1.1 BILLION NUCLEOTIDES IN THE RED SISKIN GENOME

554kb CONTIG N50
Measure of genome contiguity

DISCOVER
Differences across entire genomes between populations in Venezuela and Guyana

OTHER GOALS
- Assess the longterm viability of small, isolated populations
- Describe the phylogeographic history of the species
- Identify and exclude hybrids from captive breeding to preserve genetic identity
- Monitor and manage diversity of wild and captive populations

IDENTIFY
Genome regions associated with the ability to inhabit different environments

Percentage of core genes is as good as the two GOLD STANDARD bird genomes

50% of the total genome is assembled into segments of 554kb or longer