



Microarray Core  
Genome Sequencing Center  
4444 Forest Park Parkway  
St. Louis, MO 63108  
314-286-1452  
csawyer@watson.wustl.edu  
mheinz@watson.wustl.edu

## **Instructions for DNA submission for Golden Gate Genotyping**

The Genome Sequencing Center Microarray Core will provide you with the following:

- Enough bar-coded stickers to label all your sample plates.
- A Microsoft Excel Spread sheet to enter barcodes that are on your PCR sample plates.

Dissolve your samples in TE or water. TE is recommended for best storage, but is not required. DNA concentration must be  $>50\text{ng}/\mu\text{L}$ . Concentration can be as high as  $250\text{ng}/\mu\text{L}$ ; however we cannot guarantee results with lower concentrations. The total volume should be at least 10ul per OPA used. For example, if 2 separate sets of SNPs are being interrogated using 2 OPA's, we would need 20ul of the sample. Any remaining material can be returned if the submitter requests it. Please quantify your samples. We recommend using PicoGreen DNA Quantification. We will not re-quantify your DNA. You are responsible for providing DNA at the appropriate concentration.

2. Please transfer the DNAs into a bar-coded PCR plate. We reference your study DNAs by the plate number and well position. This allows for an interface with our robotic processes and retains sample anonymity. For human studies please leave wells A01, B01, C01, and D01 empty. These slots will be used for our laboratory controls.

3. Please seal and freeze the DNA plates with foil tape. It is the investigator's responsibility to make certain the plates are sealed properly to avoid evaporation.

4. Please prepare DNA manifest and send the completed file electronically to Chris Sawyer (csawyer@watson.wustl.edu). It is very important to fill out that manifest completely and accurately. We cannot accept DNA from you until we have received and approved your manifest.

5. If sending human RNA from patient, you must include a copy of the IRB.