

STATISTICAL METHODS

12 or 10 tissue samples

**Limma F-test
BH= 0.00001**

**2115 or 850 differentially
expressed transcripts**

**Classification
for transcripts
PAM_HCL**

**Classification
for samples
PAM_HAC**

**Clusters defined
by PAM vs HCL**

**Clusters defined
by PAM vs HAC**

**Contingency
table**

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table**

**Transcripts clusters
5 (1772) or 3 (721)**

**Samples clusters
7 or 5
transcriptional units**

Annotation

**Gene Ontology
term enrichment**

7 or 5 transcriptional units

**SMVar T-test
BH= 0.00001**

**Transcripts overexpressed
in one unit**

**Single unit of
overexpresion**

**1243 or 558 transcripts
preferentially overexpressed**

Annotation

**Common
transcripts**

Potential markers