



Analysis of HapMap Lymphoblastic Cell Line Surface Protein Expression

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Summer Research Program in Genomics

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Project Overview

- Approach: use the HapMap lymphoblastic cell lines as a model system to study gene expression
- Goals: Correlate genetic variation captured by the HapMap with:
 1. cell surface protein expression
 2. poly-marker immunological expression

Data Collection: The Samples

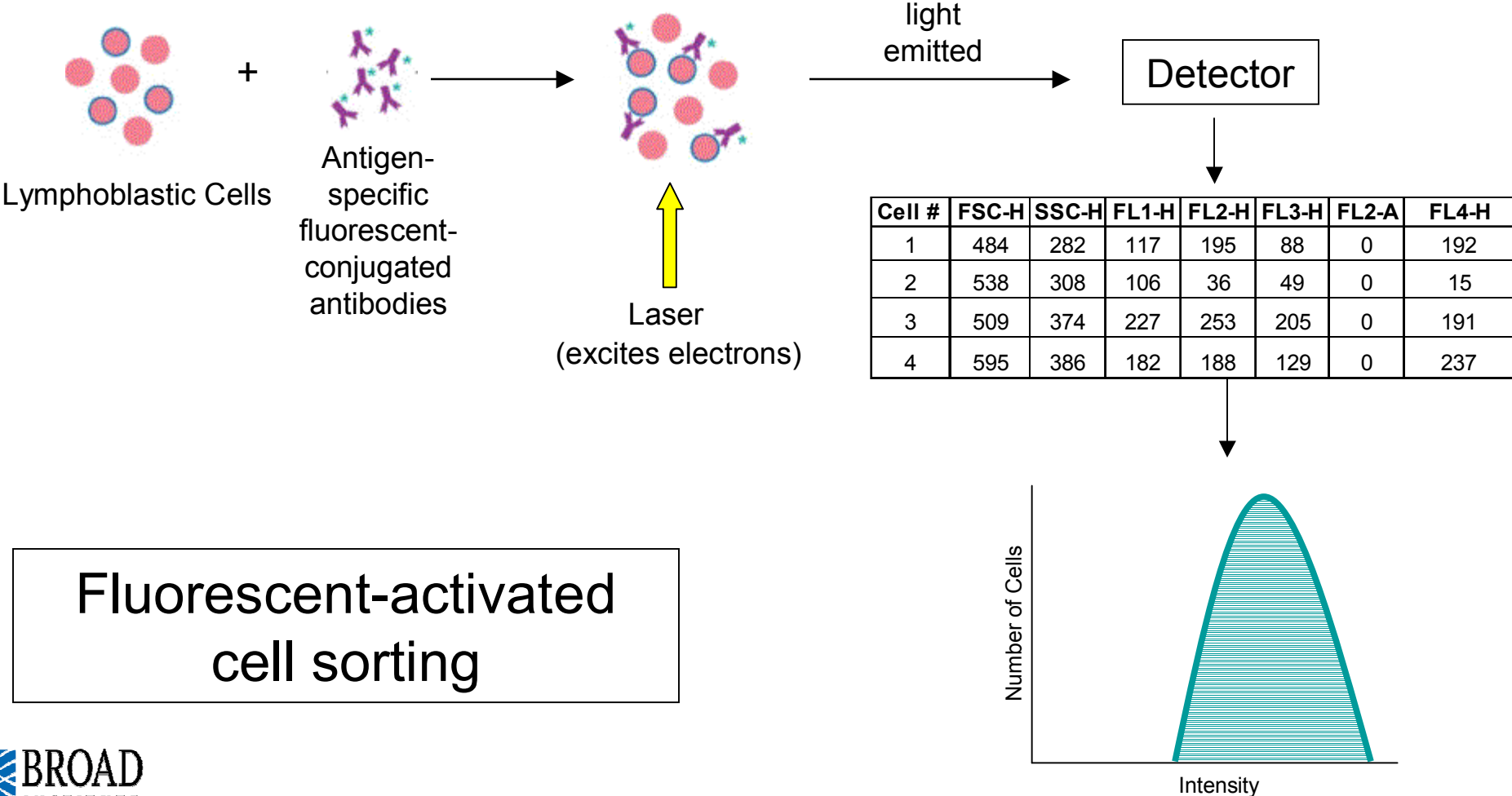
- HapMap Cell Lines (270 Total Samples)
 - 30 Yoruban Trios (YRI)
 - 45 Japanese Individuals (JPT)
 - 45 Han Chinese Individuals (CHB)
 - 30 U.S. Trios (CEU)

Data Collection: The Markers

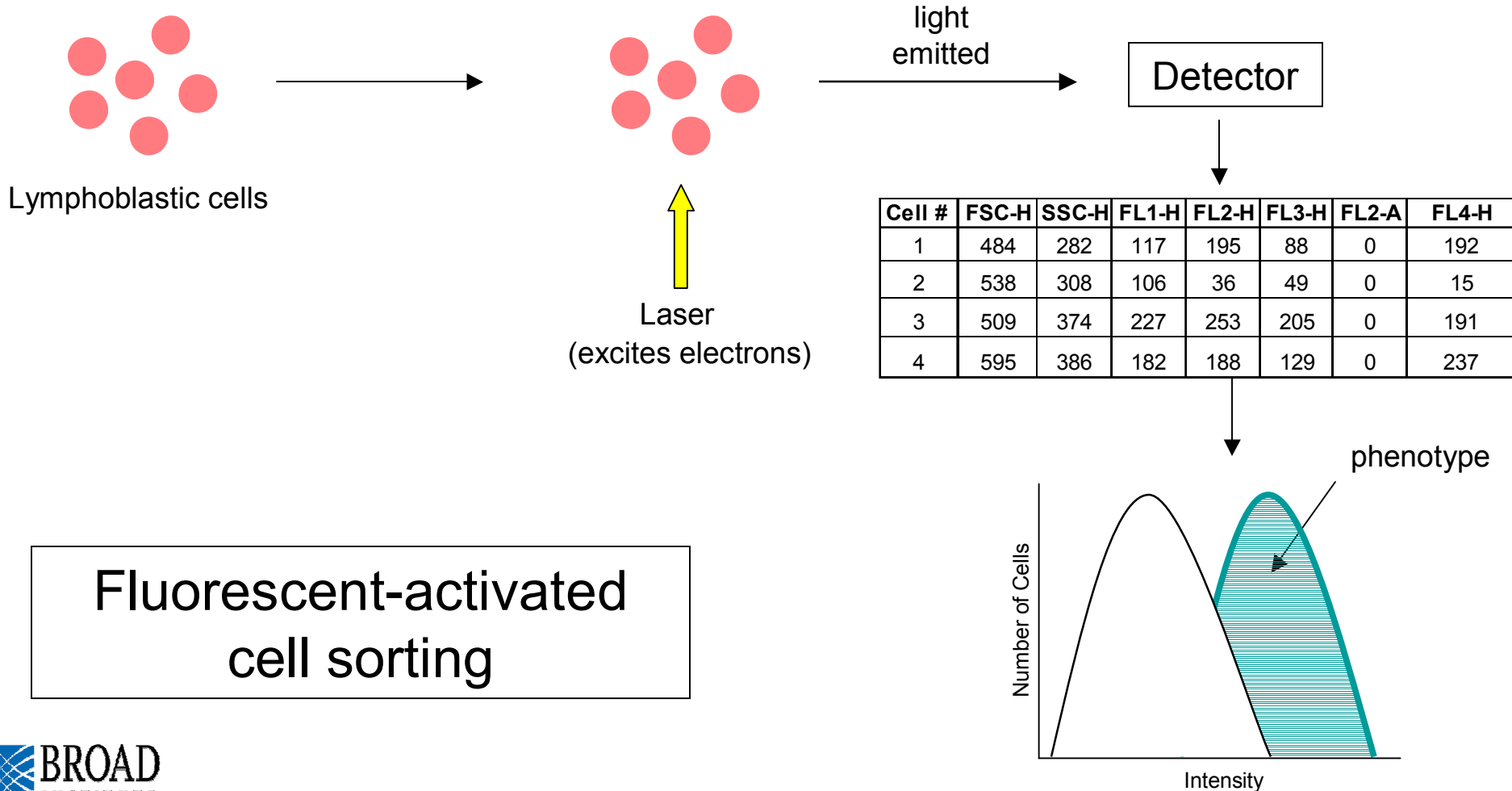
1. B-cell specific markers
2. Markers expressed on B-cells that showed evidence of heritability in previous RNA expression studies

CD19	CD20
IL6R	IgD
HLA-DQ	HLA-DR
CD227	CD21
CD40	IgG
IgM	CD58
CD95	CD86
CD80	

Data Collection: The Method



Data Collection: The Method



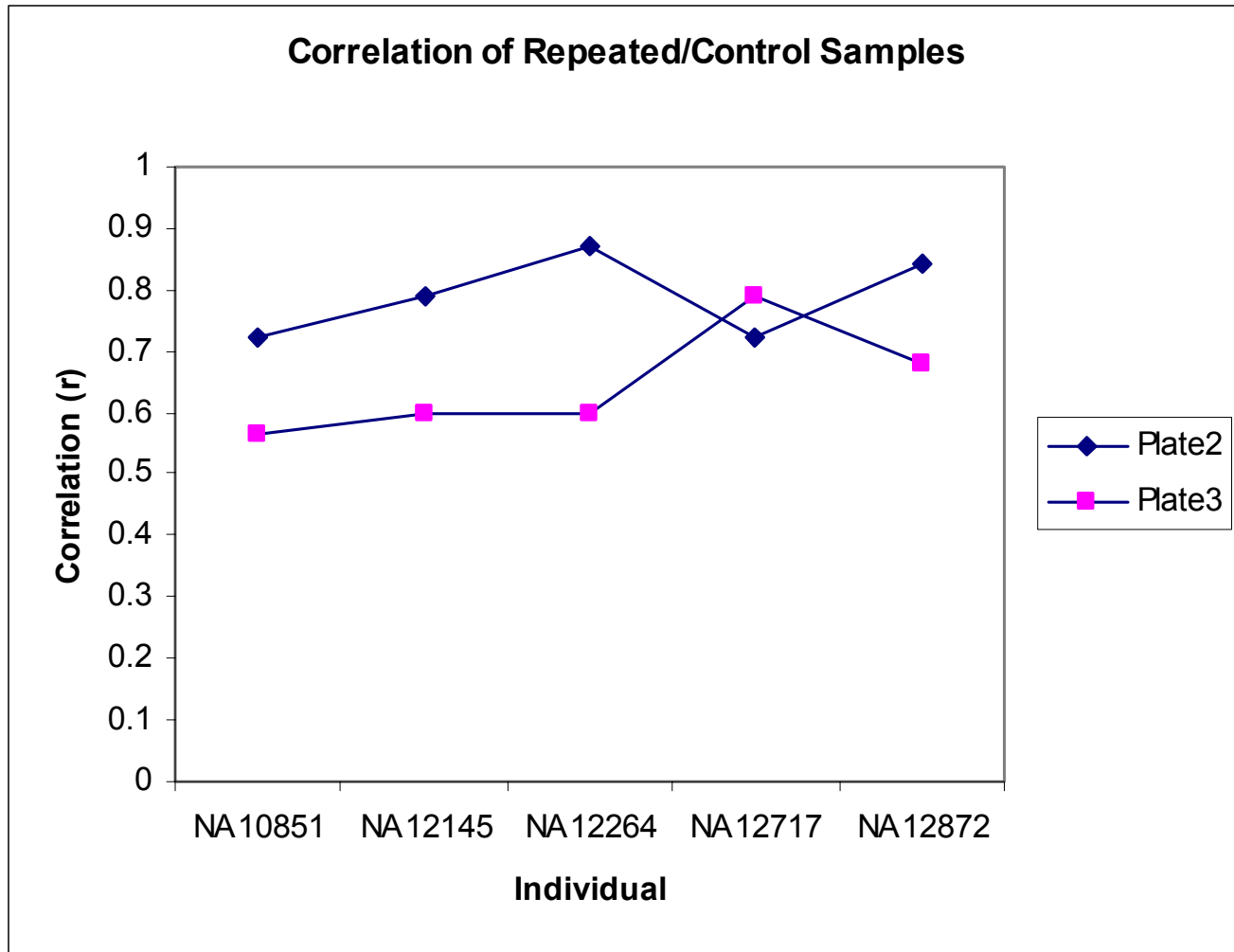
Data Processing and Analysis

1. Perform quality control analysis
2. Correlate marker expression with genetic variants
3. Define poly-marker immunological expression profiles
4. Correlate immunological expression profiles with genetic variants

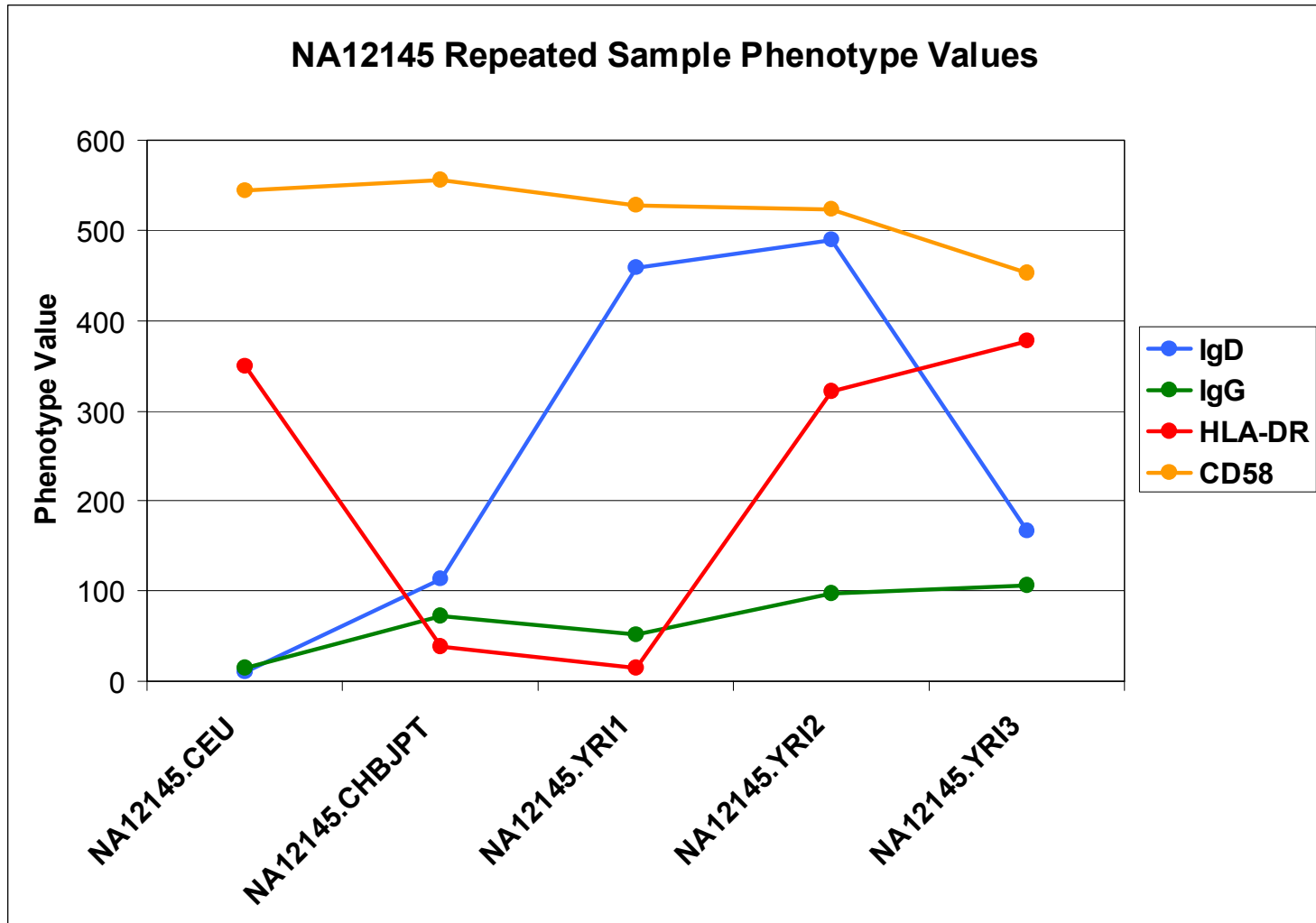
Sources of Variation

- Manual handling of samples (staining protocol/loading FACS machine)
- Cell count (sampling)
- Other (cell culture, user manipulation required during detection)

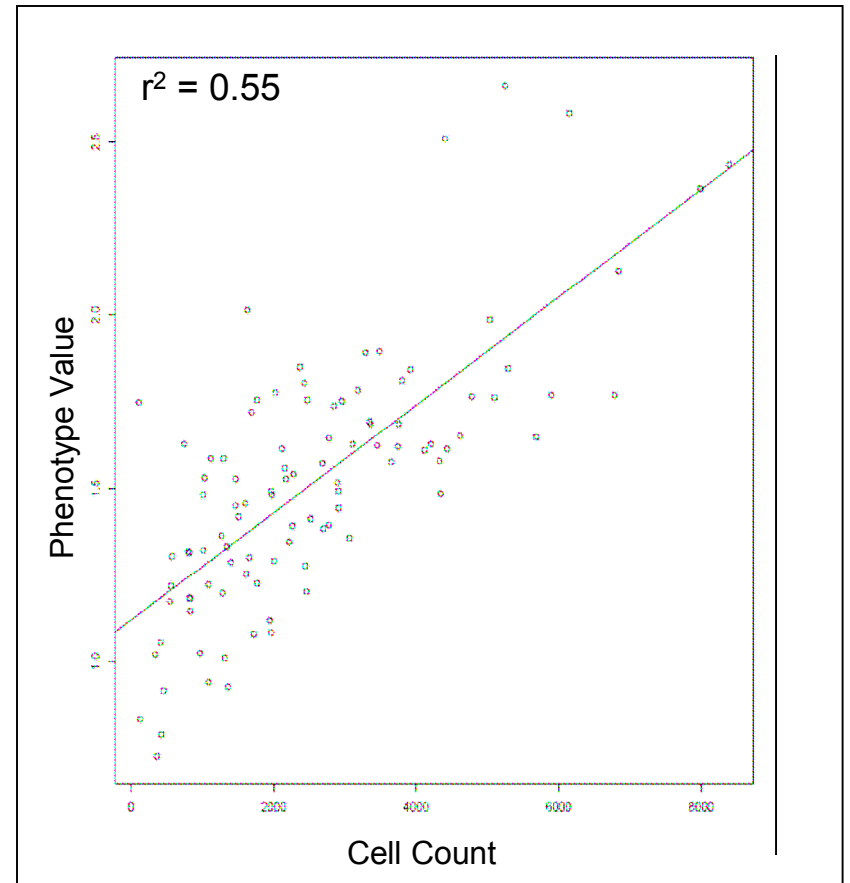
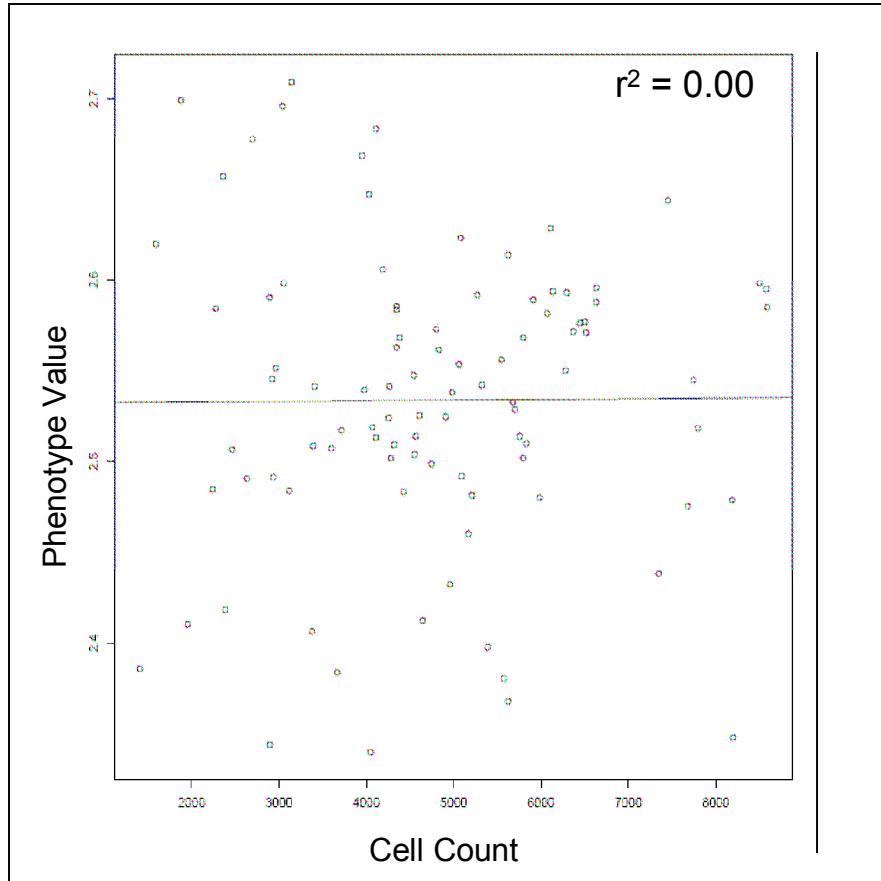
Correlation of Repeated/Control Samples



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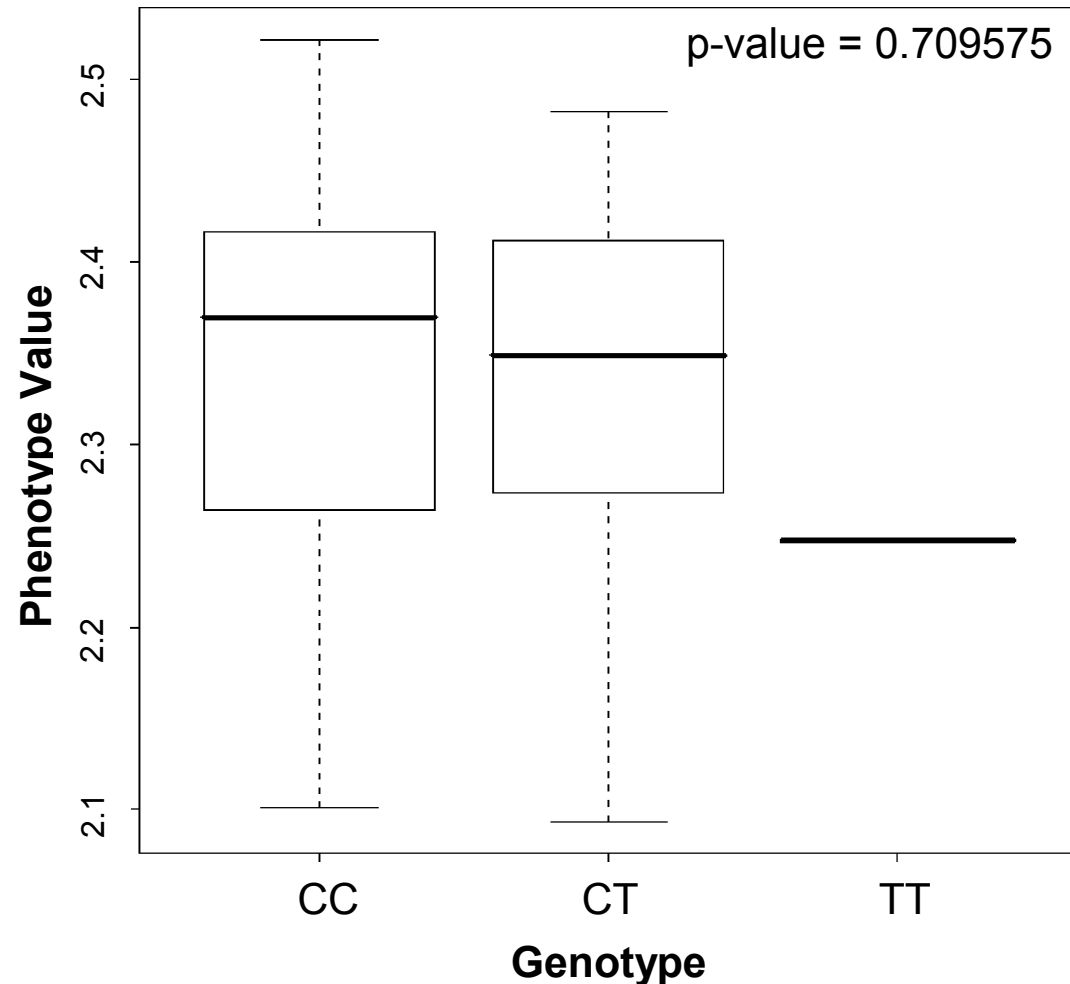
Phenotype vs. Cell Count



Markers that Passed QC in CEU

CD19	CD20
IL6R	IgD
HLA-DQ	HLA-DR
CD227	CD21
CD40	IgG
IgM	CD58
CD95	CD86
CD80	

Correlate Marker Expression with Genetic Variation

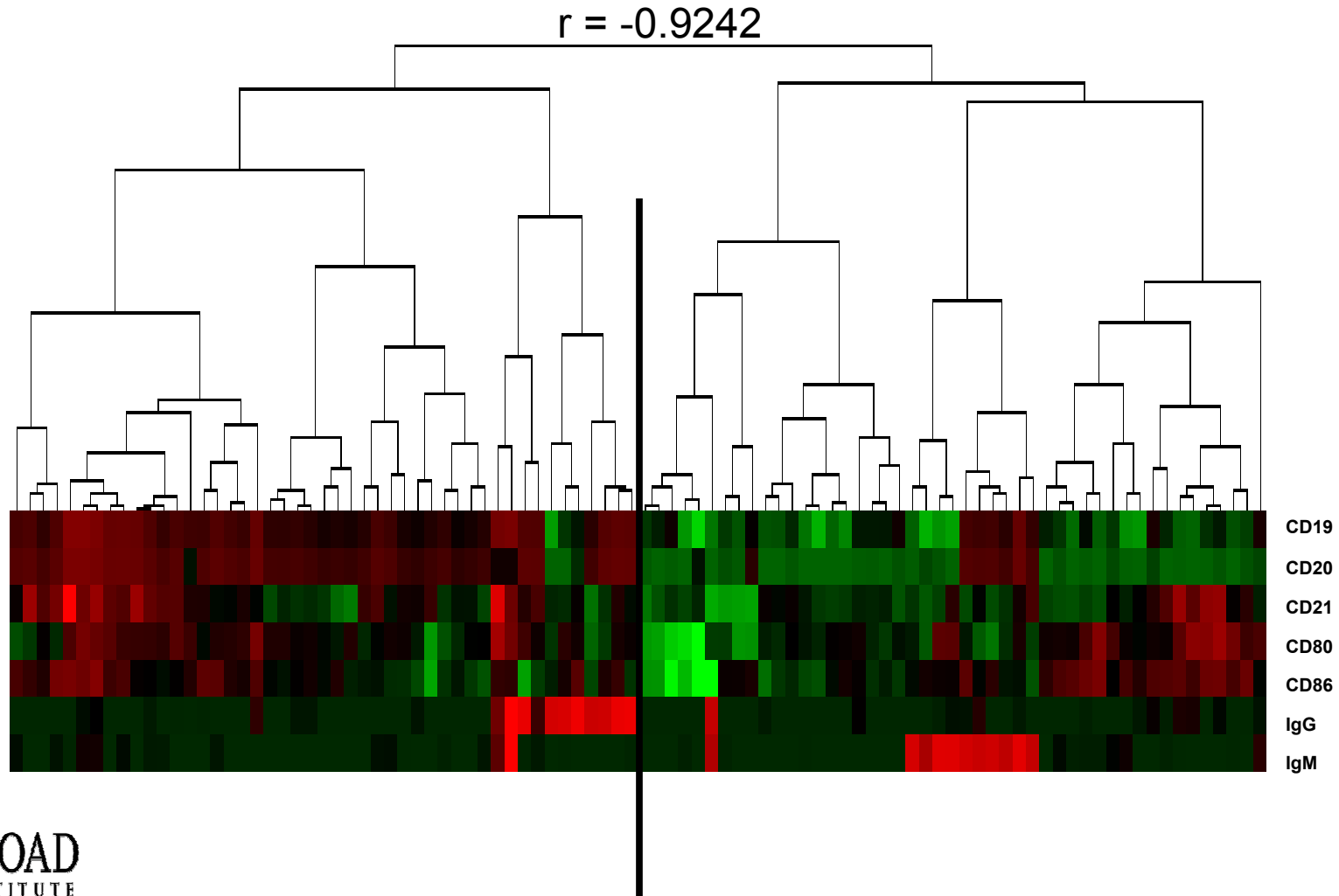


Attempt to validate a known correlation between CD40 protein expression and dose of the rs1883832^C allele (in Kozak sequence)

C allele = susceptibility to Grave's disease, high protein expression (*in vitro* & B cells *ex vivo* – 23 individuals)

T allele = low expression

Define poly-marker immunological expression profiles



Conclusion

- Completed quality control analysis
 - Defined a curated marker set
- Sub-populations of cell lines that share particular immunological profiles may exist

Future Work

- Further define poly-marker immunological expression profiles
- Further correlate marker expression phenotype with genetic variation
- Correlate marker expression phenotype with other relevant phenotypes

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