STATISTICAL METHODS

12 or 10 tissue samples
- Limma F-test BH= 0.00001
- 2115 or 850 differentially expressed transcripts
- Classification for transcripts PAM_HCL
- Clusters defined by PAM vs HCL
- Contingency table
- Transcripts clusters 5 (1772) or 3 (721)
- Annotation
- Gene Ontology term enrichment

7 or 5 transcriptional units
- SMVar T-test BH= 0.00001
- Transcripts overexpressed in one unit
- Single unit of overexpression
- 1243 or 558 transcripts preferentially overexpressed
- Annotation

Common transcripts
Potential markers