

[Subject Line] NCI Requests Input on Scientific Challenges & Opportunities for Understanding the Path from Genetic Variation to Cancer Phenotype (by November 15, 2023)

Research conducted over the past 15 years has identified thousands of common genetic variants associated with risk for cancer. However, understanding how genetic variation impacts the molecular mechanisms and biology underlying cancer risk has been challenging.

NCI is planning a virtual meeting for February 2023, “Variation to Biology: Optimizing Functional Analysis of Cancer Risk Variants,” to identify and discuss **how best to address scientific challenges and opportunities for understanding the path from genetic variation to cancer phenotype**. Day 1 of the meeting will feature a half-day of brief presentations focused on 5-6 challenges, with discussion. Day 2 will feature breakout sessions focused on ways to address the challenges discussed during Day 1.

The meeting Planning Committee would like to invite you to participate in a survey to solicit challenges for discussion during this meeting. For example:

- Is it possible or desirable to create reproducibility standards for functional validation?
- How do we decide if a variant is fully characterized? Could a minimal set of techniques/processes be established that would be required to call a variant fully characterized?
- Can the community agree on standard intermediate endpoints (in vivo or mouse model based)?
- Are there tools, infrastructure, or networking needs in this field?

This survey also includes an opportunity for you to indicate if you would be willing to serve as speaker/lead discussant for a specific challenge. This would take place on the first day; each session would include ~5 minutes of presentation and ~15 minutes of discussion including all attendees.

We welcome any feedback you would like to provide by November 15, 2023. If you have any questions about this survey, please contact us at NCIEpiCommunications@mail.nih.gov.

Your contributions will help us move the research forward—thank you!

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