Genotype Data Quality Assessment

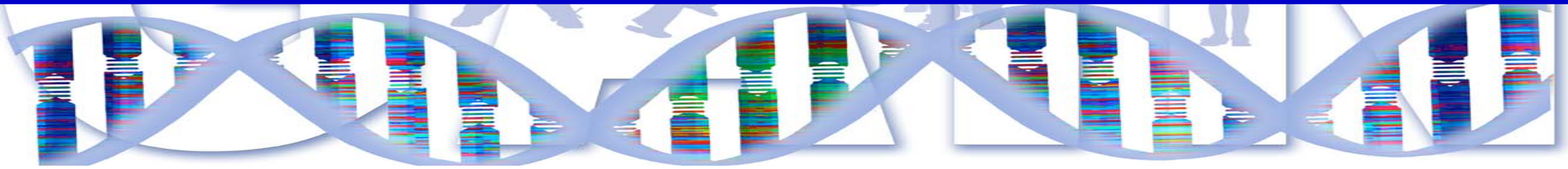
Lisa Brooks, Ph.D.

NHGRI

GENETIC ASSOCIATION INFORMATION NETWORK

Genotype Data QA/QC

- GAIN Genotyping Group
- HapMap samples initially
- QA samples for each study
- QC for genotyping
- NCBI QA check
- Genotype data quality standards



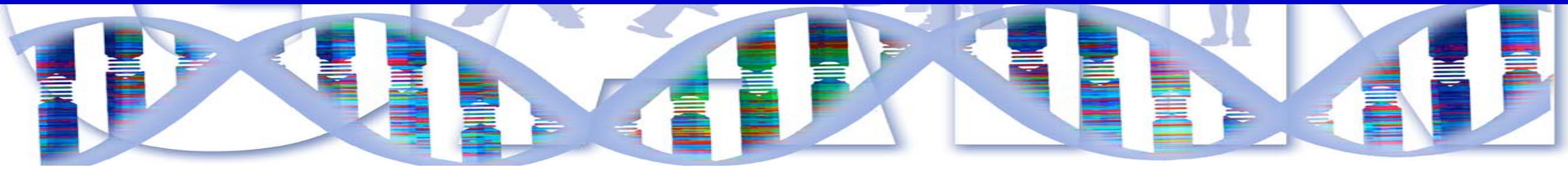
GAIN Genotyping Group

Gonçalo Abecasis (Chair)	Michigan
Dennis Ballinger	Perlegen
John Thompson	Pfizer
Stacey Gabriel, Mark Daly	Broad
Steve Lincoln	Affymetrix
Elizabeth Pugh	CIDR
Peter Donnelly	WTCCC
Stephen Sherry, Michael Feolo	NCBI
James Battey	NIDCD
Lisa Brooks, Teri Manolio, Emily Harris	NHGRI
David Wholley	FNIH

HapMap Samples Initially

Both centers are genotyping all 270 HapMap samples on the GAIN platforms and SNPs, to show:

- The SNPs that work.
- Genomic coverage of the SNPs.
- Completeness and concordance with HapMap genotypes.

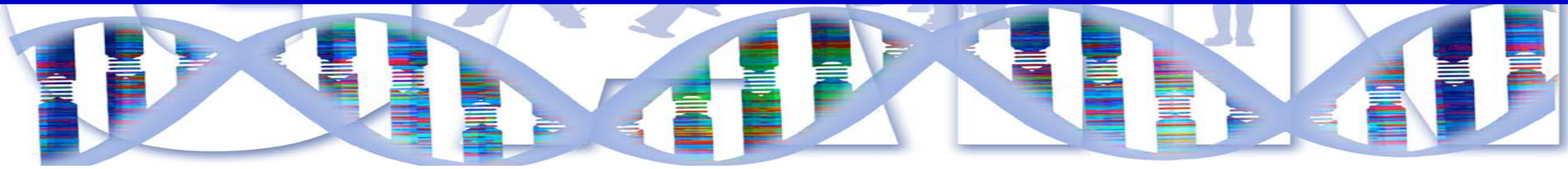


QA Samples for Each Study

- Study trio samples (Faraone ADHD)
- QA trio samples related to study samples (some studies)
- HapMap CEPH sample(s) (all studies)
- HapMap Yoruba samples (AA studies)
- Study duplicates (all studies)

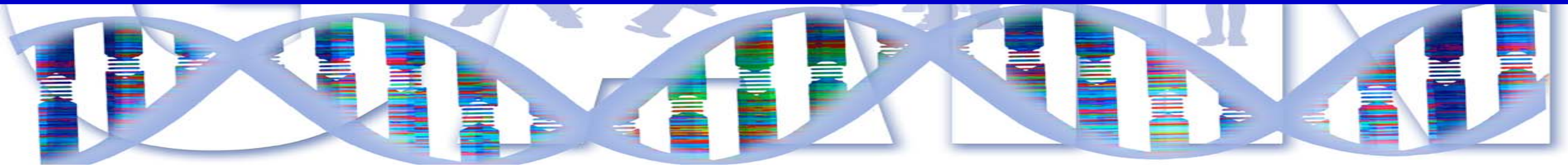
QC for Genotyping

- More QA samples for studies with unrelated samples, multiple collection sites or DNA extraction methods, more ethnic diversity.
- Cases and controls on same plates and done at same time; plates differ in sample layouts (sexes, duplicate samples).
- QC process for each genotyping center.



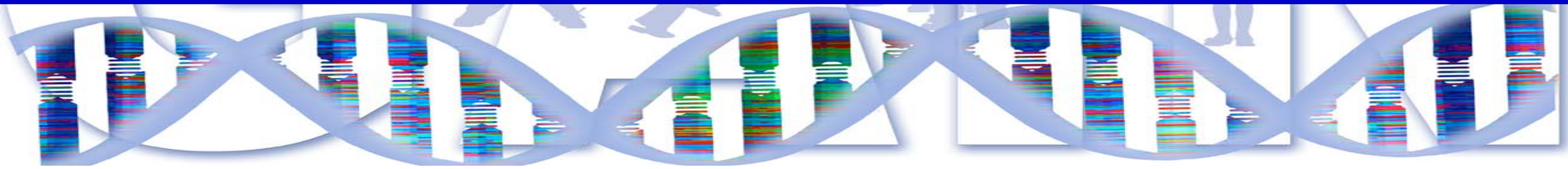
NCBI QA Check

- Gonçalo Abecasis is developing a software pipeline to assess genotype data quality.
- NCBI will apply it to each GAIN study.
- Any issues will be resolved between the genotyping centers, study PIs, and NCBI.



Genotype Data Quality

- Number of SNPs, genomic coverage.
- Completeness, and in HapMap QA samples by hets and homs.
- Concordance with HapMap samples and between duplicates.
- Concordance in family samples.



Data Quality Standards

Remove samples with < 80% of SNPs called.

Of ≥ 480k for Perlegen and 500k for Broad, ≥ 90% of SNPs will be good:

- any SNPs out of HW will not count as good,
- call rate minimum = 90% and average ≥ 97%,
- for HapMap QA samples the average call rates for hets and homs both ≥ 97%,
- concordance in duplicates of ≥ 99.5%.