In hereditary cancers, insight into genomic risk factors helps steer improved patient care. Circulogene’s cutting-edge bioinformatics applies artificial intelligence, machine-learning and database-driven algorithms to deliver highest quality and most accurate SNV, INDEL and structural variant analysis and classification to clinic.

### Aggregated Data From Diverse, First-Class Sources
- Automated, validated and up to date with built-in quality systems
- Data from diverse, first-class data sources aggregated, organized, aligned, annotated and classified
- Constant variant reclassification every 3 weeks

### Advanced and Fully Integrated AI Greatly Enhances Confident Calls.
- Machine-educated variant calling of pathogenic, likely pathogenic, VUS variants, including automatic pre-classification
- Approx. 200,000 “global inter-lab” calling data sets, on top of eight major public databases to achieve unparalleled accuracy

### Big Data-Sharing With Global Medical Community
- Fast, accurate raw data analysis and data sharing with variant calling and annotation
- Regular upload of our reported variants to share with broader medical community

### Comprehensive Intuitive Report
- Variant details
- Clinically relevant and actionable information
- Follows ACMG and AMP guidelines for all mutation types
- Simplified data mining correlates millions of internal and external medical data sources, (both public & private)

### Complete End-to-End Solution
- Patient centric
- Data analysis
- Classification
- Interpretation and reporting

### Security and Privacy
- HIPAA compliant
- Long-term cloud storage
- Clinical grade security, privacy and compliance

### OVER 2 MILLION VARIANT CALL DATA
Unlike most labs that use free, public databases, or rely on their own public-inaccessible databases, Circulogene has built a proprietary aggregate integrating the 8 largest public databases with a global community variant-calling atlas.

### HUMAN GENETIC VARIANT DATABASES:

- **The Genome Aggregation Database (gnomAD)**
  - Variants of 15,496 genomes and 123,136 exomes from seven populations worldwide

- **ClinVar**
  - Currently holds >160,000 submitted interpretations, representing >130,000 variants, affecting >26,000 genes

- **COSMIC**
  - >170,000 mutations, >2.9 million experiments, >500,000 tumors

- **ExAC**
  - 60,706 exomes from seven populations

- **ESP**
  - 6,503 exomes from European Americans and African Americans

- **1000 Genomes Project**
  - Genomic data for 2,504 individuals from five populations

- **CG69**
  - 69 individuals with complete genomes

- **dbNSFP**
  - 83,422,341 nsSNVs and ssSNVs (splicing-site SNVs)