Abstract

The Arizona Genomics Institute (AGI) has played significant roles in numerous genome projects over the past 15 years, including Asian and African rice and its 20 wild relatives, maize, wheat, *Brachypodium*, barley, date palm, sugarcane, citrus, cacao, soybean and its wild relatives, brassicas, tomato, hemp, tree nuts, etc. AGI’s expertise is not limited to plants, and includes model species like Drosophila (19 genomes), zebra finch, *Biomphalaria*, dingo and nurse shark, as examples. AGI’s philosophy is that the first genome sequence of any species should be as high a quality as possible.

We operate a Pacific Biosciences (Pacbio) Sequel platform for high quality, LONG READ sequencing. We average 35kb read length N50 with more than 10Gb raw data per cell. A critical key to our success lies in our ability to isolate and handle high-quality, high-molecular weight DNA that is vital as sequencing substrates. Our methods have been used to produce high quality substrates for a variety of different applications such as Pacbio, Nanopore, Bionano, Illumina, RNAseq, 10x Genomics, Dovetail, BAC library construction, etc.

This poster presents some of our services and some examples of our completed projects.