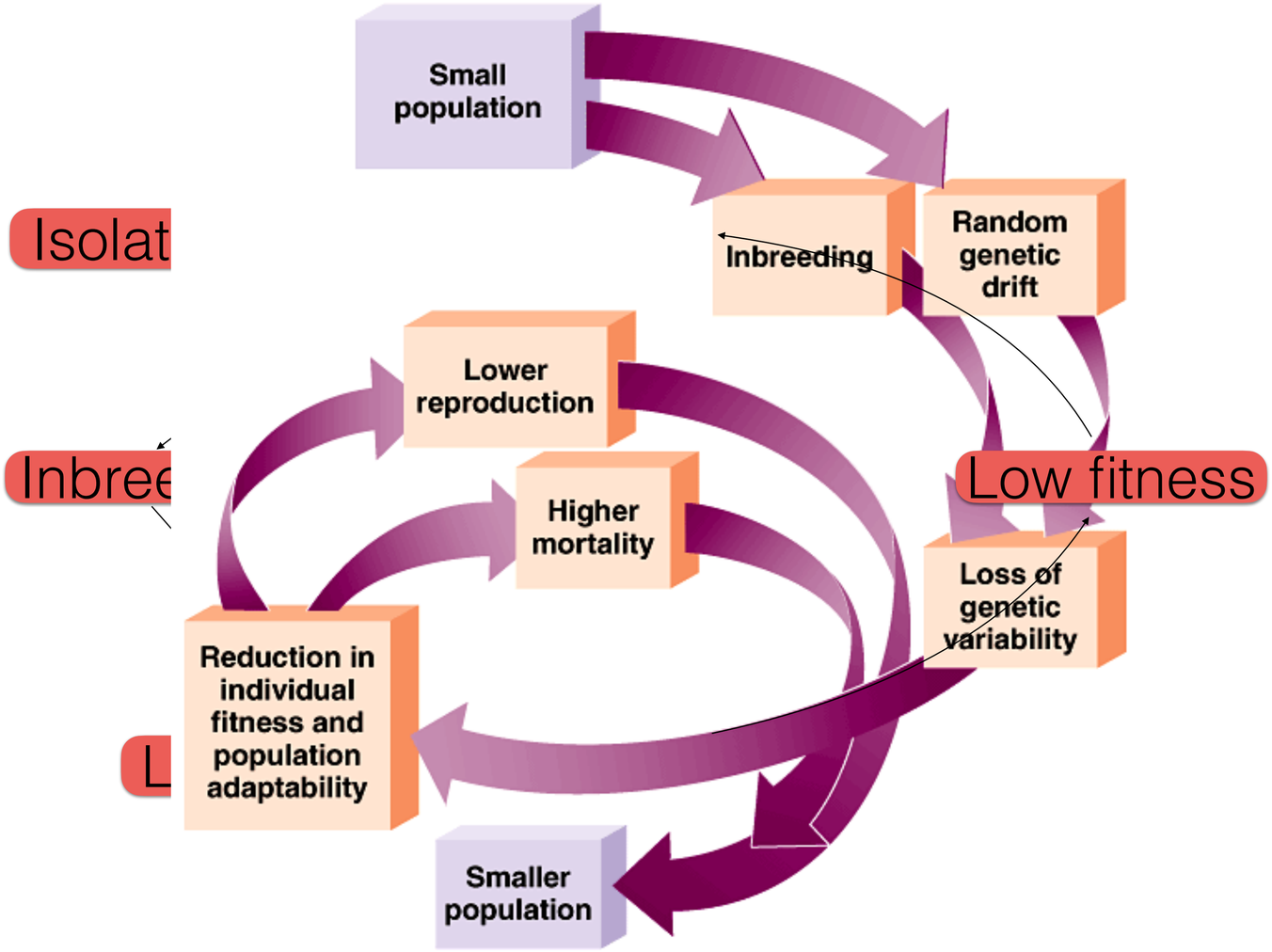
# Case: Soay sheeps


St Kilda
ATLANTIC OCEAN
Hirta
Soay
Dùn
Boreray
Stac an Armin
Stac Lee
Stac Levenish
Orkneys
SCOTLAND
Outer Hebrides
0 100 km
0 60 mi
430 m
400 m
300 m
200 m
100 m
0
summit
village ruins
Projection UTM - WGS84 datum
Estimated scale : 1:250 000
(precise to about 62.5 m)
196 m
An t-Sail
Rubha Bhriste
Mullach an Eilein
384 m
Clesgor
172 m
Creagan na Rubhaig Bana
Sgarbhstac
Rubha Bhrengadal
Am Plastair
Poll Adinet
Stac Biorach
Stac Shoalgh
Cnoc Glas
376 m
Gob a' Ghaill
Lianish
Gob Phursan
Stac Dona
216 m
Gob na h-Airde
Bradastac
Mina Stac
Baie Glen
Leac Mhina Stac
Sgeir Dhomhnuill
Mullach Mòr
361 m
Conachair
430 m
Stac a' Langa
Poll a' Choire
Sgeir nan Sgarbh
Oiseval
290 m
Mullach Bi
358 m
Village Bay
Rubha an Uisge
Gob Chathaill
Rubha Challa
Loch Hiort
Rubha Mhuirich
Ruival
An Torc
Bioda Mor
178 m
Sgeir Mhòr
Gob na Muce
Hamalan
Sgeir Cùll an Rubha
62 m
Na Bedhan
0 (km) 5
0 (mi) 3
8° 38'
8° 36'
8° 34'
8° 32'
8° 30'
8° 28'
57° 53'
57° 52'
57° 51'
57° 50'
57° 49'
57° 48'


A
1.11
1.08
1.05
1.02
0.99
0.96
39
165
84
140
131
98
Untreated
B
1.20
1.15
1.10
1.05
1.00
0.95
0.90
6
39
11
45
20
0
Antihelminth treated
Heterozygosity
1989
1992
1995
Year
Dead sheep
Live sheep

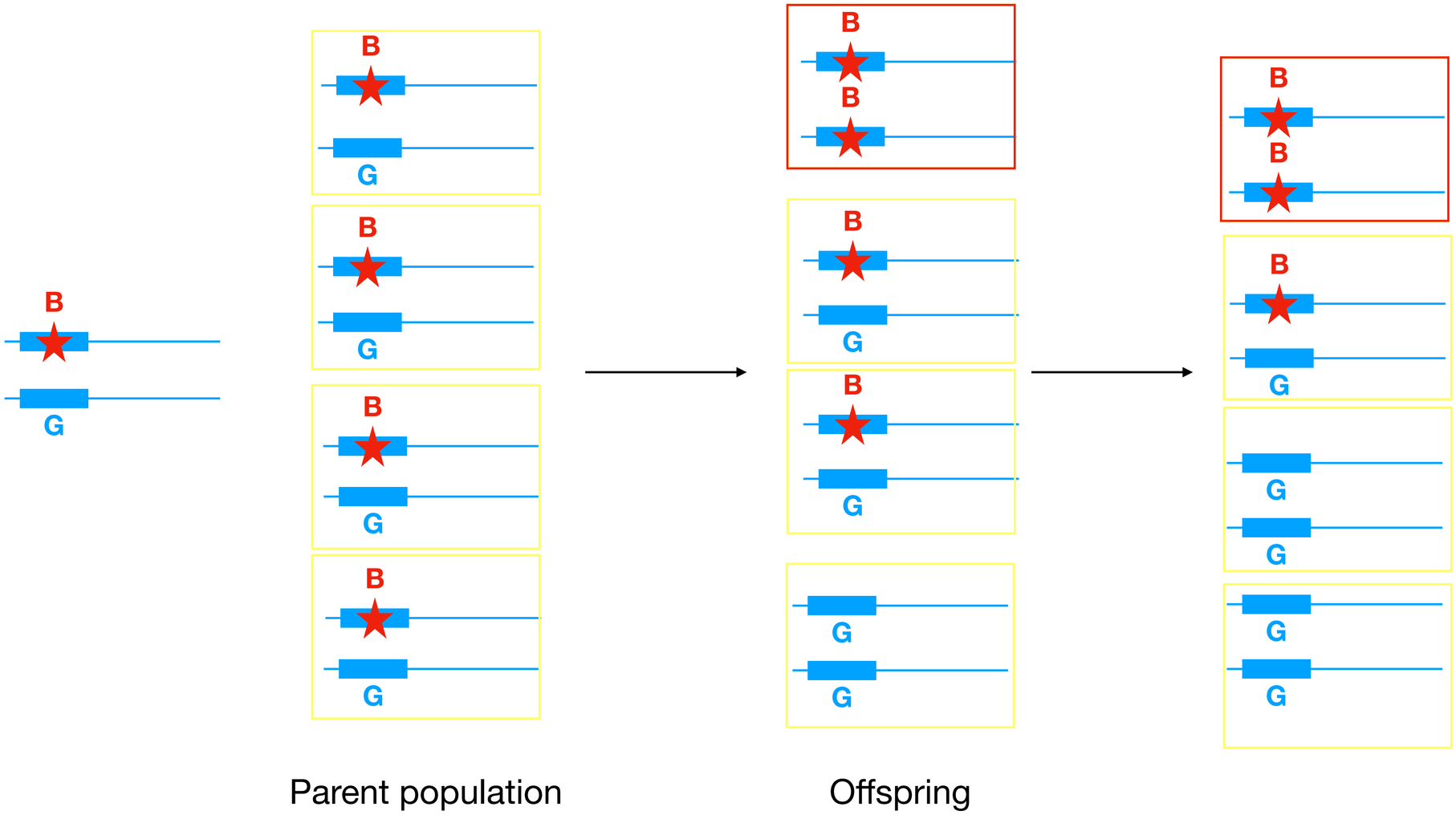
# Deleterious alleles and Purging

# Isolated small populations - a problem




Fagan and Holmes 2006

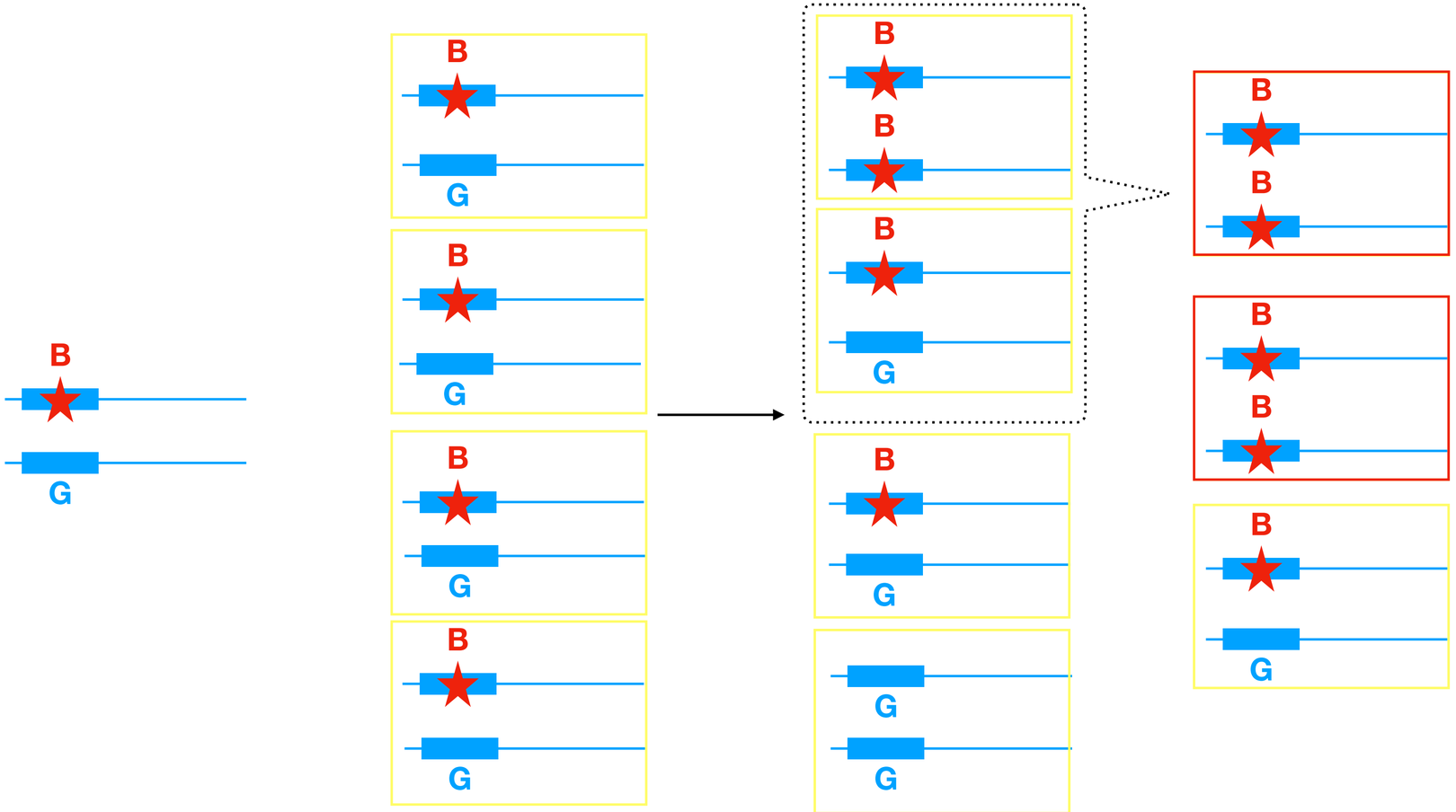
# Large population




Parent population

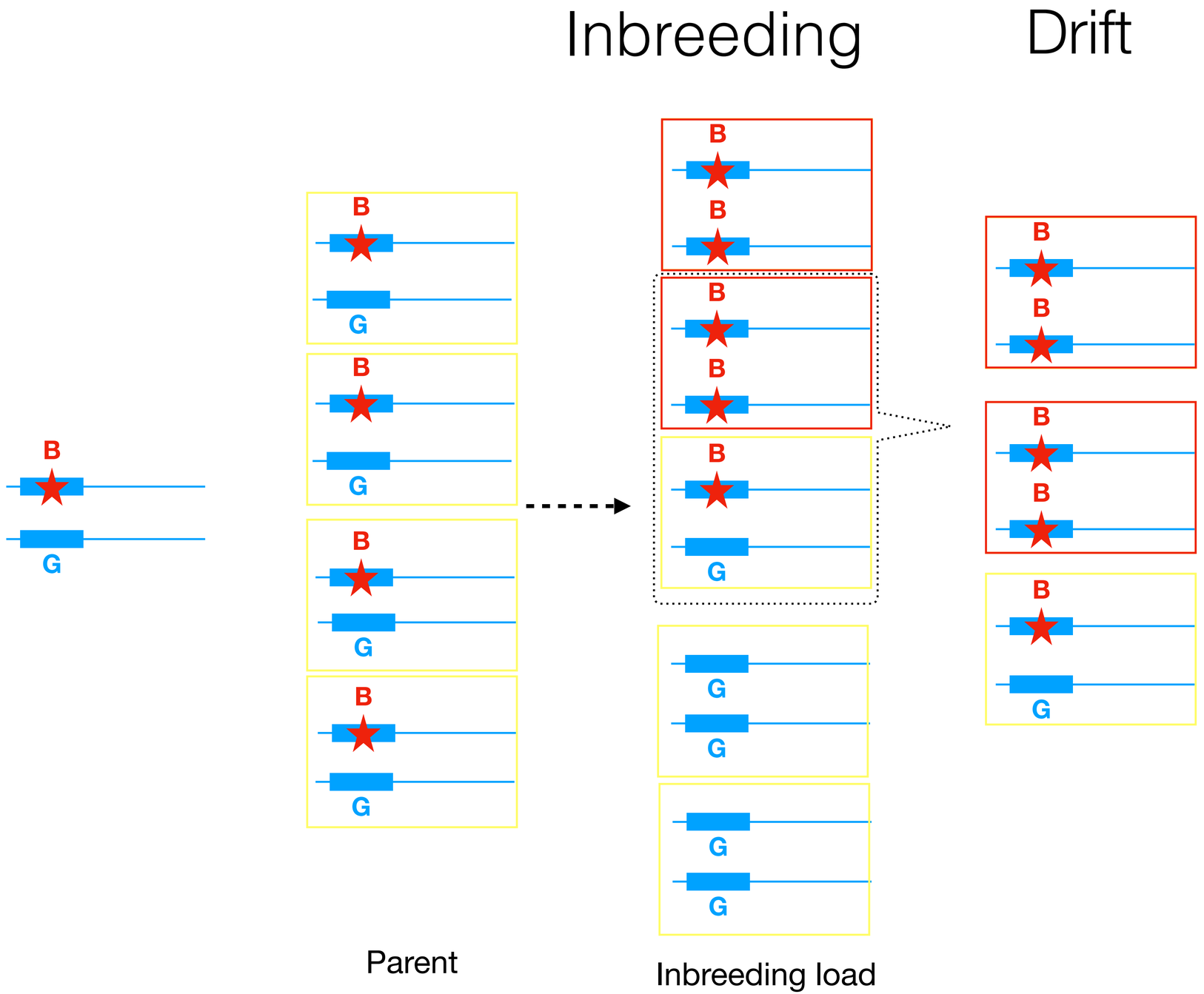
Offspring

# Small population




Parent population

Offspring


Inbreeding
Drift
B
G
Parent
Inbreeding load

## Historical Genomes Reveal the Genomic Consequences of Recent Population Decline in Eastern Gorillas

Tom van der Valk,[1] David Díez-del-Molino,[2] Tomas Marques-Bonet,[3,4,5,6] Katerina Guschanski,[1,7,8,9,*] and Love Dalén[2,7,8,*]

**2019**

## Purging of Strongly Deleterious Mutations Explains Long-Term Persistence and Absence of Inbreeding Depression in Island Foxes

Jacqueline A. Robinson,[1,4,6,*] Caitlin Brown,[1] Bernard Y. Kim,[1] Kirk E. Lohmueller,[1,2,3,5] and Robert K. Wayne[1,5]

**2018**

## Purging of highly deleterious mutations through severe bottlenecks in Alpine ibex

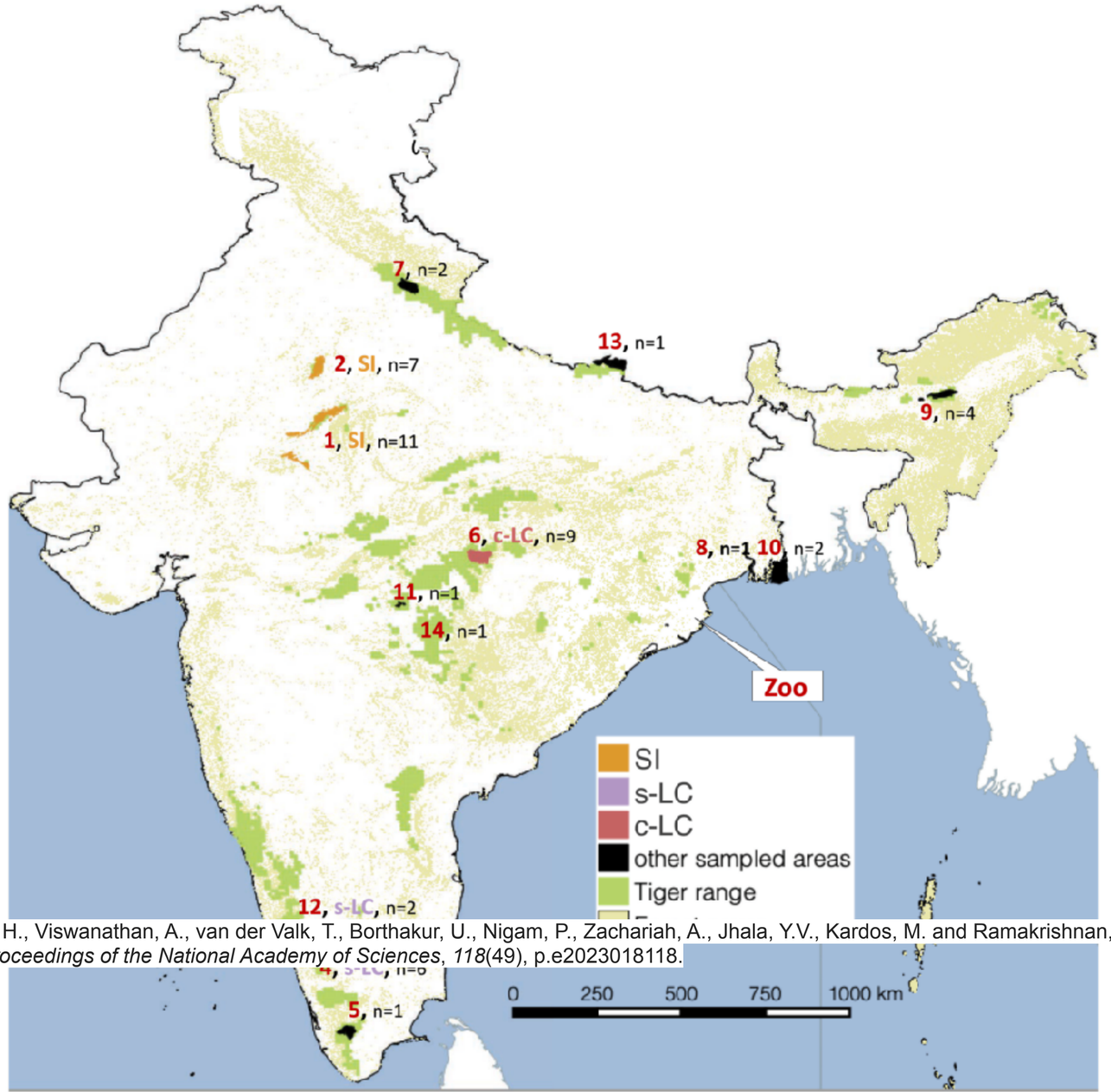
Christine Grossen[1✉], Frédéric Guillaume[1], Lukas F. Keller[1,2] & Daniel Croll[3✉]

**2020**

## Genomic insights into the conservation status of the world's last remaining Sumatran rhinoceros populations

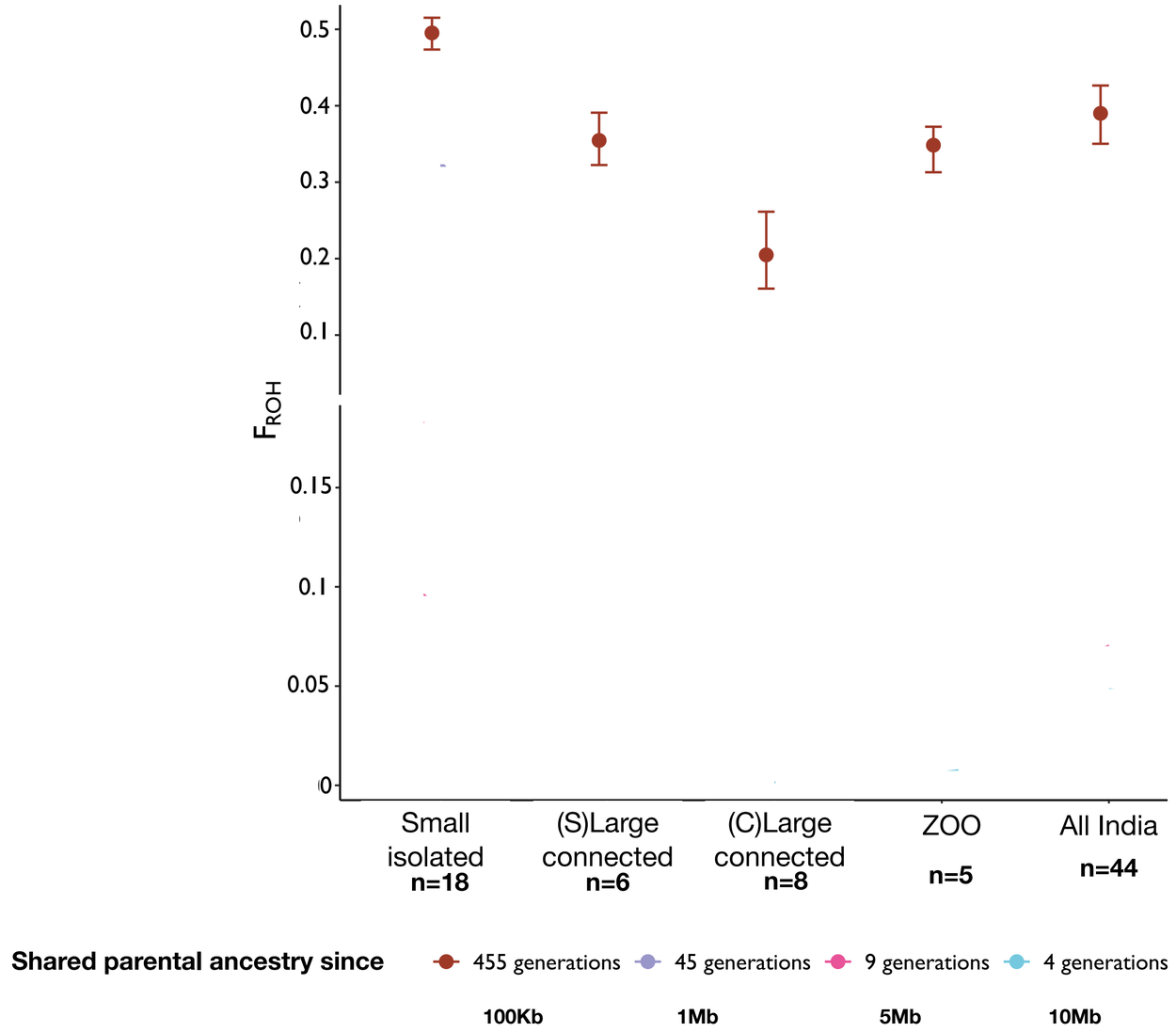
**2021**

# Sampling



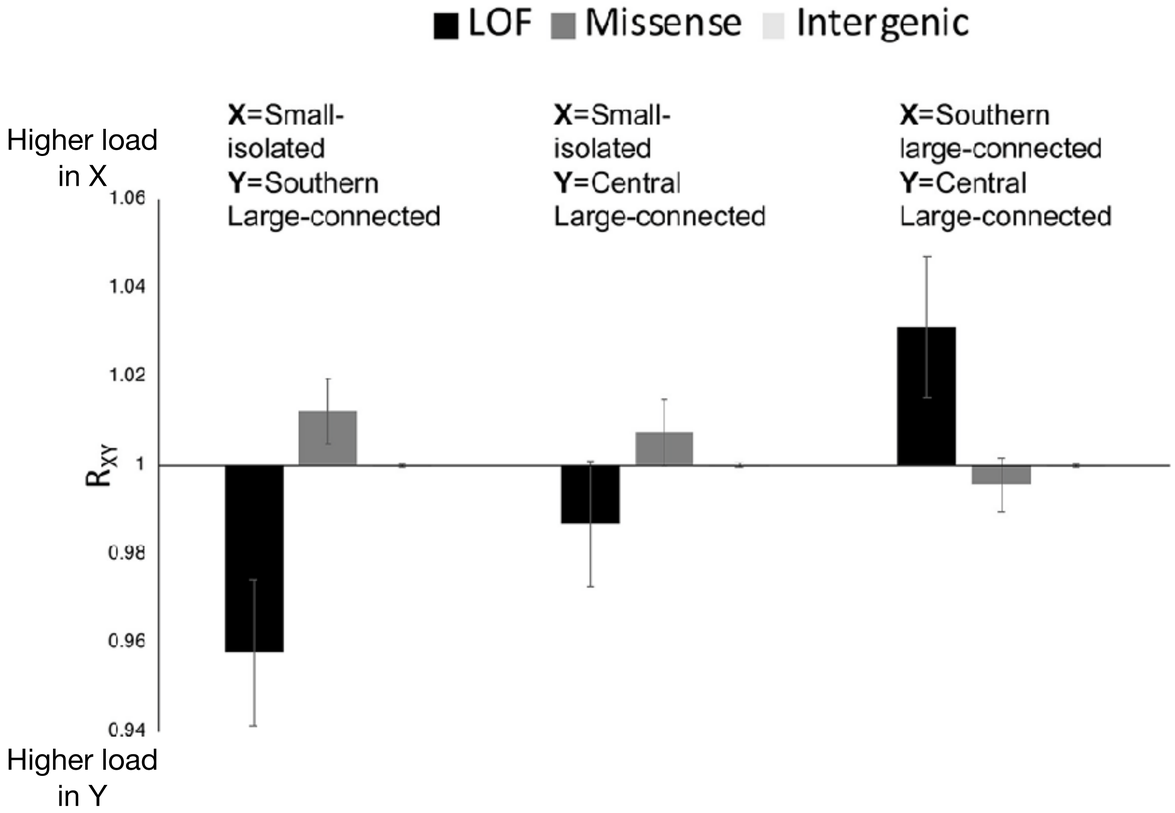

Khan, A., Patel, K., Shukla, H., Viswanathan, A., van der Valk, T., Borthakur, U., Nigam, P., Zachariah, A., Jhala, Y.V., Kardos, M. and Ramakrishnan, U., 2021. Genomic evidence for inbreeding depressio variation in Indian tigers. *Proceedings of the National Academy of Sciences*, *118*(49), p.e2023018118.

# Individuals from small isolated population are more inbred



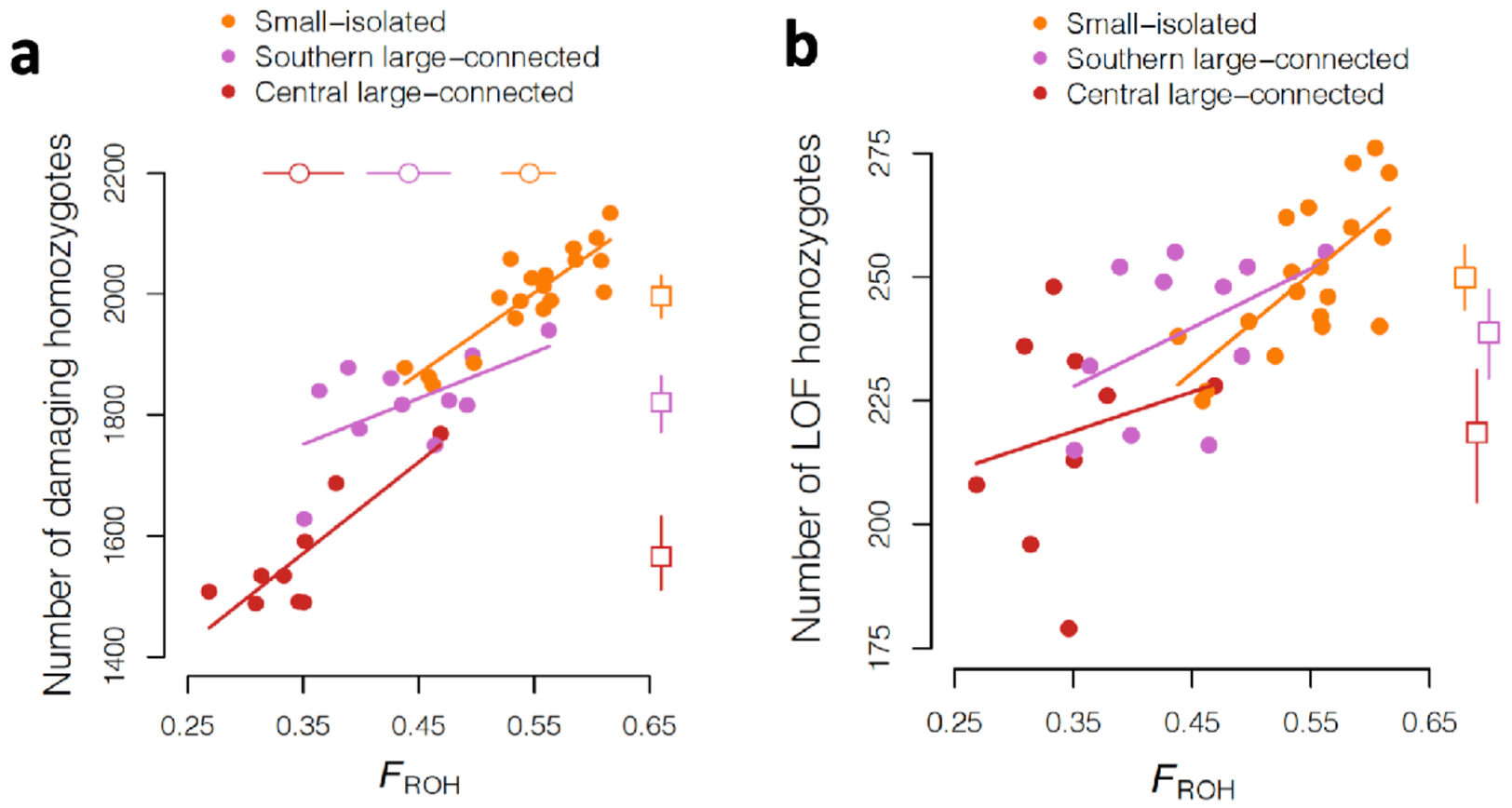

Khan et al. 2022, PNAS

# Isolated populations have lower deleterious allele load

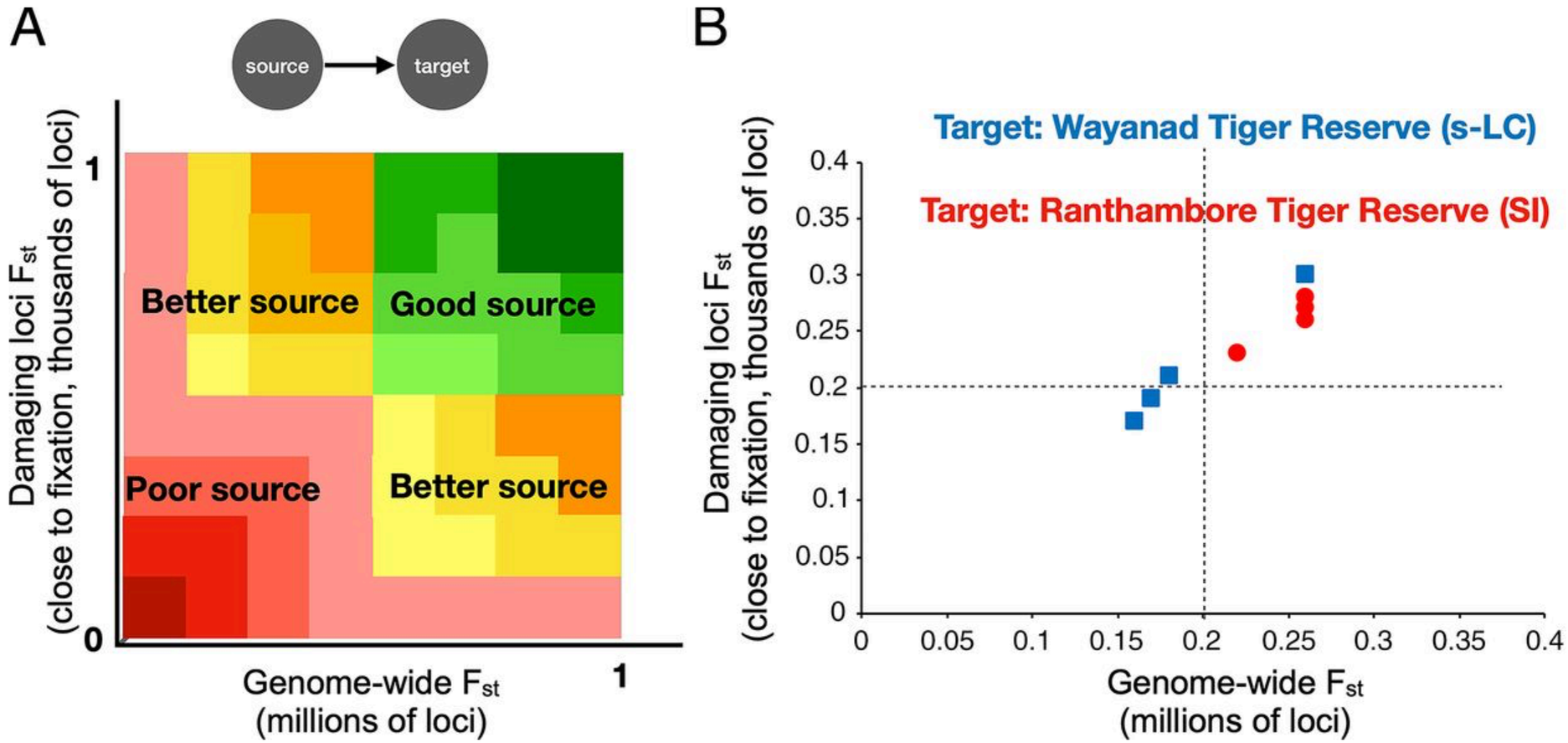

Khan et al. 2022, PNAS

# Isolated populations have high homozygosity for deleterious alleles




Khan et al. 2022, PNAS

# Genome-wide genetic distance may predict genetic rescue




Khan et al. 2022, PNAS