# An assessment of q-PCR accuracy based on RNA-seq

presented by V. Sherina

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# Introduction

The **National Center for Biotechnology Information** (NCBI) is part of the United States National Library of Medicine (NLM), a branch of the National Institutes of Health.

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# GEO

**GEO** is a public functional genomics data repository supporting MIAME-compliant data submissions. Array- and sequence-based data are accepted.
Tools are provided to help users query and download experiments and curated gene expression profiles.

# Motivation

- "A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the sequencing quality control consortium." Nature Biotechnology (2014), by SEQC/MAQC-III Consortium.
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# Results

The Sequencing Quality Control (SEQC) project is coordinated by the US FDA. Examining Illumina HiSeq, Life Technologies SOLiD and Roche 454 platforms at multiple laboratory sites using reference RNA samples with built-in controls, authors

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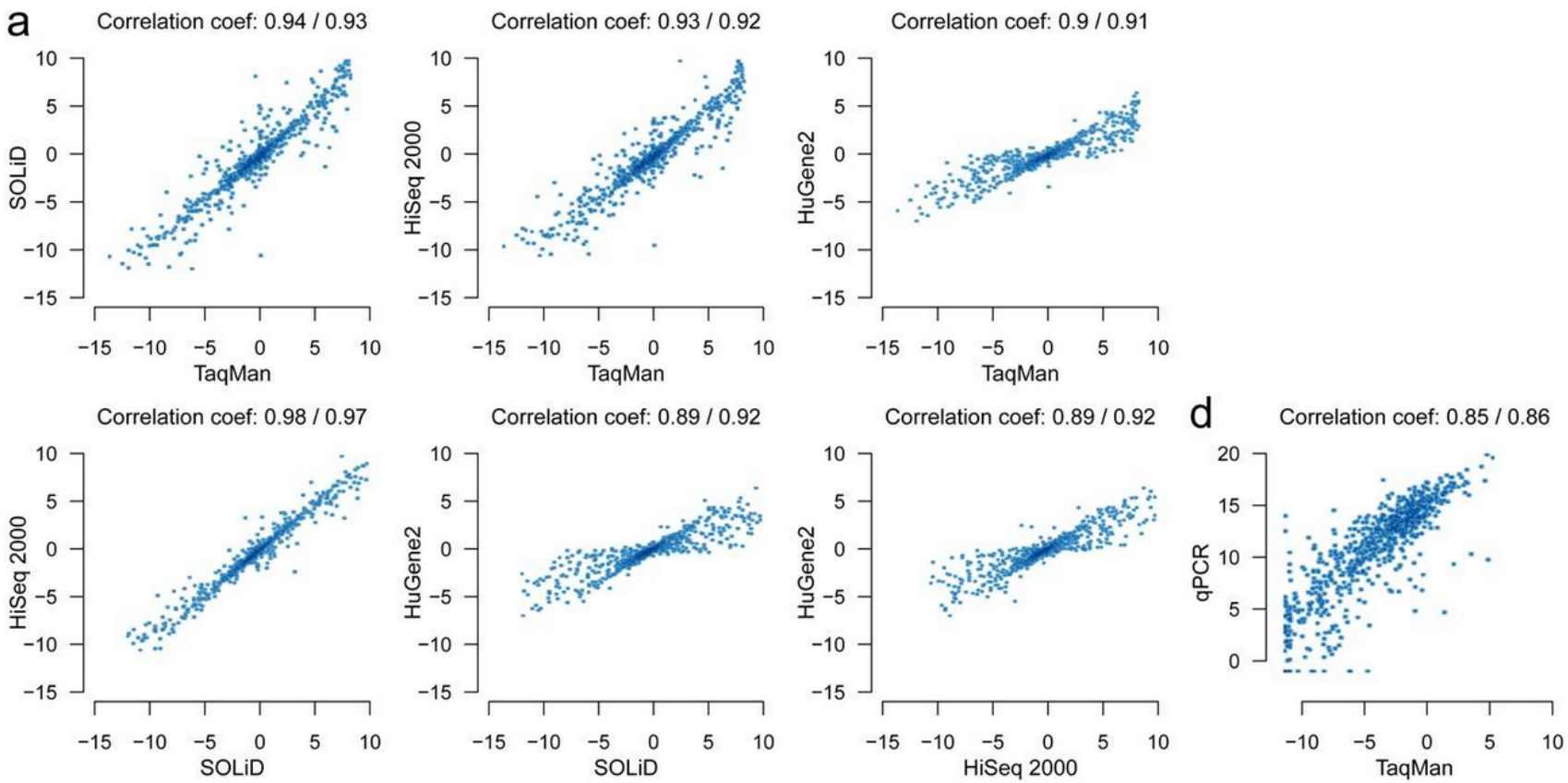
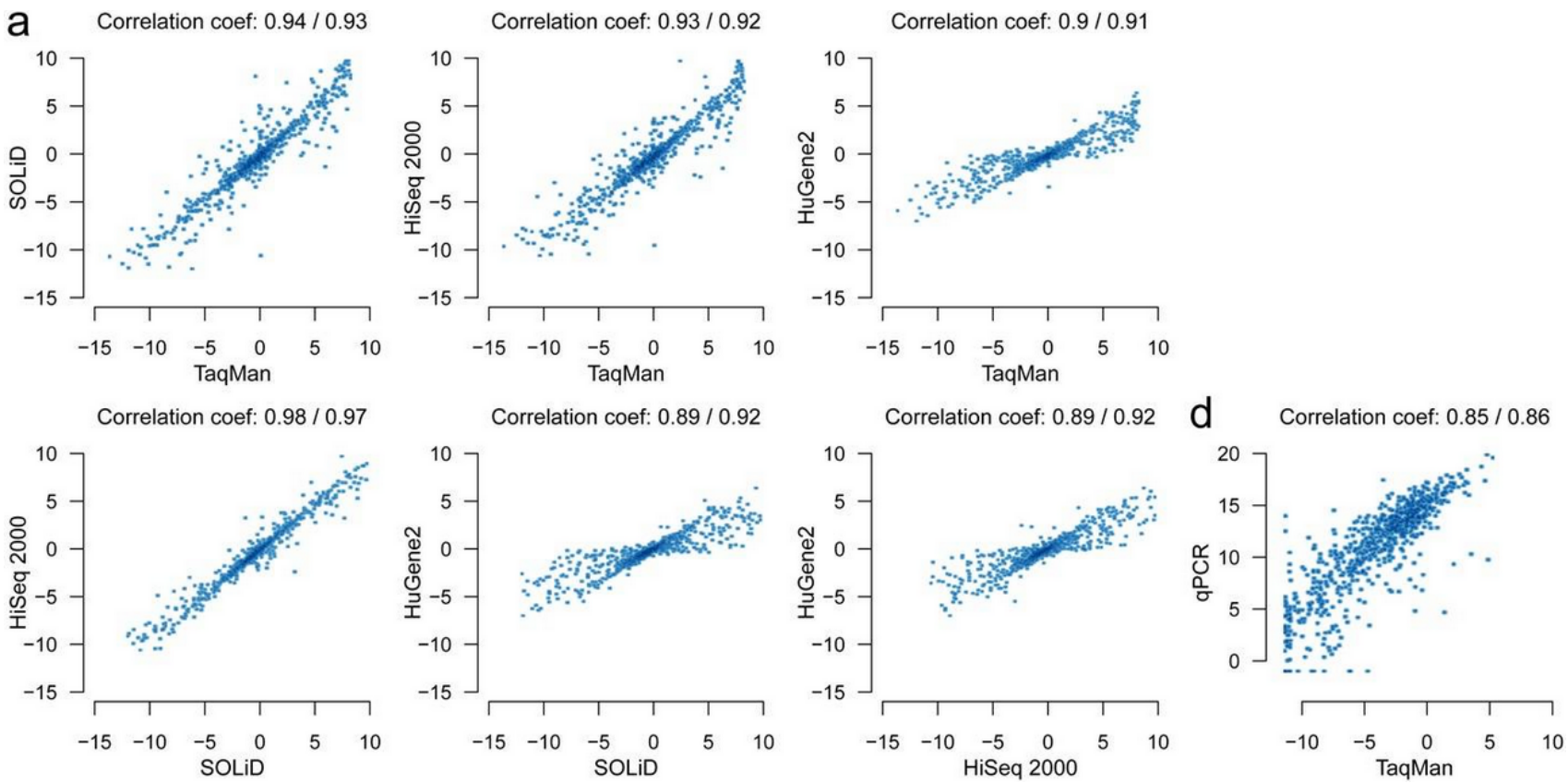
# Cross-platform agreement of expression levels

(a) Comparison of log2 fold-change estimates for 843 selected genes. Good and similar concordances were observed between relative expression measures from the MAQC-III HiSeq 2000 and SOLiD sequencing platforms, MAQC-I TaqMan and the MAQC-III Affymetrix HuGene2 arrays (Pearson and Spearman correlation) (d) Comparison of TaqMan and

PrimePCR for 843 selected genes.




Expression estimates vary considerably for individual genes, with some genes showing high expression in one platform but are not detected at all by the other.

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# References


SEQC/MAQC-III Consortium *A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium* Nature Biotechnology 32, 903914, 2014.

M.N. McCall, H.R. McMurray, H. Land and A. Almudevar *On non-detects in Quantitative real-time PCR data.* Bioinformatics V. 30 no. 16, 2310-2316, 2014.

# Thank you for your attention!

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