***Oncogene.iobio*: a web app for real-time, integrative examination and functional prioritization of tumor mutations**

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Genetic testing and clinical tumor sequencing are rapidly becoming part of the standard of care for a large subset of cancers. At present, a scattered framework of resources, often requiring expensive hardware and heavy computational skills, exists to aid clinicians and researchers in the bioinformatic analysis process. To assist in addressing the need for a comprehensive tool that operates intuitively, and at the pace of critical therapeutic timelines, we have developed *oncogene.iobio*. Utilizing our novel *iobio* analysis ecosystem (https://iobio.io), *oncogene.iobio* visualizes genomic, transcriptomic, and epigenetic data to aid in the discovery of variants with the highest potential for association with the patient's cancer.

Oncogene.iobio consumes primary sequencing data (in bam, vcf, fasta/fastq formats) sourced from local, or cloud-based repositories. In real-time, variants are identified and annotated on a gene-by-gene basis, and prioritized using functional annotations (sourced from SNPEFF, VEP, SIFT, PolyPhen) and cancer databases (COSMIC, cBioPortal). Uniquely, *oncogene.iobio* identifies compound heterozygotes between inherited cancer-implicated variants and somatically-acquired tumor mutations, dynamically filters mutations by allele frequency, and analyzes somatic variants within areas of chromosomal CNVs or LOH. Areas with large transcriptional change or allele-specific expression are highlighted when RNAseq data is present, along with hypo- or hyper-methylated sites given bisulfate-treated DNA sequencing reads. Ranked, candidate gene lists (sourced from ICGC, cBioPortal), as well as cancer-associated variants (sourced from GEMINI), are provided by *oncogene.iobio* to guide users in the analysis process, and to quickly elucidate suspect loci.

Some analyses may benefit from the more advanced features of *oncogene.iobio*, such as the ability to recall variants in real-time, using our Freebayes algorithm attuned with tumor-specific parameters. This workflow assists in discovering false negatives, and large-scale deletions and duplications, normally missed in low-coverage areas analyzed using canonical methods. Additionally, *oncogene.iobio* provides the ability to corroborate true positives and reduce reference mapping biases using our graph-based adjudication tool GRAPHITE (https://github.com/dillonl/graphite). In conjunction with the rapidly-informative and visually-intuitive primary features, these options allow for critical biomedical findings sourced from high-confidence data.

With extensive integration and immediate feedback, *oncogene.iobio* aims to aid the discovery of impactful variants in oncological research and diagnostic care.