Genomic characterization of triple negative breast cancers with high-resolution SNP 6.0 Affymetrix arrays

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• The histopathological absence of ER, PR and HER2 defines a subgroup of breast cancers named "triple negative", characterized by aggressive behaviour and poor prognosis.

• No targeted therapies are yet available.

**Data set and analysis design**

**Tumor somatic data**

- **Triple-Negative Tumors**
  - 72 ER-, PR-, HER2-

- **Non-Triple-Negative Tumors**
  - 7 ER- HER2+
  - 17 ER+ HER2-

**Patients germ-line data (baseline)**

- 18 patient’s blood samples
Aberrant regions: Triple-Negative vs Non-Triple-Negative Tumors

Triple negatives

Non-Triple-Negatives

Triple-Negative and Non-Triple-Negative specific aberrations

TN specific

-\log_{10} \text{Fisher p-value}

NTN specific
TN specific aberrations harbor cancer-related miRNAs

> TN specifically deleted or gained/amplified regions harbour a number of cancer-related miRNAs, including miR-135a, miR-let7g (3p) and miR-95 (4p)
**Frequently gained/amplified genes**

- TN: 758 genes
- NTN: 1.436 genes
- Overlapping: 6 genes

**Frequently deleted genes**

- TN: 1.615 genes
- NTN: 49 genes
- NTN: 55 genes

**Gained/Ampified Gene Pathways**

- Different pathways for Triple-Negative and Non-Triple-Negative categories

**Deleted Gene Pathways**

- Different pathways for Triple-Negative and Non-Triple-Negative categories
Heatmaps of Non-Random Co-Aberrations

co-deletions with odds-ratio > 1

co-amplifications with odds-ratio > 1

co-amplification-deletions with odds-ratio > 1

-log10 p-value

-compensatory

-synergistic

-compensatory

-synergistic

-compensatory