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**Title:** Prediction of "BRCAness" in breast cancer by array comparative genomic hybridization  
**Issue Date:** 2012-03-27
PROPOSITIONS
accompanying the thesis

*Prediction of "BRCAness" in breast cancer by array comparative genomic hybridization*

by Simon A. Joosse

1. Array CGH is a powerful technique to study a tumor's genetic makeup and divide breast cancer patients into clinically relevant subgroups (*this thesis*)

2. BRCA1 deficiency leads to a typical pattern of chromosomal aberrations in hereditary and sporadic breast cancer (*this thesis*)

3. Aneuploidy of chromosomes and chromosomal subregions can be effectively used to predict "BRCAness" in hereditary and sporadic breast cancer in the clinic (*this thesis*)

4. Although signature chromosomal aberrations can assign tumors to a subgroup, each tumor remains a unique entity (*this thesis*)

5. All triple-negative breast tumors should be tested for BRCA1 deficiency (*this thesis*)

6. To metastasize, tumor cells undergo epithelial-to-mesenchymal transition to enter the bloodstream (*Ledford. Nature 2011; 472:273*)

7. Genomic instability is an active process that drives tumor evolution (*Navin, et al. Genome Res 2010; 20:68-80*)

8. Tumor initiation as a result of BRCA1 deficiency can only occur before stem cell differentiation (*Lim, et al. Nat Med 2009; 15:907-13*)

9. Clinical management will be solely directed by the tumor's genetic makeup in the near future (*Majewski & Bernards. Nat Med 2011; 17:304-12*)

10. Our current high-throughput, whole-genome experiments drown us in information, but without proper bioinformatics we are still starving for knowledge

11. Facts are stubborn things, but statistics are more pliable (*Mark Twain*)