

*Abstract #1574*

**Title:** Biopsy Cavities in Breast Cancer Specimens: Impact on Quantitative RT-PCR Gene Expression Profiles and Recurrence Risk Assessment

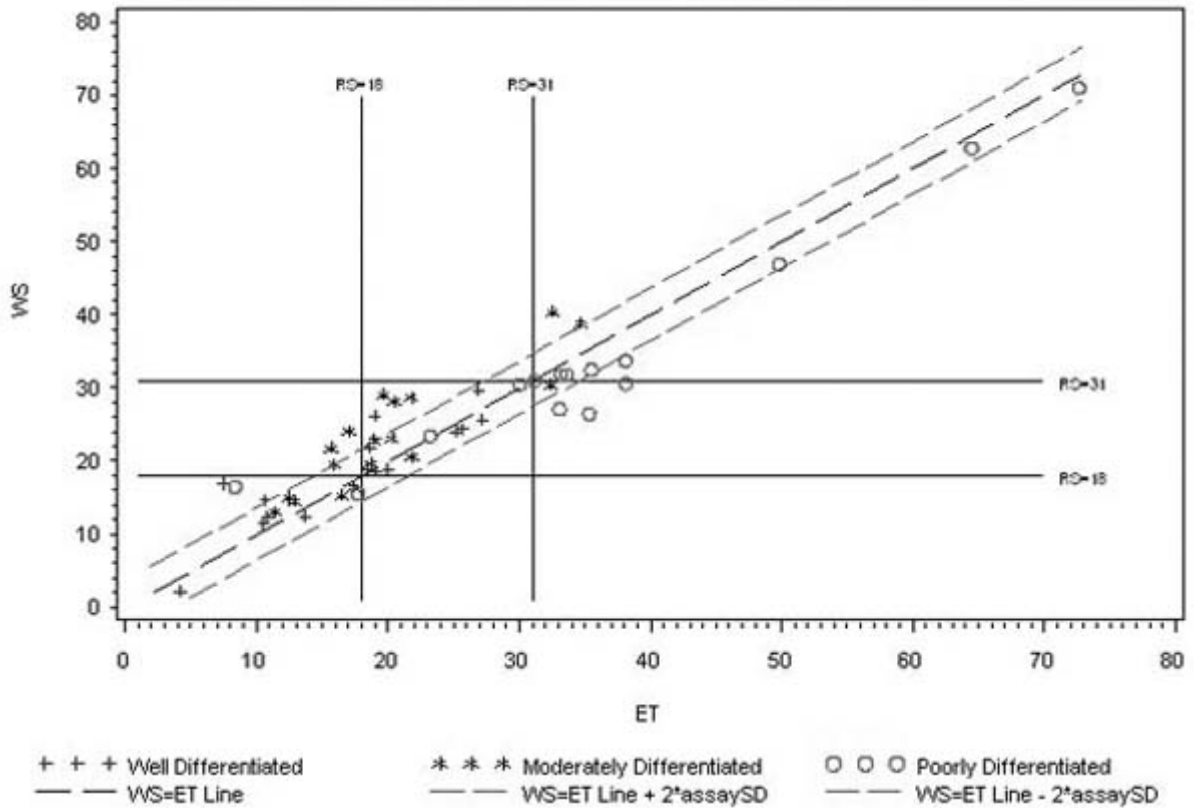
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**Background:** The 21-gene recurrence score assay is prognostically and predictively important in ER+ breast cancer. Manual microdissection is performed in cases where biopsy cavities (BxC) are present. The objective of this study was to characterize by quantitative RT-PCR the impact of BxC on 21 gene expression profiles and the Recurrence Score (RS).

**Design:** 48 (15 well, 18 moderate, and 15 poorly differentiated) invasive breast carcinomas were evaluated for differences in gene expression between whole sections (WS; which contained BxC) and enriched tumor (ET; where BxC were excluded by manual microdissection). Standardized quantitative RT-PCR analysis for the 21 genes was performed; reference normalized gene expression measurements ranged from 0 to 15, where each 1-unit reflects an approximate 2-fold change in RNA. Analyses of individual genes and RS were performed on the entire sample set and stratified by tumor grade. Correlation analyses used Pearson's R, concordance analysis by Lin's sample concordance and paired t-tests to characterize differences.

**Results:** Of the 16 cancer-related genes there were statistically significant differences in reference normalized gene expression between ET and WS in 6 genes: BAG1 (ET-WS: 0.13 units,  $p=0.0025$ ), CD68 (ET-WS: -0.64 units,  $p<0.0001$ ), ER (ET-WS: 0.29 units,  $p=0.0012$ ), GSTM1 (ET-WS: 0.18 units  $p=0.0025$ ), STK15 (ET-WS: -0.18 units,  $p=0.0041$ ) and STMY3 (ET-WS: 0.62 units,  $p<0.0001$ ). Expression of CD68 was higher and ER was lower in WS containing BxC. The correlation (0.95) and concordance (0.92) were generally high between WS and ET for RS overall; however, among moderately differentially tumors, there was a statistically significant mean increase in RS for WS of 3.3 units ( $p = 0.0012$ ) while among poorly differentiated tumors, there was a trend toward a statistically significant decrease in RS for WS of 2.2 units ( $p=0.0569$ ).

Recurrence Score®: WS vs. ET



**Conclusions:** The inclusion of BxC in breast cancer specimens is associated with significant changes in the expression of individual genes and can impact the RS. The removal of BxC by manual microdissection from breast cancer specimens assessed for gene expression levels is warranted.

Category: Breast

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Poster Session VI # 33, Wednesday Afternoon