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The National Cancer Institute is planning a virtual meeting to identify and discuss how best to address scientific challenges and opportunities for understanding the path from genetic variation to cancer phenotype. The goal of this survey is to solicit challenges for discussion at 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?

What is a significant challenge for functional characterization of genomic variants?
(Please include any relevant details.)

Are you interested in speaking or leading the discussion for a specific challenge at the meeting?

YES, I am interested in speaking or leading a discussion at the meeting

NO, I am not interested in speaking or leading a discussion at the meeting

If you answered "YES," please share the following information.

First Name	<input type="text"/>
Last Name	<input type="text"/>
Institution/Organization	<input type="text"/>
Areas of Interest or Expertise	<input type="text"/>
email address	<input type="text"/>