

Resource Summary Report

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Breast Cancer Somatic Genetics Study

RRID:SCR_003832

Type: Tool

Proper Citation

Breast Cancer Somatic Genetics Study (RRID:SCR_003832)

Resource Information

URL: <http://www.basisproject.eu/>

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Description: Consortium to generate complete catalogs of somatic mutations in 500 breast cancers, of the ER+ve HER2- subclass, under the International Cancer Genome Consortium model by high coverage, shotgun genome sequencing of both tumor and normal DNA. The strategy is to collect, store, review, quality control and extract DNA and RNA from breast cancer and normal tissues from 500 ER+, HER2- breast cancer cases which will be subjected to a coordinated series of genomic analyses including whole genome shotgun sequencing, genome-wide copy number analysis, mRNA expression analysis, miRNA expression analysis and genome-wide methylation analysis. A comprehensive catalogue of somatic mutations will be generated from each cancer. Somatic mutation catalogues from the 500 cancers will be analysed and integrated with expression and methylation data to identify novel cancer genes, characterize subverted biological pathways that are operative, describe patterns of somatic mutation and explore early translational applications of personalized somatic genomic data for patients with ER+, HER2- breast cancer. The results will impact the understanding of the causes and biology of breast cancer and will lead to major advances in detection, prevention and treatment in one of the most common diseases and causes of death in the developed world. The Consortium has completed a number of investigative exercises into the experimental protocols and technological practices relating to whole genome sequencing, epigenetics and transcriptomics including: * Completion of extensive testing of current RNA-seq protocol. * Designed and implemented a new, improved RNA-seq protocol which utilizes RNA samples regardless of their RNA Integrity Number. * Completed pilot testing of the Infinium 450k array and associated bi-sulfite sequencing. * Refined the whole genome sequencing library production protocols to produce more robust libraries. * Improved the primary variant-calling algorithms (for substitutions, insertions / deletions and rearrangements) * Developed new analytical algorithms to explore the resulting high-quality variants. As such, variant calling of whole genome sequencing data and secondary downstream analysis can begin in earnest in a trackable and automated fashion.

Abbreviations: BASIS

Resource Type: data or information resource, portal, organization portal, consortium

Keywords: oncology, biomarker, somatic mutation, whole genome sequencing, dna, rna, rna-seq, mrna expression, mirna expression, methylation, copy number, gene expression, mrna, mirna, epigenetics

Funding: European Union FP7 242006

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Alternate IDs: nlx_158147

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Record Last Update: 20260808T185805+0000

Ratings and Alerts

No rating or validation information has been found for Breast Cancer Somatic Genetics Study.

No alerts have been found for Breast Cancer Somatic Genetics Study.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.