

Progress on pink salmon genetic markers

Alaska Department of Fish & Game
Gene Conservation Lab



University of Washington
Seeb Lab for Ecological Genomics



March 2016 AHRP Meeting
Anchorage, AK

Background

- Need ~200 highly variable SNPs for parentage

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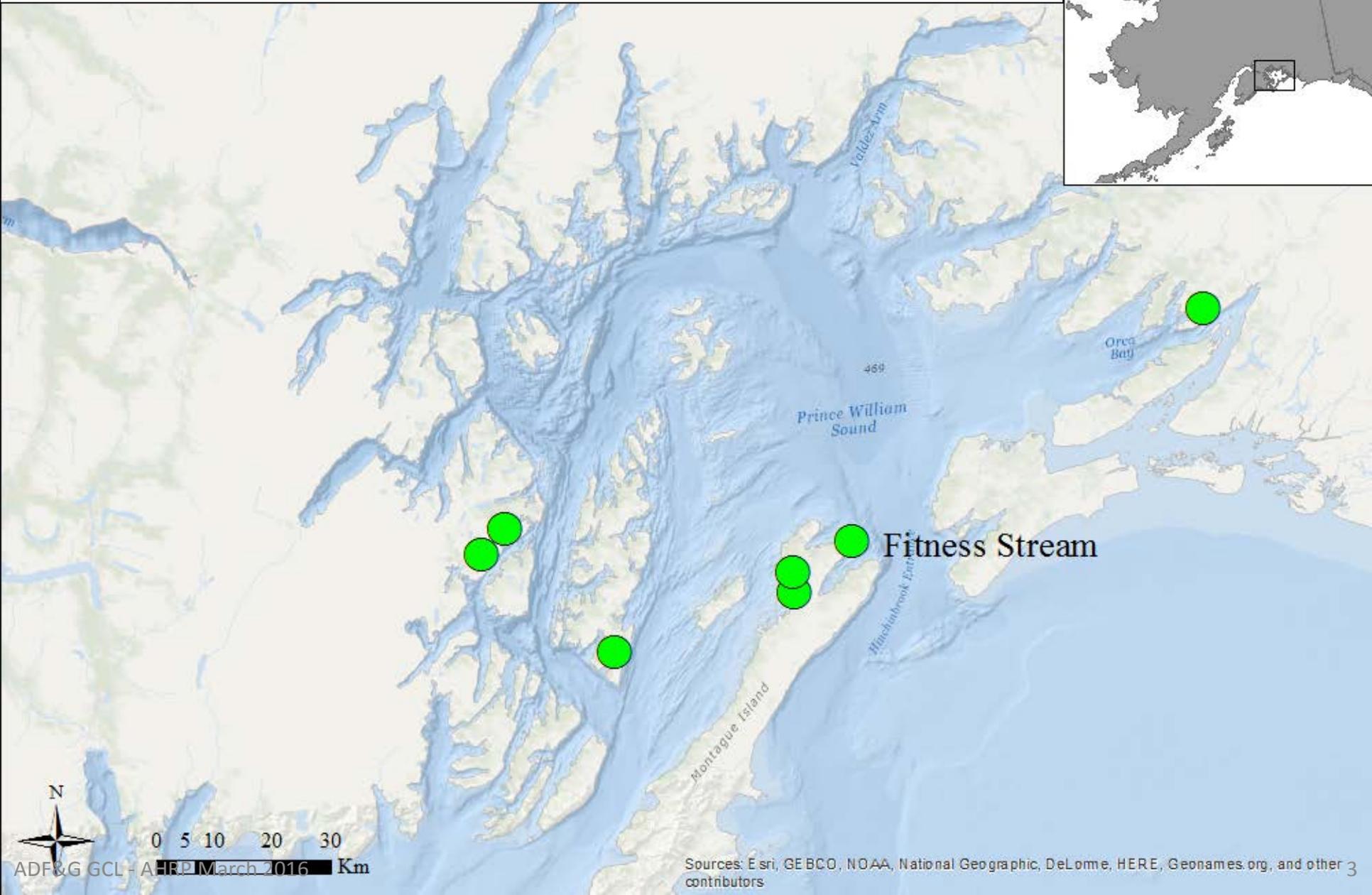
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- RAD sequencing best approach to develop SNPs
- Selecting SNPs in context of a linkage map is useful as it maximizes informational value of data
- **Development contracted to UW, analysis by UW/ADF&G staff**

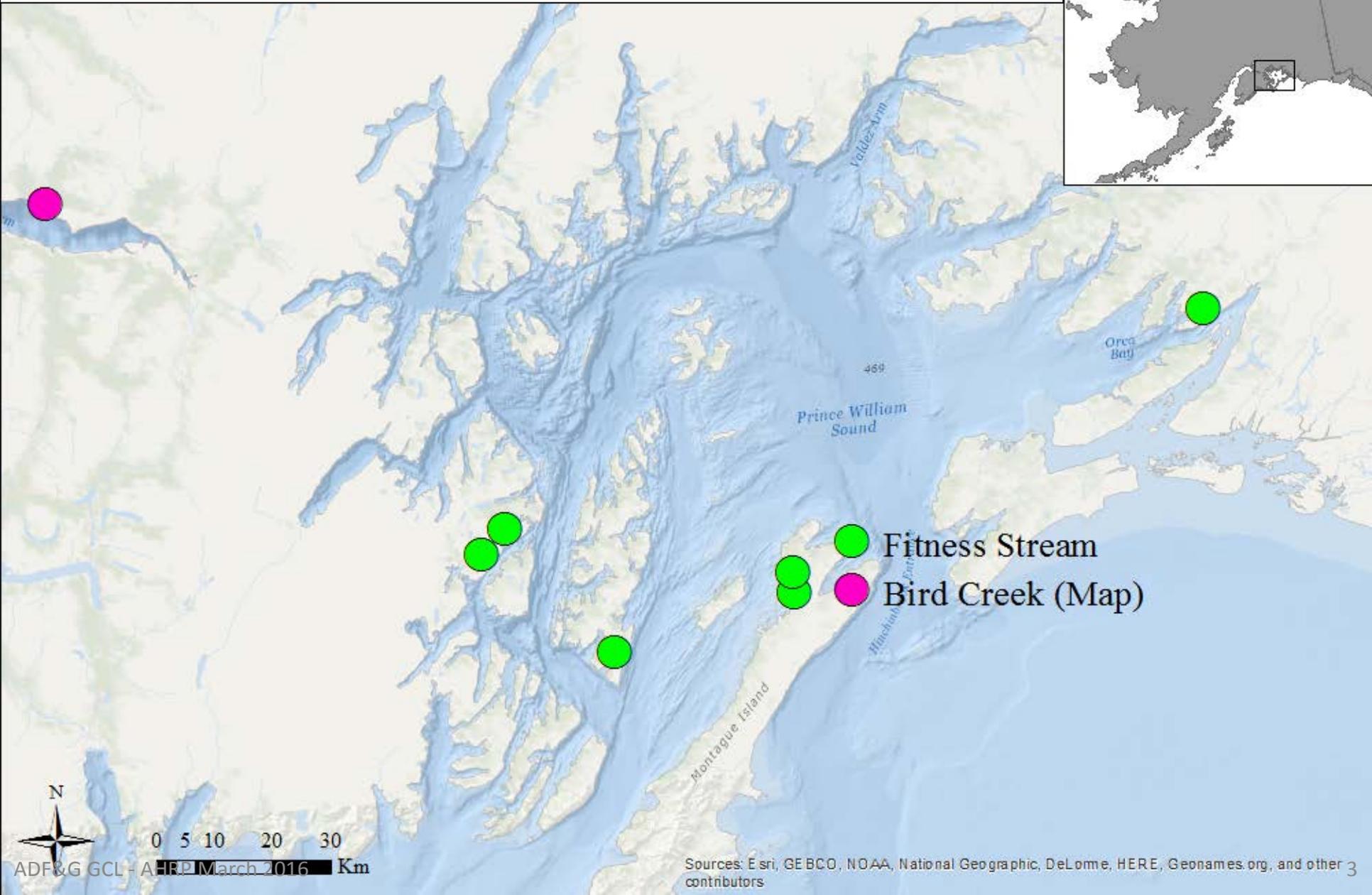
Review of experimental design



N
0 5 10 20 30
ADF&G GCL - AHRP March 2016 Km

Sources: Esri, GEBCO, NOAA, National Geographic, DeLorme, HERE, Geonames.org, and other 3 contributors

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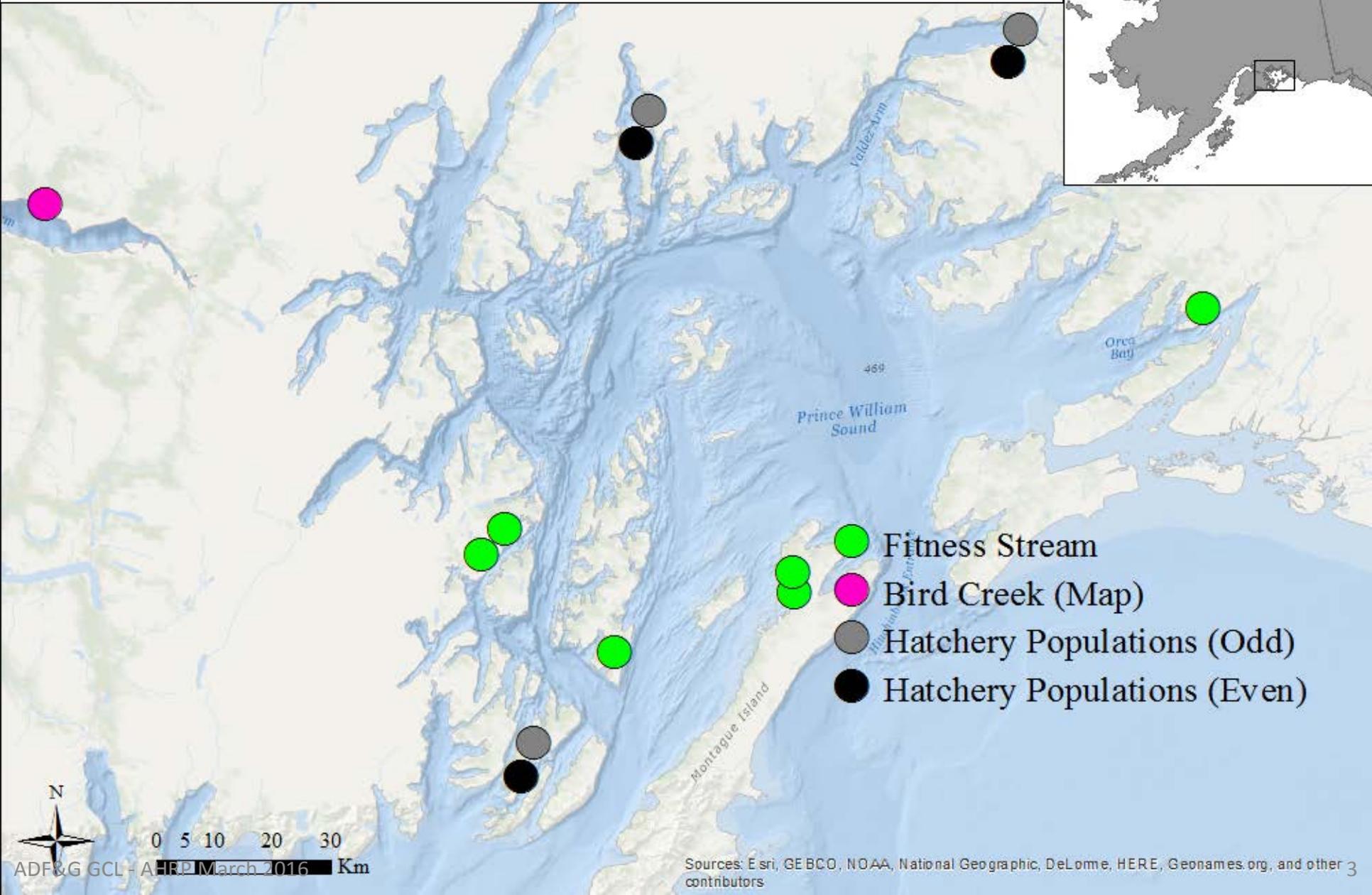
Fitness Stream

Bird Creek (Map)

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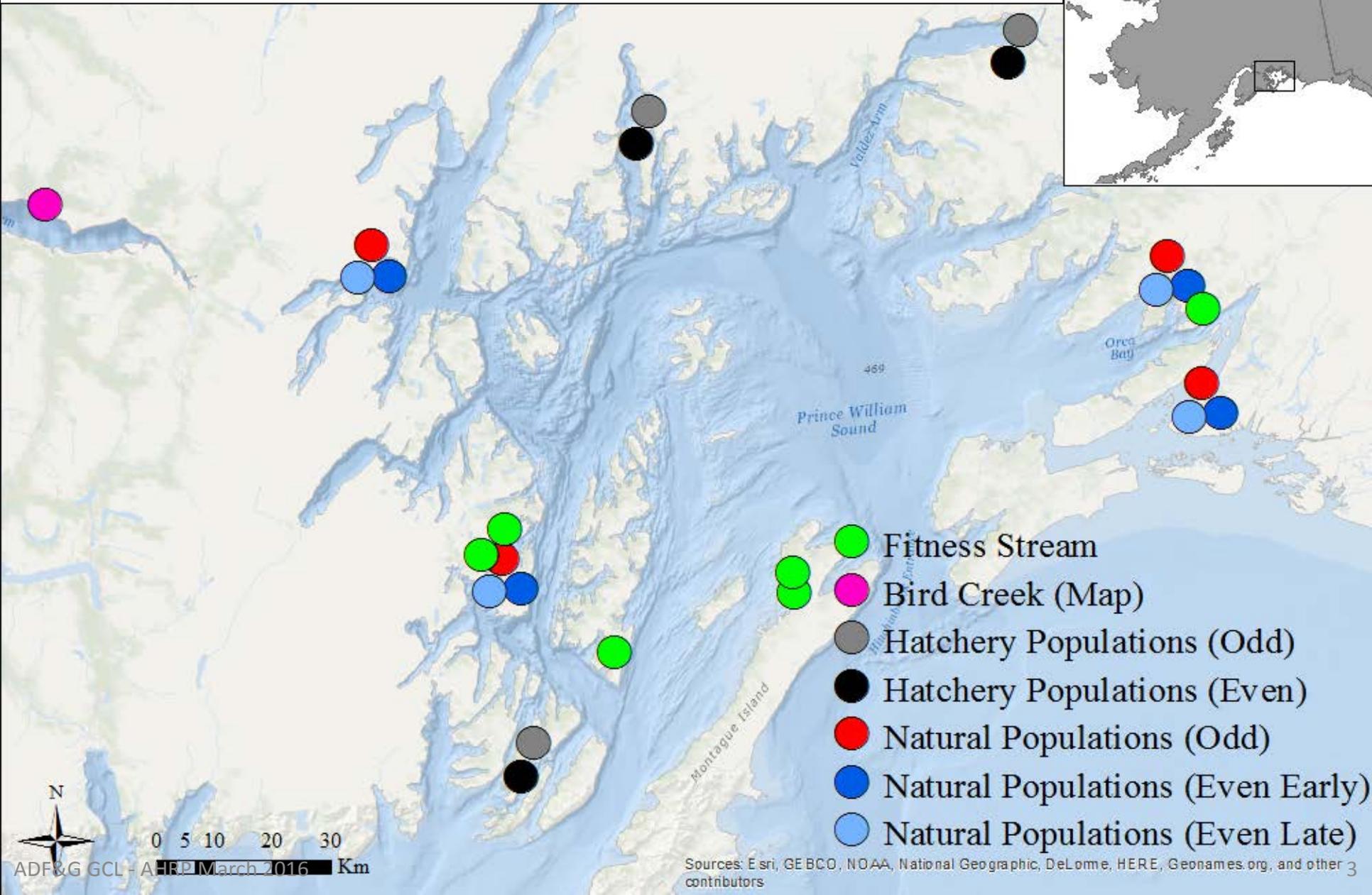
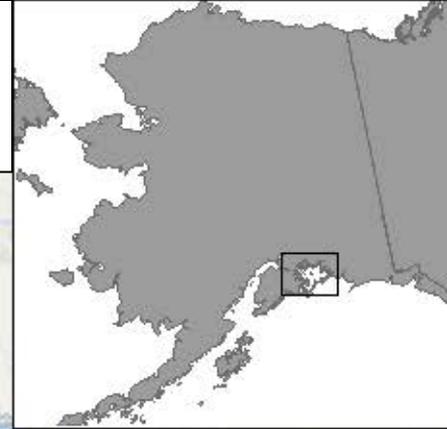


- Fitness Stream
- Bird Creek (Map)
- Hatchery Populations (Odd)
- Hatchery Populations (Even)

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- Fitness Stream
- Bird Creek (Map)
- Hatchery Populations (Odd)
- Hatchery Populations (Even)
- Natural Populations (Odd)
- Natural Populations (Even Early)
- Natural Populations (Even Late)

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Results

~70,000-80,000

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Results

Present in 4+ pops
Global MAF > 0.05
Genotyped ½ fish within pops

40,617 Even / 37,542 Odd
51,406 Total (26,675 Common)

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Global MAF > 0.05
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Missing call rates > ¼ fish *

18,358 Even / 15,347 Odd

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* Also filtered poor quality fish

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HWE $P > 0.05$ in ½ of pops
Population MAF > 0.05 all pops

14,405 Even / 12,854 Odd

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8,738

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Single SNP/RAD tag

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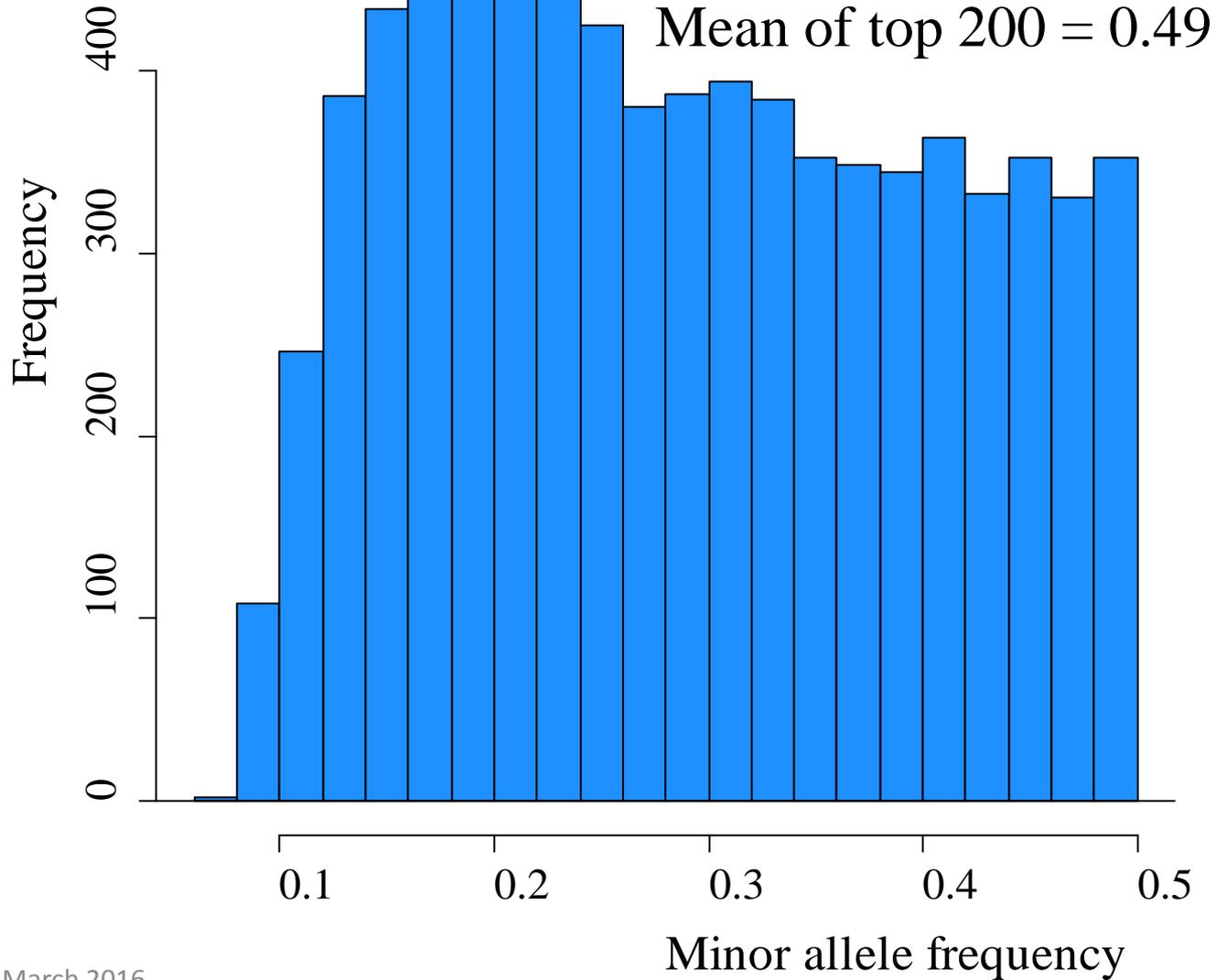
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Minor allele frequency



Summary

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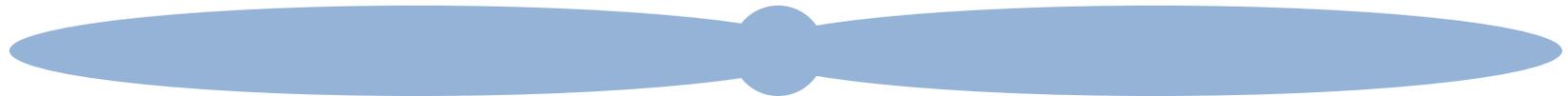
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- Final selection:
 - Discount for variation among populations
 - Locate on map and select independent SNPs



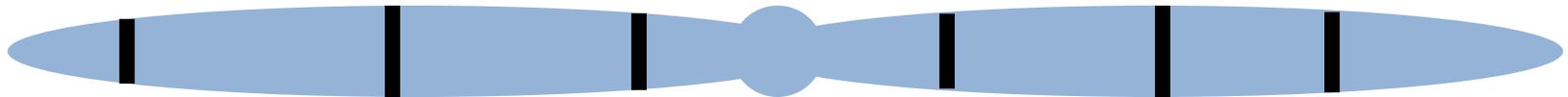
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Timeline

		2016		
Task	Funding	Q2	Q3	Q4
Pink SNP Development	Funded	2	4	5

Key:

Stages of completion	1	2	3	4	5
SNP Development	Data collection	Data filtering	Location on map	SNP selection	Optimization