**RESOURCE SHARING PLANS**

Research tools and resources will be made available in full accordance with the NIH Grants Policy Statement, the Principles and Guidelines for Recipients of NIH Research Grants and Contracts, and the NIH Genomic Data Sharing Policy. Each of the JAX CSVA Principal Investigators has significant experience participating in large-scale genome sequencing projects, and has an established record of sharing unique resources generated with NIH support with the academic research community, through publications and submission to data repositories without any license or research restrictions.

All genomic data (large-scale data as defined in the NIH Genomic Data Sharing Policy) resulting from the proposed JAX CSVA, as well as relevant phenotype-associated data, will be made available in a timely manner in full accordance with the NIH Final Genomic Data Sharing (GDS) Policy as well as any distributions plans established by NHGRI Genome Sequencing Program (GSP). In particular, the catalog of structural variations identified from the individuals sequenced as part of the NHGRI-supported GSP by JAX CSVA investigators will be made publicly available within the timelines required by the GDS Policy and Supplemental Information. JAX CSVA investigators that download unrestricted-access data from NIH-designated data repositories will acknowledge the specific data sets or applicable accession numbers(s) and the NIH-designated data repository. It is anticipated that genomic data made available from the GSP will be de-identified, and therefore, the derived data will meet the standards set forth in the HHS Regulations for the Protection of Human Subjects. All de-identified metadata and phenotype information received from the GSP will be stored securely at servers at one of the three participating institutions, The Jackson Laboratory, Washington University at St. Louis and Yale University. In addition, this project will be registered in the Database of Genotypes and Phenotypes (dbGaP) <http://www.ncbi.nih.gov/gap> and the human genomic data will be submitted to the relevant NIH-designated, as well as other public data archives (e.g., dbGaP, Database of Genomic Variants (DGV) [http://dgv.tcag.ca](http://dgv.tcag.ca/%22%20%5Ct%20%22pmc_ext), Database of Genomic Structural Variation (dbVar) <http://www.ncbi.nlm.nih.gov/dbvar> and ClinVar [http://www.ncbi.nlm.nih.gov/clinvar/](http://www.ncbi.nlm.nih.gov/clinvar/%22%20%5Ct%20%22pmc_ext), as appropriate.) In addition, the various methods developed for identification, annotation and association of Structural Variants will be disseminated to the research community through public code sharing repositories such as GitHub.