New non-redundant structural variant (NR-SV) datasets to aid variant interpretation and disease discovery including deletions, duplications, and insertions.

**How to Use dbVar Non-Redundant Data**

- Available in three formats – BED (for easy upload to genome browsers), BEDPE (complete with metadata for more detailed analyses), and TSV (custom tab-delimited format for downstream annotation and analysis).
- Review QuickStart.md and/or ToolGuide.md for use case examples
- Intersect dbVar’s non-redundant (NR) files with other genomic interval files using popular tools and browsers, such as NCBI’s Sequence Viewer, Bedtools, Galaxy, and UCSC Genome Browser
- Run a comparison or workflow using your custom data and dbVar NR-SV files. For example, use dbVar’s NR-SV data to generate a map of ClinVar loci where SV has been implicated.

Your best source for the latest and most complete sets of human structural variants

160+ Studies

3M+ non-redundant structural variants

updated monthly