**BAYLOR COLLEGE OF MEDICINE**

**CURRICULUM VITAE**

SEPTEMBER 26, 2026

## PERSONAL STATEMENT

I am an Assistant Professor in the Department of Medicine, Epidemiology and Population Science Section at Baylor College of Medicine. My research program integrates genomics, systems biology, and network medicine to elucidate gene regulatory processes that drive disease development and therapeutic response, particularly in lung cancer and chronic lung disease, with the goal of advancing sex-aware, mechanism-based precision medicine.

My training spans experimental molecular biology, genomics, and computational and systems biology. I earned a master's degree in Medical Physiopathology from UNICAMP and a PhD in Science (Oncology) from the A.C. Camargo Cancer Center, where I identified molecular mechanisms of treatment response and predictive biomarkers in rectal cancer. During my postdoctoral fellowship at Harvard, Dana-Farber Cancer Institute, and Brigham and Women's Hospital, I worked with omic data and applied network methods to a wide range of problems, including PD1 pathway regulation in glioblastoma, regulatory differences between cell lines and primary tissues, and sex differences in healthy tissues and cancer. These publicly available network resources continue to support broader investigations into network disruptions that underlie disease.

As Principal Investigator, I have leveraged these systems approaches to define sex-, age-, and smoking-related regulatory programs in lung cancer, COPD, and Alpha-1 Antitrypsin Deficiency, supported by the American Lung Association, the Alpha-1 Foundation, and an NIH K01. My recent work has shown that sex, aging, and tobacco exposure reshape gene regulatory architectures in ways that influence lung cancer risk, tumor biology, and survival, providing a foundation for sex-aware preventive and therapeutic strategies.

Teaching and mentoring are central to my mission. I have co-directed for 8 years the course "Introductory Genomics & Bioinformatics for Health Research" at Harvard. I develop interactive, cloud-based training materials, and mentor trainees across disciplines with a particular emphasis on genomics, sex differences, and gene regulatory networks. Across my research, education, and clinical collaborations, my overarching goal is to leverage integrative multi-omics, network medicine, and clinical data to transform our understanding of lung disease heterogeneity, prevent or delay progression from chronic lung disease to lung cancer, and improve outcomes for patients with pulmonary disease.

## I. GENERAL BIOGRAPHICAL INFORMATION

### A. Personal

1. Full Name: Camila Miranda Lopes-Ramos
2. Citizenship: Brazilian

### B. Education

**1. Undergraduate Education**

2004–2007 BS, Biological Sciences, University of Campinas (UNICAMP), Campinas, Brazil

**2. Graduate Education**

2010–2014 PhD, Science (Oncology), A.C. Camargo Cancer Center, São Paulo, Brazil
*Advisor*: Raphael Parmigiani
*Dissertation*: Identification and expression study of polyadenylation variants and miRNAs through large scale sequencing in colorectal tumor samples

2008–2010 MS, Medical Physiopathology, University of Campinas (UNICAMP), Campinas, Brazil
*Advisor*: Iscia Lopes-Cendes
*Dissertation*: Development of an *in vitro* model of the cytotoxic effects of expanded ataxin-3 and evaluation of different therapeutic strategies to control these effects

**3. Postgraduate Training**

2021–2023 Postdoctoral Fellow, Network Medicine
*PI:* Dawn DeMeo
*Support:* NIH T32 (2021-2023)
Channing Division of Network Medicine, Brigham and Women's Hospital and Harvard Medical School, Boston

2015–2018 Postdoctoral Fellow, Computational Biology
*PI:* John Quackenbush
*Support:* FAPESP (2015-2016)
Dana-Farber Cancer Institute and Harvard T.H. Chan School of Public Health, Boston

2014–2015 Postdoctoral Fellow, Genomics and Molecular Biology
*PI:* Raphael Parmigiani
Hospital Sírio-Libanês, São Paulo, Brazil

**C. Academic Appointments**

**1. Current Faculty Positions**

08/2026–present Assistant Professor, Department of Medicine, Epidemiology and Population Science Section, Baylor College of Medicine

**2. Previous Faculty / Research Positions at Other Institutions**

2026 Assistant Professor in Medicine, Department of Medicine, Harvard Medical School, Boston

2023–2026 Instructor in Medicine, Department of Medicine, Harvard Medical School, Boston

2023–2026 Associate Scientist (Investigator), Department of Medicine, Channing Division of Network Medicine, Brigham and Women's Hospital, Boston

2021–2026 Instructor in Biostatistics, Department of Biostatistics, Harvard T.H. Chan School of Public Health, Boston

2021–2023 Research Scientist, Department of Medicine, Channing Division of Network Medicine, Brigham and Women's Hospital, Boston

2018–2021 Research Scientist, Department of Biostatistics, Harvard T.H. Chan School of Public Health, Boston

**D. Other Advanced Training/Experience**

**1. Formal Sabbatical Leave**

None

**2. Other Specialized Training Following Academic Appointment**

2022 Careers through Mentoring in Omics and Data for Early-stage Investigators (Career MODE) Program, Columbia University – Scholarship award

2022 Epigenetics Boot Camp, Columbia University – Professional development / tuition award

2014 X Summer Course Bioinformatics – R and Bioconductor, University of São Paulo – Travel award

**E. Other Information**

**1. Honors or Awards**

2026 Poster Award, Connors-MGB Research Collaborative Symposium, Brigham and Women's Hospital

2025 Research Excellence Award, Connors-MGBRI Center for Women's Health and Sex Differences, Brigham and Women's Hospital

2024 Lung Research Day Distinguished Abstract Award, Lung Research Center, Brigham and Women's Hospital

2023 Department of Medicine Research Performance Incentive Program, Brigham and Women's Hospital

2023 Incorporating Sex and Gender Into Research Featured Speaker Award, Connors-BRI Research Center, Brigham and Women's Hospital

2022 Charles J. Epstein Trainee Awards for Excellence in Human Genetics Research, Semifinalist, American Society of Human Genetics

2022 Scholarship award, Careers through Mentoring in Omics and Data for Early-stage Investigators (Career MODE) Program, Columbia University

2022 Professional Development Scholarship, Epigenetics Boot Camp, Columbia University

2021-2023 Postdoctoral Training Award, NIH T32 HL007427

2016 Travel award, Transatlantic Data Science Workshop, NIH

2015–2016 Fellowship for Abroad Research, São Paulo Research Foundation (FAPESP)

2014 Travel award, X Summer Course Bioinformatics – R and Bioconductor, University of São Paulo

2010–2014 PhD Scholarship, São Paulo Research Foundation (FAPESP)

2008–2010 MS Scholarship, São Paulo Research Foundation (FAPESP)

## II. RESEARCH INFORMATION

### A. Research Support

**ACTIVE RESEARCH SUPPORT**

2026-2030
Understanding the Role of the X Chromosome in COPD through Integrated Multi-Omic Approaches
NIH/NHLBI
K01 HL186417
PI
Annual Direct Cost: $165,000; Total Direct Cost: $660,000
The goal of this project is to understand the role of X chromosome and genetic variation driving COPD onset and heterogeneity using integrated multi-omic approaches.

2026-2028
Using multi-omic and network analysis to understand gene dosage effect in COPD
NIH/NHLBI
R03 HL185156
PI
Annual Direct Cost: $75,000; Total Direct Cost: $150,000
The goal of this project is to generate network maps of X-linked transcription factor regulatory interactions in COPD, identifying key genetic and epigenetic changes that influence transcription factor–gene regulation and contribute to disease heterogeneity.

2026
Multi-Omic Signatures Underlying COPD and Lung Cancer Comorbidity
Francis Family Foundation
Research Opportunity Award
PI
Annual Direct Cost: $5,000; Total Direct Cost: $5,000
The goal of this project is to identify both shared and distinct multi-omic signatures between COPD alone and COPD comorbid with lung cancer, and ultimately provide mechanistic insights and potential biomarkers for early detection and personalized intervention in individuals with COPD who are at high risk for developing lung cancer.
*I was selected for the full 4-year Parker B. Francis Fellowship ($225,000), which changed to a Research Opportunity Award ($5,000) after I received an NIH K01 grant.*

2024-2029
Minority Faculty Career Development Award

Brigham and Women's Hospital
PI
Annual Direct Cost: $20,000; Total Direct Cost: $100,000
The goal of this award proposal is to support Dr. Lopes-Ramos' career development to a fully independent investigator with expertise in integrative omic analysis and network medicine to advance sex-aware strategies to prevent and treat pulmonary diseases.

2024-2026 Multi-omic Sex Differences in Alpha 1 Antitrypsin Deficiency Associated COPD
Alpha-1 Foundation
Research Grant Award ID 1253216
PI
Annual Direct Cost: $100,000; Total Direct Cost: $200,000
The goal of this study is to understand the molecular mechanisms associated with sex-based differences in individuals with AATD-associated COPD by investigating sex hormones, proteomics, and DNA methylation patterns.

**COMPLETED RESEARCH SUPPORT**

2023-2025 Sex chromosome gene regulatory networks and COPD
NIH/NHLBI
K01 HL166376
PI
Annual Direct Cost: $162,000; Total Direct Cost: $324,000
The goal of this project was to integrate X chromosome multi-omic data, X chromosome inactivation patterns, and network analysis to better understand sex-biased regulation of X chromosome genes in COPD onset and heterogeneity.
*Subject to mass termination in May 2025 as part of the U.S. government's action.*

2021-2023 Identifying therapeutic targets through sex-specific regulatory networks in lung cancer
American Lung Association
Lung Cancer Discovery Award LCD-821824
PI
Annual Direct Cost: $100,000; Total Direct Cost: $200,000
The goal of this project was to determine sex differences in gene regulatory processes of lung adenocarcinoma and new therapeutic targets that consider sex-based differences.

## B. National Scientific Participation

### 1. Editorial Contributions

*Ad Hoc Reviewer:*

- Bioinformatics
- Biology of Sex Differences
- BMC Genomics
- Brazilian Journal of Medical and Biological Research

- British Journal of Cancer
- Cancer Research
- Cancers
- Cell Communication and Signaling
- Cell Genomics
- Cell Reports
- Genetics and Molecular Biology
- Journal of Molecular Medicine
- Life
- Molecular and Cellular Probes
- npj Aging
- PeerJ
- PLOS One
- PNAS Nexus
- Respiratory Research
- 3Biotech

*Other Editorial Roles:*

2022 Special Issue Editor, Cancers
Special Issue: "Gene Regulatory Networks in Cancers"

**2. Review Panels and Selection Committees**

2024 Ad hoc reviewer, Rosetrees Out of Round Applications, Rosetrees Trust, United Kingdom

2022 Ad hoc reviewer, Translational Innovator – "The Five Senses: Input & Response", Harvard Catalyst

**3. Professional Societies**

2025–present American Association for Cancer Research – Active Member

2023–present American Thoracic Society – Active Member

2022–present American Society of Human Genetics – Active Member

2019 Organization for the Study of Sex Differences – Past Member

**4. Elected Positions**

None.

**5. Invited Lectures, Presentations, Seminars**

**a. International**

2026 Understanding sex differences through the lens of biological networks
PhD Program in Artificial Intelligence, Biomedical Engineering and Computer Science,
Università degli Studi Magna Graecia di Catanzaro
Catanzaro, Italy (Virtual)

2025 Using gene regulatory networks to advance sex-specific approaches in personalized medicine
70º CBG Genetica 2025 | International Congress of the Brazilian Genetics Society
Belém, Pará, Brazil

2024 Understanding Sex and Gender Differences Through the Lens of Biologic Networks.
Artificial Intelligence and Network Medicine: Path to Precision Medicine
Milan, Italy

**b. National**

2026 Precision Medicine Through the Lens of Multi-Omics and Network Biology
Baylor College of Medicine, Houston, TX.

2025 Chromosome Inactivation and SDOH on COPD Outcomes in Women.
COPDGene Spring Investigator Meeting, San Francisco, CA.

2023 X Chromosome Methylation Patterns and Sex-Dosage Imbalance: Implications for COPD Susceptibility and Severity.
COPDGene Fall Investigator Meeting, Boston, MA.

2023 Career MODE Final Symposia Panel
Columbia University, New York, NY (Virtual)

2022 Using gene regulatory networks to understand sex differences.
Genetics Virtual Week, Labroots, Yorba Linda, CA (Virtual).

2020 Sex differences in drug metabolism.
American Association for Cancer Research Annual Meeting, Philadelphia, PA (Virtual).

2019 Gene Regulatory Network Analysis Identifies Sex-linked Differences in Colon Cancer Drug Metabolism Processes
Organization for the Study of Sex Differences and International Gender Medicine Society Meeting (OSSD/IGM), Washington, DC

**c. Regional / Local**

2026 Multi-omic Sex Differences in Alpha 1 Antitrypsin Deficiency Associated COPD.
SGGU/SP Unit Meeting, CDNM, Brigham and Women's Hospital

2025 Using gene regulatory networks to understand lung aging.
CDNM Retreat, Brigham and Women's Hospital

2025 Panel Discussion on non-HHS grants. Invited panelist.
CDNM Division-wide Seminar Series, Brigham and Women's Hospital

2025 The Impact of X Chromosome Inactivation Patterns on COPDOutcomes.
SGGU/SP Unit Meeting, CDNM, Brigham and Women's Hospital

2024 Understanding Sex and Gender Differences Through the Lens of Biologic Networks.
Radcliffe Exploratory Seminar: Sex and Gender at the Crossroads of the 21st Century Precision Medicine, Harvard Radcliffe Institute

2024 Multi-omic Sex Differences in Alpha 1 Antitrypsin Deficiency Associated COPD.
Alpha-1 Research Retreat, CDNM, Brigham and Women's Hospital

2024 The Impact of X Chromosome Inactivation Patterns on COPD Outcomes in Women.
Network Science Working Group, Department of Biostatistics, Harvard TH Chan School of Public Health

2024 X Chromosome Methylation Patterns and Sex-Dosage Imbalance: Implications for COPD Susceptibility and Severity.
SGGU/SP Unit Meeting, CDNM, Brigham and Women's Hospital

2019 Using gene regulatory networks to understand sex differences.
Bioinformatics Seminar, Department of Immunology, Harvard Medical School

2018 Using regulatory networks to understand sex differences.
Lightning Talks, Department of Biostatistics, Harvard T.H. Chan School of Public Health

2017 Using gene regulatory networks to understand sex differences.
Program in Quantitative Genomics Working Group Series, Department of Biostatistics, Harvard T.H. Chan School of Public Health

2017 Sexual dimorphism in colon cancer revealed by gene regulatory networks.
Cancer Biology Seminar, Department of Cancer Biology, Dana-Farber Cancer Institute

2017 Regulatory network changes between cell lines and their tissues of origin.
Genomics Get Together, Department of Data Science, Dana-Farber Cancer Institute

2016 Transcriptional landscape of cell lines and their tissues of origin.
Statistical Genetics and Network Science Meeting, CDNM, Brigham and Women's Hospital

2013 Predicting response to neoadjuvant chemoradiation treatment in rectal cancer through miRNA expression profile.
Hospital Sírio-Libanês, São Paulo, Brazil

**C. Publications**

**1. Full Papers in Peer Reviewed Journals**

**a. Published – Research Investigations**

*authors contributed equally to this work

1. Guebila MB, Saha E, Shapoval M, Chen C, Micheletti S, Eicher TD, Fanfani V, Fischer J, Shutta KH, Mandros P, Kuijjer ML, **Lopes-Ramos CM**, Quackenbush J. Deploying a JupyterHub Server for Academic Research Using Netbooks as an Example. Curr Protoc. 2026 Jun;6(6):e70396. PMID: 42273923. DOI: 10.1002/cpz1.70396.

2. Adebari T, Fanfani V, Guebila MB, DeConti D, Shutta KH, **Lopes-Ramos CM**, Hsu L, DeMeo DL, Quackenbush J, Eicher T. Gene regulatory network analysis identifies dysregulation of hypoxia pathways as contributing to glioblastoma treatment resistance in females. Biol Sex Differ. 2026 May 21. PMID: 42169093. DOI: 10.1186/s13293-026-00927-4.

3. **Lopes-Ramos CM**, Burkholz R, Ben Guebila M, Fanfani V, Saha E, Shutta KH, Glass K, Quackenbush J, DeMeo DL. Sex differences in gene regulation and its impact on cancer incidence. iScience. 2026 May;29(5):115570. PMID: 42023161. DOI: https://doi.org/10.1016/j.isci.2026.115570.

4. Pinheiro CCG, **Lopes-Ramos CM**, Inagaki T, Asprino PF, Ferreira JRM, de Mattos YGF, Campos HCG, Shibli JA, Parmigiani RB, Jarrahy R, Hokugo A, Faria AVS, Bueno DF. Intrinsic microRNA regulatory programs define lineage-specific differentiation in human mesenchymal stem cells of different origin - dental pulp- and fat tissue-derived. Stem Cell Rev Rep. 2026 May;22(4):1946-1957. PMID: 41865109. DOI: 10.1007/s12015-026-11107-7.

5. Chen C, Saha E, Fischer J, Ben Guebila M, Fanfani V, Shutta KH, Padi M, Glass K, DeMeo DL, **Lopes-Ramos CM**, Quackenbush J. Multi-omics protein signaling networks identify sex-specific therapeutic candidates in lung adenocarcinoma. Biol Sex Differ. 2025 Sep 29;16(1):71. PMID: 41024254; PMCID: PMC12482505. DOI: 10.1186/s13293-025-00752-1.

6. Cruz L, Ferreira FM, **Lopes-Ramos CM**, Wei Z, Hendriks WT, Jinnah HA, Nakaya HI, Bragg DC, Krichevsky AM, Breakefield XO, Hohmuth Lopes M. Intracellular and Extracellular Vesicle miRNA Signatures in Human iPSC-Derived Neural Stem Cells and Floor Plate Progenitors. FASEB J. 2025 Aug 31;39(16):e70958. PMID: 40873389; PMCID: PMC12392061. DOI: 10.1096/fj.202501157R.

7. Saha E, Guebila MB, Fanfani V, Shutta KH, DeMeo DL, Quackenbush J, **Lopes-Ramos CM**. Aging-associated Alterations in Gene Regulatory Networks Associate with Risk, Prognosis and Response to Therapy in Lung Adenocarcinoma. NPJ Aging. 2025 Jul 9;11(1):61. PMID: 40634311. PMCID: PMC12241614. DOI: 10.1038/s41514-025-00247-8.

8. Fanfani V, Shutta KH, Mandros P, Fischer J, Saha E, Micheletti S, Chen C, Guebila MB, **Lopes-Ramos CM,** Quackenbush J. Reproducible processing of TCGA regulatory networks. Gigascience. 2025 Oct 20:giaf126. PMID: 41114645. DOI: 10.1093/gigascience/giaf126.

9. Saha E, Fanfani V, Mandros P, Ben Guebila M, Fischer J, Shutta KH, DeMeo DL, **Lopes-Ramos CM**, Quackenbush J. Bayesian inference of sample-specific coexpression networks. Genome Res. 2024 Oct 11;34(9):1397-1410. PMID: 39134413. PMCID: PMC11529861. DOI: 10.1101/gr.279117.124.

10. Saha E, Ben Guebila M, Fanfani V, Fischer J, Shutta KH, Mandros P, DeMeo DL, Quackenbush J, **Lopes-Ramos CM**. Gene regulatory networks reveal sex difference in lung adenocarcinoma. Biol Sex Differ. 2024 Aug 6;15(1):62. PMID: 39107837 PMCID: PMC11302009. DOI: 10.1186/s13293-024-00634-y.

11. **Lopes-Ramos CM**, Shutta KH, Ryu MH, Huang Y, Saha E, Ziniti J, Chase R, Hobbs BD, Yun JH, Castaldi P, Hersh CP, Glass K, Silverman EK, Quackenbush J, DeMeo DL. Sex-biased Regulation of Extracellular Matrix Genes in Chronic Obstructive Pulmonary Disease. Am J Respir Cell Mol Biol. 2024 Aug 5;72(1):72-81. PMID: 39102858. PMCID: PMC11707671. DOI: 10.1165/rcmb.2024-0226OC.
    - *Commentary:* Shim YM, MacLeod JL. Sex Matters: A Deep Dive into Sex Differences in COPD. Am J Respir Cell Mol Biol. 2024 Aug 13;72(1):10-11.

12. Hsieh PH, **Lopes-Ramos CM**, Zucknick M, Sandve GK, Glass K, Kuijjer ML. Adjustment of spurious correlations in co-expression measurements from RNA-Sequencing data. Bioinformatics. 2023 Oct 3;39(10):btad610. PMID: 37802917. PMCID: PMC10598588. DOI:10.1093/bioinformatics/btad610.

13. Ben Guebila M, Wang T, **Lopes-Ramos CM**, Fanfani V, Weighill D, Burkholz R, Schlauch D, Paulson JN, Altenbuchinger M, Shutta KH, Sonawane AR, Lim J, Calderer G, van IJzendoorn DGP, Morgan D, Marin A, Chen CY, Song Q, Saha E, DeMeo DL, Padi M, Platig J, Kuijjer ML, Glass K, Quackenbush J. The Network Zoo: a multilingual package for the inference and analysis of gene regulatory networks. Genome Biol. 2023 Mar 9;24(1):45. PMID: 36894939. PMCID: PMC9999668. DOI: 10.1186/s13059-023-02877-1.

14. Hayden LP, Hobbs BD, Busch R, Cho MH, Liu M, **Lopes-Ramos CM**, Lomas DA, Bakke P, Gulsvik A, Silverman EK, Crapo JD, Beaty TH, Laird NM, Lange C, DeMeo DL. X Chromosome Associations with Chronic Obstructive Pulmonary Disease and Related Phenotypes: An X Chromosome-wide Association Study. Respir Res. 2023 Feb 1;24(1):38. PMID: 36726148. PMCID: PMC9891756. DOI: 10.1186/s12931-023-02337-1.

15. Ben Guebila M*, **Lopes-Ramos CM***, Weighill D, Sonawane AR, Burkholz R, Shamsaei B, Platig J, Glass K, Kuijjer ML, Quackenbush J. GRAND: A database of gene regulatory network models across human conditions. Nucleic Acids Res. 2022 Jan 7;50(D1):D610-D621. PMID: 34508353. PMCID: PMC8728257. DOI: 10.1093/nar/gkab778.

16. Ben Guebila M, Weighill D, **Lopes-Ramos CM**, Burkholz R, Pop RT, Palepu K, Shapoval M, Fagny M, Schlauch D, Glass K, Altenbuchinger M, Kuijjer ML, Platig J, Quackenbush J. An online notebook resource for reproducible inference, analysis, and publication of gene regulatory networks. Nat Methods. 2022 May;19(5):511-513. PMID: 35459940. PMCID: PMC9239854. DOI: 10.1038/s41592-022-01479-2.

17. **Lopes-Ramos CM**, Quackenbush J, DeMeo DL. Genome-Wide Sex and Gender Differences in Cancer. Front Oncol. 2020 Nov 23;10:597788. PMID: 33330090. PMCID: PMC7719817. DOI: 10.3389/fonc.2020.597788.

18. **Lopes-Ramos CM**, Chen C-Y, Kuijjer M L, Paulson JN, Sonawane AR, Fagny M, Platig J, Glass K, Quackenbush J, DeMeo DL. Sex differences in gene expression and regulatory

networks across twenty-nine human tissues. Cell Rep. 2020 Jun 23;31(12):107795. PMID: 32579922 PMCID: PMC7898458. DOI: 10.1016/j.celrep.2020.107795.

19. Rocha AL, de Lima TI, de Souza GP, Corrêa RO, Ferrucci DL, Rodrigues B, **Lopes-Ramos CM,** Nilsson D, Knittel TL, Castro PR, Fernandes MF, Dos Santos Martins F, Parmigiani RB, Silveira LR, Carvalho HF, Auwerx J, Vinolo MAR, Boucher J, Mori MA. Enoxacin induces oxidative metabolism and mitigates obesity by regulating adipose tissue miRNA expression. Sci Adv. 2020 Dec 2;6(49):eabc6250. PMID: 33268375. PMCID: PMC7710362. DOI: 10.1126/sciadv.abc6250.

20. Campbell PT, Ambrosone CB, Nishihara R, Aerts HJWL, Bondy M, Chatterjee N, Garcia-Closas M, Giannakis M, Golden JA, Heng YJ, Kip NS, Koshiol J, Liu XS, **Lopes-Ramos CM**, Mucci LA, Nowak JA, Phipps AI, Quackenbush J, Schoen RE, Sholl LM, Tamimi RM, Wang M, Weijenberg MP, Wu CJ, Wu K, Yao S, Yu KH, Zhang X, Rebbeck TR, Ogino S. Proceedings of the fourth international molecular pathological epidemiology (MPE) meeting. Cancer Causes Control. 2019 Aug;30(8):799-811. PMID: 31069578. PMCID: PMC6614001. DOI: 10.1007/s10552-019-01177-z.

21. **Lopes-Ramos CM**, Marieke L Kuijjer, Shuji Ogino, Charles S Fuchs, Dawn L DeMeo, Kimberly Glass, John Quackenbush. Gene regulatory network analysis identifies sex-linked differences in colon cancer drug metabolism. Cancer Res. 2018 Oct 1;78(19):5538-5547. PMID: 30275053. PMCID: PMC6169995. DOI: 10.1158/0008-5472.CAN-18-0454.
    • *Commentary:* Arnold AP and Disteche CM. Sexual Inequality in the Cancer Cell. Cancer Res. 2018 Oct 1;78(19):5504-5505.

22. Pinto S, Sato VN, De-Souza EA, Ferraz RC, Camara H, Pinca APF, Mazzotti DR, Lovci MT, Tonon G, **Lopes-Ramos CM**, Parmigiani RB, Wurtele M, Massirer KB, Mori MA. Enoxacin extends lifespan of C. elegans by inhibiting miR-34-5p and promoting mitohormesis. Redox Biol. 2018 Sep:18:84-92. PMID: 29986212. PMCID: PMC6037660. DOI: 10.1016/j.redox.2018.06.006.

23. Koyama FC, **Lopes-Ramos CM**, Fernandes JM, Ledesma F, Alves VAF, Perez RO, Camargo AA. Effect of Akt-activation and experimental pharmacological inhibition on responses to neoadjuvant chemoradiotherapy in rectal cancer. Br J Surg. 2018 Jan;105(2):e192-e203. PMID: 29341150. DOI: 10.1002/bjs.10695.

24. Sonawane AR, Platig J, Fagny M, Chen CY, Paulson JN, **Lopes-Ramos CM**, DeMeo DL, Quackenbush J, Glass K, Kuijjer ML. Understanding Tissue-Specific Gene Regulation. Cell Rep. 2017 Oct 24;21(4):1077-1088. PMID: 29069589. PMCID: PMC5828531. DOI: 10.1016/j.celrep.2017.10.001.

25. Fagny M, Paulson JN, Kuijjer ML, Sonawane AR, Chen CY, **Lopes-Ramos CM**, Glass K, Quackenbush J, Platig J. Exploring regulation in tissues with eQTL networks. Proc Natl Acad Sci U S A. 2017 Sep 12;114(37):E7841-E7850. PMID: 28851834. PMCID: PMC5604022. DOI: 10.1073/pnas.1707375114.

26. Paulson JN, Chen CY, **Lopes-Ramos CM**, Kuijjer ML, Platig J, Sonawane AR, Fagny M, Glass K, Quackenbush J. Tissue-aware RNA-Seq processing and normalization for heterogeneous and

sparse data. BMC Bioinformatics. 2017 Oct 3;18(1):437. PMID: 28974199. PMCID: PMC5627434. DOI: 10.1186/s12859-017-1847-x.

27. **Lopes-Ramos CM***, Paulson JN*, Chen CY, Kuijjer ML, Fagny M, Platig J, Sonawane AR, DeMeo DL, Quackenbush J, Glass K. Regulatory network changes between cell lines and their tissues of origin. BMC Genomics. 2017 Sep 12;18(1):723. PMID: 28899340. PMCID: PMC5596945. DOI: 10.1186/s12864-017-4111-x.

28. **Lopes-Ramos CM**, Barros BP, Koyama FC, Carpinetti PA, Pezuk J, Doimo NTS, Habr-Gama A, Perez RO, Parmigiani RB. E2F1 somatic mutation within miRNA target site impairs gene regulation in colorectal cancer. PLoS One. 2017 Jul 13;12(7):e0181153. PMID: 28704519. PMCID: PMC5509303. DOI: 10.1371/journal.pone.0181153.

29. **Lopes-Ramos CM**, Pereira TC, Dogini DB, Gilioli R, Lopes-Cendes I. Lithium carbonate and coenzyme Q10 reduce cell death in a cell model of Machado-Joseph disease. Braz J Med Biol Res. 2016 Nov 21;49(12):e5805. PMID: 27878228. PMCID: PMC5188859. DOI: 10.1590/1414-431X20165805.

30. Marçola M, **Lopes-Ramos CM**, Pereira EP, Cecon E, Fernandes PA, Tamura EK, Camargo AA, Parmigiani RB, Markus RP. Light/Dark Environmental Cycle Imposes a Daily Profile in the Expression of microRNAs in Rat CD133+ Cells. J Cell Physiol. 2016 Sep;231(9):1953-63. PMID: 26728119. DOI: 10.1002/jcp.25300.

31. **Lopes-Ramos CM***, Koyama FC*, Habr-Gama A, Salim ACM, Bettoni F, Asprino P, França GS, Gama-Rodrigues J, Parmigiani RB, Perez RO, Galante PAF, Camargo AA. Comprehensive evaluation of the effectiveness of gene expression signatures to predict complete response to nCRT and guide surgical intervention in rectal cancer. Cancer Genet. 2015 Jun;208(6):319-26. PMID: 25963525. DOI: 10.1016/j.cancergen.2015.03.010.

32. **Lopes-Ramos CM**, Habr-Gama A, Quevedo BS, Felício NM, Bettoni F, Koyama FC, Asprino P, Galante PAF, Gama-Rodrigues J, Camargo AA, Perez RO, Parmigiani RB. Overexpression of miR-21-5p as a predictive marker for complete tumor regression to neoadjuvant chemoradiotherapy in rectal cancer patients. BMC Med Genomics. 2014 Dec 11;7:68. PMID: 25496125. PMCID: PMC4279677. DOI: 10.1186/s12920-014-0068-7.

33. Hinske LC, França GS, Torres HAM, **Lopes-Ramos CM**, Heyn J, Ohno-Machado J, Kreth S, Galante PAF. miRIAD – integrating microRNA inter- and intragenic data. Database (Oxford). 2014 Oct 6:2014:bau099. PMID: 25288656. PMCID: PMC4186326. DOI: 10.1093/database/bau099.

34. França MC, Yasuda CL, Pereira FR, D'Abreu A, **Lopes-Ramos CM**, Rosa MV, Cendes F, Lopes-Cendes I. White and grey matter abnormalities in patients with SPG11 mutations. J Neurol Neurosurg Psychiatry. 2012 Aug;83(8):828-33. PMID: 22696581. DOI: 10.1136/jnnp-2011-300129.

**b. Accepted / In Press**

1. Phillips EK, Regan E, Hoth KF, Patchen B, Saw W-Y, **Lopes-Ramos CM**, Make B, Bon J, Yohannes AM, Hanania NA, Washko G, Silverman E, Crapo J, Bowler R, Carey V, DeMeo DL. Lung function change and quantitative CT measurements associate with prospective frailty. ERJ Open Res 2026; in press (https://doi.org/10.1183/23120541.00470-2026).

**2. Full Papers Without Peer Review**

1. Fischer J, Shutta KH, Chen C, Fanfani V, Saha E, Mandros P, Ben Guebila M, Xiu J, Nieva J, Liu S, Uprety D, Spetzler D, **Lopes-Ramos CM**, DeMeo D, Quackenbush J. Selective loss of Y chromosomes in lung adenocarcinoma modulates the tumor immune environment through cancer/testis antigens. bioRxiv. 2024 Sep 22;. doi: 10.1101/2024.09.19.613876. PubMed PMID: 39345481; PubMed Central PMCID: PMC11430018.

**3. Abstracts Given During Last Three Years**

1. **Lopes-Ramos CM**, Moll M, Hobbs BD, Stoller JK, Sandhaus RA, McElvaney G, Rennard SI, Brantly ML, Barker A, Campbell EJ, Eden E, Strange C, Silverman EK, DeMeo DL. Sex Hormones and Inflammatory Proteins Impact Disease Heterogeneity in Alpha-1 Antitrypsin Deficiency-Associated COPD. American Thoracic Society International Conference, Orlando, 2026.

2. **Lopes-Ramos CM**, Moll M, Hobbs BD, Stoller JK, Sandhaus RA, McElvaney G, Rennard SI, Brantly ML, Barker A, Campbell EJ, Eden E, Strange C, Silverman EK, DeMeo DL. Sex Hormones and Inflammatory Proteins Impact Disease Heterogeneity in Alpha-1 Antitrypsin Deficiency-Associated COPD. Connors-MGB Research Collaborative Symposium, Boston, 2026. Poster Award.

3. **Lopes-Ramos CM**, Quackenbush J, DeMeo DL. Transcription Factors Orchestrate Sex-Specific Regulatory Networks Across Human Tissues. American Society of Human Genetics Annual Meeting, Boston, 2025.

4. **Lopes-Ramos CM**, Saha E, Yun JH, Hersh CP, Silverman EK, DeMeo DL, Quackenbush J, Glass K. Lung cancer gene regulatory networks reflect smoking history and age-related metabolic pathway alterations. American Association of Cancer Research, Chicago, 2025.

5. **Lopes-Ramos CM**, Huang Y, Saw W-Y, Hersh CP, Silverman EK, Quackenbush J, DeMeo DL. The Impact of X Chromosome Inactivation Patterns and Social Determinants of Health on COPD Outcomes in Women, American Thoracic Society International Conference, San Francisco, 2025.

6. **Lopes-Ramos CM**, Huang Y, Saw W-Y, Hersh CP, Silverman EK, Quackenbush J, DeMeo DL. The Impact of X Chromosome Inactivation Patterns on COPD Outcome. Connors-MGBRI Center Symposium, Boston, 2025. Poster Award.

7. **Lopes-Ramos CM**, Huang Y, Shutta KH, Silverman EK, DeMeo DL. X Chromosome Methylation Patterns and Sex-Dosage Imbalance: Implications for COPD Susceptibility and Severity. Brigham Lung Research Day, Boston, 2024. Distinguished Abstract Award.

**Abstract Oral Presentations**

1. X Chromosome Methylation Patterns and Sex-Dosage Imbalance: Implications for COPD Susceptibility and Severity
   American Thoracic Society International Conference, San Diego, CA, 2024.

2. Using Gene Regulatory Networks to Understand Sex Differences in Lung Cancer Gene Regulation
   American Thoracic Society International Conference, Washington D.C., 2023.

3. Regulatory network approaches reveal sex differences in cancer gene regulation
   Charles J. Epstein Trainee Awards for Excellence in Human Genetics Research, semifinalist
   American Society of Human Genetics Annual Meeting, Los Angeles, CA 2022.

4. Global miRNA expression study to predict complete tumor regression to neoadjuvant chemoradiotherapy in rectal cancer patients
   Challenges and Solutions in Cancer Research and Treatment, Rio de Janeiro, Brazil, 2014.

5. Predicting response to neoadjuvant therapy in patients with rectal cancer through global miRNA expression study
   X Summer Course Bioinformatics - R and Bioconductor, USP, Ribeirão Preto, Brazil, 2014.

6. Construction and evaluation of an in vitro model of expanded ataxin-3 cytotoxic effects
   IX Meeting of the Brazilian Society of Neurological Research (SBIN), Curitiba, Brazil, 2009.

7. Low frequency of SPG11 mutation in Brazilian patients with hereditary spastic paraplegia with thin corpus callosum
   IX Meeting of the Brazilian Society of Neurological Research (SBIN), Curitiba, Brazil, 2009.

**4. Books**

**a. Complete Books Written**

None.

**b. Books Edited**

None.

**c. Book Chapters Written**

1. Canal D, Carpinetti-Oliveira PA, **Lopes-Ramos CM,** Brustolini OJB, Ferreira MFS. Capítulo 13. RNA-SEQ: Principais conceitos e cuidados [Chapter 13. RNA-SEQ: Concepts and Precautions]. In Tópicos Especiais em Genética e Melhoramento II [Special Topics in Genetics and Breeding II]. Alegre, ES : CCA-UFES; 2018. p. 274-297. (Published in Portuguese)

**5. Other Works Communicating Research Results to Scientific Colleagues**

1. Network Zoo: Softwares for network generation and analyses.
   [https://netzoo.github.io]

2. netBooks: a cloud notebook server for network analysis [web resource].
   [http://netbooks.networkmedicine.org]

3. Identification and expression study of polyadenylation variants and miRNAs through large scale sequencing in colorectal tumor samples [dissertation].
   São Paulo (SP, Brazil): A.C. Camargo Cancer Center; 2014.
   [http://accamargo.phlnet.com.br/Doutorado/2014/CamilaLopes/CamilaLopes.pdf]

**6. Other Works Communicating Research Results to General Public**

2026 Press Interview – "Lung cancer in women emerges as a distinct disease"
Nature 653, S76–S77 (2026)

**D. Innovation and Commercialization**

**1. Patents**

None.

**2. Device, Software or Other Development**

| | |
|---|---|
| Web-based resource for gene regulatory networks and drug repurposing | GRAND: Gene Regulatory Network Database<br>https://grand.networkmedicine.org/<br>Current version: 1.7.0. Last update: 7/31/2025.<br>GRAND is a collection of gene regulatory networks built from human tissues, cancers, and cell lines, and it also provides analytic tools for analyzing networks and drug repurposing. Researchers use GRAND internationally; they can download these networks to answer various scientific questions using data from a variety of normal tissues and cancer types, as well as to identify potential therapeutic drugs. |
| Software for analyzing RNA Sequencing data from multiple conditions or tissues | YARN: Robust Multi-Condition RNA-Seq Preprocessing and Normalization<br>R package version 1.7.0 (2018)<br>https://www.bioconductor.org/packages/devel/bioc/html/yarn.html<br>Paulson JN, Chen C, Lopes-Ramos C, Kuijjer M, Platig J, Sonawane A, Fagny M, Glass K, Quackenbush J<br>YARN is a software tool used by researchers internationally. My colleagues and I developed this tool to analyze RNA sequencing data sets from multiple conditions or tissues. It helps improve data quality and normalization, making it easier to accurately compare gene expression across different conditions. |
| Dataset of gene regulatory networks across tissues | Gene regulatory networks for 38 human tissues [Data set]. Zenodo. 2017.<br>[http://doi.org/10.5281/zenodo.838734] |

Sonawane AR, Platig J, Fagny M, Chen CY, Paulson JN, Lopes-Ramos CM, DeMeo DL, Quackenbush J, Glass K, Kuijjer ML.

## III. TEACHING INFORMATION

### A. Educational Leadership Roles

2018–present Course Co-director Instructor, "Introductory Genomics & Bioinformatics for Health Research" (BST280), Harvard T.H. Chan School of Public Health.

### B. Didactic Coursework

#### 1. Courses Taught at Current Institution

2018–present "Introductory Genomics & Bioinformatics for Health Research" (BST280), Harvard T.H. Chan School of Public Health
Course Co-director and Instructor
3 hours/week for 12 weeks
Audience: Master's students

2025 "Applied Biomarkers in Cancer Epidemiology" (EPI246), Harvard T.H. Chan School of Public Health
Invited Lecturer (90 minutes)
Audience: Master's students

#### 2. Courses Taught at Other Institutions

2014 miRNA and cancer. UNICID, São Paulo, Brazil – Invited lecturer (90 minutes)

2013 miRNA and cancer. Hospital Sírio-Libanês, São Paulo, Brazil – Invited lecturer (90 minutes)

#### 3. Courses Expected to Be Taught at BCM

To be determined.

### C. Curriculum Development Work

#### 1. Courses/Curricula

• "Introductory Genomics & Bioinformatics for Health Research" (BST280), Harvard
Full course design (lectures + labs)
Audience: Master's students

• Cloud-based notebooks and tutorials for genomics and gene regulatory network analysis (netBooks)
[http://netbooks.networkmedicine.org]

Audience: Students, postdoctoral fellows, and researchers in genomics and systems biology

## D. Non-didactic Teaching

### 1. Resident Training

None.

### 2. Clinical Fellow Training

None.

### 3. Research Fellow Training

2025–present Woei-Yuh Saw, PhD – Research Fellow, Brigham and Women's Hospital
Co-mentor with Dawn DeMeo

2025–present Tara Eicher, PhD – Research Fellow, Harvard T.H. Chan School of Public Health
Co-mentor with John Quackenbush.

2021–2024 Enakshi Saha, PhD – Research Fellow, Harvard T.H. Chan School of Public Health
(now Assistant Professor of Biostatistics, Univ. of South Carolina)
Co-mentor with John Quackenbush

### 4. Graduate Student Training

2019 - 2020 Thesis Defense Committee: Computational Biology and Quantitative Genetics Program, Department of Biostatistics, Harvard T.H. Chan School of Public Health
2019: Lucy Liu
2020: Aonia Traxler
2020: Ursula Widocki

2019 - 2020 Aonia Traxler, MSt, Computational Biology and Quantitative Genetics Master Program, Harvard T.H. Chan School of Public Health
Supervision of master thesis entitled "Sexual dimorphism in gene regulatory networks for bladder and thyroid cancer and the implications on clinical treatment." Current position: CTO, HairDAO.

2018 - 2019 Lucy Liu, MSc, Computational Biology and Quantitative Genetics Master Program, Harvard TH Chan School of Public Health
Supervision of master thesis entitled "Identification of sex differences in lung adenocarcinoma with regulatory networks." Current position: Senior Consultant, ZS Boston.

### 5. Medical Student Mentoring

None.

### E. Faculty Development or Continuing Medical Education

2025 "Non-HHS Grants." Panelist at CDNM Division-wide Seminar Series, Brigham and Women's Hospital.

2023 Career MODE Final Symposium – Invited presentation at Columbia University (Virtual) with mentoring and professional development content.

### F. Lectures and Presentations

2014 miRNAs as predictive biomarkers for rectal cancer. UNICAMP, Campinas, Brazil (2 hours)

2009 Human Genetics. UNESP, Ilha Solteira, Brazil – Invited lecturer (4 hours)

2009 Introduction to RNAi and miRNA. UNICAMP, Campinas, Brazil – Invited lecturer (2 hours)

### G. Visiting Professorships

None.

## IV. PATIENT CARE AND CLINICAL CONTRIBUTIONS

Not applicable (research-focused role).

## V. SERVICE CONTRIBUTIONS

### A. Administrative Assignments and Committees

2026 Proceedings Program Committee Member, ISMB 2026 Conference, International Society for Computational Biology

2025 Poster Prize Selection Committee Member, 70º CBG Genetica 2025 | International Congress of the Brazilian Genetics Society, Belém, Pará, Brazil

### B. National, Regional or Local Participation in Professional or Voluntary Organizations

2025 Single-Cell Multiomic Dissection of Gene Regulation in Disease
American Society of Human Genetics Annual Meeting, Boston
Role: Moderator

2022 North Carolina Community Connections, Learning About Lung Cancer
American Lung Association
Role: Panelist

Event dedicated to educating the community and answering questions about lung cancer.

2016 Behind the Breakthroughs
Dana-Farber Cancer Institute, Boston
Role: Explain scientific research to patients and donors to enhance understanding of ongoing cancer research and its impact.

## C. Other Pertinent Information (including community service)

### Press Coverage

| | | |
|---|---|---|
| 2026 | Lung cancer in women (Press Interview) | Nature: Lung cancer in women emerges as a distinct disease<br>Nature 653, S76-S77 (2026)<br>https://www.nature.com/articles/d41586-026-01459-y |
| 2020 | Sex differences in gene expression and regulatory networks across twenty-nine human tissues (Press Coverage) | GenomeWeb: Tissue Network Analysis Points to Significant Sex-Related Regulatory Differences (06/23/2020).<br>https://www.genomeweb.com/sequencing/tissue-network-analysis-points-significant-sex-related-regulatory-differences |
| 2018 | Gene regulatory network analysis identifies sex-linked differences in colon cancer drug metabolism (Press Coverage) | The ASCO Post: Sex-Linked Differences in Cancer May Identify Specific Genetic Drivers, Predict Responses to Treatment (10/4/2018).<br>American Association for Cancer Research, Medical Press: Sex-linked differences in cancer may identify gender-specific genetic drivers and predict responses to treatment (10/02/2018). https://medicalxpress.com/news/2018-10-sex-linked-differences-cancer-gender-specific-genetic.html |
| 2017 | Understanding Tissue-Specific Gene Regulation (Press Coverage) | Science Daily: Using networks to understand tissue-specific gene regulation.<br>www.sciencedaily.com/releases/2017/10/171027141537.htm<br>DoveMed: Using networks to understand tissue-specific gene regulation.<br>Phys Org: Using networks to understand tissue-specific gene regulation. https://phys.org/news/2017-10-networks-tissue-specific-gene.html |