#302 - Breast Tumours withIntermediate Histological Grade can be Reclassified into Prognostically Distinct Groups by Gene Expression Profiling

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Background

- Histological grade has long been recognized to provide significant prognostic information
- Whilst grade 1 and 3 tumours are clearly associated with different prognoses, those classified as grade 2 (~40%) represent a difficulty in clinical decision making
- Inter-observer variability results in poor reproducibility across institutions

Material and Methods

- Training set: N = 64
- Validation sets
  - 22,583 gene sets
  - 368 probe sets of "grade signature" (22 genes) FSCC-0

Defining Genomic Grade in the training set

GGI = scale \( \sum \beta_j - \sum \beta_j \cdot \) cutoff

Consistent Distribution of GGI in Different Populations and Microarrays Platforms

Comparison between the gene-expression grade index (GGI) and the 70-gene signature

Conclusions

- HG2 tumours are a mixture of HG1 and HG3 cases based on the genomic grade
- Gene-expression based grading can significantly improve current grading system for the prognosis assessment of breast cancer
- Genomic grade was highly reproducible across multiple independent datasets and across different microarray platforms