

GENOME AND BIOMEDICAL SCIENCES FACILITY

70 Faculty (>25 new)

~700 people

~20,000 mice

Six floors

225,000 sq ft

Several Med School Depts

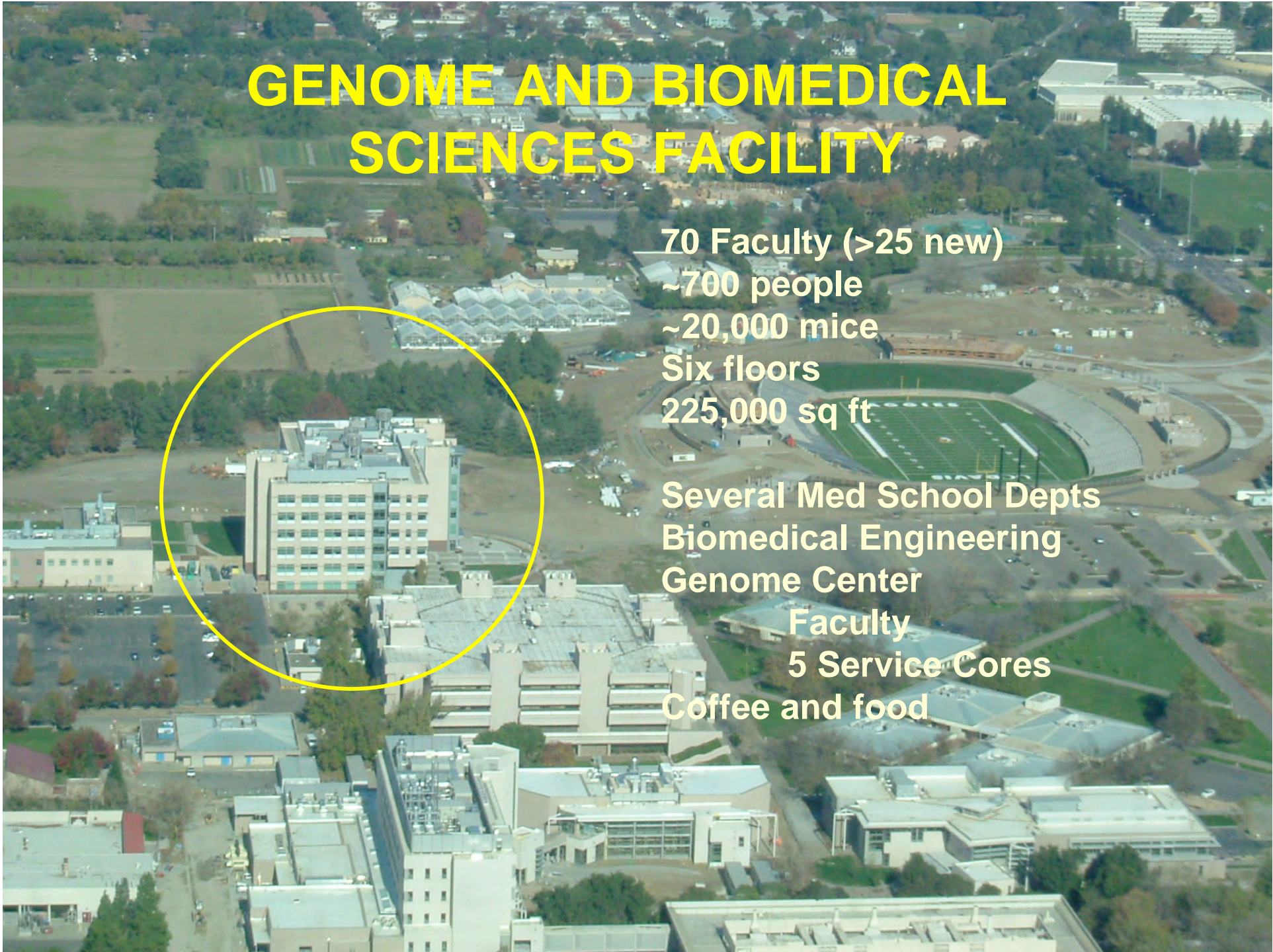
Biomedical Engineering

Genome Center

Faculty

5 Service Cores

Coffee and food



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- [Core Home](#)
- [Find Us](#)
- [Contact Us](#)
- [Links](#)
- [Log In](#)
- [Prices](#)
- [Bioinformatics](#)
- [Equipment](#)

UC DAVIS GENOME CENTER

Expression Analysis Core

Expression Analysis Core Facility

The mission of the Expression Analysis Core at the UC Davis Genome Center is to provide services and technologies for gene expression analyses at the genomic level, without duplicating services readily available elsewhere on campus. We are currently focused on exploiting ultra high throughput sequencing, chromatin immunoprecipitation, and varying array platforms including NimbleGen custom arrays and Illumina Expression arrays. Tutorials and seminars in these technologies are an important part of facility

operations. We also offer access to microarray scanners, liquid handlers, and nucleic acid analyzers to facilitate your experiments.

Getting Started in the Expression Analysis Core

Our Services

- New Technology:** Ultra High Throughput Sequencing
- Microarrays:** Illumina Gene Expression Nimblegen & Other Array Platforms
- Techniques:** Chromatin Immunoprecipitation
- Workshops:** Chromatin & Methylated DNA Immunoprecipitation Workshops
- Equipment Access:** Scanners Bioanalyzer Chromatin Sonication
Array Hybridizer Liquid Handlers Nanodrop

Contact Information

Facility Manager



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-  [Log In](#)
-  [Prices](#)
-  [Bioinformatics](#)
-  [Equipment](#)

DNA Technologies Core Facility



The mission of the DNA Technologies Core at the UC Davis Genome Center is to provide DNA analytical services to campus and other researchers. We are currently focused on single nucleotide polymorphism (SNP) genotyping. Our goal is to enable access to high throughput, genome-wide analyses at economical recharge rates, as a functional extension of your laboratory. The services offered by the Genome Center complement other UC Davis facilities in order to provide access to numerous technologies for molecular marker analysis.

Getting Started at the DNA Technologies Core

Facility Services

Illumina Golden Gate SNP Genotyping Ultra High Throughput Sequencing

Infinium Genotyping BeadXpress Genotyping

Equipment & training

Analyst Plate Reader Robotic Liquid Handlers

Find out more about getting trained

Contact Information

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Staff Research Associate



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FAX: 530-754-9658

We're located in Rm 4212A, Genome and Biomedical Sciences Facility

Using the BeadXpress to Genotype Earth's Diversity



Vertebrate Animals

Mammals	5,416
Birds	9,956
Reptiles	8,240
Amphibians	6,199
Total Vertebrates	59,811

Invertebrate Animals

Insects	950,000
Molluscs	81,000
Crustaceans	40,000
Corals	2,175
Others	130,200
Total Invertebrates	1,203,375

Plants

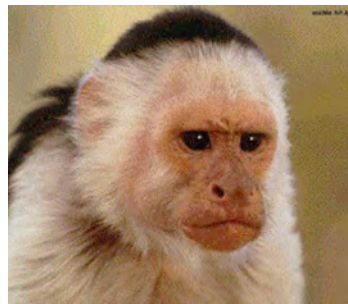
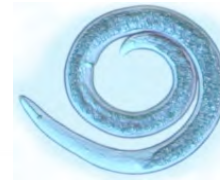
Flowering plants (angiosperms)	258,650
Conifers (gymnosperms)	980
Ferns and horsetails	13,025
Mosses	15,000
Red and green algae	9,671
Total Plants	297,326

Others


Lichens	10,000
Mushrooms	16,000
Brown algae	2,849
Total Others	28,849

TOTAL SPECIES 1,589,361

Species Genotyped in the DNA Technologies Core using the Illumina Golden Gate Assay



Genotyping with the BeadXpress



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BeadXpress System

The BeadXpress system from Illumina offers a cost effective platform for assaying 1 to 384 SNPs in essentially any number of individuals. The BeadXpress platform primarily uses the Golden Gate SNP genotyping assay that we currently use in conjunction with the Bead Array Reader (for more information on Golden Gate, see our Illumina Golden Gate genotyping [web page](#)). The main advantages of the BeadXpress platform compared to the Bead Array reader are that the costs/SNP are lower than on the Bead Array Reader, particularly at the 96 SNP/sample level, variable numbers of samples can be more easily assayed since the readout is not entirely dependent on maintaining samples in a 96 well format (with the caveat that labor costs are very similar regardless of the number of samples processed, up to a full plate), and that ASPE assays can be created for small numbers of SNPs.

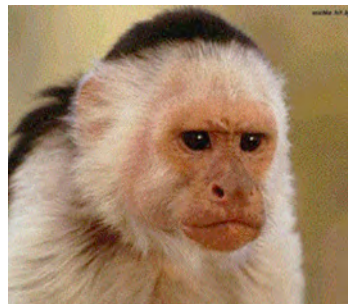
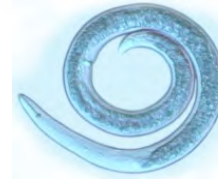


- Golden Gate assay based
- Straightforward workflow
- Convenient stopping, starting points
- Data quality matches or exceeds solid-phase hybridization assays
- Economical “project size” packages available
- Flexible plexities available
- Genome Studio (Bead Studio) software for data analysis

Genome Studio/Bead Studio

- Intuitive Interface
- Lots of ways to view, sort, export data
- Easy to learn
- Easy to teach

Species Genotyped in the DNA Technologies Core using the Illumina Golden Gate Assay





Canid Diversity and Conservation Group

Genotyping the California Red Fox

Ben Sacks, Ph.D. (& F1)

- Marker analysis for population structure delimitation, population management
- Population dynamics following the introduction of the Alaskan/Canadian Red Fox: displacement, hybridization, or both?

Red Fox SNPs

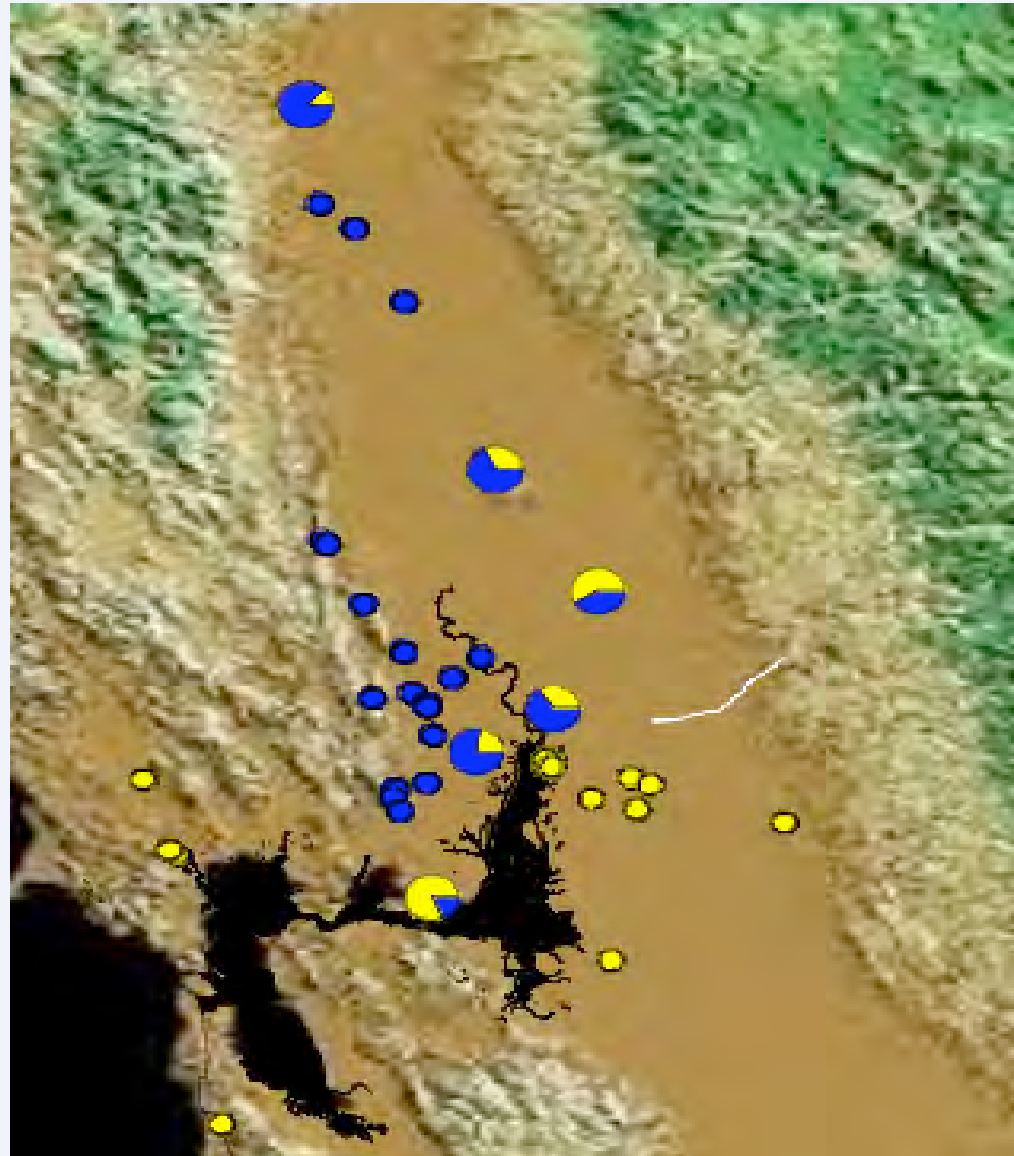
96 selected, based on:

- Linkage to STRs
- Coat color
- Sequenced regions (ESTs)
- Sex informative
- Mitochondrial (!)

Population Studies to date with STRs

- Native
- Non-native

Native species does not cross the American R./Sacramento Delta

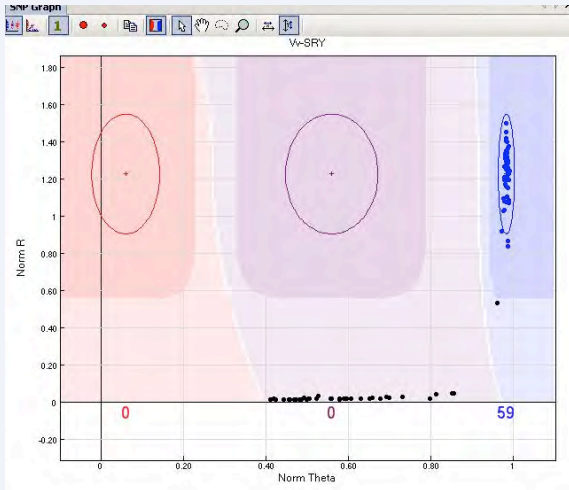


Assay Performance & Validation

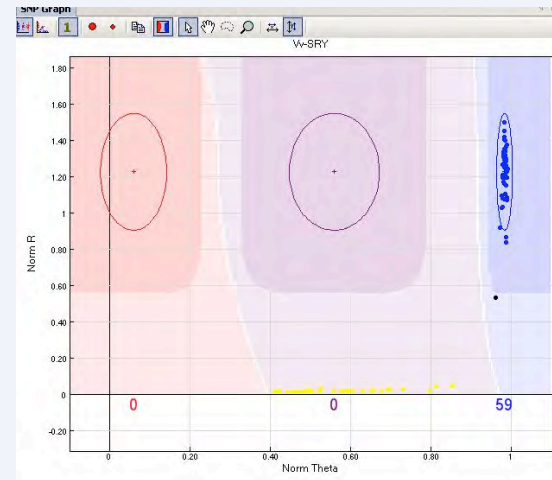
SNP set	Number indiv*loci assayed	Number indiv*loci correct	overall	AutoMarkerTotal genotype accuracy
SacksLouie markers	119	110	0.92437	0.947643979
SNP-Strs	72	71	0.98611	
Cyt B	70	70	1	*
Sex	29	27	0.93103	Suspect trappers erred in sex call!
Sex of Aussie samples	88	81	0.92045	
Coat color (wild)	156	155 red, 1 smoky red		
Coat color (fur farm)	12	11	0.91667	Need to sequence the one individ at Mc1r
**10 negative cntrl loci (1 failed)	754	752	0.99735	

Locus	Genotype			Sequence			Comment
	M5258	MAM3678	S07-0167	M5258	MAM3678	S07-0167	
O-C01.424A	AA	GG	GG	TT	CC	CC	
O-C04.140A	--	--	--				
O-C04.140B	GG	GG	GG	CC	--	--	
O-C08.618A	CG	GG	CC	GC	CC	GG	
O-C08.618B	GG	AA	GG	GG	AA	GG	
O-CPH16A	GG	GG	GG	GG	GG	GG	
O-CPH18A	GG	AG	GG	AA	AG	AA	
O-CPH2	GG	GG	GG	GG	GG	GG	
O-CPH3A	AG	AG	GG	GA	--	GG	
O-CPH8A	GG	AG	GG	--	AA	GG	clear heterozygote
O-CPH8H	GG	CC	GG	GG	CC	GG	
O-CPH9B	GG	AA	AG	GG	AA	AG	
O-FH2001	AA	GG	AA	TT	CC	--	
O-FH2004A	AA	GG	GG	AA	GG	GG	
O-FH2100B	GG	AG	AA	CC	CT	TT	
O-FH2457	AA	AC	CC	TT	GT	GG	
O-INRA021C	GG	AG	AG	GG	AG	AG	
O-INU005	GG	AA	AA	GG	AA	AA	
O-INU030	TT	AT	TT	TT	AT	TT	
O-INU055D	AG	GG	GG	CT	CC	CC	
O-INU055G	AG	AA	AA	AG	AA	AA	
O-REN105L03A	AA	GG	AA	AA	GG	AA	
O-REN105L03B	GG	AA	GG	GG	AA	GG	
O-REN162C04	GG	AG	GG	GG	AG	--	
O-REN247M23A	GG	AG	GG	CC	TC	CC	
O-REN247M23C	AA	AG	AA	AA	AG	AA	
O-REN247M23D	--	--	--	--	--	--	
O-RENS4P11A	GG	AA	AA	CC	TT	TT	
	Subtotal 143/144 alleles called correctly						0.993056

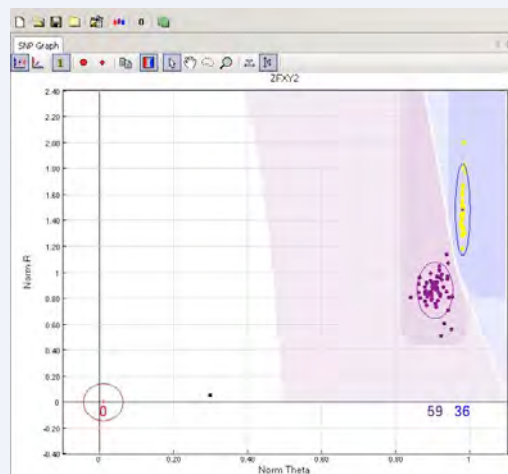
Sex Determination



SRY linked SNP

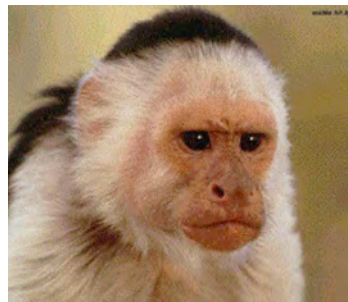
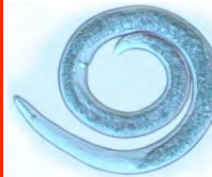


Select non-reactive individuals



X-chromosome linked SNP

Species Genotyped in the DNA Technologies Core using the Illumina Golden Gate Assay





UC DAVIS College of Biological Sciences

Department of **Evolution & Ecology**



H. Bradley Shaffer, Ph.D.

Genotyping the California Tiger Salamander



Jarrett Johnson

- Definition of genetically-based management units
- Hybridization/displacement studies with introduced barred salamander from OK, northern TX

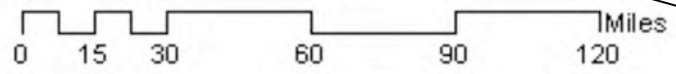
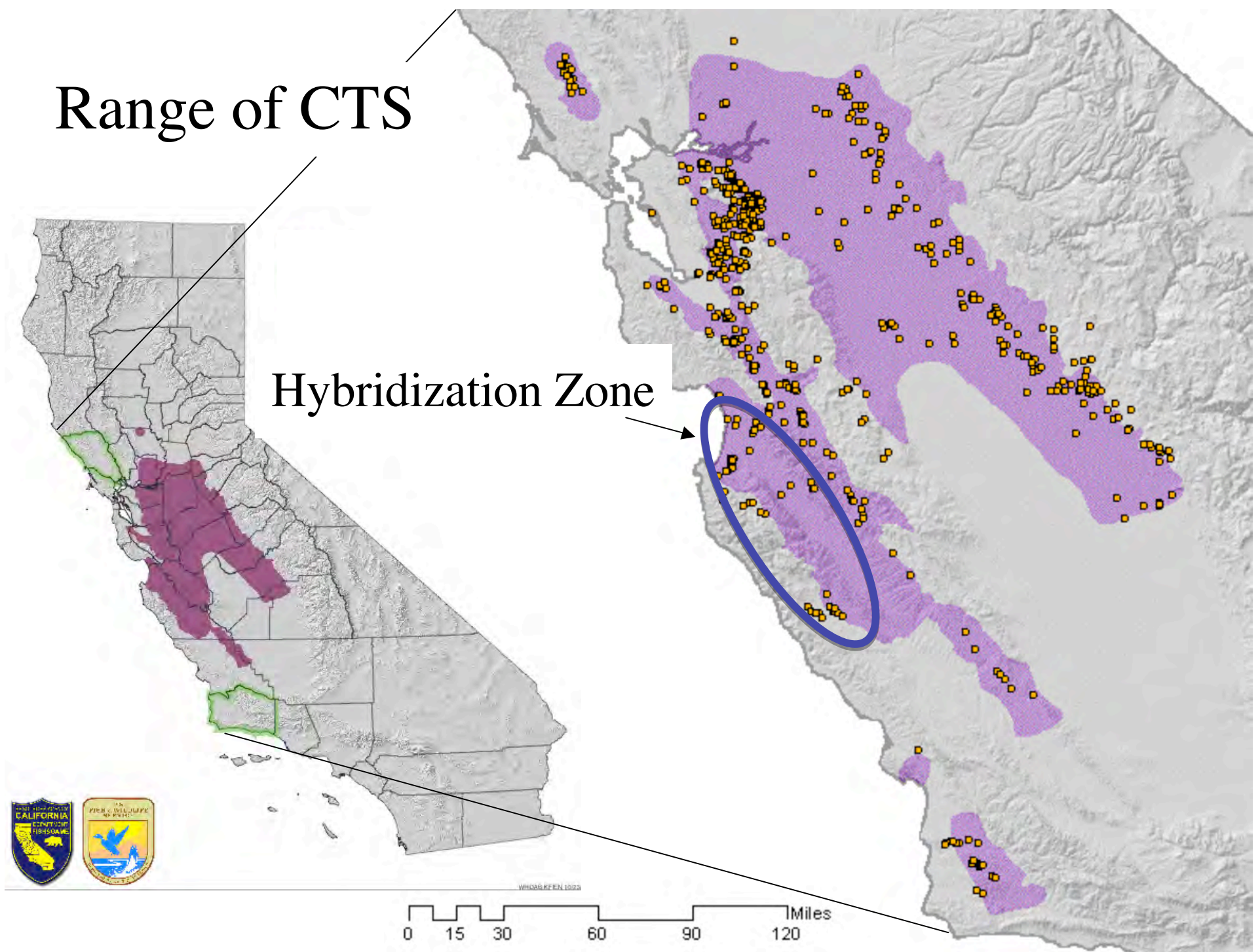
Salamander SNPs

96 selected, based on:

- Linkage to STRs
- Linkage to QTLs
- Candidate genes:
 - Development (Hox, Dlx, Fox)
 - Signalling (Gnat, Wnt)

Range of CTS

Hybridization Zone



California Tiger vs. Barred Salamanders

California Tiger Salamander (CTS) –
Ambystoma californiense



Barred Tiger Salamander (BTS)
– *Ambystoma tigrinum mavortium*



Introduced by sport fishermen as bass bait

Thousands of Potential Hybrid Genotypes



Genes 100%
californiense

0



Genes 100%
mavortium



1

most hybrid
populations

hybrid index

Investigations Utilizing SNP Analysis

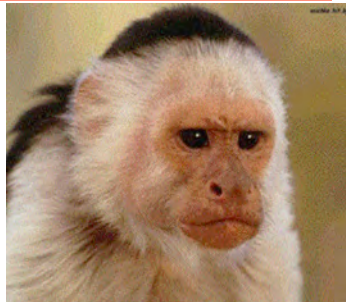
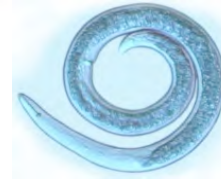
- Estimate the proportion of the genome affected by hybrid dysfunction or hybrid vigor and characterize variation in environment-dependent (e.g., pond type: seasonal, perennial) invasion success.
- Viability selection on hybrids in the lab: place observed patterns of introgression, LD, and HWD into the context of dynamics during the initial generations of contact.
- Transect sampling of 25 populations (over 100 km) to assess the stability of hybrid genotypes (over time and space using allele frequencies
- Identify deviations from Mendelian and HW expectations that indicate positive or negative selection

Story so far

- Ended up with approximately 68 SNPs: bonanza for amphibians (high “C” value makes STRs, AFLPs difficult)
- Found SNPs linked to biologically interesting QTLs controlling timing of metamorphosis
- Found SNPs in regions with significant deviations from Mendelian segregation
- Transect studies identified more introduced genes than previously suspected--high resolution analyses

SNPs will always provide this, but could easily work through 1200 individuals in a few weeks in our lab with the BeadXpress

Species Genotyped in the DNA Technologies Core using the Illumina Golden Gate Assay





Genetic Structure of Domestic Cats

Leslie Lyons, Ph.D.

ELSEVIER

ISSN 0888-7543
Volume 91, Number 1, January 2008

GENOMICS

Molecular genetic variation among cat breeds

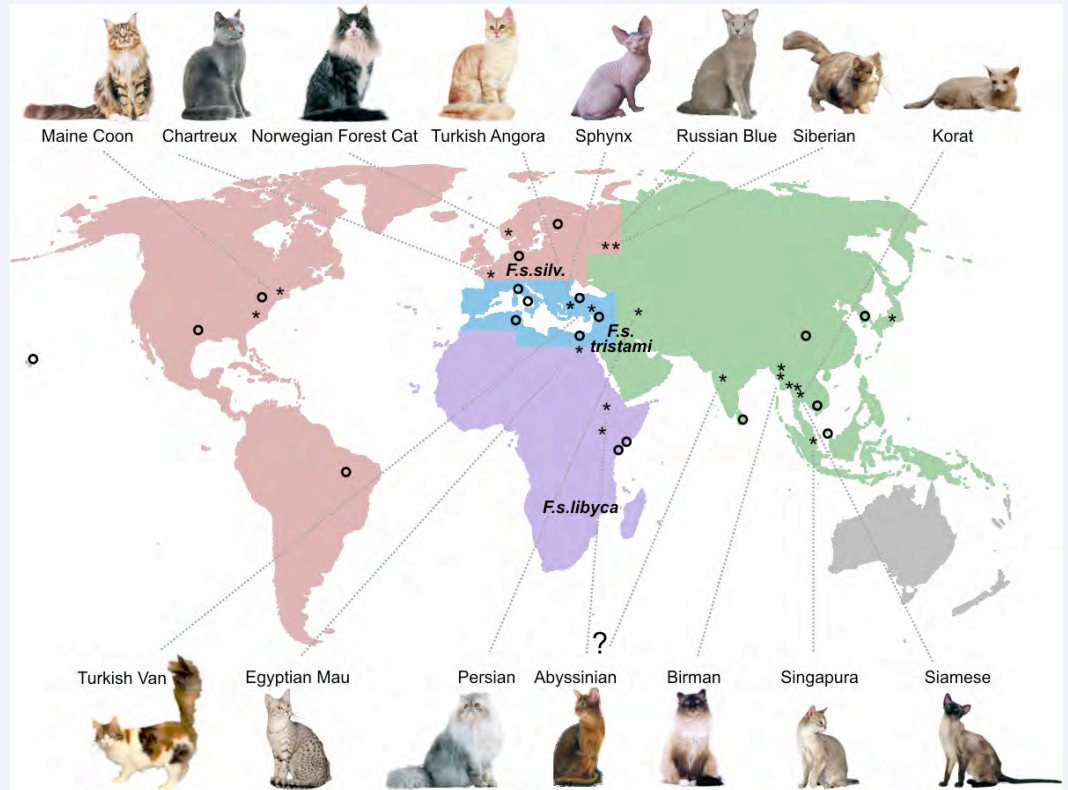
Genetics of cat breeds and random bred populations

Gene expression changes in children with autism

ST-4821 complex, a unique *Neisseria meningitidis* clone

Available online at
ScienceDirect
www.sciencedirect.com

The phylogenetic tree shows the genetic relationships between various cat breeds. The tree is rooted at the bottom and branches out to different breeds. The breeds are color-coded by geographic region: red for North and South America, blue for Europe, purple for Africa, and green for Asia. Breeds shown include: Sphynx, Norwegian Forest, Maine Coon, Siberian, Fennel, German, American SH, Chartreux, British SH, Persian, Exotic, F.s. silvestris, F.s. castra, F.s. mitami, F.s. silvestris, F.s. castra, F.s. mitami, H. Brown, Singapore, J. Bobail, Korat, Vietnam, Burmese, Siamese, H. Brown, Singapore, J. Bobail, Korat, Vietnam, Burmese, Siamese, H. Brown, Singapore, J. Bobail, Korat, Vietnam, Burmese, Siamese.



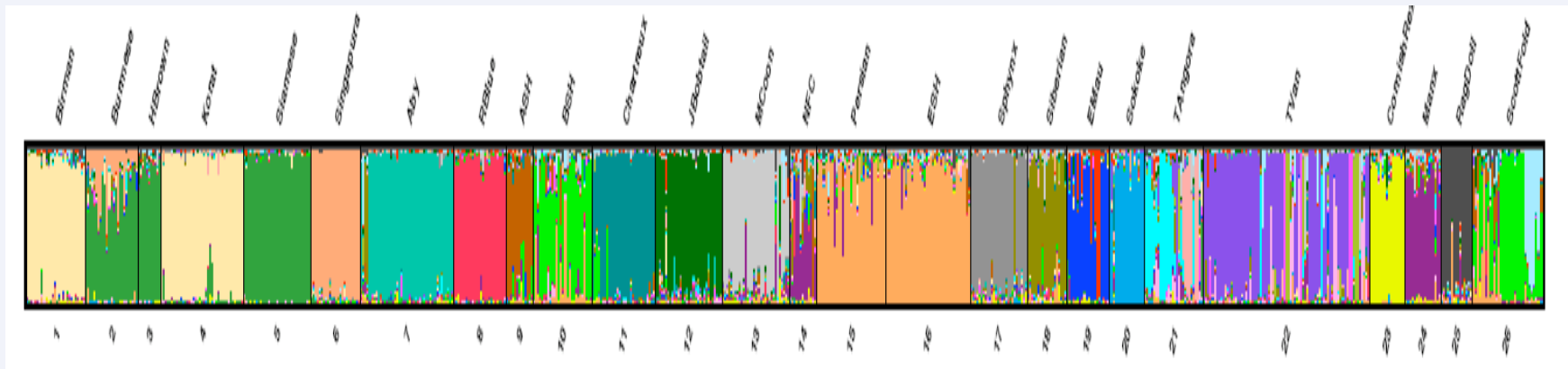
Cat SNPs

384 selected, many based on:

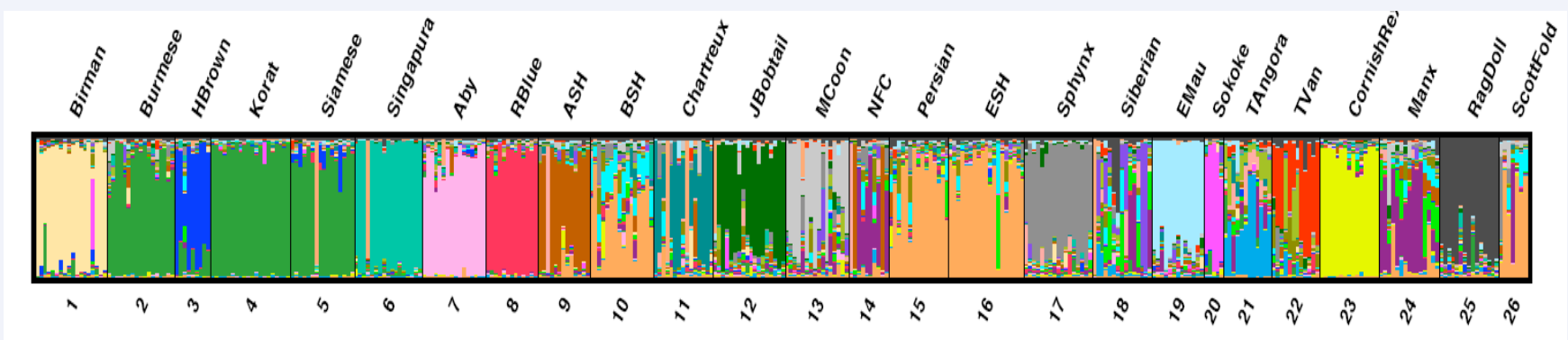
- Coat color
- Blood type
- X-chromosome linked (no SRY yet)
- Disease related
- Genome-dispersed SNPs for mapping

Microsatellites vs. SNPs in feline genetics

Microsatellites evolve too quickly to resolve random breeding individuals but do give good population structure information for purebreds

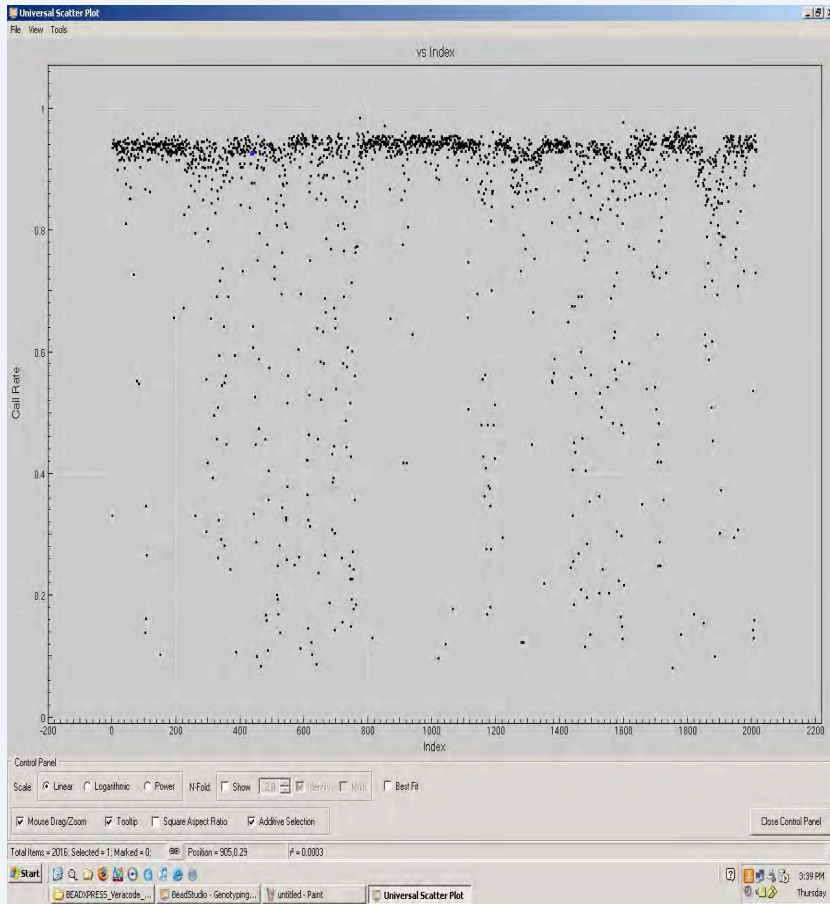


Microsats in purebred animals

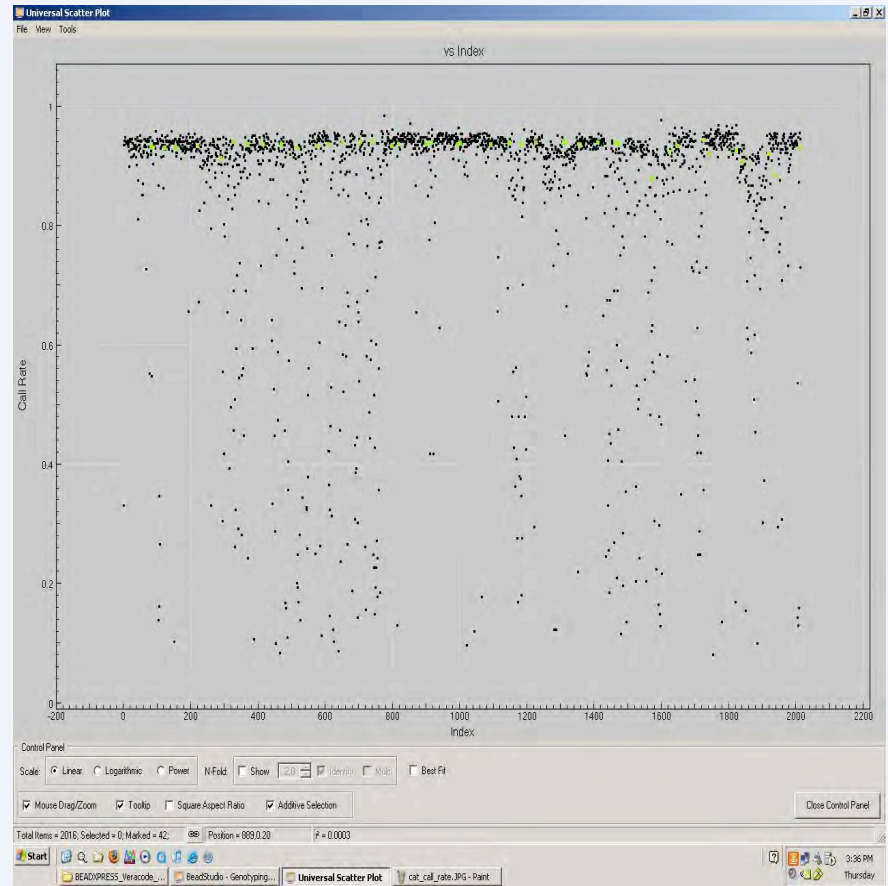


SNPs in purebred animals

Run Quality Control

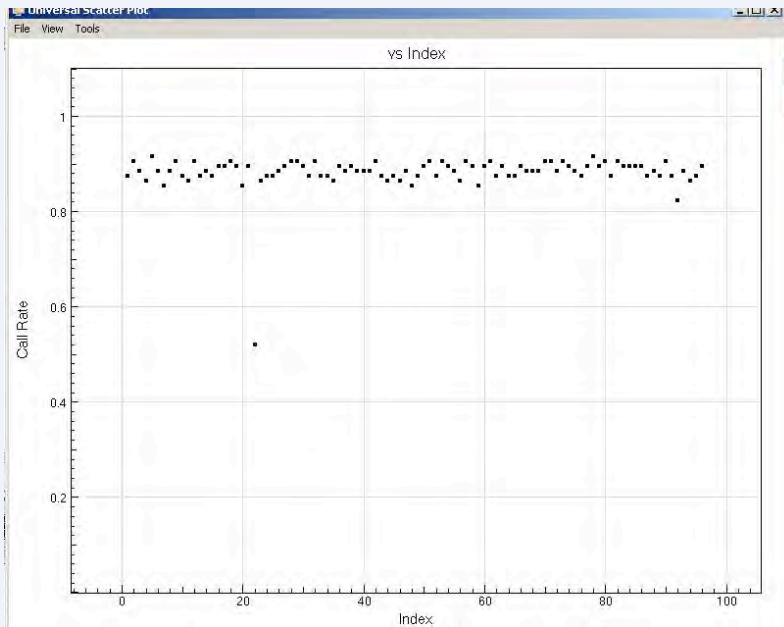


Index vs. Call Rate

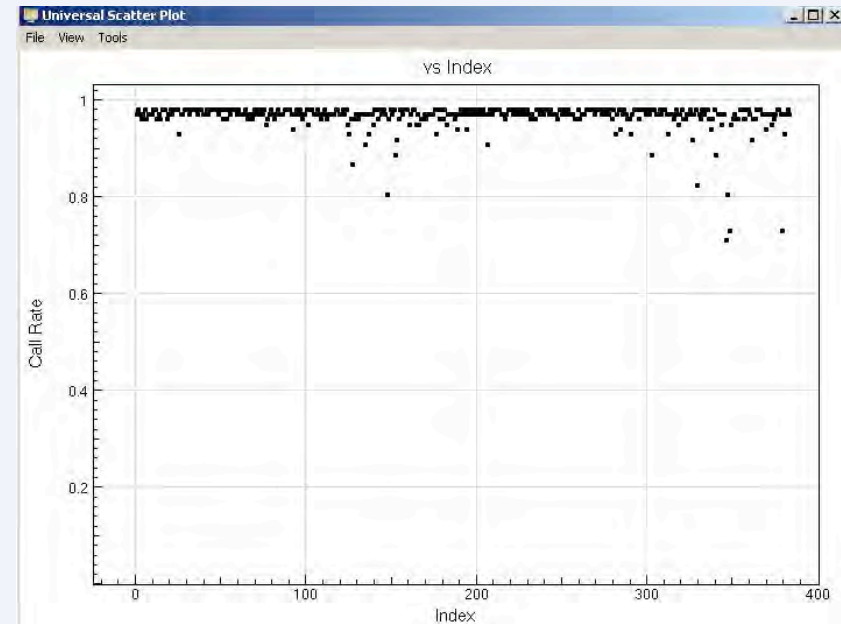


Index vs. Call Rate:
Highlight Controls

Typical Index vs. Call Rate



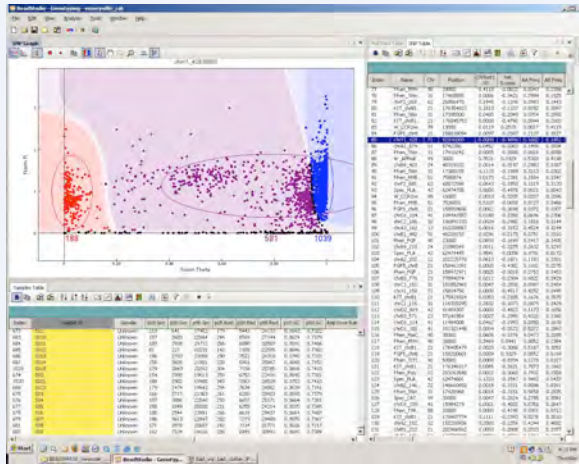
Red Fox



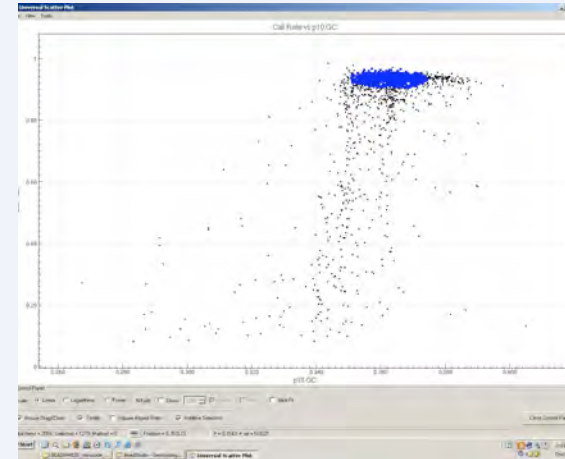
Salamander

High conversion rate in “pre-genome” organisms

Clustering Flexibility



Initial clustering with all samples

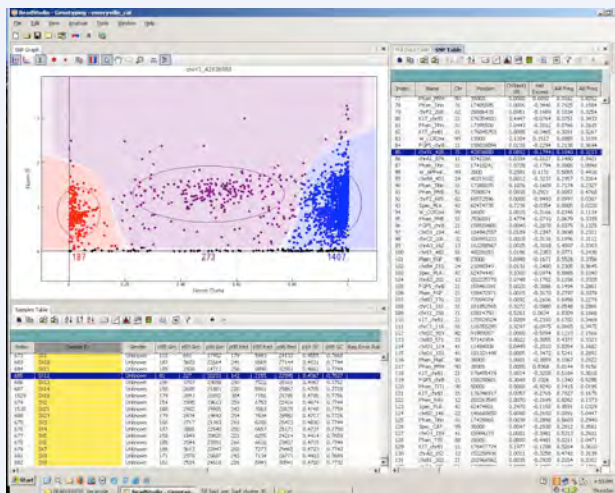


Plot Call Rate vs. 10% GC

Select best samples

Recluster based on those only

Save cluster file and re-apply to all samples



More accurate calls

Options important for non-model, “pre-genome” organisms & when sample collection less than optimal

Acknowledgements

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