Re: Variant Interpretation for Cancer Consortium Participation

Dear VICC leaders,

I would like to take this opportunity to express my commitment to participating in the Variant Interpretation for Cancer Consortium (VICC). As you know, we are one of several institutions engaged in the challenge of curating knowledge to annotate cancer genome mutations associated with evidence of pathogenicity or linked to relevant treatment options. Specifically, we have developed the [INSTITUTION RESOURCE (INSTITUTION NAME)]. While this resource serves the specific needs of our own institution, we recognize that there is **clear value in sharing knowledge of cancer-variant-treatment associations.** Such sharing will increase confidence where interpretations overlap, fill gaps, reduce redundancy, and leverage disparate domain expertise. To this end, we support your plans to coordinate global efforts for curation and help develop a community resource for cross-knowledgebase queries under the auspices of the Global Alliance for Genomics and Health (GA4GH). As a VICC participant we agree with the following data sharing principles, developed through community discussion at GA4GH meetings and calls.

- We will commit to sharing at least a minimal set of data elements for cancer variant interpretations including: gene symbol, variant name, cancer subtype (tumor type and organ), clinical implication (drug sensitivity, drug resistance, adverse response, diagnostic, or prognostic), source (e.g., PubMed identifier) and curation group.
- We agree that to avoid patient data privacy concerns, the project will focus on only clinical interpretations of variants derived from published findings (literature, conference proceedings, and clinical trial records), not individual patient/variant-level observations. Thus, there should be no possibility of linking variants to individuals.
- We agree to share [SPECIFY: all OR a significant proportion] of our interpretations (with at least the minimal required data elements) accumulated by our ongoing curation efforts.
  - This content will be released under a permissive license (free and non-exclusive for at least research use).
  - Software developed as part of this data sharing initiative will be released in public repositories (e.g., github) with open source licenses.
  - Public APIs will be developed to facilitate access to our data for use by the VICC.
  - Wherever possible, data sharing will be facilitated by use of the existing GA4GH schemas, APIs and demonstration implementations.
  - Interpretations made available by our institution will also be made available as cross-knowledgebase bulk downloads.

I look forward to working together with the Variant Interpretation for Cancer Consortium to further our common goal of improving genomics-guided precision medicine for cancer patients.

Sincerely,