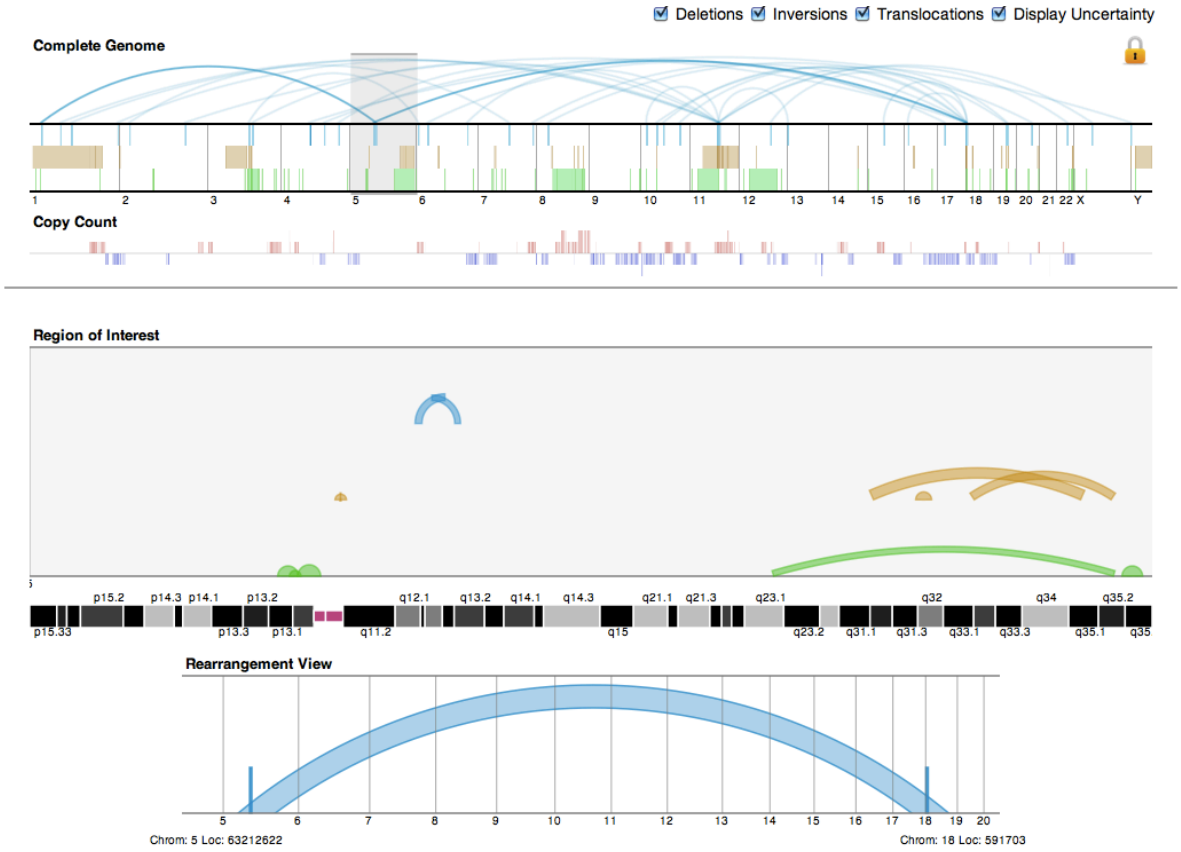
Gremlin: Genome Rearrangement Explorer with Multi-scale, Linked INteractions



Gremlin is a genome explorer that displays results from geometric rearrangement analysis. It currently focuses on three types of rearrangements: deletions (green), inversions (tan) and inter-chromosomal translocations (blue). There are three distinct views in Gremlin: Complete Genome View, Region of Interest View and Rearrangement View.

In the **Complete Genome View**, deletions are marked with green glyphs, beginning at the starting breakpoint of a deletion, and ending at the end breakpoint. Inversions are marked similarly in tan. Translocations, lacking a notion of size, are marked with uniformly sized blue glyphs positioned according to breakpoint location. Additionally, arcs are drawn atop the Genome View to indicate relationships between inter-chromosomal breakpoints.

The **Region of Interest View** is dependent on the selection windows in the Complete Genome View, which can be resized and translated along the genome. The size of the selection window determines the scale at which rearrangements are drawn in the ROI view. In this view, inversions and deletions are draw as arcs between their respective starting and ending breakpoints. Translocations are draw as uniformly sized half-arcs, pointing in the direction of their paired breakpoint.

The thickness of each arc is proportional to the number of fragments that support a rearrangement. The thicker the arc, the higher the support.

The **Rearrangement View** is dependent on the rearrangement glyph that has been left-clicked in the ROI View. In this view, only the selected rearrangement is displayed, along with its exact breakpoint locations. Clicking on breakpoints in the Rearrangement View will open a link to the UCSC Human Genome Browser, where detailed information regarding the location of the breakpoint can be cross-referenced.