Target enrichment capture methods allow scientists to rapidly interrogate important genomic regions of interest for variant discovery, including SNPs, gene isoforms, and structural variation. Custom targeted sequencing panels are important for characterizing heterogeneous, complex diseases and uncovering the genetic basis of inherited traits with more uniform coverage when compared to PCR-based strategies. With the increasing availability of high-quality reference genomes, customized gene panels are readily designed with high specificity to capture genomic regions of interest, thus enabling scientists to expand their research scope from a single individual to larger cohort studies or population-wide investigations. Coupled with PacBio® long-read sequencing, these technologies can capture 5 kb fragments of genomic DNA (gDNA), which are useful for interrogating intronic, exonic, and regulatory regions, characterizing complex structural variations, distinguishing between gene duplications and pseudogenes, and interpreting variant haplotypes. In addition, SMRT® Sequencing offers the lowest GC-bias and can sequence through repetitive regions. We demonstrate the additional insights possible by using in-depth long read capture sequencing for key immunology, drug metabolizing, and disease causing genes such as HLA, filaggrin, and cancer associated genes.