QIAGEN

Sequenced Whole Genome Data

Recruiting patients, collecting their medical histories and sequencing their genomes can be costly and time consuming. Wouldn't it be nice if you could instantly access the sample data you need?

License Inova Genomes and gain instant access to a tailored set of scientifically validated, sequenced genomes that best fit your research or clinical testing needs.

Sample to Insight

Customized Cohort Selection

The complete Inova Genomes collection includes nearly 7,000 and growing phenotypically and ethnically diverse whole genome samples from more than 2,100 consented families. All de-identified genome samples are linked to demographic and ancestral information, with more than one third of the samples linked to a clinical phenotype. With phenotypes spanning all major organ systems, it's easy to assemble custom therapeutically relevant cohorts. At the same time, the ancestral diversity and large percentage of healthy samples makes this an ideal data set for general population studies as well as control applications such as confirming rare variant status for diagnostic odyssey cases or compensating for unavailable normal-matched samples in tumor sequencing. Custom matched control cohorts are easily assembled based on demographic attributes including sex, age and ancestral background.

Fast, Easy Access

Purchased genomes can be delivered and accessed as VCF level, clinically annotated samples in Ingenuity Variant Analysis, QIAGEN's platform for causal variant analysis. Alternatively, purchased genomes can be delivered for direct download as VCF or BAM files via Amazon S3 links with clinical annotations delivered in tab-delimited format. For a subset of samples, RNA-Seq data is also available. The RNA-Seq data is delivered as tab-delimited gene and splice junction based files with RSEM and RPKM values, and upon request in FASTQ format.

For more information, contact:
bioinformaticssales@qiagen.com.

Quality You Can Trust

Inova Genomes are made available in partnership with the Inova Translational Medicine Institute (ITMI) in Falls Church, Virginia. ITMI scientists and staff are continuously developing and refining innovative methods in genomics research for application to personalized healthcare. Greater than 40X sequencing depth and rigorous QC measures backed up by leading publications ensures the quality of the sequenced samples.

Genomes	Disease Area
436	Cardiovascular Diseases
858	Congenital Disorders
712	Gastrointestinal Diseases
372	Hematological Diseases
236	Immunological Diseases
700	Metabolic Diseases
394	Respiratory Diseases

Table of Selected Disease Areas

Genomes	Region of Origin
84	Africa
394	Asia
811	Central America
131	Europe
63	Middle East
119	North America - Mexico
2284	North America – US & Canada
241	South America

Table of Selected Regions of Origin