With the rise of next generation sequencing methods, there are now a variety of tools available to researchers for the detection and genotyping of sequence variants. However, the concordance among variant sets between these disparate approaches has been shown to be poor. Recently, researchers in the machine learning community have shown that combining the output of multiple models can dramatically improve performance of a classifier. Collectively, these techniques are referred to as ensemble methods. Here we describe a variant calling approach based on an ensemble of variant calling algorithms which we call Consensus Genotype for Exome Sequencing (CGES). Our method employs a two-stage voting scheme among a set of three algorithm implementations, GATK2.0. Freebayes, and Atlas2.0, which were used to identify variant sites and determine genotypes in the study. While the ensemble method is able to accept variants from any variant calling algorithm, these were chosen for their widespread adoption and diverse strategies. We apply CGES to a dataset consisting of 123 samples sequenced at the Center for Inherited Disease Research (CIDR) using the Agilent SureSelect Exome Capture and Illumina sequencing technology. Samples were drawn from extended pedigrees allowing us to compute individual and family based quality metrics across all algorithms. The CGES approach was shown to outperform its constituent parts in many key quality metrics without a significant loss in the number of variant sites called. In particular we are able to achieve a thorough reduction in Mendelian inconsistencies between the best performing variant callers and our consensus approach (CGES ~ 0.41 and Atlas2.0 ~ 0.69 subscription times). For callers with comparable VAF scores, our CGES set of variants has an average VAF score 11% (GATK) and 70% (Freebayes) higher than the unfiltered output set of each respective variant caller. Additionally, the consensus set outperforms all individual callers in the study with regard to expected exome-wide transition/transversion ratios (CGES ~ 3:1 and Atlas2.0 ~ 2:6). For the purpose of accessible, efficient, and reproducible analysis, we provide implementation of CGES as a standalone command line tool, as well as a set of parallel Galaxy tools and workflows for accessible and efficient use by the research community (see Implementing a High Performance, Reusable Consensus Calling Pipeline for Next Generation Sequencing using Genome Generation).