CIViC: Crowdsourcing the Clinical Interpretation of Variants in Cancer

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Project Website: https://civic.genome.wustl.edu (or www.civicdb.org)
Mission Statement: https://civic.genome.wustl.edu/#/collaborate

Source Code:
https://github.com/genome/civic-server
https://github.com/genome/civic-client

The landscape of the genomics of tumorigenesis has been systematically surveyed in recent years, identifying thousands of potential cancer-driving alterations. However, few resources exist to facilitate prioritization and interpretation of these alterations in a clinical context. Interpreting the events from even a single case requires both extensive bioinformatics expertise as well as an understanding of cancer biology and clinical paradigms. Genomic aberrations must be placed in the context of therapeutic response and diagnostic or prognostic associations. The evidence for these associations must be captured and characterized so that we can achieve a principled consensus among genomic experts, pathologists, and oncologists on how best to interpret a genomic alteration in a clinical context. This interpretation step now represents a significant bottleneck, preventing the realization of personalized medicine. To this end, we present CIViC (www.civicdb.org) as a forum for the clinical interpretation of variants in cancer. We believe that to succeed, such a resource must be comprehensive, current, community-based and above all, open-access. CIViC allows curation of structured evidence coupled with free-form discussion for user-friendly interpretation of clinical actionability of genomic alterations. CIViC supports multiple lines of evidence, stratified based on the type of study, from *in vitro* studies to large clinical trials. CIViC currently contains clinical interpretations for over 135 genomic alterations in 55 genes spanning 45 cancer types and summarizing the evidence from nearly 230 publications. The CIViC interface facilitates both discovery and collaboration by allowing a user to not only search and browse the current state-of-the art interpretations but also to join the community discussion by adding, editing, or commenting on genomic events, evidence for their clinical actionability and the resulting community consensus interpretation.