



UF Center for Pharmacogenomics

Explanation of Services

Services are provided either as a price per sample or price per project, depending on the specific needs of the researcher. Basic “a la carte” services, such as DNA isolation and quantitation, are performed at the price per sample rate listed above. Researchers interested in multiple services will be provided with an estimate of charges for the entire project. As the research project progresses, researchers will be notified of the current total of expenses for their project. DNA isolation, quantitation, and/or plating can be submitted independently or done through the UF Center for Pharmacogenomics (UFCPGx). We strive to accommodate the needs of each researcher; if you do not see a service listed on our menu, please inquire.

UF Center for Pharmacogenomics Services

Price per sample services (includes labor and consumables):	
Receiving and Processing of Blood/Saliva	\$10.00 per sample (blood, includes separation of fractions and tubes) \$3.00 per sample (saliva)
Sample prep and plating (send out for sequencing or genome wide chip)	\$variable depends on the condition of your sample
DNA isolation	\$15.00 per sample (includes quantitation)
DNA quantitation (spectrophotometer)	\$1.00 per sample (minimum 50 samples)
DNA quantitation (PicoGreen)	\$8.00 per sample
PCR reaction	\$8.00 per sample
Restriction enzyme digestion	\$7.00 per sample
Whole Genome Amplification	\$25.00 per sample (~40 ug yield) \$10.00 per sample (~10 ug yield) (price includes quantification)
Price per project services (includes labor and consumables, will provide written estimate of charges):	
Genotyping using TaqMan allelic discrimination (genotyping 1 SNP, 384	*Estimated total price: \$1,200-\$1,400

samples)	
Gene Expression using TaqMan assays (1 gene including control, 384 plate run)	*Estimated total price: \$1,200-\$1,400
miRNA profiling (depends on quality and number of samples and probes, ask for details)	*Estimated total price: \$variable, please inquire
Genotyping by Pyrosequencing (genotyping 1 SNP, 96 samples)	*Estimated total price: \$700-\$900
Methylation by Pyrosequencing (1 gene, per run including bisulfite conversion, 96 samples)	*Estimated total price: \$1,200-\$1,400
Luminex 100/200 xMAP detection (variable number of analytes per run)	*Estimated total price: \$variable, please inquire
Genotyping by QuantStudio™ 12K Flex System with OpenArray™ Block (3072 reactions per run, #of SNPs and samples variable).	*Estimated total price: \$variable, please inquire
Scientific Consultation (pre- and post-project, sample and data consultation)	\$75/hour

*All genotyping projects are **estimated** totals. Investigators will be notified of any price changes prior to work being completed. Price includes all reagents and consumable unless otherwise noted. Genotypes and default settings exported into an excel file as well as Hardy-Weinberg calculations. Price does NOT include any data analysis.

UF Center for Pharmacogenomics Genotyping Platforms

We offer the following platforms at the UF Center for Pharmacogenomics. Our trained staff will help you select the platform that is best suited for your project.

Qiagen Pyromark Q96 Pyrosequencer™



Method of “sequencing in synthesis” that generates short sequence fragments up to 50 bases. Appropriate for SNP, INDEL, and microsatellite genotyping. The instrument can also be used for quantification of individual or multiple CpG sites in different genes. The instrument has medium through-put; 96 samples can be run at one time. Genotyping by the pyrosequencing method requires an initial assay design step that uses pyrosequencing software to design three compatible PCR and sequencing primers and to determine the quality of the assay. Standard and biotinylated oligonucleotides are then ordered for subsequent PCR and sequencing steps. For methylation analysis, we can provide all steps in the process including bisulfite conversion of DNA samples.

Applied Biosystems 7900 HT™



Method of genotyping that uses dye labeled probes to discriminate genotypes. Also used for gene expression and other real-time assays. Medium-high through-put; 384 samples can be run at one time. Genotyping by the TaqMan method requires the selection of appropriate probes to assay the SNP of interest. Many SNP assays are readily available from ABI (now Life Sciences) and are considered “pre-designed”. Assays that are not readily available can be designed using ABI software. These assays are highly successful but require additional design and optimization time. Both pre-designed and custom assays are then ordered from ABI.

QuantStudio™ 12K Flex System with OpenArray™ Block



The QuantStudio™ 12K Flex system is a highly flexible, comprehensive **real-time** PCR platform. The QuantStudio™ 12K Flex Real-Time PCR System includes easy-to-change blocks that can accommodate OpenArray® plates, TaqMan® array cards, 384-well, 96-well, and FAST 96-well plates allowing you to select the format that is right for your project. OpenArray plates are used for performing 3072 genotyping reactions simultaneously. These plates are customizable and ideal for researchers who have a large number of samples and SNPs of interest. The DNA requirements for OpenArray per sample is 20 ul of 50 ng/ul, all other applications require 20 ul of 20ng/ul.

Luminex 100/200™



The Luminex 100/200 System is a flexible analyzer based on the principles of flow cytometry. The system enables you to multiplex (simultaneously measure) up to 100 analytes in a single microplate well, using very small sample volumes. The system delivers fast and cost-effective bioassay results on many assay formats including nucleic acid assays, receptor-ligand assays, immunoassays and enzymatic assays. Used with a variety of RUO kits including the xTAG® CYP2D6 Kit which features genotyping and copy number variants of important CYP2D6 variants.

Submission requirements

DNA

DNA can be isolated at UFCPgx from buccal cells, blood, or tissue. Please provide samples that are clearly labeled, accompanied with a spreadsheet inventory of the samples. If DNA has already been isolated and plated, please provide the DNA samples in 96-well plates. We reserve the last two wells of the 96-well plate (positions H11 and H12) for the controls, so please leave those two wells empty. The plate(s) needs to be clearly labeled. Please provide a chart that shows the locations of all the samples along with their IDs. If samples have not been quantitated and normalized, we will do so using either the Quant-IT PicoGreen method of quantitation (see explanation of services) or standard UV absorbance. If DNA has already been quantitated, please normalize the DNA samples to ~20ng/ul if using the pyrosequencing or TaqMan methods. QuantStudio OpenArray genotyping requires a minimum of 50ng/ul. If submitting for send-out sequencing or a genome wide chip study, we will work with you and the core facility to make sure submission requirements are met. Any remaining DNA will be returned after the genotyping is completed.

Copy of informed consent and approval letter

To ensure that all genetic analyses we conduct are done under appropriate informed consent processes, we require a copy of the approval letter and a blank consent form under which the samples were collected. This document must be in place in our laboratory before we will proceed with any genotyping.

Turnaround time

We will work closely with you to provide insight into the turnaround time and expense you should expect. This will be influenced by the number of SNPs genotyped, number of samples for genotyping, and whether or not the SNP assays are validated in house. Additionally, backlog in the laboratory may influence turnaround time. SNPs for which an assay needs to be developed will take longer, but assays can typically be developed in a matter of weeks, with samples processed quickly thereafter.

Transmission of Results

The genotyping data will be sent to you electronically in excel spreadsheets or other appropriate format. Genotypes and default settings will be exported into an excel file as well as Hardy-Weinberg calculations.

For more information about UF Center for Pharmacogenomics services please contact:

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