UF Center for Pharmacogenomics Genotyping Platforms

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

Pyrosequencing (PSQ HS 96A System)

Method of "sequencing in synthesis" generates short sequence fragments up to 50 bases. Appropriate for SNP, INDEL, and microsatellite genotyping. Medium through-put, 96 samples are can be run at one time.

TaqMan (TaqMan 7900 HT)

Method of genotyping that uses dye labeled probes to discriminate genotypes. Appropriate only for SNPs. Medium-high through-put, 384 samples can be run at one time.

Illumina BeadXpress Reader

Method of genotyping that uses VeraCode technology and Golden Gate assays for multiplex reactions. Appropriate only for SNPs. High through-put, 96 samples and up to 384 SNPs can be run at one time.

UF Center for Pharmacogenomics Services

Service	Price	Unit
DNA isolation, quantitation, plating, and archiving	$15.00	1 sample
DNA quantitation and plating	$5.00	1 sample
Genotyping by Pyrosequencing Method		
Genotyping < 200 samples	$3.50	1 genotype
Genotyping > 200 samples	$3.00	1 genotype
Pyrosequencing Genotyping Assay Design fee	$500.00	1 assay
Genotyping by TaqMan Method		
Genotyping < 200 samples	$3.50	1 genotype
Genotyping 200-500 samples	$3.00	1 genotype
Genotyping > 500 samples	$2.50	1 genotype
TaqMan® Pre-Designed SNP Genotyping Assays	$263.50	1 probe
Custom TaqMan® SNP Genotyping Assays	$263.50	1 probe
TaqMan probe order and design fee	$200.00	1 probe
Genotyping by Illumina VeraCode Method		
DNA quantitation and plating	$5.00	1 sample
Illumina genotyping	$7.00	1 sample
Illumina supplied OPA and reagents (480 samples)	$12.48 $0.26	1 sample 1 genotype
Illumina supplied OPA and reagents (960 samples)	$10.50 $0.24	1 sample 1 genotype
Illumina supplied OPA and reagents (≥ 1440 samples)	$8.64 $0.22	1 sample 1 genotype
OPA design fee*	$250.00-$1000.00	1 OPA
*** optional service**		

Explanation of Services

All DNA samples must be quantitated and plated prior to genotyping. DNA isolation, quantitation, plating and archiving can be done independently or through the UF Center for Pharmacogenomics (UFCPgx). Our quantitation method uses Quant-iT™ PicoGreen® reagent, a highly sensitive fluorescent nucleic acid stain for quantitating double-stranded DNA.

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. All of these services are included in the Pyrosequencing assay design fee. The reagents, equipment, and labor comprise the price per genotype.

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". These assays do not require the TaqMan assay set-up and probe design fees. 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. The reagents, equipment, and labor comprise the price per genotype.

Genotyping by the Illumina VeraCode method requires the design of an oligonucleotides pool assay (OPA). Illumina genotyping is the most expensive genotyping in total price but is the least expensive in price per genotype. This is the only assay that multiplexes up to 96 SNPs per run. Since this assay multiplexes 96 SNPs in the same reaction there is great deal of effort involved in the OPA design process. SNPs of interest are selected and then submitted to Illumina for compatibility. Those SNPs that fail the compatibility test are then replaced by either tag SNPs or entirely different SNPs. The trial and error process is different for each OPA design and is reflected in the range of OPA design fees. Once the OPA has been designed the Illumina supplied reagents and OPA are purchased. All samples must be plated and quantitated by the UF Center for Pharmacogenomics prior to genotyping. This requirement is due to the increased DNA requirements (minimum of 50ng/ul) and the sensitivity of the instrument to variations in DNA quantity. The reagents, equipment, and labor comprise the price per genotype.

Submission requirements

DNA

DNA can be isolated at UFCPgx from buccal cells, blood, and tissue. Please provide samples in cryovials or 1.5 mL tubes that are clearly labeled accompanied with a spreadsheet inventory of the samples. If DNA has already been isolated 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 the Quant-IT PicoGreen method of quantitation (see explanation of services). If DNA has already been quantitated, please normalize the DNA samples to ~20ng/ul if using the pyrosequencing or TaqMan methods. Illumina genotyping requires a minimum of 50ng/ul. Up to 50 to 100ng of genomic DNA may be used for each PCR reaction. Send at least 50 to 75 ul of each sample to facilitate the use of our liquid handling robots. Any remaining DNA will be returned after the genotyping is completed.

Copy of informed consent

To insure that all genetic analyses we conduct are done under appropriate informed consent processes, we will need a copy of the 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 you should expect. This will be influenced by the number of SNPs you need to be genotyped, the 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. Those SNPs for which we need to develop an assay 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.

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

Taimour Y. Langaee, MSPH, Ph.D.
Research Associate Professor
Dept. of Pharmacy Practice and Pharmaceutics
Director, UF Center for Pharmacogenomics
Genotyping Core Laboratory
Tel: (352)273-6357
langaee@cop.ufl.edu