The Integrative Genomics Core (IGC) within the Beckman Research Institute at City of Hope is a powerful, shared resource that provides not only high throughput sequencing and microarray analysis of DNA and RNA, but also data analysis and interpretation that can be used in grant and manuscript preparation. Armed with the Illumina Hiseq2500 and the Life Tech’s Ion Proton, the core can sequence more than 109 RNA or DNA molecules in one eleven-day run. For perspective, sequencing the entire human genome originally took multiple institutions over ten years to complete. Now, with state-of-the-art instrumentation, our core can complete a process of this magnitude 30 times in one eleven-day run. IGC also provides microarray services to perform transcriptome, genome and epigenome analysis. Many of these technologies work well with low quality and low quantity samples, particularly archived paraffin embedded tissue samples (FFPE) and serum/plasma samples. These samples are extremely useful for large scale and clinical trial studies but may be challenging to work with because of potential DNA/RNA degradation within the sample. IGC has conducted thorough testing and developed protocols to work consistently well with these samples. The impressive capabilities of our IGC are currently expanding as the newly acquired Fluidigm C1 Single-Cell Autoprep system comes online. The new system enables the capture of single cells by microfluidics. This technique facilitates genomic analysis of individual cells as opposed to an analysis of the average genome over a piece of tissue, which contains a mixture of different cell populations. These powerful techniques, which facilitate testing the entire genome and transcriptome simultaneously, have revolutionized and expedited discovery in basic, translational, and clinical settings.

This revolution has in part been achieved by acquiring large amounts of high quality data quickly. With the IGC’s team of experienced lab scientists and research associates, led by Dr. Jinhui Wang, manager of the IGC, efficient sample handling, library preparation and rigorous quality control steps are routinely implemented to ensure data quality. In this context, perhaps one of the most compelling and unique features of the City of Hope IGC is its outstanding data analysis service. Our core director, Dr. Xiwei Wu, completed his training as an MD in China and then moved to the United States in 1997 to pursue a Ph.D. program in molecular genetics studying the transcriptional co-activator lens epithelium-derived growth factor. He subsequently completed postdoctoral work in bioinformatics and computational biology analyzing microarray data and gene regulation. Dr. Wu’s background and experience in genomics and bioinformatics, in combination with his team of bioinformaticians, leaves the core uniquely poised to perform high-level data interpretation for our researchers who require deep sequencing or transcriptome analysis to advance their area of study. In essence, the IGC at City of Hope can be considered a convenient, one-stop “genomics services shop” for our investigators.

One of the many IGC success stories involves a translational effort with Dr. Huiqing Wu, a professor in the Department of Pathology at City of Hope, to identify very small non-coding RNA molecules, called miRNAs, that are associated with metastasis in clear cell renal cell carcinoma (ccRCC). Metastasis of ccRCC is extremely difficult to predict reliably (there is currently no clinical molecular assay) and is associated with extremely poor prognosis. In this context, the team of investigators used microarray, real time PCR, and whole genome deep sequencing miRNA analysis to compared 78 benign kidney, localized ccRCC, and metastatic ccRCC samples and identified four particular miRNAs (miR-10b, miR-130b, miR-139-5p, and miR-199b-5p) that displayed a unique expression level signature in metastatic samples (Xiwei Wu et al., Plosone, 2012, 5, e35661). This unique miRNA signature was then validated using an independent, 40 patient sample set of different ccRCC stages, and it successfully identified both metastatic patients and patients who may undergo metastasis in the future. Thus, the signature provides the capability to make early predictions that can significantly improve treatment options. Dr. Xiwei Wu, Dr. Huiqing Wu, and the team are currently validating these results with a larger cohort of tissue samples towards moving this potentially transformative technology into clinical practice.