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Variant Interpretation: UCSC Genome Browser Recommended Track Sets

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Abstract

The UCSC Genome Browser has been an important tool for genomics and clinical genetics since the sequence of the human genome was first released in 2000. As it has grown in scope to display more types of data it has also grown more complicated. The data, which are dispersed at many locations worldwide, are collected into one view on the Browser, where the graphical interface presents the data in one location. This supports the expertise of the researcher to interpret variants in the genome. Because the analysis of Single Nucleotide Variants (SNVs) and Copy Number Variants (CNVs) require interpretation of data at very different genomic scales, different data resources are required. We present here several Recommended Track Sets designed to facilitate the interpretation of variants in the clinic, offering quick access to datasets relevant to the appropriate scale.

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