The Third

MicroArray Quality Control

Project Meeting

December 1-2, 2005

Palo Alto, California

http://edkb.fda.gov/MAQC/

Co-sponsored by:

Contents of the Meeting Handout:

1. Meeting Agenda
2. Introduction to the MAQC Project
    - Overview
    - Implementation and progress
    - Participating organizations
    - Publication plan
    - Timeline
3. List of Registered Meeting Participants

Notes:

1. The results to be presented at the MAQC project meeting should be considered preliminary and do not necessarily represent the final conclusions of the MAQC project.
2. The main objectives of the MAQC project meeting are:
    - To allow participants an opportunity to review the datasets, exchange ideas about data analysis and QC metrics/thresholds based on the preliminary analysis results;
    - To decide on the next phase of the MAQC project (rat or mouse);
    - To discuss the proposed publication plan and to decide additional analyses that need to be performed for each manuscript.
3. The entire MAQC project meeting (including discussion sessions) will be recorded.
4. Information presented at the MAQC meeting should be considered confidential and should not be distributed beyond participants of the MAQC meeting.

The MAQC Project Meeting Agenda

December 1-2, 2005, Cyprus Room, Crowne Plaza Cabana, Palo Alto, CA

Day One: Thursday, December 1, 2005 Chair: Yvonne Dragan (FDA/NCTR)		
8:00 am	Chair's remarks	Yvonne Dragan
8:05 am	Welcome	Ronald Davis (Stanford)
8:10 am	Overview of the MAQC project	Leming Shi (FDA/NCTR)
8:20 am	MAQC reference RNA samples	James Fuscoe (FDA/NCTR)
Seven Microarray Platforms*		Co-chairs: Mike Wilson (Ambion)/Federico Goodsaid (CDER)
8:30 am	Inter-site reproducibility	Xu Guo (Affymetrix)
8:45 am	Cross-site performance of one- and two-color platforms	Jim Collins (Agilent)
9:00 am	ABI expression array data comparison	Yongming Sun (Applied Biosystems)
9:15 am	DualChip platform: concept	Francoise de Longueville (Eppendorf)
9:30 am	GEH:	Richard Shippy (GE Healthcare)
9:45 am	Performance metrics for cross-platform studies	Eugene Chudin (Illumina)
10:00 am	Analysis of NCI home brew 70mer arrays	Ernest Kawasaki (NCI)
10:15 am	**Break**	
Three Alternative Technology Platforms*		Co-chairs: Federico Goodsaid/Mike Wilson
10:30 am	TaqMan® gene expression assays for microarray validation	Kathy Lee (Applied Biosystems)
10:45 am	Cross-platform comparison based on 245 genes	Yuling Luo (Genospectra)
11:00 am	Numerical calibration of 205 genes	James Willey (Gene Express)
11:15 am **Discussion** (10 platform providers)	1. Quality of data from your test sites 2. Lessons learned: challenges & pitfalls 3. Cost ($ & time) and value to your org. 4. Suggestions for the MAQC project 5. Comments from external test sites	**Panel**: Shawn Baker, Jim Collins, Francoise de Longueville, Xu Guo, Ernest Kawasaki, Kathy Lee, Yuling Luo, Richard Shippy, Yongming Sun, James Willey
12:00 pm	**Lunch** (on your own)	
Ten Data Analysis Sites (I)*		Co-chairs: Roderick Jensen (UMB)/Marc Salit (NIST)
1:15 pm	Intra-platform, inter-laboratory variation	Walter Liggett (NIST)
1:30 pm	Correlation estimation from a random effects model	Sheng Zhong (UIUC)
1:45 pm	Assessing consistency of the MAQC platforms	Wenjun Bao/Tzu-Ming Chu (SAS)
2:00 pm	Repeatability, reproducibility, and inter-platform consistency	Wendell Jones (Expr. Analysis)
2:15 pm	Integrating the MAQC project into clinical diagnostic applications: Lessons from the clinical laboratories	Hanlee Ji (Stanford)
2:30 pm	QRI image analysis of Affymetrix GeneChip .DAT files	Cecilie Boysen (ViaLogy)
2:45 pm	An extensive survey of analysis methods	*Lisa Croner (Biogen Idec)*
3:00 pm	QC metrics/thresholds & analysis methods	Leming Shi/Weida Tong (FDA/NCTR)
3:15 pm	**Break**	
Ten Data Analysis Sites (II)*		Co-chairs: Marc Salit/Roderick Jensen/
3:30 pm	Cross-platform probe mapping and quality metrics for the 1000 chosen genes	Roderick Jensen (UMB)
3:45 pm	Mapping probes to RefSeq transcripts	Damir Herman (NCBI)
4:00 pm	Probe design and alternative splicing on data consistency	*Jean Thierry-Mieg (NCBI)*
4:15 pm **Discussion** (10 analysis sites)	1. Probe-target mapping & master indices 2. Performance metrics and thresholds 3. Normalization & gene selection methods 4. Flagged spots and outlier arrays 5. Future directions of data analysis 6. Biogen Idec's request for data access	**Panel**: Wenjun Bao, Cecilie Boysen, Lisa Croner, Damir Herman, Walter Liggett, Roderick Jensen, Hanlee Ji, Wendel Jones, Jean Thierry-Mieg, Weida Tong, Chunlin Xiao, Sheng Zhong
5:00 pm	Adjourn	

*Each speaker has 10 minutes for presentation and 5 minutes for questions/discussion.

Day Two: Friday, December 2, 2005 Chair: William Slikker, Jr. (FDA/NCTR)		
8:00 am	Chair's remarks	William Slikker, Jr.
8:10 am	**Keynote address**: Data quality in genomics	Ronald Davis
Invited Presentations	Chair: William Slikker, Jr.	
8:50 am	ERCC: The External RNA Controls Consortium	Janet Warrington (Affymetrix)
9:00 am	The Metrology for Gene Expression Program	Marc Salit (NIST)
9:10 am	Array standardization and the MfB Programme	Carole Foy (LGC, UK)
9:20 am	Rat reference RNAs for proficiency testing	Karol Thompson (FDA/CDER)
9:30 am	Study design and analysis of multiple platforms (mouse)	Winston Kuo (Harvard)
9:40 am	Proficiency testing using MTRRM and MAQC samples	Laura Reid (Expr. Analysis)
9:50 am	10th Anniversary of *Science* 95' paper	Mark Schena (TeleChem ArrayIt)
10:00 am	MAQC rat mini pilot project: preliminary data	Hongzhu Ren (EPA)
10:05 am	Preliminary results using rat RNA samples	James Fuscoe (FDA)
10:10 am	**MAQC for rat and/or mouse?** 1. Survey of interest: platform providers, test sites 2. RNA samples 3. Experimental design 4. Timeline	Federico Goodsaid
10:30 am	**Break**	
Regulatory Perspectives:	Co-chairs: Yvonne Dragan/Federico Goodsaid	
10:45 am	Hybridization standards for regulatory review	Federico Goodsaid
10:55 am	1. Expected uses of the MAQC datasets 2. Proficiency tests 3. External spike-in controls 4. Remaining challenges (prior to RNA) 5. Guidance on QC and data analysis	**Panel**: Yvonne Dragan, Federico Goodsaid, Francis Kalush, Scott Pine, Hongzhu Ren, Weida Tong
Planning for MAQC Manuscripts	Chair: Leming Shi	
11:30 am	1. Editorial 2. FDA's VGDS and IPRG 3. MAQC main manuscript 4. Reference RNA samples 5. Sequence-based cross-platform mapping 6. Normalization & gene selection methods 7. Validation by alternative technologies 8. Titration datasets 9. Inter-laboratory variations 10. Cross-hybridization 11. One-color versus two-color platforms 12. Informatics tools for regulatory review *13. Other topics to be suggested* Manuscript-drafting teams Timeline Journal	Janet Woodcock/Dan Casciano Felix Frueh/Federico/Sponsors Leming Shi (MAQC Team) James Fuscoe/Mike Wilson Damir Herman/Roderick Jensen Leming Shi/Jim Chen Federico Goodsaid Richard Shippy Walter Liggett/Marc Salit Zoltan Szallasi/Roderick Jensen Tucker Patterson/Jim Collins Weida Tong *Participants*
12:55 pm	Concluding remarks	Leming Shi
1:00 pm	Adjourn	
The Cyprus conference room will be available until 4:00 pm for participants to continue discussion.		

Location:
The meeting will be held on December 1-2, 2005 at the **Cyprus Room**, Crowne Plaza Cabana, 4290 El Camino Real, Palo Alto, CA 94306. Telephone: 650-857-0787; FAX: 650-496-1939; Website: http://www.cppaloalto.crowneplaza.com/. Please note the change of meeting venue.

Registration:
Registration is free but required. Contact Leming Shi, National Center for Toxicological Research, US FDA, 3900 NCTR Road, Jefferson, AR 72079. Tel: 870-543-7387; leming.shi@fda.hhs.gov.

Conference Call:
A conference call has been set up to allow interested people to join the meeting by telephone throughout the entire MAQC meeting. **Dial-in number: 888-566-5020** (international: +1-210-795-9594), **Passcode: 33297**. In fairness to the expected large audience in the Palo Alto conference room, callers are asked to minimize the number and length of their questions/comments because the audio quality may be less than satisfactory. However, callers are encouraged to send their questions/comments by e-mailing weida.tong@fda.hhs.gov and leming.shi@fda.hhs.gov. We reserve the right to disconnect the conference call if the audience in the Palo Alto conference room decides that there is too much disruption by the calls. Thanks in advance for your understanding.

MAQC:
http://edkb.fda.gov/MAQC/ or
http://www.fda.gov/nctr/science/centers/toxicoinformatics/maqc/.

ArrayTrack:
http://www.fda.gov/nctr/science/centers/toxicoinformatics/ArrayTrack/

Genomics @FDA:
http://www.fda.gov/cder/genomics/

Stanford Genome Technology Center (SGTC):
http://med.stanford.edu/sgtc/

ERRC (The External RNA Controls Consortium):
http://www.cstl.nist.gov/biotech/ERCC/testplan.htm

NIST's Metrology for Gene Expression Program:
http://www.cstl.nist.gov/biotech/Cell&TissueMeasurements/GeneExpression.htm

Co-sponsors: The MAQC (MicroArray Quality Control) project meeting is co-sponsored by the US Food and Drug Administration and Stanford Genome Technology Center of Stanford University.

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

FDA's Critical Path Initiative (http://www.fda.gov/oc/initiatives/criticalpath/) identifies pharmacogenomics as a key opportunity in advancing medical product development and personalized medicine. FDA issued the "*Guidance for Industry: Pharmacogenomic Data Submissions*" (http://www.fda.gov/cder/guidance/6400fnl.pdf) to facilitate scientific progress in the field of pharmacogenomics and to facilitate the use of pharmacogenomic data in drug development and medical diagnostics. Microarrays represent a core technology in pharmacogenomics; however, before this technology can successfully and reliably be applied in clinical practice and regulatory decision-making, standards and quality measures need to be developed.

The MicroArray Quality Control (MAQC) project involves six FDA Centers, major providers of microarray platforms and RNA samples, government agencies, academic laboratories, and other stakeholders. The MAQC project (Figure 1) aims to evaluate QC metrics and thresholds for objectively assessing the performance achievable by various microarray platforms and evaluating the advantages and disadvantages of various data analysis methods. Two RNA samples will be selected for three species (*i.e.*, human, rat, and mouse), and differential gene expression levels between the two samples will be calibrated with microarrays and other technologies (*e.g.*, QRT-PCR). The resulting microarray datasets will be used for assessing the precision and cross-platform/laboratory comparability of microarrays, and the QRT-PCR datasets will enable evaluation of the nature and magnitude of any systematic biases that may exist between microarrays and QRT-PCR. The availability of the calibrated RNA samples and the resulting microarray and QRT-PCR datasets, which will be made readily accessible to the microarray community, will allow individual laboratories to more easily identify and correct procedural failures. The implementation and progress of the MAQC project is shown in Figure 2. The MAQC project will help improve the microarray technology and foster its proper applications in discovery, development and review of FDA regulated products.

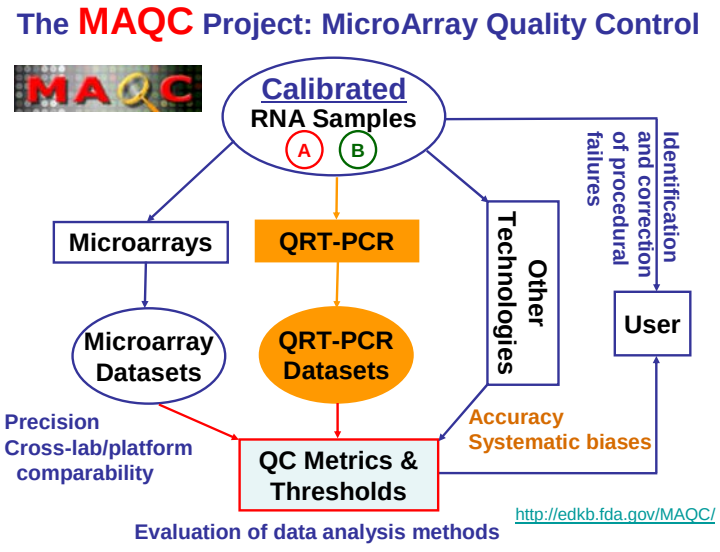

Figure 1: An overview of the MAQC project.

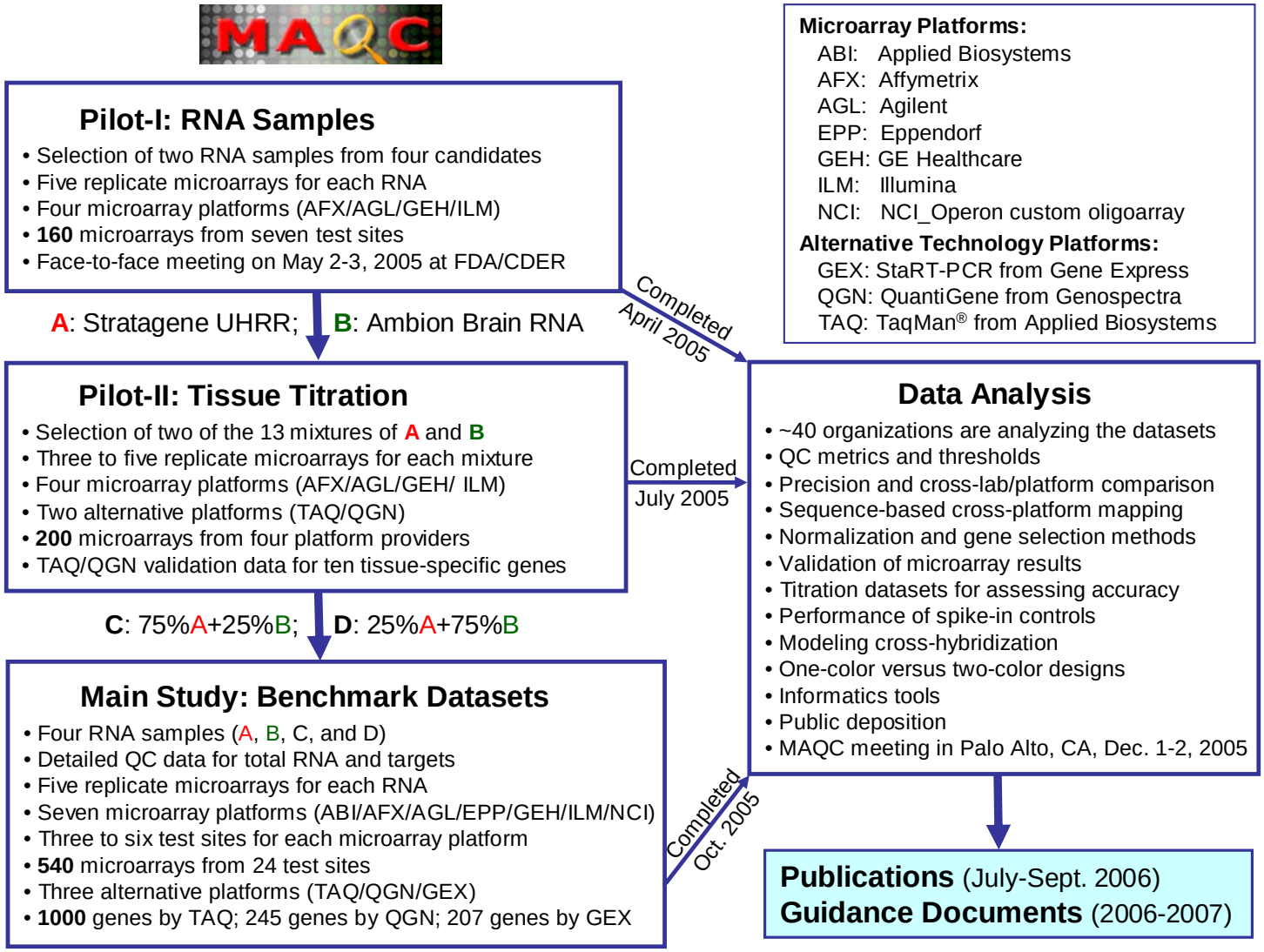

Figure 2: The implementation and progress of the MAQC project.

MAQC Participating Organizations

Government Agencies (4):
FDA (six Centers)
EPA
NIH (NCBI and NCI)
NIST

Platform Providers (10):
Affymetrix (AFX)
Agilent (AGL)
Applied Biosystems (ABI)
Eppendorf (EPP)
GE Healthcare (GEH)
Illumina (ILM)
National Cancer Institute (NCI)
Applied Biosystems' TaqMan (TAQ)
Gene Express' StaRT-PCR (GEX)
Genospectra's QuantiGene (QGN)

RNA Sample Providers (3):
Ambion
Clontech
Stratagene

http://edkb.fda.gov/MAQC/

Test Sites (27):
ABI_1: Applied Biosystems
ABI_2: EPA
ABI_3: Vanderbilt University
AFX_1: Affymetrix
AFX_2: FDA/CDER
AFX_3: Ambion
AFX_4: EPA
AFX_5: Novartis
AFX_6: UCLA/Cedars-Sinai
AGL_1: Agilent
AGL_2: FDA/NCTR
AGL_3: Icoria
EPP_1: Eppendorf
EPP_2: MD Anderson
EPP_3: CSHL
GEH_1: GE Healthcare
GEH_2: UMass Boston
GEH_3: GenUs BioSystems
ILM_1: Illumina
ILM_2: UTSW
ILM_3: Burnham Institute
NCI_1: NIH/NCI
NCI_2: FDA/NCTR
NCI_3: FDA/CBER
TAQ_1: Applied Biosystems
QGN_1: Genospectra
GEX_1: Gene Express

Data Analysis Sites (10):
Expression Analysis
FDA/NCTR
Harvard University
NIH/NCBI
NIST
SAS
Stanford University
UIUC
UMass Boston
ViaLogy
(More organizations are requesting to be included as an analysis site.)

MAQC "Observers":
Over 200 people from >70 organizations

ERCC

Thank you!

Figure 3: Participants in the MAQC project.

Table 1. An outline of manuscripts proposed as a special journal issue on Microarray Quality Control (draft; for discussion only)

No.	Tentative Title	Contents	Manuscript Team
1	Pharmacogenomics and the US FDA's Critical Path Initiative to Medical Product Development: Technology-driven Innovations	• Editorial to this Special Issue on microarray quality control; • The importance of pharmacogenomics in medical product development and personalized medicine (as stated in the FDA's Critical Path Initiative); • The reliability of technologies is essential to realize the promises of pharmacogenomics.	**Janet Woodcock** (Deputy Commissioner, FDA) Dan Casciano (Director, FDA/NCTR)
2	Implementation of the FDA's Voluntary Genomic Data Submissions (VGDS) Mechanism: Guidelines on microarray quality control and data analysis are essential	• Implementation of the VGDS mechanism at the FDA for sponsors to voluntarily submit genomic data (including data management, analysis, visualization, and interpretation; training of FDA reviewers; interactions between FDA and sponsors); • Lessens learned from several VGDS case studies; • Illustration of the challenges in the regulatory review of pharmacogenomic data: quality control of microarray experiments and guidance on data analysis.	**Felix Frueh** Federico Goodsaid Weida Tong Sponsors
3	The MAQC Project: Establishing Calibrated RNA Samples, Reference Datasets, and QC Metrics/Threshold for MicroArray Quality Control ("MAQC Main Manuscript")	• Overview of the MAQC project: Pilot-I; Pilot-II; Main Study (~1000 arrays); • Uniqueness and deliverables of the MAQC project; • Quality control metrics and thresholds for assessing the performance of each platform; • Microarray cross-platform comparability; • Concordance with alternative technologies (TaqMan, QuantiGene, and StaRT-PCR); • Correlation of step-by-step QC data with overall quality of microarray data; • Relative accuracy based on titration datasets; • Next steps for the MAQC project: mouse and rat; beyond total RNA.	**Leming Shi** Mike Wilson Uwe Scherf Laura Reid
4	Establishing Well-calibrated Reference RNA Samples as an Efficient Quality Control Tool for Quantitative Gene Expression Profiling	• MAQC Pilot-I: Selection of two RNA samples as the reference materials using six objective criteria (based on data from 160 arrays on four microarray platforms): (A) Stratagene Universal Human Reference RNA and (B) Ambion Human Brain Reference RNA were selected; • Characteristics of the two RNAs: quality, purity, stability, availability, and reproducibility; • Characterization by microarray gene expression profiling; • Protocols on the applications of the reference RNA samples.	**Jim Fuscoe** Mike Wilson Gavin Fischer
5	Probe Sequence Based Mapping across Microarray Platforms: "Are they measuring the same things?"	• Mapping probe sequences of each platform to the 9/26/2005 release of RefSeq database; • Statistics on the probe-target mapping; • Handling different mapping scenarios: (A) one probe – one target; (B) multiple probes – one target; (C) one probe – multiple targets; and (D) multiple probes – multiple targets; • Relationship between proximity of probes from different platforms and cross-platform consistency; • Web access to probe sequences and cross-platform mapping indices.	**Damir Herman** Rick Jensen Scott Pine Zoltan Szallasi
6	Impact of Normalization and Gene Selection Methods on Microarray Studies	• Normalization methods: raw; total (mean) intensity; median intensity; quantile; Affymetrix specific – MAS5, dCHIP, RMA, PLIER, and their variants; • Gene selection methods: fold change, *p*-value, fold change + *p*-value, SAM, FDR, Others; • Impact of the different combinations of normalization and gene selection methods on the stability of the "significant gene list" from the same platform; • Impact on microarray cross-platform comparability; • Identification of a reliable/stable "significant gene list"; • Impact of different ways of handling background and offset values.	**Leming Shi** Xu Guo Wenjun Bao Rick Jensen *Lisa Croner* *Rafael Irizarry* Jim Chen
7	Validation of Microarray	• Unbiased selection of 1000 genes for TaqMan validation;	**Federico Goodsaid**

	Results with Alternative Technologies	• Unbiased selection of 200 genes for QuantiGene and StaRT-PCR validation; • Consistency across technology platforms; • Identification of the most discordant genes across platforms; • Design of new assays for explaining the discrepancies.	Kathy Lee Yuling Luo Jim Willey
8	The Use of Titration Datasets to Assess the Accuracy of Microarray Platforms	• MAQC Pilot-II: Selecting two of the 13 titration points for the main study (200 arrays plus TaqMan and QuantiGene assays for 10 genes); • MAQC Main Study: Two titration points (75:25 and 25:75, SUHRR:ABHRR); • Expected versus observed fold changes (including mathematical formulas); • The use of titration data to evaluate normalization methods.	**Rich Shippy** Shawn Baker Paul Wolber Yuling Luo Rick Jensen
9	Characterization of Intra-platform, Inter-laboratory Variability	• Sources of technical variation that affect many genes; • Inter-laboratory comparison approaches that encompass many genes; • Surprising aspects of inter-laboratory differences; • Confirmation by manufacturer spike-ins (if this contributes to the characterization).	**Walter Liggett** David Duewer Marc Salit
10	Modeling Cross-hybridization of Microarray Experiments	• Probe sequence based models to estimate the affinity between probe and target; • Probe sequence based models to estimate the level of tendency of cross hybridization; • Target sequence based methods to estimate the effect of secondary structure of microarray hybridization.	**Zoltan Szallasi** Rick Jensen
11	One-color versus Two-color Designs in Microarray Experiments	• Philosophical considerations on microarray experimental designs: two-color vs one-color; • Common reference design vs sample-pairing design; • Dye biases and dye-swaps; • One-color hybridizations run on a two-color platform; • Ratio- and intensity-based data analysis for two-color design.	**Tucker Patterson** Jim Collins Francoise de Longueville Hong Fang Tao Han Jing Han Ernie Kawasaki
12	Informatics Tools for Utilizing the MAQC Datasets for Microarray Quality Control	• ArrayTrack as a tool for regulatory review of pharmacogenomic data submissions; • Assessing laboratory proficiency by comparing its data against the MAQC benchmark datasets; • Assessing the quality of individual arrays by examining the performance of spike-in controls.	**Weida Tong** Hong Fang Federico Goodsaid

Timeline:

1. **May 31, 2006**: Submission of MAQC manuscripts; Public release of MAQC datasets.
2. **July-September 2006**: Publication of MAQC manuscripts.

MAQC Timeline

3. **April 28, 2004**: Leming Shi submitted a Concept Paper (brief proposal) to FDA/NCTR director on "*Establishing Quality Assurance and Quality Control (QA/QC) Criteria for DNA Microarray Measurements*". Multiple FDA Centers were invited to participate.
4. **June 10, 2004**: The Microarray QC concept paper was approved (project#: E0720701).
5. **September 24, 2004**: Felix Frueh and Federico Goodsaid (FDA/CDER) were invited to visit FDA/NCTR. A wide range of issues and challenges regarding the use of genomic data in regulatory review were extensively discussed.
6. **October 2004**: Major microarray platform providers and RNA companies were invited.
7. **October 22, 2004**: *Science* published "Getting the noise out of gene arrays", raising concerns about the reliability of microarray data.
8. **February 11, 2005**: The first face-to-face meeting was held at FDA/NCTR, Jefferson, Arkansas. In the meeting summary (dated February 16, 2005), Leming Shi named the project as "MAQC" (MicroArray Quality Control). Regular biweekly teleconferences have been set up to keep track of the MAQC project.
9. **March 22, 2005**: FDA released the final version the "*Guidance for Industry: Pharmacogenomic Data Submissions*" (http://www.fda.gov/cder/guidance/6400fnl.pdf) to facilitate scientific progress in the field of pharmacogenomics and to facilitate the use of pharmacogenomic data in drug development and medical diagnostics.
10. **March 27, 2005**: Full proposal under the title "The MAQC (Microarray Quality Control) Project" was submitted to FDA/NCTR director.
11. **April 2005**: Pilot-I (RNA Sample Selection) data generation was completed.
12. **May 2-3, 2005**: The second face-to-face meeting was held at FDA/CDER, Rockville, MD. Decisions were made on RNA sample selection and the design of the main study.
13. **May 3, 2005**: The full MAQC protocol was approved by FDA/NCTR director.
14. **June 2005**: The MAQC website was set up: http://edkb.fda.gov/MAQC/.
15. **July 2005**: Pilot-II (Tissue Titration) data generation was completed.
16. **July 15, 2005**: "Cross-platform comparability of microarray technology: intra-platform consistency and appropriate data analysis procedures are essential" (Shi L. *et al*.) was published in *BMC Bioinformatics*, illustrating the importance of the MAQC project on quality control and data analysis.
17. **August 22, 2005**: Main study RNA samples were shipped to test sites.
18. **October 21, 2005**: Main study data were generated and submitted to FDA/NCTR.
19. **October 25, 2005**: Data from AFX, AGL, ABI, GEH, and ILM were distributed to 27 test sites and 10 data analysis sites.
20. **November 4, 2005**: Data from EPP, NCI, TAQ, QGN, and GEX were distributed.
21. **November 28, 2005**: Agilent one-color data (AG1) were distributed.
22. **December 1-2, 2005**: The third face-to-face meeting will be held in Palo Alto, CA to discuss results on the analysis of the MAQC datasets and plans for publications.
23. **May 31, 2006**: Submission of MAQC manuscripts; Public release of the datasets.
24. **July-September 2006**: Publication of MAQC manuscripts.
25. **December 2006**: Public meeting on microarray quality control and data analysis.
26. **December 2007**: Guidance on microarray quality control and data analysis.

Table 2. List of Registered MAQC Meeting Participants

As of 7:00 AM PST, November-29-2005, 100 people have registered to attend the MAQC project meeting in Palo Alto, CA. For those who plan to attend the meeting via conference call, please contact Leming.Shi@fda.hhs.gov so that your name will be added to the list of participants in the meeting summary.

No.	Name	Organization	E-mail
1	Aschheim, Kathy	Nature Biotechnology	k.aschheim@natureny.com
2	Austermiller, Bradley	Ohio Medical University	
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13	Chen, Michelle	Agilent	
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25	Dick, Daren	TeleChem ArrayIt	daren@biosearchtech.com
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39	Ji, Hanlee	Stanford University	hanleeji@stanford.edu
40	Jokhadze, George	PhalanxBio	
41	Jones, Wendell	Expression Analysis	wjones@expressionanalysis.com
42	Kalush, Francis	FDA/CDRH	fxk@cdrh.fda.gov
43	Kao, Pail	PhalanxBio	
44	Kawasaki, Ernest S.	NIH/NCI	kawasake@mail.nih.gov
45	Knight, Charles	Ohio Medical University	
46	Kohne, Connie	Jaden BioScience	ckohne@san.rr.com
47	Kohne, David	Jaden BioScience	drkohne@gmail.com
48	Kumm, Jochen	Stanford University	Jochen.kumm@stanford.edu
49	Kuo, Winston	Harvard University	wkuo@genetics.med.harvard.edu
50	Lee, Kathy Y.	Applied Biosystems	kathy.y.lee@appliedbiosystems.com

51	Li, Li	Stanford University	l3li@stanford.edu
52	Li, Quan	UT Southwestern	quan.li@utsouthwestern.edu
53	Liggett, Walter	NIST	walter.liggett@nist.gov
54	Liu, Chunmei	Affymetrix	chunmei_liu@affymetrix.com
55	Liu, Wei-min	Roche	wei-min.liu@roche.com
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58	Luo, Yuling	Genospectra	yluo@genospectra.com
59	Ma, Charles	PhalanxBio	charlesma@phalanxbiotech.com
60	Ma, Yunqing	Genospectra	yma@genospectra.com
61	Magnuson, Scott R.	GenUs BioSystems	smagnuson@genusbiosystems.com
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64	Mehta, Kshama	Agilent	
65	O'Leary, Dan	Nichols Institute Diagnostics	olearyd@nicholsdiag.com
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