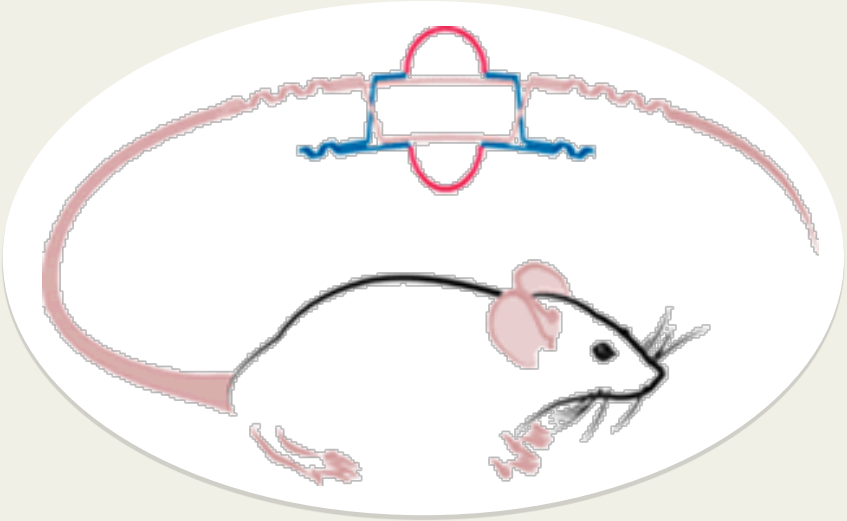
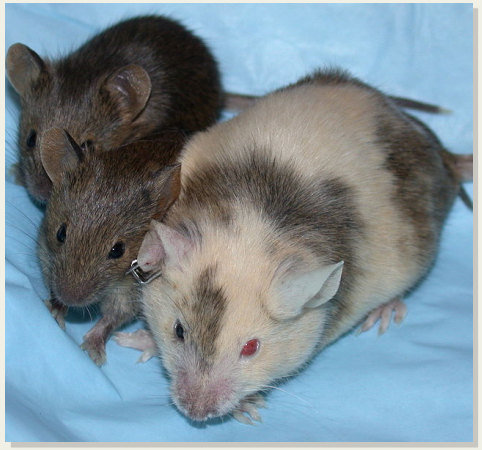
# *The Knockout Mouse Project (KOMP)*
# *&*
# *KOMP Phenotyping (KOMP$^2$)*

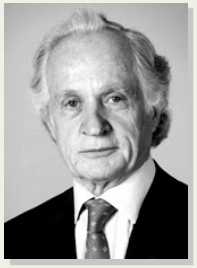


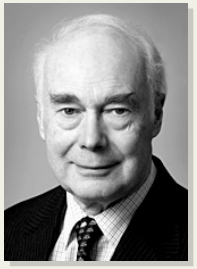
Jane Peterson, Ph.D.
June 6, 2010

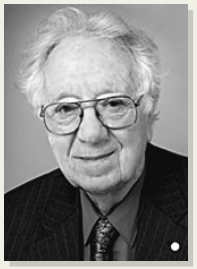
# *Mice in Biomedical Research*

- The laboratory mouse has been considered the premiere experimental model of human biology and disease since 1902 when it was first used to demonstrate how genetic traits could be transferred from parents to offspring via classical or “Mendelian” inheritance in mammals.
- In just over a century, an impressive array of genetic tools, reagents and processes has been developed in the mouse, including:
  - Homozygous inbred strains
  - Recombinant inbred and consomic strains
  - Transgenic and knockout methods
  - Monoclonal antibodies
  - iPS cells
- Evidence that mice have played a key role in biomedical research is provided by the fact that at least 18 Nobel prizes have been awarded for work done using the mouse. Most recently, the 2007 Nobel Prize was awarded to Mario Capecchi, Martin Evans, and Oliver Smithies for their discovery of the "principles for introducing specific gene modifications in mice by the use of embryonic stem (ES) cells.”

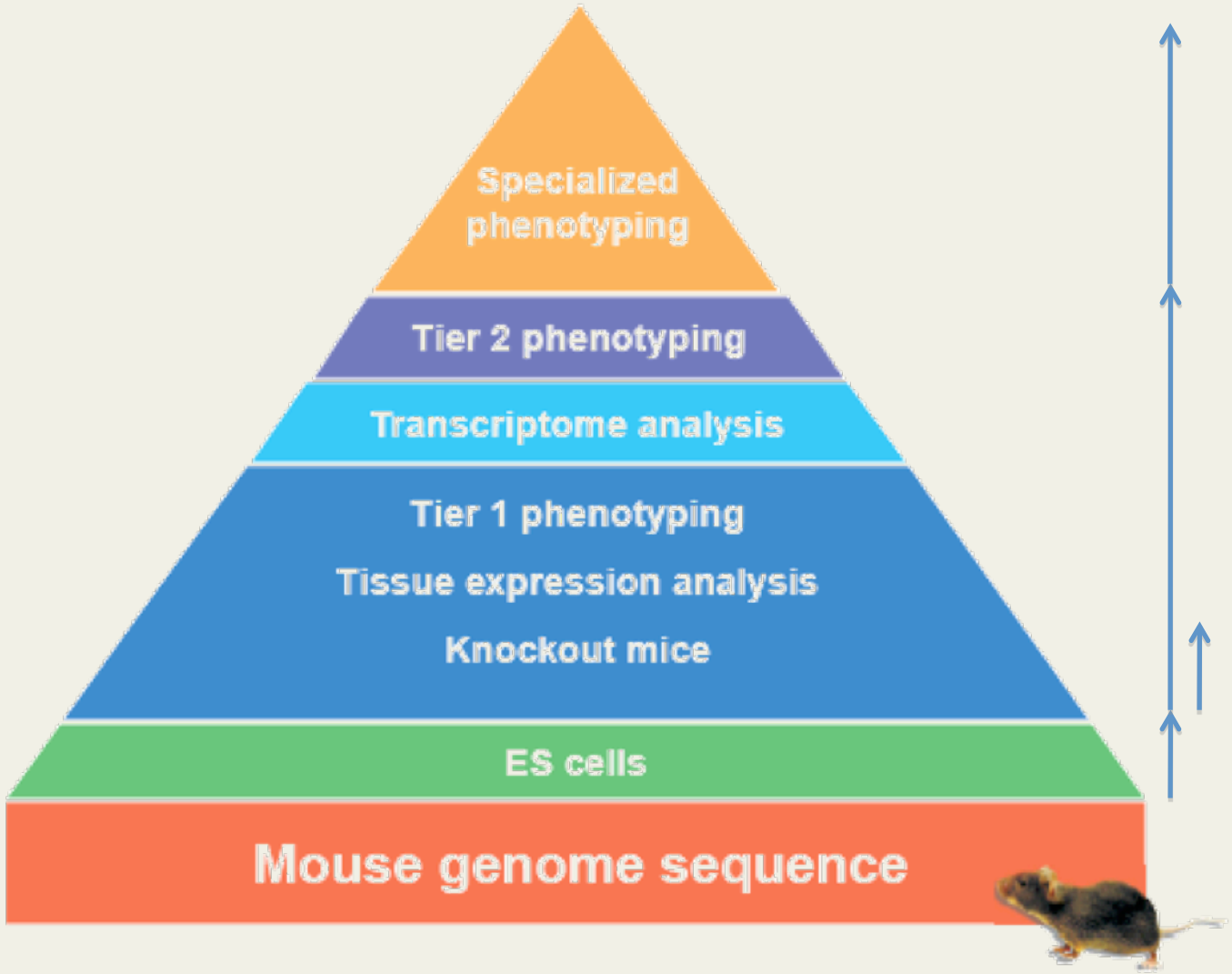






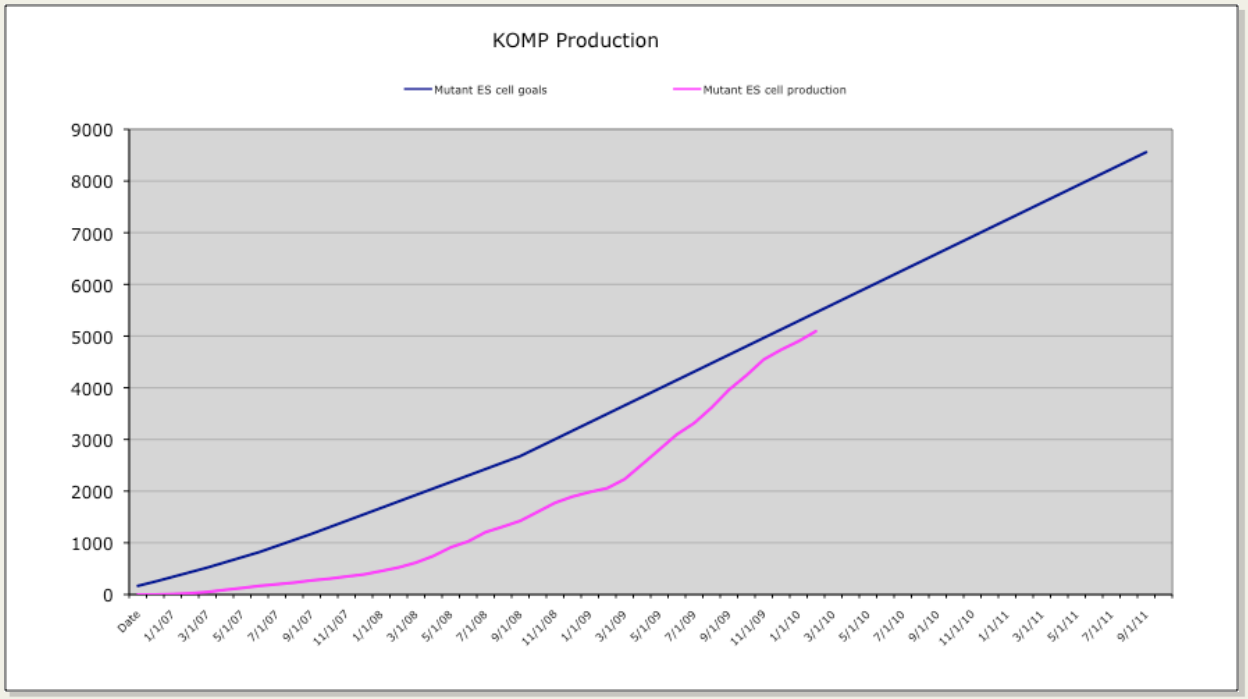


# KOMP Vision



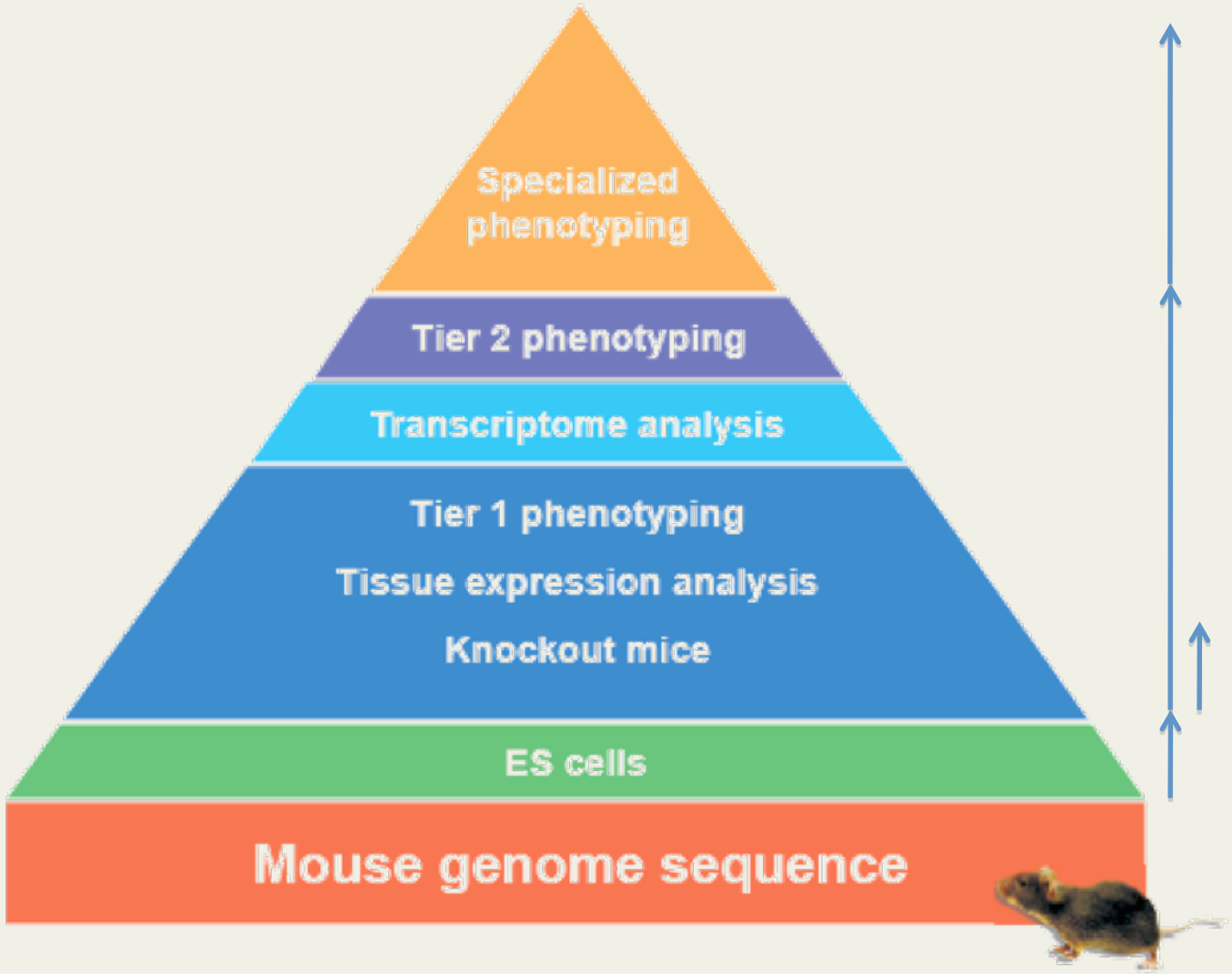

*Austin et al., Nature Genetics, 2004*

# Goals and Progress



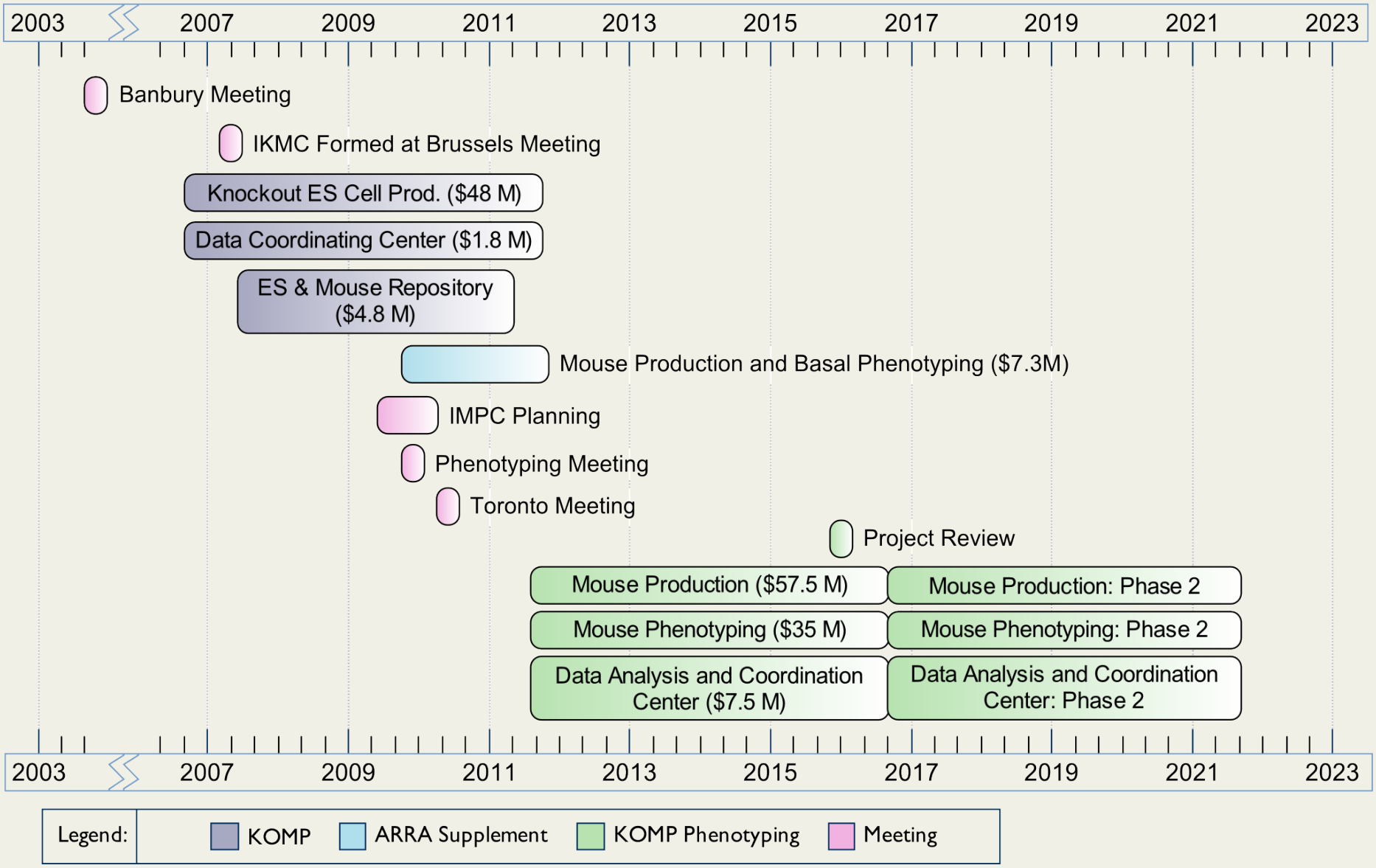

| | CSD | Regeneron | EuCOMM | NorCOMM | TIGM | Total |
|---|---|---|---|---|---|---|
| Goal (ES) | 5,000 | 3,500 | 8,000 | 500 | | 17,000 |
| Vectors | 4991 | 3116 | 4271 | 596 | | |
| Targeted ES | 3064 | 2038 | 2883 | 236 | | 8,221 |
| Mice | 189 | 160 | 351 | 12 | | 700 |

# KOMP Vision



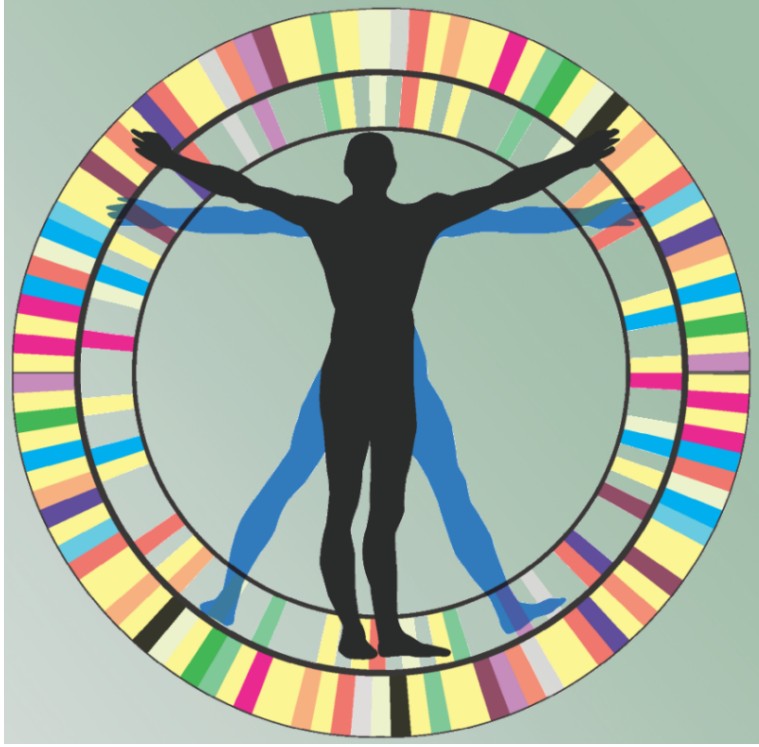

*Austin et al., Nature Genetics, 2004*

# KOMP – KOMP$^2$ Timeline




Goal: Phenotype 2,500 mice in Phase 1 and 6,000 in Phase 2

# NIH Roadmap Human Microbiome Project



# NIH Human Microbiome Project

**Goal**:

1. **Catalog the microbes that inhabit the human body**
2. **Examine whether changes in the microbiome can be related to health and disease**
3. **Generate a community resource to support and enable metagenomics-based projects that investigate the role of microbial communities in human health.**

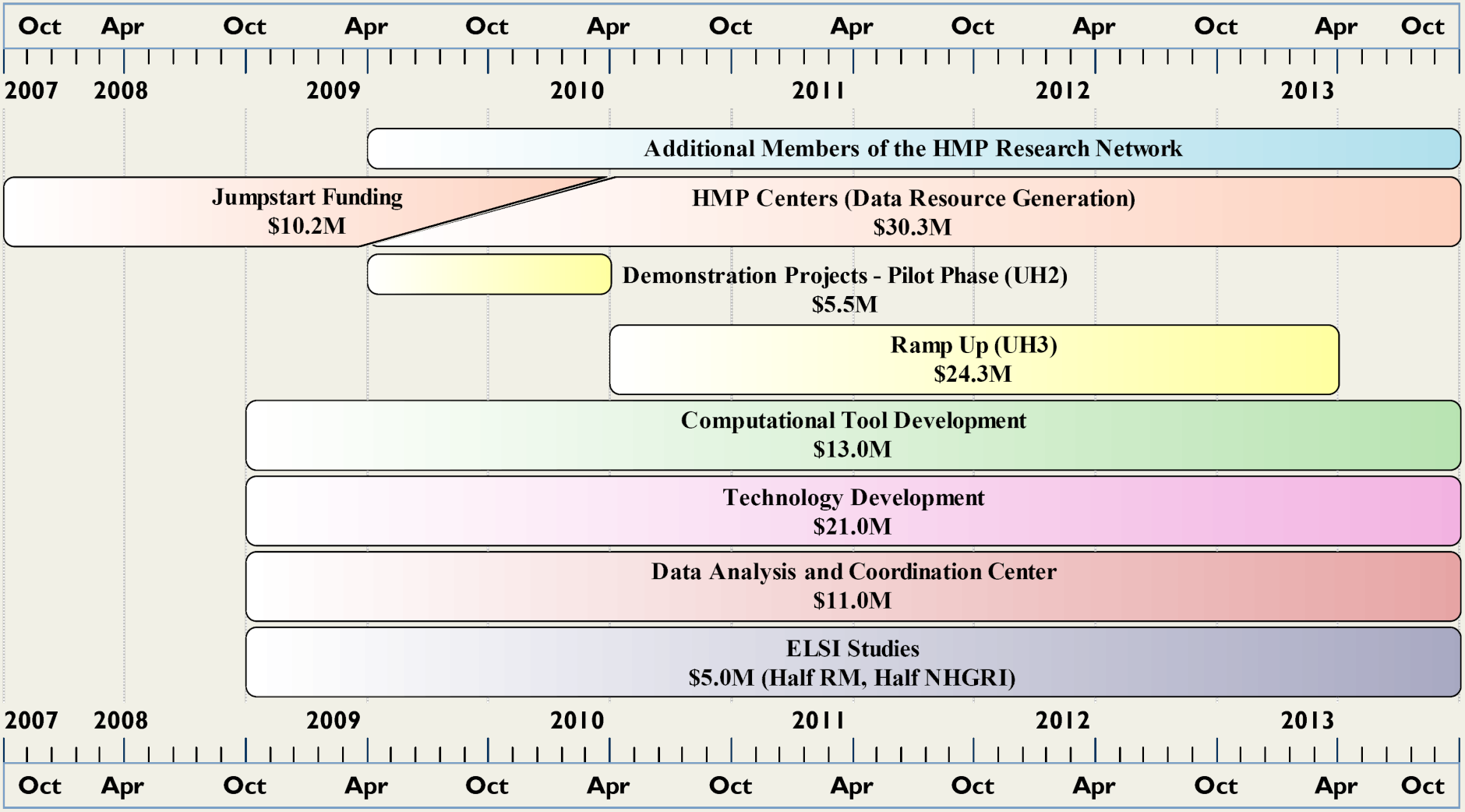
- **Timeline: five-year project**
- **Budget: $157 million**
- **Data Release: All data and resources will be released immediately (community resource project).**

**URLs: http://nihroadmap.nih.gov/hmp/**

**http://hmp.nih.gov**

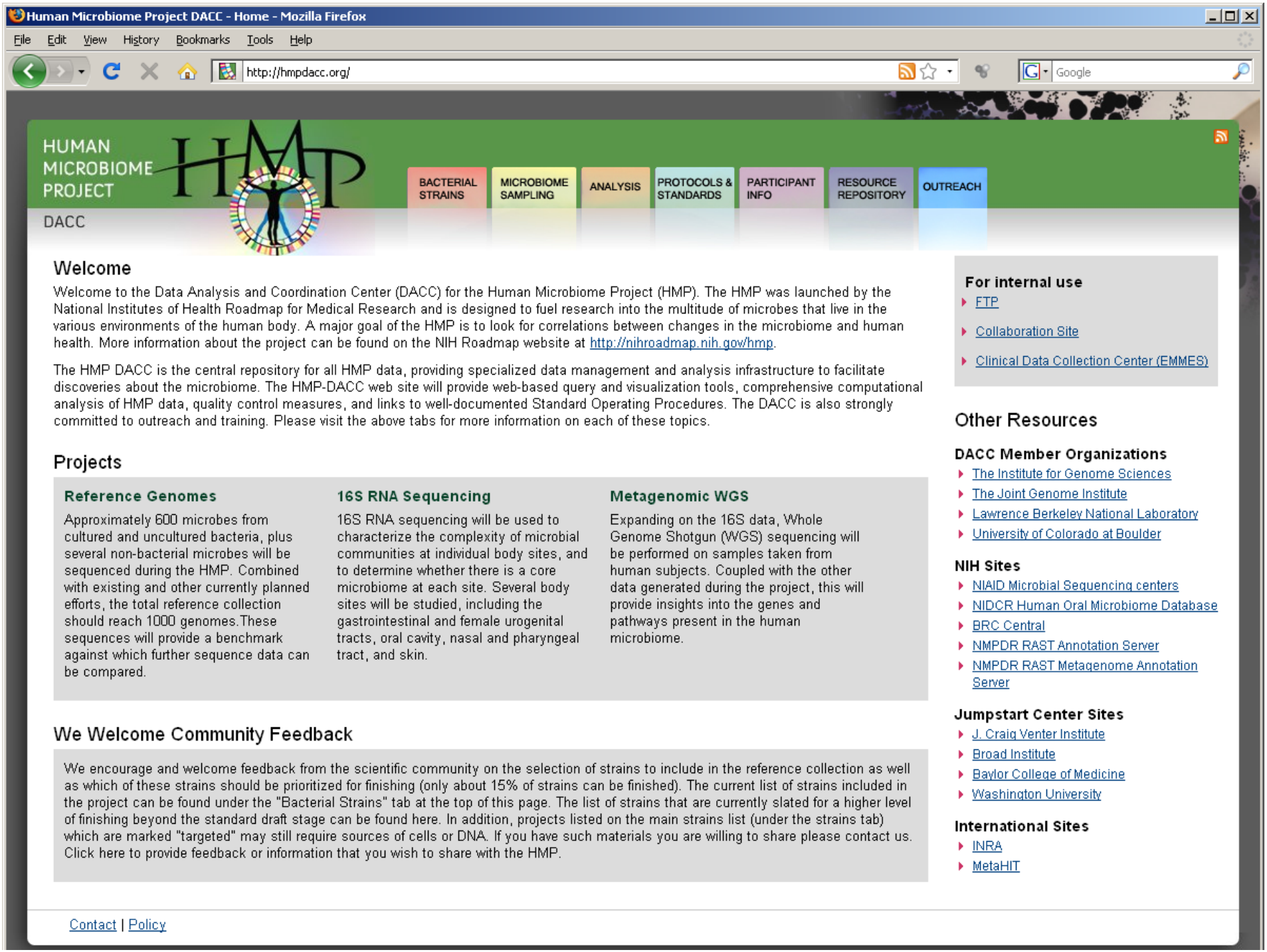
**http://www.hmpdacc.org**

# HMP Initiatives



| Contact PI | Application Title |
|---|---|
| Blaser, Martin | Evaluation of the cutaneous microbiome in psoriasis |
| Storch, Gregory | The human virome in children and its relationship to febrile illness |
| Fraser-Liggett, Claire | The thrifty microbiome: The role of the gut microbiota in obesity in the Amish |
| Li, Huiying | Metagenomic study of the human skin microbiome associated with acne |
| Wu, Gary | Diet, genetic factors, and the gut microbiome in Crohn's disease |
| Fortenberry, Dennis | Urethral microbiome of adolescent males |
| Tarr, Phillip | The neonatal microbiome and necrotizing enterocolitis |
| Pei, Zhiheng | Foregut microbiome in development of esophageal adenocarcinoma |

| Contact PI | Application Title |
|---|---|
| Ravel, Jacques | The microbial ecology of bacterial vaginosis: A fine scale resolution metagenomic analysis |
| Li, Ellen | Effect of Crohn's disease risk alleles on enteric microbiota |
| Young, Vincent | The role of the gut microbiota in ulcerative colitis |
| Versalovic, James | The Human Microbiome in Pediatric Abdominal Pain & Intestinal Inflammation |
| Segre, Julia | Skin Microbiome in Disease States: Atopic Dermatitis and Immunodeficiency |
| Buck, Gregory | The Vaginal Microbiome: Disease, Genetics and the Environment |
| Fraser-Liggett, Claire | Metagenomic Analysis of the Structure and Function of the Human Gut Microbiota in Crohn's Disease |


Human Microbiome Project DACC - Home - Mozilla Firefox
File Edit View History Bookmarks Tools Help
http://hmpdacc.org/
Google
HUMAN MICROBIOME PROJECT
DACC
BACTERIAL STRAINS
MICROBIOME SAMPLING
ANALYSIS
PROTOCOLS & STANDARDS
PARTICIPANT INFO
RESOURCE REPOSITORY
OUTREACH
Welcome
Welcome to the Data Analysis and Coordination Center (DACC) for the Human Microbiome Project (HMP). The HMP was launched by the National Institutes of Health Roadmap for Medical Research and is designed to fuel research into the multitude of microbes that live in the various environments of the human body. A major goal of the HMP is to look for correlations between changes in the microbiome and human health. More information about the project can be found on the NIH Roadmap website at http://nihroadmap.nih.gov/hmp.
The HMP DACC is the central repository for all HMP data, providing specialized data management and analysis infrastructure to facilitate discoveries about the microbiome. The HMP-DACC web site will provide web-based query and visualization tools, comprehensive computational analysis of HMP data, quality control measures, and links to well-documented Standard Operating Procedures. The DACC is also strongly committed to outreach and training. Please visit the above tabs for more information on each of these topics.
Projects
Reference Genomes
Approximately 600 microbes from cultured and uncultured bacteria, plus several non-bacterial microbes will be sequenced during the HMP. Combined with existing and other currently planned efforts, the total reference collection should reach 1000 genomes.These sequences will provide a benchmark against which further sequence data can be compared.
16S RNA Sequencing
16S RNA sequencing will be used to characterize the complexity of microbial communities at individual body sites, and to determine whether there is a core microbiome at each site. Several body sites will be studied, including the gastrointestinal and female urogenital tracts, oral cavity, nasal and pharyngeal tract, and skin.
Metagenomic WGS
Expanding on the 16S data, Whole Genome Shotgun (WGS) sequencing will be performed on samples taken from human subjects. Coupled with the other data generated during the project, this will provide insights into the genes and pathways present in the human microbiome.
We Welcome Community Feedback
We encourage and welcome feedback from the scientific community on the selection of strains to include in the reference collection as well as which of these strains should be prioritized for finishing (only about 15% of strains can be finished). The current list of strains included in the project can be found under the "Bacterial Strains" tab at the top of this page. The list of strains that are currently slated for a higher level of finishing beyond the standard draft stage can be found here. In addition, projects listed on the main strains list (under the strains tab) which are marked "targeted" may still require sources of cells or DNA. If you have such materials you are willing to share please contact us. Click here to provide feedback or information that you wish to share with the HMP.
For internal use
FTP
Collaboration Site
Clinical Data Collection Center (EMMES)
Other Resources
DACC Member Organizations
The Institute for Genome Sciences
The Joint Genome Institute
Lawrence Berkeley National Laboratory
University of Colorado at Boulder
NIH Sites
NIAID Microbial Sequencing centers
NIDCR Human Oral Microbiome Database
BRC Central
NMPDR RAST Annotation Server
NMPDR RAST Metagenome Annotation Server
Jumpstart Center Sites
J. Craig Venter Institute
Broad Institute
Baylor College of Medicine
Washington University
International Sites
INRA
MetaHIT
Contact | Policy