

## **P035 Quantitative RT-PCR gene expression in the special histologic subtypes of invasive breast cancer**

Poster Abstracts I

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**Goals:** ER+ special histologic breast cancer subtypes are prognostically significant. Here we report the special histologic subtypes of ER+ breast carcinoma and associated patterns of observed gene expression as measured by the 21 gene OncotypeDX assay.

**Methods:** All tumors from 6/1/04–5/31/13 were included in analyses. Central path used WHO criteria. Ductal NOS (DC), tubular (TC), cribriform (CC), mucinous (MC) and papillary (PC) carcinomas were included. Quantitative expression of 16 cancer related genes was measured on a scale from 2 to 15 (relative to reference genes) where a 1 unit increment is associated with 2-fold change in expression. Recurrence Score (RS) was calculated as published. Descriptive stats for the RS and individual genes [ER, PR, invasion gene group (IGG) and proliferation gene group (PGG)] were obtained. Comparisons of means were adjusted to control the overall error rate under any complete or partial null hypothesis.

**Results:** DC accounted for 95.1%, TC 0.7%, CC 0.4%, MC 3.1% and PC 0.7% of 307,175 cases. For all histological subtypes a wide continuous range of RS was noted. DC had the highest mean RS, followed in decreasing order by MC, TC, CC and PC. PC had the highest ER; PC and CC had the highest PR; TC had the lowest ER. ER was not different between CC and MC but PR was. The proportion with ER+/PR- phenotype was different among the subtypes: TC (8.2%) and CC (6.8%) had the lowest incidence whereas MC (12.7%) and PC (9.5%) were more similar to DC (13.8%). TC had lowest PGG expression. MC and PC had lower IGG expression compared to other subtypes.

Histologic subtype