Goals: Classic lobular carcinoma is characterized by a distinctive morphology, loss of E-cadherin commonly due to mutation or deletion of CDH1 on chromosome 16q, and a variable clinical course (Pestalozzi JCO 2008 26: 3006). Variants (pleomorphic, solid and alveolar) with distinct morphologies and potential differences in outcome have been described (Rosen 2009). We provide a 9-year update of the patterns of quantitative gene expression as measured by the 21 gene Oncotype DX® assay for ductal NOS (DC) and classic and variant lobular carcinomas.

Methods: All tumors analyzed in the Genomic Health laboratory from 6/04–5/13 were included. Central path used WHO criteria for classification of classic lobular (CL), solid and alveolar lobular (SAL), and pleomorphic lobular (PL) carcinomas. 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 an ?2-fold change in expression. Descriptive statistics for RS and individual genes [ER, PR, invasion gene group (IGG) and proliferation gene group (PGG)] among the different subtypes were obtained. Comparisons of means among the subtypes were adjusted to control the overall error rate under any complete or partial null hypothesis.