Development of an Integrated Core for NCS Genomics, Gene Expression and Proteomics

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Rigorous operational assessment of nucleic acids and proteins requires state of the art technology and developmental capacities for genetic and epigenetic analysis. Macromolecule isolation, total and micro-RNA expression, DNA methylation, genotyping, and diverse proteomic analyses are all part of Integrated Core offerings. These high throughput services are provided by microarrays, deep sequence and mass spectrometry approaches. This study shows that flexible technology choice, consistent sample handling and quality assurance of genetic, epigenetic, and protein analysis can be robustly supplied by integrating discrete full-service cores. In year 1, the CWRU Integrated NCS Core has established a LIMS system to bring together core studies extending from sample coding to final data mining provided by a dedicated data analysis team. Core development has also included work on the ethics evaluation for all these analyses and FISMA compliant approaches to data /sample storage, acquisition and transmission.

Core Laboratory studies have defined conditions for analytical baselines using readily available, anonymous materials of umbilical cord and cord blood samples from healthy newborns. Development of sample collection methodologies has focused on defining protocols and conditions to obtain optimal quality and quantity of macromolecules for analysis from samples collected under diverse sub-optimal conditions. Initial studies have characterized specific macromolecular phenotypes by differentially analyzing vein and arteries from umbilical cords and Ficoll-purified buffy coat from cord blood. Study design also incorporates developmental methods to define individual differences in methylation-correlated regulation of gene expression, and novel proteomics approaches to defining individual differences in immune cells of the subjects.