IGB terminology

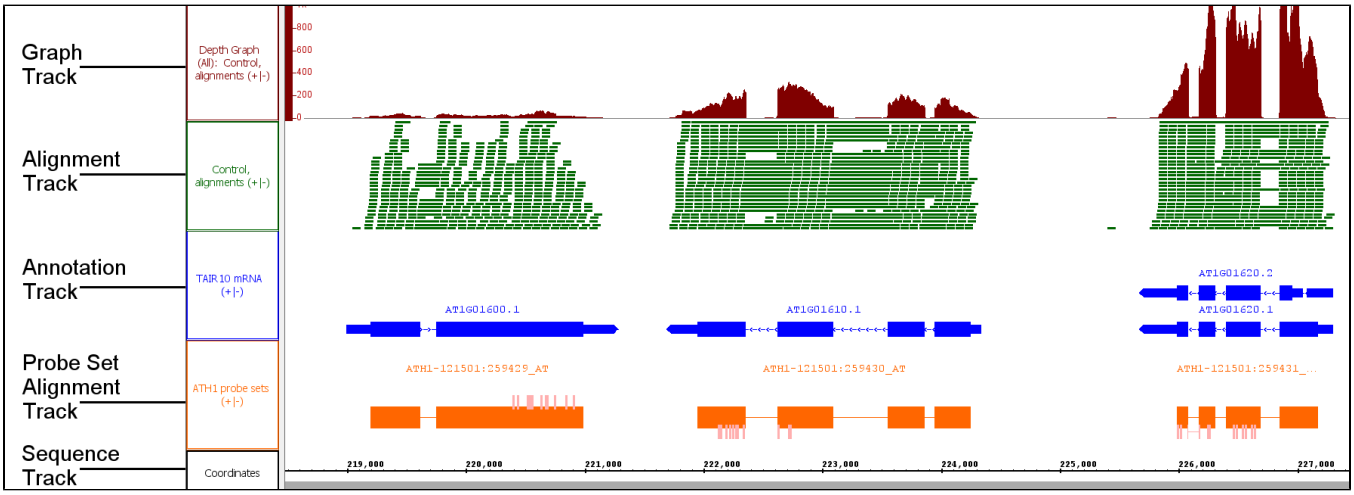
Genomes and chromosomes

Chromosomes, also called **contigs** or **reference sequences**, refer to one or more annotated sequences that form a genome assembly. For completed genome projects, these correspond to the sequence of a physical chromosome. For less complete genomes, they may represent assembled contigs that correspond to parts of a physical chromosome.

Genome, genome version, or **assembly** refer to a group of annotated sequences corresponding to the genome sequence of an organism. IGB designates these using the month and year they were published or made publicly available.

Tracks

Tracks are rows of data read from the same file or data set. When you open a file, the data within the file will appear in one or more tracks. Older versions of IGB referred to tracks as "tiers" and so you may see this term used elsewhere in the User's guide. There are three main types of tracks: **Graph** tracks, **A nnotation** tracks, and **Reference Sequence** tracks. **Alignment** tracks and **Probe Set** tracks are types of Annotation Track.

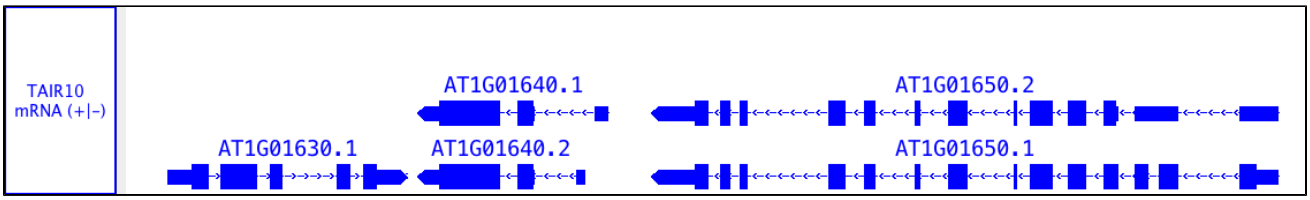


Annotation tracks

Annotations indicate the known or suspected locations of genomic features such as genes, exons, promoter regions, pseudogenes, and so forth. Annotations may consist of a single coordinate, a single span with a start and end positions, or a collection of spans. Most annotations reside on either the plus or minus strand of a chromosome, but some do not.

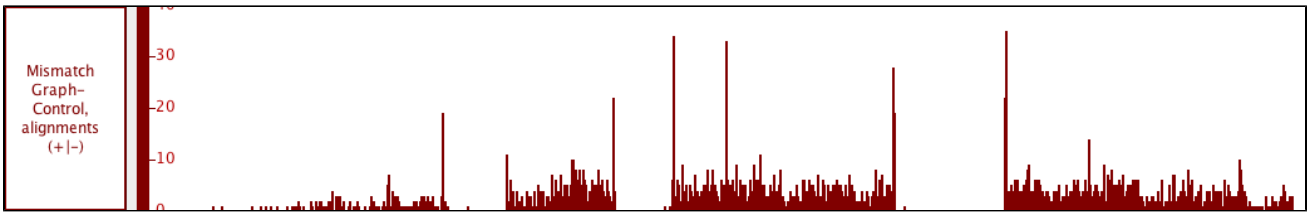
Examples of annotations include:

- **single-coordinate feature**: splice site
- **single-span feature, with strand**: an exon
- **single-span feature, no strand**: sequence recognized by a restriction enzyme
- **multi-span feature, with strand**: a gene model



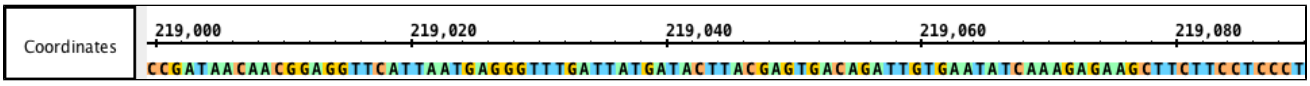
Graphs tracks

Graphs are numeric data associated with regions or single-base positions in a chromosome.



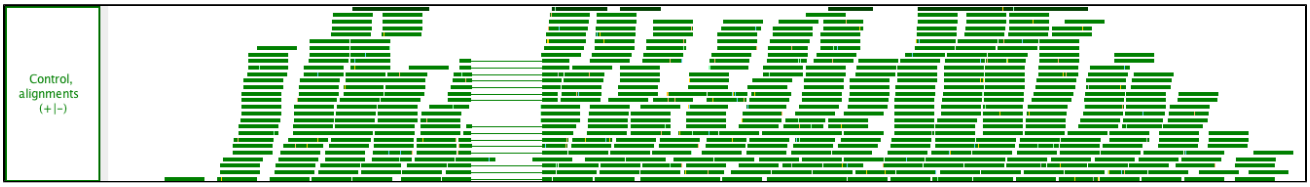
Sequence track

Sequences are DNA residues from a chromosomes or contigs that together make an assembly. Sequences can be fully or partially loaded from local files, Quickload sites, or Distributed Annotation Servers. You can view sequence data in the **Coordinates** track or by opening the **Sequence Viewer**.



Alignments

Alignments represent how sequences obtained from an experiment (such as sequence reads from an RNA-Seq experiment) align onto a reference sequence. At low zoom they look like annotations, with marks representing mismatches, insertions, or deletions. At higher zoom, the aligned sequence bases become visible.



Probe set alignments

Probe set alignments consist of Affymetrix probe set target sequences aligned onto the reference with probe locations indicated as annotations on the target sequence alignments. The probes are kind of annotation on an annotation.

These data are Affymetrix specific.