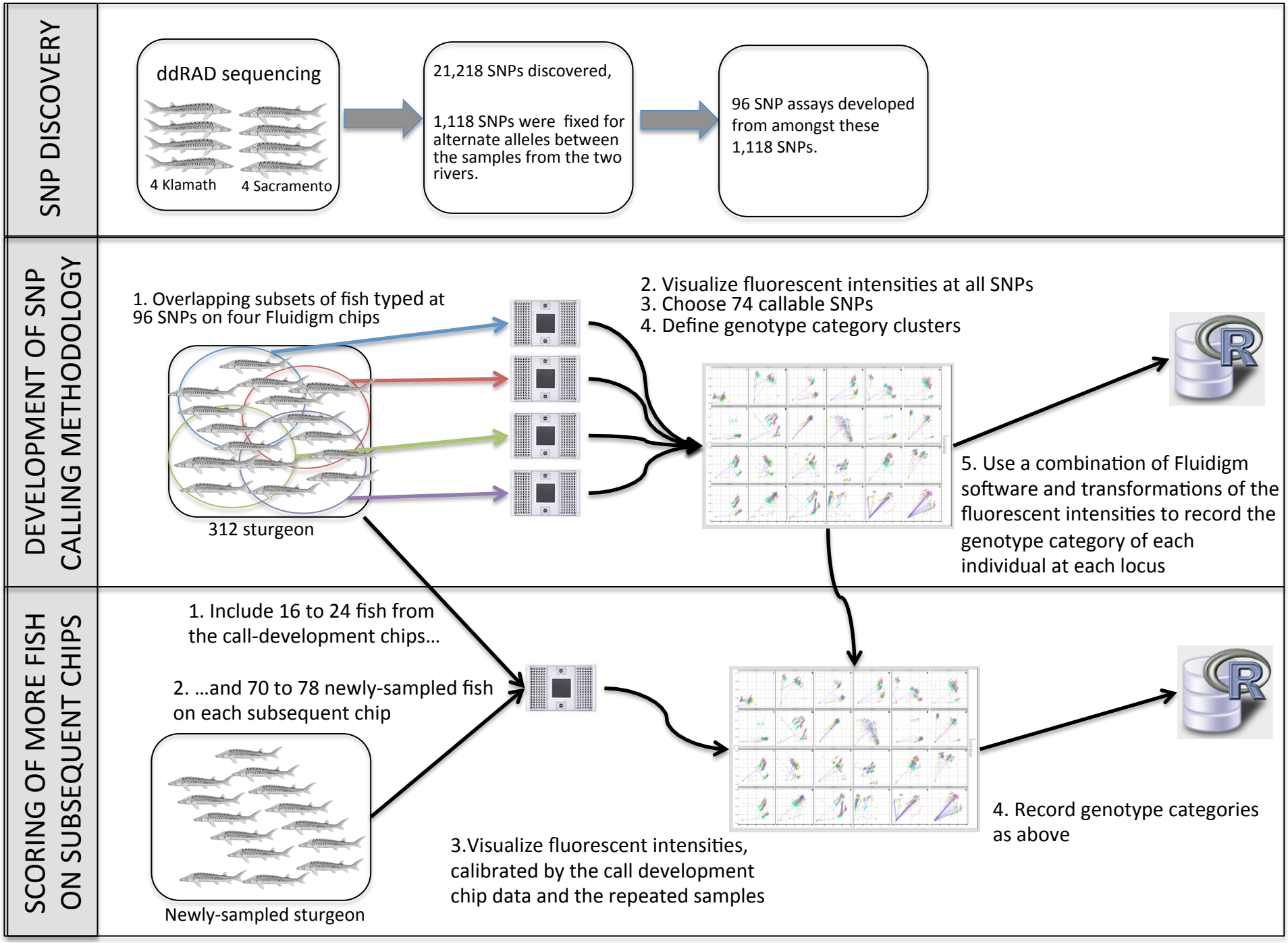
SNP DISCOVERY
ddRAD sequencing
4 Klamath
4 Sacramento
21,218 SNPs discovered,
1,118 SNPs were fixed for alternate alleles between the samples from the two rivers.
96 SNP assays developed from amongst these 1,118 SNPs.
DEVELOPMENT OF SNP CALLING METHODOLOGY
1. Overlapping subsets of fish typed at 96 SNPs on four Fluidigm chips
312 sturgeon
2. Visualize fluorescent intensities at all SNPs
3. Choose 74 callable SNPs
4. Define genotype category clusters
5. Use a combination of Fluidigm software and transformations of the fluorescent intensities to record the genotype category of each individual at each locus
SCORING OF MORE FISH ON SUBSEQUENT CHIPS
1. Include 16 to 24 fish from the call-development chips…
2. …and 70 to 78 newly-sampled fish on each subsequent chip
Newly-sampled sturgeon
3.Visualize fluorescent intensities, calibrated by the call development chip data and the repeated samples
4. Record genotype categories as above