

## **Integrated Genomics for Rapid Marker Development and Targeted Crop Improvement**

**J. CLEVENGER\***; W. KORANI; C. VALERIO; Z. MYERS. Hudson Alpha Institute for Biotechnology, 601 Genome Way Huntsville, AL 35806

High throughput marker technologies weigh cost, accuracy, precision, scalability, throughput, and reproducibility. The available technologies provide an advantage on some metrics while sacrificing others. For example, capture-based sequencing technologies are highly accurate, cost efficient, high throughput, but lack precision because they are focused on a small number of common markers. Alternatively, whole genome sequencing is highly precise, yet has been cost prohibitive and low throughput. Using a random oligo-based library prep which can multiplex up to 960 samples, we have reduced the cost of whole genome sequencing to levels comparable with array and capture-based genotyping technologies. Combined with the informatics platform, Khufu, highly accurate analysis of low coverage sequencing data maintains throughput. Because whole genome variants are assayed that are population-specific, there is no ascertainment bias that accompanies fixed marker sets. Multiple outcomes are possible after data generation, including diversity analysis, purity assessment, population genotyping, foreground and background marker-assisted selection, and genomic selection. We have bundled the sequencing and analysis into Khufu, an affordable and scalable genotyping and analysis platform. Khufu is currently being used widely across plant and animal species, but was developed specifically for peanut. The informatics are uniquely tuned to deliver genomics to any sized research program.