

Resource Summary Report

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Core Genotyping Facility

RRID:SCR_008438

Type: Tool

Proper Citation

Core Genotyping Facility (RRID:SCR_008438)

Resource Information

URL: <http://cgf.nci.nih.gov>

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Description: With remarkable advances in genomic technologies, the National Cancer Institute established the Core Genotyping Facility (CGF) to investigate the contribution of germline genetic variation to cancer susceptibility and outcomes. Working in concert with epidemiologists, biostatisticians and basic research scientists in the intramural research program, the CGF has developed the capacity to conduct genome-wide association studies and candidate gene approaches to identify the heritable determinants of various forms of cancer. In order to ensure the accuracy and timely completion of all CGF provided operations, the following Information Systems were developed. While the investigator does not have direct access to these systems, their availability to CGF staff members greatly aids in their querying and reporting capabilities. In turn this provides benefit to the investigator by providing the most up to date reporting possible. The Core Genotyping Facility (CGF) offers a wide variety of sample preparation and genotyping operations. All samples received must meet minimum requirements and are taken through the Sample Handling pipeline prior to completing any genotyping. The Sample Handling pipeline includes DNA quantification and genetic fingerprinting. Also offered are Whole Genome Amplification (WGA) assays, to get the most yield out of low quantity DNA samples. Their genotyping products cover a wide-range of assay sizes. The CGF operates the Illumina BeadLab system which supports Illumina assay technologies including the whole genome genotyping Infinium assays, custom GoldenGate OPA assays, and Custom Infinium (iSelect) assays. In addition, the CGF offers Affymetrix GeneChip arrays and uniplex TaqMan genotyping. Sponsors: CGF is supported by the SAIC-Frederick. :Keywords: Genomic, Technology, Cancer, Genotyping, Germline, Genetic, Epidemiologist, Biostatistician, Research, Gene, Assay, Genotype, Pipeline, Genome, DNA, :

Synonyms: CGF

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

Resource Name: Core Genotyping Facility

Resource ID: SCR_008438

Alternate IDs: nif-0000-30251

Record Creation Time: 20220129T080247+0000

Record Last Update: 20260912T200013+0000

Ratings and Alerts

No rating or validation information has been found for Core Genotyping Facility.

No alerts have been found for Core Genotyping Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

Shi J, et al. (2014) Rare missense variants in POT1 predispose to familial cutaneous malignant melanoma. Nature genetics, 46(5), 482.

Brenner AV, et al. (2013) Common single nucleotide polymorphisms in genes related to immune function and risk of papillary thyroid cancer. PLoS one, 8(3), e57243.

Savage SA, et al. (2013) Genome-wide association study identifies two susceptibility loci for osteosarcoma. Nature genetics, 45(7), 799.

Zhu G, et al. (2011) Polymorphisms in Th1/Th2 cytokine genes, hormone replacement therapy, and risk of non-Hodgkin lymphoma. Frontiers in oncology, 1(21).

Hsiung CA, et al. (2010) The 5p15.33 locus is associated with risk of lung adenocarcinoma in never-smoking females in Asia. PLoS genetics, 6(8).

Rodríguez-Santiago B, et al. (2010) Mosaic uniparental disomies and aneuploidies as large structural variants of the human genome. American journal of human genetics, 87(1), 129.

Wang SS, et al. (2009) Polymorphisms in DNA repair and one-carbon metabolism genes and overall survival in diffuse large B-cell lymphoma and follicular lymphoma. Leukemia, 23(3), 596.

Chang MH, et al. (2009) Prevalence in the United States of selected candidate gene variants: Third National Health and Nutrition Examination Survey, 1991-1994. American

journal of epidemiology, 169(1), 54.

Savage SA, et al. (2008) TIN2, a component of the shelterin telomere protection complex, is mutated in dyskeratosis congenita. American journal of human genetics, 82(2), 501.

Chatterjee N, et al. (2006) Powerful multilocus tests of genetic association in the presence of gene-gene and gene-environment interactions. American journal of human genetics, 79(6), 1002.