



Summary of the MAQC June-16-2005 Teleconference

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

Meeting Date: June 16, 2005 (9 am PDT / 11 am CDT / 12 pm EDT / 16:00 GMT)

Meeting Place: Teleconference

Summary Date: June 20, 2005

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1. **Brain RNA:** Mike Wilson updated the group on the manufacturing of the brain RNA sample. The availability date has been pushed back to the end of July.
2. **Pilot Titration Study:** Rich Shippy and others briefed the group on progress to date. Affymetrix and Illumina have completed the microarray work on the titration study and are in the process of data analysis. GEHealthcare, Agilent, and Combimatrix have the study in-progress and expect to complete it soon. Analysis is estimated to take 1-2 weeks. Ten RefSeq sets from for the Brain and Stratagene UHRR were selected, based upon the MAQC pilot project, for qRT-PCR and Genospectra analysis. The 10 RefSeqs were initially selected by Jim Collins based on the Agilent pilot datasets and then ranked by other participants in the MAQC pilot study. Individual rankings were averaged and the selections will be confirmed by the participants in the Pilot Titration Study in the next few days. The RefSeqs were chosen based on their highly differentiated expression pattern between the 2 samples.
3. **Sequence-based Mapping Across Platforms:** Zoltan Szallasi and Scott Pine updated the group on progress. All microarray providers, except for ABI, indicated probe sequences would be made available to the MAQC. Lu Zhang said ABI would provide 120-base sequences that would include the probe. Zoltan gave a brief summary of his results that suggest a problem with about 10% of the probes if the 120-base sequence is used instead of the exact probe. This has to do with sequences that span the coding and 3' UTR. Lu said she would check with her management to find out if the exact sequences could be provided. Follow-up after the meeting resulted in ABI's willingness to provide the exact sequences under a non-disclosure agreement. Agilent has agreed in principle to releasing the probe sequence data and Jim Collins will confirm with upper management. With the exception of ABI and Agilent, probe sequences from all providers have been obtained, including Affymetrix, GEHealthcare, Illumina, and Combimatrix. Eppendorf Array Technologies will also participate in the MAQC main study and will provide exact probe sequences.
4. **Selection of Test Sites:** Each platform provider has agreed to select 3 sites for evaluation of the 2 sample RNAs in the MAQC Main Study. The sites should be

chosen for their known ability to produce high quality data. These reference datasets will be important in development of QC metrics/thresholds for microarray quality control as well as for evaluation of data analysis methods. Test sites should be selected soon and it was agreed that they would be invited to participate in the MAQC. Platform providers will also develop detailed recommended protocols that will be followed by all test sites for a given platform. These protocols can be posted at the new MAQC web site as described below.

5. **MAQC Web Site:** The MAQC website is set up and can be found at <http://www.fda.gov/nctr/science/centers/toxicoinformatics/maqc/index.htm>. The minutes, news and presentations about this project will be available from the website. Weida Tong indicated that presentation slides will also be available from the website (although presenters can choose not to have them posted). Janet Warrington suggested that the experimental protocols used in the main study should be also included in the website and the suggestion was approved.

The next MAQC Teleconference:

Thursday, June 30, 2005 (9 am PDT / 11 am CDT / 12 pm EDT / 16:00 GMT),
Jim Fuscoe (FDA/NCTR) will be moderating the discussions.