**Genomics Core pilot project list 2017 – 2020:**

**Title Researcher Inst. Type Year**

Effects of Early-Life Antipsychotic Drug Administration on RNA expression Bardgett, Mark NKU Rat brain RNA-Seq 2020

32 samples

The effect of the estrus cycle on microbiota composition and the Listeria Pirece, Marcia EKU Mouse fecal microbiome 2020

Monocytogenes infectious process in murine models 16S- RNA-Seq;

45 samples

Transcriptome profiling of pancreatic cancer cells treated with novel Clark, Geoffrey UofL Human RNA-Seq 2020

Ras inhibitors 12 samples

Single Cell Sequencing of Ocular Immune Cells in a Model of Uveitis Pre-and Donninger, Howard UofL Mouse ocular cells 2020

Post-Anti- IL-6 Treatment Sc-RNA-Seq 2 samples

Unveiling transcriptome changes in lymphatic cells from lymph fluid Hao, Hongying UofL Human lymph cells 2020

sc-RNA-Seq 4 samples

Transcriptome profiling of cancer associated fibroblasts Donninger, Howard UofL Human RNA-Seq 2019

9 samples

Differential Expression of Unconventional Targets for Type 1 Shirwan, Haval UofL Mouse RNA-Seq 2019

24 samples

Urine Microbiome of Persons with Pneumo coccal Pneumonia Using NGS - Wolf, Leslie UofL Human urine microbiome; 2019

60 samples

Sex differences in neural effects of prenatal cigarette smoke exposure Corbitt, Cynthia UofL Mouse RNA-Seq 2019

24 samples

Differential Gene Expression in Checkpoint and S-Adenosyl Methionine Strome, Erin NKU Yeast RNA-Seq 2019

Synthetase Mutants 24 samples

Next Generation Sequencing to Reveal Novel Platinum Compound-Induced Smith, Michael WKU Human RNA-Seq 2018

Cancer Cell Death Pathways 27 samples

Transcriptional response to the loss of Shoc2 in zebrafish Galperin, Emilia UK Zebrafish RNA-Seq 2018

12 samples

Differential Regulation of Zn Transporters Associated with Zn Thompson, David NKU Squirrelfish RNA- Seq; 2018

Hyperaccumulation 24 samples

Whole Exome and T-cell Receptor Repertoire Sequencing in Immunotherapy- Yaddanapudi, Kavitha UofL Human Amplicon- Seq; 2018

treated Cancer Patients 12 samples

Identifying Gene Expression Differences in S-Adenosyl Methionine Synthetase Strome, Erin NKU Yeast RNA-Seq 2017

Mutants. 40 samples

Identification of HNRNPA2B1-regulated miRNA targets in breast cancer cells Klinge, Carolyn UofL Human RNA-Seq 2017

12 samples

PSAT1 Mediated Changes in Gene Expression in EGF-Stimulated Clem, Brian UofL Human RNA-Seq 2017

Lung Cancer 18 samples

Transcriptomic Analysis of Macrophages Persistently Infected by Sokoloski, Kevin UofL Human RNA-Seq 2017

Arthrogenic Alphaviruses. 6 samples

Identifying Risks Associated with Antibiotic Resistant Bacteria in Himes, Paul UofL Microbiome DNA- Seq; 2017

Louisville Environments. 10 samples

Transcriptome Analysis of Novel Hepatitis C Vaccines in Human Mester, Joseph NKU Human RNA-Seq 2017

Dendritic Cells 30 samples

Transcriptomic response of nucleated red blood cells to lipopolysaccharide Ashley, Noah WKU Zebrafinch RNA- Seq; 2017

(LPS)challenge in Zebrafinch (Taeniopygia guttata) 12 samples