



## Summary of the MAQC August-25-2005 Teleconference

### The MAQC Project: Calibrated RNA Samples, Reference Datasets, and QC Metrics/Thresholds for Microarray Quality Control

Teleconference Date: August 25, 2005 (9 am PDT/11 am CDT/12 pm EDT/16:00 GMT)

Summary Date: August 29, 2005

Author: Leming Shi, FDA/NCTR, +1-870-543-7387, [Leming.Shi@fda.hhs.gov](mailto:Leming.Shi@fda.hhs.gov)

MAQC URL: <http://edkb.fda.gov/MAQC/>

The Main Study Guidance Document and manufacturers' SOPs can be viewed at <http://www.fda.gov/nctr/science/centers/toxicoinformatics/maqc/studyguidance-sops.html>.

- 1. Shipment of RNA Samples:** The four RNA samples have been shipped to 25 of the 28 test sites from Ambion on Monday (Aug-22-2005) and Wednesday (Aug-24-2005) based on the time that confirmation of test site's acceptance to the MAQC Main Study Guidance Document was received. To ensure timely delivery, samples for Eppendorf (Belgium, EPP\_1) will be shipped on Monday (Aug-29-2005). Samples to FDA/CBER (NCI\_3) will also be shipped when the receiver returns from abroad. Participation of Stanford University (CMB\_3) as the third test site for the Combimatrix platform is still under legal review by the HHMI. If this review process does not go through very soon, Combimatrix will need to use an alternative test site.
- 2. Independent Replicates:** The five replicates for each RNA sample should be replicated totally independently from the start to the end just as if they were different samples. No pooling-splitting should be involved. The PI of each test site should make sure that the person who is actually performing the task in the laboratory understands this policy.
- 3. Guidance Document and SOPs:** Test sites were urged to follow the Main Study Guidance Document and the manufacturer's SOP in performing quality assessment of total RNA and targets, naming files, and submitting all types of files. The dataset from each test site should be directly sent to FDA/NCTR and should not be shared between the test sites of the same platform until the data distribution phase.
- 4. Selection of Genes for TaqMan Validation:** The strategy for gene selection was sent to the MAQC group on Aug-23-2005 and extensively discussed during the TC and in e-mail exchanges. It appeared that some of the concerns (*e.g.*, probes targeting negative strand or locating too far away from the 3'-end) raised by Rich Shippy (GEH) were resulting from the use of an earlier version of GEH's array annotation file from which the initial list of 9,442 (9K) common RefSeq's was derived. To avoid any further confusion and/or concerns, it was requested (Aug-27-2005) that each array provider sends its current array annotation file for its product being used in the main study to the MAQC and confirms that the same annotation information is available to its customers as of Aug-25-2005. Based on the new annotation files from AFX, AGL, ABI, CMB, GEH, ILM, and NCI (*i.e.*, according to what the customers are being told by the manufacturers via the annotation files), an updated list of common RefSeq's that each manufacturer is trying to detect will be created. This list

will be used as the basis to select ~1,000 RefSeqs for TaqMan validation and will serve as the starting point for cross-platform comparison. **The deadline for submitting updated array annotation file is 6:00 pm PDT, Tuesday, Aug-30-2005.** In order to select the TaqMan gene list as unbiased as possible, probe distance to the 3'-end and probe sequence proximity among platforms will NOT be considered as selection criteria, but the impact of such factors will be investigated during data analysis. In addition, as agreed upon by ABI, Genospectra and Stratagene, the "trouble-shooting" of a subset of ~20 discordant genes will be conducted after the main study datasets have been collected and consensus is reached on the selection of such discordant genes.

5. **StaRT-PCR from Gene Express Inc.:** On Aug-25-2005 (after the TC), a representative from Gene Express Inc. contacted Leming Shi and expressed interest in participating in the MAQC study by providing StaRT-PCR data on the four MAQC samples for ~200 genes. This request will be discussed during the next MAQC teleconference.

**The next MAQC Teleconference:**

Thursday, September 8, 2005 (9 am PDT / 11 am CDT / 12 pm EDT / 16:00 GMT)

USA Toll Free Number: **888-566-5020**

International caller: +1-210-795-9594

PASSCODE: **79451**