Objectives:

1. Discuss the scientific questions and opportunities for better understanding genome function and applying that knowledge to basic biological questions and disease studies through large-scale genomics studies.

2. Consider options for future NHGRI projects that would address these questions and opportunities.

**Tuesday, March 10, 2015**

1:00 p.m.   **Welcome and Setting the Context**  Eric Green

1:15 p.m.   **Purpose of Workshop: Background and Planning Process for Future Initiatives**  Elise Feingold

1:35 p.m.   **From Genome Function to Biomedical Insights: Defining the Scientific Challenges**  Ewan Birney

2:05 p.m.   **Discussion**

2:30 p.m.   **Break**

3:00 p.m.   **Genome Function Circa 2016: Updates from Related Projects**
Moderator: Daniel Gilchrist

**ENCODE**  Michael Snyder

**REMC/IHEC/BLUEPRINT**  Michael Pazin

PsychENCODE

Genomics of Gene Regulation (GGR)

4D Nucleome

FunVar
4:00 p.m. **Proposals for Future Directions**  
ENCODE PIs’ Vision for Functional Genomics  
Joseph Ecker

Recommendations related to genome function from NHGRI’s Planning Workshop on the Future Opportunities for Genome Sequencing and Beyond  
Mark Gerstein

Richard Myers

5:00 p.m. **General Discussion**

6:00 p.m. **Working Dinner**

7:00 p.m. **Topic #1: Identifying and characterizing functional elements**  
Moderator: Carol Bult

7:00 p.m. – 7:30 p.m.  
The regulatory landscape: where are the gaps?  
Ross Hardison

7:30 p.m. – 7:45 p.m.  
Creating a framework for mechanistic studies  
B. Franklin Pugh

7:45 p.m. – 8:00 p.m.  
ENCODE 2.0: improving the syntax for understanding functional elements in the genome  
Laurie Boyer

8:00 p.m. – 8:15 p.m.  
Genomics at the "quantum" level: new directions for genomic data generation and functional validation  
William Greenleaf

8:15 p.m. **Topic #1 Discussion**

9:00 p.m. **Adjourn**

**Wednesday, March 11, 2015**

8:00 a.m. **Topic #2: Using genomic assays of function to interpret the role of genetic variation in disease**  
Moderator: Eric Boerwinkle

8:00 a.m. – 8:25 a.m.  
Leveraging whole genome annotation for genotype-phenotype association studies  
Eric Boerwinkle
8:25 a.m. – 8:50 a.m.
Hirschsprung disease consequent to mutations in the RET gene regulatory network
Aravinda Chakravarti

8:50 a.m. – 9:05 a.m.
Genetically predicted endophenotypes: getting to the next level in understanding how genome variation drives disease
Nancy Cox

9:05 a.m. – 9:20 a.m.
Identification of regulatory variation important for maternal metabolism during pregnancy
William Lowe

9:20 a.m.  Topic #2 Discussion

10:05 a.m.  Break

10:30 a.m.  Topic #3: Using genomic assays of function to study basic biological questions
Moderator: Aviv Regev

10:30 a.m. – 10:50 a.m.
Understanding basic biology using functional genomics: solving the genotype-phenotype problem
Brenda Andrews

10:50 a.m. – 11:10 a.m.
Fundamental insights into gene regulation from genomic analyses: past successes and future challenges
Karen Adelman

11:10 a.m. – 11:30 a.m.
Analyzing cytosine modifications in genomic DNA
Anjana Rao

11:30 a.m. – 11:50 a.m.
Ask not what you can do for ENCODE – ask what ENCODE can do for you
John O'Shea

11:50 a.m.  Topic #3 Discussion

12:30 p.m.  Lunch

1:30 p.m.  Discussion
Moderators: Eric Boerwinkle, Carol Bult, Aviv Regev

2:30 p.m.  Final Recommendations, including priorities and balance of activities
Moderators: NHGRI

3:30 p.m.  Adjourn