

Tiffany M. Delhomme

Ph.D.

2 Rue Garibaldi, 69006 Lyon, France

✉ tiffany.delhomme@irbbarcelona.org | [tidelhomme](https://www.linkedin.com/company/tidelhomme) | [@tm_delhomme](https://twitter.com/tm_delhomme)

Experience

Postdoctoral researcher (Juan de la Cierva fellow)

[IRB Barcelona, Spain](#)

GENOME DATA SCIENCE LAB (PI: PR. SUPEK)

Jan. 2020 - present

- Scientific projects: mining genomics data in order to explore how exogenous and endogenous factors can impact mutational processes in the soma

Ph.D. in Computational Cancer Genomics

[Lyon, France](#)

INTERNATIONAL AGENCY FOR RESEARCH ON CANCER (IARC)

Nov. 2015 - July 2019

- Thesis: Using the systematic nature of errors in NGS data in order to efficiently detect mutations. Computational methods and application to early cancer detection.

Education

Ph.D. in Computational Cancer Genomics

[Lyon, France](#)

INTERNATIONAL AGENCY FOR RESEARCH ON CANCER (IARC)

Nov. 2015 - July 2019

- Thesis: Using the systematic nature of errors in NGS data in order to efficiently detect mutations. Computational methods and application to early cancer detection.

M.Sc. in Theoretical Computer Science

[Lyon, France](#)

ENS LYON, IXXI (RHONE-ALPES COMPLEX SYSTEMS INSTITUTE)

Sept. 2014 - July. 2015

- Major in complex system modelisation, minor in algorithms

M.Sc. in Bioinformatics and Evolutionary Biology

[Lyon, France](#)

UNIVERSITE CLAUDE BERNARD

Sept. 2012 - June. 2014

- Major in Bioinformatics and biostatistics, minor in evolution and biometry

Skills

Omics	NGS, somatic and germline variant calling and filtering, RNA-seq analysis, TCGA data
Cancer Evolution	Neutral tumor evolution, repeated tumor evolution
Cancer Biomarkers	Circulating tumor DNA for early cancer detection
Machine Learning	Supervised learning and semi-supervised learning (random forest) Unsupervised learning (cluster-then-label)
Statistics	Hypothesis testing and probability theory, bayesian inference, (generalized) linear models
Discrete Mathematics	Graph theory, clustering, biological networks
Programming	Bash, Python, cloud computing (SevenBridges Genomics platform)
Statistical Programming Languages	R
Scientific Reproducibility	Docker, DockerHub, Singularity, SingularityHub, Git, GitHub
Workflow writing and data format	Nextflow, CWL, JSON, YAML
Language	French: native, English: good writing and communication, Spanish: notions

Publications

TP53 Targeted Deep Sequencing of Cell-Free DNA in Esophageal Squamous Cell Carcinoma Using Low-Quality Serum: Concordance with Tumor Mutation

[Int. J. Mol. Sci.](#)

Dariush Nasrollahzadeh, Gholamreza Roshandel, **Tiffany M Delhomme** *et al.*

May 2021

[link](#)

The PI3K/mTOR Pathway Is Targeted by Rare Germline Variants in Patients with Both Melanoma and Renal Cell Carcinoma

[Cancers](#)

Jean-Noël Hubert, Voreak Suybeng, Maxime Vallée, **Tiffany M Delhomme** *et al.*

2021

[link](#)

Development of sensitive droplet digital PCR assays for detecting urinary TERT promoter mutations as non-invasive biomarkers for detection of urothelial cancer

Ismail Hosen, Nathalie Forey, Geoffroy Durand, Catherine Voegelé, Selin Bilici, Patrice H. Avogbe, **Tiffany M Delhomme** *et al.*

[Cancers](#)

2020

[link](#)

needlestack: an ultra-sensitive variant caller for multi-sample deep next generation sequencing data

Tiffany M. Delhomme, Patrice H. Avogbe, Aurelie AA. Gabriel *et al.*

[Nucleic Acid Res. - Genomics and Bioinformatics](#)

June 2020

[link](#)

Integrative and comparative genomic analyses identify clinically relevant groups of pulmonary carcinoids and unveil the existence of supra-carcinoids

Nicolas Alcalá*, Noémie Leblay*, Aurelie Gabriel*, Lise Mangiante, David Hervás Marin, Theo Giffon, Anne-Sophie Sertier, Anthony Ferrari, Jules Derks, Akram Ghantous, **Tiffany M. Delhomme** *et al.*

[Nat. Commun.](#)

Aug. 2019

Urinary TERT promoter mutations as non-invasive biomarkers for the comprehensive detection of urothelial cancer

Patrice H. Avogbe, Arnaud Manel, Emmanuel Vian, Geoffroy Durand, Nathalie Forey, Catherine Voegelé, Maria Zvereva, Ismail Hosen, Sonia Meziani, Berengere De Tilly, Gilles Polo, Olesia Lole, Pauline Francois, **Tiffany M. Delhomme** *et al.*

[EBioMedicine](#)

June 2019

[link](#)

Integrative genomic profiling of large-cell neuroendocrine carcinomas reveals distinct subtypes of high-grade neuroendocrine lung tumors

Julie George, Vonn Walter, Martin Peifer, Ludmil B. Alexandrov, Danila Seidel, Frauke Leenders, Lukas Maas, Christian Müller, Ilona Dahmen, **Tiffany M. Delhomme** *et al.*

[Nature Communications](#)

Mar. 2018

[link](#)

KRAS mutations in blood circulating cell-free DNA: a pancreatic cancer case-control study

Florence Le Calvez-Kelm, Matthieu Foll, Magdalena B. Wozniak, **Tiffany M. Delhomme** *et al.*

[Oncotarget](#)

Oct. 2016

[link](#)

Identification of Circulating Tumor DNA for the Early Detection of Small-cell Lung Cancer

Lynnette Fernandez-Cuesta*, Sandra Perdomo*, Patrice H. Avogbe*, Noémie Leblay, **Tiffany M. Delhomme** *et al.*

[EBioMedicine](#)

Aug. 2016

Contribution: development of needlestack, an highly sensitive variant caller that can detect low abundance mutations such as tumor-derived mutations from circulating tumor DNA data. In this study, we applied needlestack to Small-cell Lung Cancer cases and matched controls in order to use circulating tumor DNA as an early cancer biomarker.

[link](#)

SUBMITTED

Malignant Pleural Mesothelioma heterogeneity disentangled through deep integrative genomic analyses

Lise Mangiante*, Nicolas Alcalá*, Alex Di Genova*, Alexandra Sexton-Oates*, [+14], **Tiffany M. Delhomme** *et al.*

Aug. 2019

IN PREPARATION

Assessment of the diagnostic value of circulating RB1 and TP53 mutations for early detection of small cell lung cancers

Patrice H. Avogbe*, **Tiffany M. Delhomme*** *et al.*

expected sub. Dec. 2021

Communications

POSTERS

needlestack: an ultra-sensitive variant caller for multisample deep next generation sequencing data

Journées Ouvertes Biologie, Informatique et Mathématiques (JOBIM), Clermont Ferrand, France

June 2015

needlestack: an ultra-sensitive variant caller for multisample deep next generation sequencing data

RECOMB-Computational Cancer Biology, Paris, France

Apr. 2018

TALKS

needlestack: an ultra-sensitive variant caller for multisample deep next generation sequencing data

Journées Ouvertes Biologie, Informatique et Mathématiques (JOBIM), Lyon, France

Aug. 2016

IARC nextflow pipelines: toward efficient cancer genomics analyses

Nextflow workshop, **invited speaker**, Barcelona, Spain

Nov. 2018

Honors & Awards

FELLOWSHIPS

Postdoctoral Fellowship, "Juan de la Cierva", Spanish Ministry of Science

2020-2022

Ph.D. Fellowship, La Ligue Nationale Contre le Cancer

2015-2018

Referees

Dr. Matthieu Foll

GEN/GCS group

International Agency for Research on Cancer

Lyon, France

✉ FollM@iarc.fr

+334-72-73-85-37

Dr. James McKay

GEN/GCS group

International Agency for Research on Cancer

Lyon, France

✉ McKayJ@iarc.fr

+334-72-73-80-93

Pr. Fran Supek

PI Genome Data Science Lab

IRB Barcelona

Spain

✉ fran.supek@irbbarcelona.org

+34-934-039-942