

# **FAANG Steering Committee December 10, 2025\_Minutes**

(HZ's revision of AI Companion output).

Attending: C.K.Tuggle, E. Giuffra, C. Kasper, CKühn, B. Murdoch, H. Zhou, E. Clark, T. Kalbfleisch, C. Gondro, H. Cheng, D. Lourenco, M. Calus, L. Fang

Regrets: G. Tosser-Klopp, G. Plastow,

## **Agenda:**

1. Approval of previous minutes; review of outstanding Next Steps
2. Updates from Task Forces (Comparative Genomics, Farm Prediction, FAANG Data, Single Cell, MetaFAIR, HTP)
3. Planning the FAANG Workshop at PAG and 2026 Coordination
4. Data Integration, SNP Annotation System, and Pangenome Strategy
5. Next steps

## **Minutes**

### **1. Approval of Previous Minutes & Review of Action Items**

The minutes from the previous meeting were approved. The committee revisited outstanding action items, particularly the alignment of task force activities ahead of the January meeting. This December call was intended to consolidate updates from all task forces and prepare for the FAANG workshop at PAG, following the structure outlined in prior meetings.

Christopher will confirm with Zhiliang that the Comparative Genomics TF mailing list is functional.

### **2. Task Force Updates**

#### **Comparative Genomics TF**

Brenda and Emily reported limited activity, noting fragmentation of research efforts compared to earlier FAANG years. While overlap exists with other consortia, the group agreed that facilitating shared webinars remains a worthwhile role.

Chris suggested focusing on clearly defined tasks rather than serving primarily as a communications hub.

#### **Farm Prediction Task Force (Hao, Daniela, Mario)**

Hao provided updates on the bi-monthly seminar series, including upcoming talks in March. Recent cattle-breeding seminar recording will be posted publicly. The task force proposed developing a centralized cross-species SNP documentation/annotation resource, leveraging existing work and avoiding duplication. Several members emphasized building a concise, interoperable resource that summarizes functional annotations across species.

The group reaffirmed its goal to integrate molecular data with quantitative genetics to demonstrate the value of FAANG resources to funding agencies and industry. A centralized annotated SNP database is envisioned, enabling downstream genomic prediction and demonstrating return on investment through seminar case studies and publications.

Lingzhao asked how FAANG annotation could support gene editing interventions; Chris recommended that the first step is robust labeling of regulatory information at SNPs the FAANG community already has data for.

### **FarmGTEx TF**

Lingzhao shared current progress on FarmGTEx: Sheep GTEx data is available now and goat GTEx will be available in a few months and other species such as rabbit, camel will be available. Bimonthly seminar is being arranged.

### **Single Cell TF**

Chris reported ongoing development of training modules for single-cell analysis, in collaboration with plant communities. The committee discussed potential use of RCN funds for cross-training, enabling international participation while respecting U.S. funding restrictions.

### **MetaFAIR TF**

Ted and Emily updated the group on the data portal's progress. After January, the team will deliver a virtual training course on new submission and validation tools, reusing materials evolved from earlier workshops.

### **HTP TF**

Cedric shared plans to coordinate with Deb and the Prediction Task Force on a USDA workshop proposal, ultimately contributing to a white paper on the use of pangenomes for prediction. European alignment efforts are underway as well. The TF may shift the direction to data integration and analysis in coordinating with other TFs such as Prediction and MetaFAIR TFs.

## **3. Planning the FAANG Workshop at PAG**

The committee emphasized reducing the time spent summarizing task force activities during PAG, allowing more time for **structured discussion on:**

- Data integration strategies
- Formation of cross-task force teams
- Identifying action items and volunteer leads
- Mechanisms for enabling collaboration under data-access restrictions

Huaijun will prepare and circulate structured discussion points for the workshop.

Task forces are asked to **submit updated reports if any** for online posting prior to PAG, with a one-week window for revisions Due on December 17, 2025.

## **4. Data Integration, SNP Annotation System, Pangenome Strategy**

### **Centralized SNP Documentation System**

The committee discussed the technical and scientific considerations of building a centralized SNP annotation resource:

- Hao emphasized adopting a lightweight, modular design.
- Lingzhao proposed incorporating human genetic data to infer conserved regulatory importance.
- Emily clarified that community-generated pangenomes can be displayed on Ensembl; Ted noted NCBI's progress on their comparative viewer.

## **5. Cross-Task Force Seminar Coordination**

Huaijun proposed establishing a **rotating bi-monthly FAANG seminar series**, with each task force hosting one seminar per year. This would:

- Reduce duplication across task forces
- Increase participation
- Encourage broader topic integration

The committee agreed this coordinated approach would better utilize community time and support cross-topic dialogue.

## **6. Next Steps**

### **Huaijun**

- Coordinate with task forces on seminar schedules to prevent overlap.
- Prepare structured discussion points and action-item prompts for the PAG workshop.
- Summarize and share all task force reports online for review.

### **Task Force Leaders**

- Review and update task force reports within one week.
- Identify bimonthly speakers/topics that support cross-task force alignment.