Background:
• Many types of gene expression profiling have been explored
• Transcriptome methods were used to examine the concordance between Her-2 status from pathology reports vs. gene expression ERBB2
• High risk cancers underwent whole transcriptome gene expression profiling

Methods/Materials:
• For 48 patients the concordance between Her-2 pathology reporting and ERBB2 as determined via RNA sequencing
• Twenty luminal B patients (via Mammoprint or Blueprint) underwent stratification based on whole transcriptome gene expression

Results:
• High concordance between HER-2 and ERBB2 was seen with high gene expression levels
• Discrepancies occurred with lower gene expression levels
• High-risk luminal breast cancer patients found 2 distinct sub-populations, 1 of which is more like triple negative and the other is more like triple positive patients.

Conclusions:
• Treatment changes can be enacted by incorporating transcriptome genetics combined with clinical studies
• Many luminal B patients may benefit from chemotherapy traditionally used for TNC or triple positive patients
• Clinical correlations are underway to explore these findings