## UOC-BC: expression - Illumina HT-12 v3, microarray

## **Analysis Description:**

Data output is from the Caldas Laboratory at the University of Cambridge . Full details can be found in the paper Bruna et al., Cell 167, 260 - 274 (2016) .

RNA expression was analyzed using the Illumina HT-12 v3 platform. Raw data were processed with the beadarray package. The BASH algorithm was employed to correct for spatial artifacts. Summarization and probe selection based on quality was performed on the bead-level data using the detection thresholds recommended in the package and the re-annotation of the Illumina HT-12v3 platform as described previously (Curtis et al., 2012). The samples were classified into the intrinsic subtypes using PAM50, and the Three Gene classifier. ER, Her2 and PR status was inferred fitting a mixture model with the package mclust.