Lorena Pantano, Ph.D.

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Summary

Computational biologist expert in high-dimensional data, from sequencing data to microscope screening. 13 years of experience in biological data analysis using the most well-established tools and contributing to novel algorithms to improve the quantification and visualization of genomic data. I approach scientific projects with passion and believe that a team and not an individual alone can successfully conquer them.

Competences

Building Partnerships, Building Trust, Continuous Learning, Decision Making, Delivers Results, Interpersonal Skills, Planning and Organizing, Problem Analysis and Problem Solving, Pursues Excellence, Teamwork and Collaboration, Time Management, Valuing Diversity

Education

Coursera **2020**.
Certificate in *Neural Networks and Deep Learning*

Center for Genomic Regulation, Barcelona, Spain **2011**
Ph.D. in *Biomedicine*
Full characterization of the small RNA transcriptome using novel computational methods for high-throughput sequencing data: study of miRNA variability in eukaryote organisms

University of Pompeu Fabra, Barcelona, Spain **2008**
M.S. in *Bioinformatics for health science*

University of Granada, Granada, Spain **2005**
B.S *Biochemistry*

Experience

Axcella Health, Cambridge, MA **2020 - to date**
Principal Scientist in Computational Biology

- Leading R&D pipelines with computational strategies
- Integrating genomic/metabolimic/transcriptomic data to understand gene regulation
- Leading visualization plarform to boost biological interpretation
- Developing bioinformatic infrastructure to ensure reproducibility and scalability in the cloud
- Experience with CROs
- Senior Manager and Mentor

eGenesis, Cambridge, MA **2019 - 2020**
Senior Computational Biologist

- Responsable of the internal next generation sequencing team with oxford nanopore and illumina sequencers

- Research of putative chromatine opening genomic elements to enforce expression of transgenes through machine learning methods
- Technical lead in the quality control of modified pigs from genomic data
- Develop small RNAseq, (Single Cell and bulk) RNA-seq, and ChIP-seq pipelines as part of the nf-core community
- System Architect for the computational infrastructure based on the cloud
- Help with manuscript materials
- Mentor junior researchers in the group

Picower Institute of MIT, Cambridge, MA **2019**
Research Scientist - Bioinformatics Core Supervisor

- Organize and maintain bioinformatics pipelines for researchers
- Help with grant and manuscript materials
- Develop small RNAseq, (Single Cell and bulk) RNA-seq, and ChIP-seq pipelines as part of the nf-core community
- Develop variant calling pipeline as part of the bcbio-nextgen
- Develop supervised and unsupervised clustering, differential expression, and visualization analyses in python frameworks and the Bioconductor platform
- Mentor junior researchers in the group

Boehringer Ingelheim, **2016 - 2019**
Computational Biologist - Fellowship, 80%

- Lead the bioinformatic analysis (at Harvard) in a international collaboration for the study of fibrosis across organs
- Design and analyze the RNAseq and smallRNAseq data in a pre-clinical NASH study
- Design, automatize and optimize the high-throughput screening pipeline of small molecules in three cell models
- Manage junior bioinformatician

Harvard T.H. Chan School of Public Health, Boston, MA **2017 - 2019**
Research Scientist

- Organize the data science research in the small RNA-seq field inside the (**miRTOP**) group
- Lead the bioinformatic analysis in the cross organ fibrosis project collaboration between Harvard University and Boehringer Ingelheim
- Develop tools for NGS data analysis: small RNAseq, (Single Cell and bulk) RNA-seq, ChIP-seq, WholeGenome-seq as part of the bcbio-nextgen python framework and Bioconductor platform
- Mentor junior researchers in the group

Harvard T.H. Chan School of Public Health, Boston, MA **2014-2017**
Research Associate

- Developed the visualization and integration of multi-omics data
- Developed pipelines for NGS data analysis (ATACseq, ChIPseq, RNAseq) inside the bcbio-nextgen python framework
- Developed co-correlation methods to detect transcriptional modules from transcriptome data

Institute of Biotechnology and Biomedicine, Barcelona, Spain **2013 - 2014**
Post-doctoral fellow

- Detected de-novo transcripts as effect of inversion in the HapMap population
- Expression quantitive trait loci analysis of inversion in the HapMap population
- Developed inversion database back-end

ASCIDEA, Barcelona, Spain **2011-2014**
Co-founder and CTO

- Led a group of 3 bioinformaticians
- Supervised cloud computing systems
- Developed computational pipelines

Institute of Predictive and Personalized Medicine of Cancer, Barcelona, Sapin **2011–2013**
Post-doctoral fellow

- Determined small RNA characterization in human sperm samples

Bioinformatics tools

seqcluster: python package for smallRNA detection and quantification

seqclusterViz: Web-app for smallRNAseq visualization

isomiRs: R/Bioconductor package for isomiR detection and quantification

DEGreport: R/Bioconductor package for Differential Expressed results analysis and visualization

nf-core: community driven pipelines

bcbio-nextgen: python framework for the analysis of sequencing data

cloudbiolinux: python framework for the installation of specific tools related to a given bioinformatic analysis

bioconda: package manager for the installation of bioinformatics tools

multiqc: python package for the generation of reports

Instructor activities

Small RNAseq analysis, Harvard T.H. Chan School of Public Health, Boston, MA	2015-2018
Data visualization, PRBB, Spain	2013
Workshop of ChIP-Seq analysis, University of Vic, Spain	2013
Workshop of Metagenomic, University of Vic, Spain	2013
Workshop of small RNA analysis, CRG, Spain	2010

Reviewer experience

Editor at JOSS	2019-todate
RNA journal	2018
NAR journal	2017-2018
Scientific Reports journal	2018
Bioinformatics journal	2018-2019
BMC Genomics journal	2017
BOSC program committee	2014-2018
Student Council Symposium program committee	2010-2012

Leadership activities

Program committee, Bioconductor Conference	2019
Founder and Co-organizer of women in bioinformatics MeetUp, Cambridge, MA	2014-to date
Program committee, Bioinformatics Open Source Conference	2014-to date
Co-founder of RSG Spain, the Spanish student group of ISCB student council	2010
Former member of ISCB student council	2010-2014

Awards and Honors

Leadership Award (eGenesis)	2020
Research Scientist Award (Harvard Chan School)	2018
Travel Fellowship for Student Council Organization	2011
Travel Fellowship for ISMB participation	2010
Training University Lecturers fellowship	2008-2011
University Schoolarship	2000-2005

Work presented at International Conferences

Great Lakes Bioinformatics Consortioum	2017-Chicago
Bioinformatics Open Source Conference	2018-Orlando, 2016-Florida
CodeFest Hacklaton	2016-Florida, 2010-Boston
Bioconductor Annual Conference	2015-Boston, 2017-Boston
Intelligent System for Molecula Biology Annual Conference	2011-Vienna, 2010-Boston

Event Organization

Mind the Gap Barcelona, Co-Chair 2013

ISCB Student Council Symposium Long Beach, Travel fellowship chair 2012

Spain, Portugal and North Africa Student Symposium Barcelona, Program committee chair 2012

ISCB Student Council Symposium Vienna, Co-Chair 2012

Spain, Portugal and North Africa Student Symposium Malaga, Co-Chair 2011

Computational skills

Programming languages: Python (bioconda packages), R (Bioconductor), Java, Bash, LaTeX

Visualization: HTML, CSS, javascript (D3, Charts, jquery)

Databases: MySQL, sqlite3

AWS cloud: EC2, S3, RDS, dynamoDB, SQS, Batch

Control version system: git, svn

High performance computing: Slurm, LSF, SGE

Courses

Improving Deep Neural Networks: Hyperparameter tuning, Regularization and Optimization @ Coursera 2020

Neural Networks and Deep Learning @ Coursera 2020

Structuring Machine Learning Projects @ Coursera 2020

Neural Networks and Deep Learning @ Coursera 2020

Materials Characterization and Analysis for Scientists and Engineers @ Harvard Extension School 2018

Initiating and Planning Projects @ Coursera 2018

Fundamentals and Applications of Microfluidics @ Harvard Extension School 2018

Tissue Engineering for Clinical Applications @ Harvard Extension School 2017

Principles of fMRI 1 @ Coursera 2016

Practical Machine Learning @ Coursera 2016

Calculus One @ Coursera 2015

Regression Model @ Coursera 2014

Analysis of high-throughput sequencing data @ EMBL-EBI 2012

Web applications @ Udacity (CS253) 2012

Machine learning @ Coursera 2012

Introduction to Artificial Intelligence (www.ai-class.org) 2011

Advance R @ CRG 2008

Languages skills

Language	Speech	Writing	Reading
Spanish	Native	Native	Native
English	Proficient	Proficient	Proficient
Catalan	Conversant	Good	Conversant

Selected Publications

5. Podnar, J. W., **Pantano, L.,** Zeller, M. J., Kolling, F. W., Zhang, Y., Alekseyev, Y. O., Niece, J., Deiderick, H., Fan, J., Xuei, X., *et al.* Cross-Site Evaluation of Commercial Sanger Sequencing Chemistries. *Journal of Biomolecular Techniques: JBT* **31,** 88 (2020).
6. Santos, D. M., **Pantano, L.,** Pronzati, G., Grasberger, P., Probst, C. K., Black, K. E., Spinney, J. J., Hariri, L. P., Nichols, R., Lin, Y., *et al.* Screening for YAP Inhibitors Identifies Statins as Modulators of Fibrosis. *American Journal of Respiratory Cell and Molecular Biology* (2020).
7. Desvignes, T., Loher, P., Eilbeck, K., Ma, J., Urgese, G., Fromm, B., Sydes, J., Aparicio-Puerta, E., Barrera, V., Espin, R., *et al.* Unification of miRNA and isomiR research: the mirGFF3 format and the mirtop API. *Bioinformatics* (2019).
13. Pavkovic, M., **Pantano, L.,** Gerlach, C. V., Brutus, S., Boswell, S. A., Everley, R. A., Shah, J. V., Sui, S. H. & Vaidya, V. S. Multi omics analysis of fibrotic kidneys in two mouse models. *Scientific data* **6,** 92 (June 2019).
18. Steinhauser, M. L., Olenchock, B. A., OKeefe, J., Lun, M., Pierce, K. A., Lee, H., **Pantano, L.,** Klibanski, A., Shulman, G. I., Clish, C. B. & Fazeli, P. K. The circulating metabolome of human starvation. *JCI Insight* **3** (Aug. 2018).
20. Carmona, J. J., Accomando, W. P., Binder, A. M., Hutchinson, J. N., **Pantano, L.,** Izzi, B., Just, A. C., Lin, X., Schwartz, J., Vokonas, P. S., Amr, S. S., Baccarelli, A. A. & Michels, K. B. Empirical comparison of reduced representation bisulfite sequencing and Infinium BeadChip reproducibility and coverage of DNA methylation in humans. *npj Genomic Medicine* **2** (2017).
30. **Pantano, L.,** Friedlander, M. R., Escaramis, G., Lizano, E., Pallares-Albanell, J., Ferrer, I., Estivill, X. & Marti, E. Specific small-RNA signatures in the amygdala at premotor and motor stages of Parkinson's disease revealed by deep sequencing analysis. *Bioinformatics (Oxford, England)* (Nov. 2015).
31. **Pantano, L.,** Jodar, M., Bak, M., Ballesca, J. L., Tommerup, N., Oliva, R. & Vavouri, T. The small RNA content of human sperm reveals pseudogene-derived piRNAs complementary to protein-coding genes. *RNA (New York, N.Y.)* **21,** 1085–95 (June 2015).
39. **Pantano, L.,** Estivill, X. & Martí, E. A non-biased framework for the annotation and classification of the non-miRNA small RNA transcriptome. *Bioinformatics (Oxford, England)* **27,** 3202–3 (Nov. 2011).
40. Martí, E., **Pantano, L.,** Bañez-Coronel, M., Llorens, F., Miñones-Moyano, E., Porta, S., Sumoy, L., Ferrer, I. & Estivill, X. A myriad of miRNA variants in control and Huntington's disease brain regions detected by massively parallel sequencing. *Nucleic Acids Research* **38,** 7219–7235 (2010).
41. **Pantano, L.,** Estivill, X. & Martí, E. SeqBuster, a bioinformatic tool for the processing and analysis of small RNAs datasets, reveals ubiquitous miRNA modifications in human embryonic cells. *Nucleic Acids Research* **38,** e34 (2010).

Publications

1. Creus-Muncunill, J., Guisado-Corcoll, A., Venturi, V., **Pantano, L.,** Escarams, G., de Herreros, M. G., Solaguren-Beascoa, M., Gomez-Valero, A., Navarrete, C., Masana, M., *et al.* Huntington's disease brain-derived small RNAs recapitulate associated neuropathology in mice. *Acta Neuropathologica,* 1–20 (2021).
2. Gupta, H., Rubio, M., Sitoe, A., Varo, R., Cistero, P., Madrid, L., Cuamba, I., Jimenez, A., Martinez-Vendrell, X., Barrios, D., *et al.* Plasma MicroRNA Profiling of Plasmodium falciparum Biomass and Association with Severity of Malaria Disease. *Emerging Infectious Diseases* **27,** 430 (2021).
3. Alsamman, S., Christenson, S. A., Yu, A., Ayad, N. M., Mooring, M. S., Segal, J. M., Hu, J. K.-H., Schaub, J. R., Ho, S. S., Rao, V., *et al.* Targeting acid ceramidase inhibits YAP/TAZ signaling to reduce fibrosis in mice. *Science Translational Medicine* **12** (2020).
4. Pao, P.-C., Patnaik, D., Watson, L. A., Gao, F., Pan, L., Wang, J., Adaikkan, C., Penney, J., Cam, H. P., Huang, W.-C., *et al.* HDAC1 modulates OGG1-initiated oxidative DNA damage repair in the aging brain and Alzheimer's disease. *Nature communications* **11,** 1–17 (2020).
5. Podnar, J. W., **Pantano, L.,** Zeller, M. J., Kolling, F. W., Zhang, Y., Alekseyev, Y. O., Niece, J., Deiderick, H., Fan, J., Xuei, X., *et al.* Cross-Site Evaluation of Commercial Sanger Sequencing Chemistries. *Journal of Biomolecular Techniques: JBT* **31,** 88 (2020).
6. Santos, D. M., **Pantano, L.,** Pronzati, G., Grasberger, P., Probst, C. K., Black, K. E., Spinney, J. J., Hariri, L. P., Nichols, R., Lin, Y., *et al.* Screening for YAP Inhibitors Identifies Statins as Modulators of Fibrosis. *American Journal of Respiratory Cell and Molecular Biology* (2020).
7. Desvignes, T., Loher, P., Eilbeck, K., Ma, J., Urgese, G., Fromm, B., Sydes, J., Aparicio-Puerta, E., Barrera, V., Espin, R., *et al.* Unification of miRNA and isomiR research: the mirGFF3 format and the mirtop API. *Bioinformatics* (2019).
8. Engeland, W. C., Massman, L., Miller, L., Leng, S., Pignatti, E., **Pantano, L.,** Carlone, D. L., Kofuji, P. & Breault, D. T. Sex Differences in Adrenal Bmal1 Deletion–Induced Augmentation of Glucocorticoid Responses to Stress and ACTH in Mice. *Endocrinology* **160,** 2215–2229 (2019).
9. Giner-Delgado, C., Villatoro, S., Lerga-Jaso, J., Gayà-Vidal, M., Oliva, M., Castellano, D., **Pantano, L.,** Bitarello, B. D., Izquierdo, D., Noguera, I., *et al.* Evolutionary and functional impact of common polymorphic inversions in the human genome. *Nature communications* **10,** 1–14 (2019).
10. Hanlon, K., Thompson, A., **Pantano, L.,** Hutchinson, J. N., Al-Obeidi, A., Wang, S., Bliss-Moreau, M., Helble, J., Alexe, G., Stegmaier, K., *et al.* Single-cell cloning of human T-cell lines reveals clonal variation in cell death responses to chemotherapeutics. *Cancer genetics* **237,** 69–77 (2019).
11. Mavrikaki, M., **Pantano, L.,** Potter, D. N., Rogers-Grazado, M. A., Anastasiadou, E., Amr, S., Slack, F. J., Ressler, K. J., Daskalakis, N. P. & Chartoff, E. Sex-dependent changes in miRNA expression in the bed nucleus of the stria terminalis following stress. *Frontiers in molecular neuroscience* **12,** 236 (2019).
12. **Pantano, L.,** Pantano, F., Marti, E. & Sui, S. H. Visualization of the small RNA transcriptome using seqclusterViz. *F1000Research* **8** (2019).

13. Pavkovic, M., **Pantano, L.,** Gerlach, C. V., Brutus, S., Boswell, S. A., Everley, R. A., Shah, J. V., Sui, S. H. & Vaidya, V. S. Multi omics analysis of fibrotic kidneys in two mouse models. *Scientific data* **6,** 92 (June 2019).

14. Podnar, J. W., Kolling, F. W., Zeller, M. J., Zhang, Y., Thimmapuram, J., Alekseyev, Y. O., Deiulio, A., Niece, J., Deiderick, H., Fan, J., *et al.* Cross Site Evaluation of Sanger Sequencing Dye Chemistries. *Journal of biomolecular techniques: JBT* **30,** S46 (2019).

15. Sui, S. H., Kirchner, R., Steinbaugh, M., Boswell, S., Piper, M., Barrera, V., **Pantano, L.,** Khetani, R., Mistry, M., Rutherford, K., *et al.* Supporting Single Cell RNA-seq Analysis at Harvard-A Community Approach. *Journal of Biomolecular Techniques: JBT* **30,** S39 (2019).

16. Rubio, M., Bustamante, M., Hernandez-Ferrer, C., Fernandez-Orth, D., **Pantano, L.,** Sarria, Y., Pique-Borras, M., Vellve, K., Agramunt, S., Carreras, R., Estivill, X., Gonzalez, J. R. & Mayor, A. Circulating miRNAs, isomiRs and small RNA clusters in human plasma and breast milk. *PLoS ONE* **13** (2018).

17. Rubio Martinez, M., Bustamante Pineda, M., Hernandez-Ferrer, C., Fernandez-Orth, D., **Pantano, L.,** Sarria-Trujillo, Y., Pique-Borras, M., Vellve del Amo, K., Agramunt, S., Carreras Collado, R., *et al.* Circulating miRNAs, isomiRs and small RNA clusters in human plasma and breast milk (2018).

18. Steinhauser, M. L., Olenchock, B. A., OKeefe, J., Lun, M., Pierce, K. A., Lee, H., **Pantano, L.,** Klibanski, A., Shulman, G. I., Clish, C. B. & Fazeli, P. K. The circulating metabolome of human starvation. *JCI Insight* **3** (Aug. 2018).

19. Busby, B., Weitz, E., **Pantano, L.,** Zhu, J. & Upton, B. Viewing RNA-seq data on the entire human genome. *F1000Research* **6** (2017).

20. Carmona, J. J., Accomando, W. P., Binder, A. M., Hutchinson, J. N., **Pantano, L.,** Izzi, B., Just, A. C., Lin, X., Schwartz, J., Vokonas, P. S., Amr, S. S., Baccarelli, A. A. & Michels, K. B. Empirical comparison of reduced representation bisulfite sequencing and Infinium BeadChip reproducibility and coverage of DNA methylation in humans. *npj Genomic Medicine* **2** (2017).

21. Daily, K., Ho Sui, S. J., Schriml, L. M., Dexheimer, P. J., Salomonis, N., Schroll, R., Bush, S., Keddache, M., Mayhew, C., Lotia, S., Perumal, T. M., Dang, K., **Pantano, L.,** Pico, A. R., Grassman, E., Nordling, D., Hide, W., Hatzopoulos, A. K., Malik, P., Cancelas, J. A., Lutzko, C., Aronow, B. J. & Omberg, L. Molecular, phenotypic, and sample-associated data to describe pluripotent stem cell lines and derivatives. *Scientific Data* **4,** 170030 (Mar. 2017).

22. Daily, K., Sui, S. J. H., Schriml, L. M., Dexheimer, P. J., Salomonis, N., Schroll, R., Bush, S., Keddache, M., Mayhew, C., Lotia, S., *et al.* Molecular, phenotypic, and sample-associated data to describe pluripotent stem cell lines and derivatives. *Scientific data* **4,** 1–10 (2017).

23. Mehta, S., Cronkite, D. A., Basavappa, M., Saunders, T. L., Adiliaghdam, F., Amatullah, H., Morrison, S. A., Pagan, J. D., Anthony, R. M., Tonnerre, P., *et al.* Maintenance of macrophage transcriptional programs and intestinal homeostasis by epigenetic reader SP140. *Science immunology* **2** (2017).

24. Mehta, S., Cronkite, D. A., Basavappa, M., Saunders, T. L., Adiliaghdam, F., Amatullah, H., Morrison, S. A., Pagan, J. D., Anthony, R. M., Tonnerre, P., Lauer, G. M., Lee, J. C., Digumarthi, S., **Pantano, L.,** Ho Sui, S. J., Ji, F., Sadreyev, R., Zhou, C., Mullen, A. C., Kumar, V., Li, Y., Wijmenga, C., Xavier, R. J., Means, T. K. & Jeffrey, K. L. Maintenance of macrophage transcriptional programs and intestinal homeostasis by epigenetic reader SP140. *Science Immunology* **2,** eaag3160 (Mar. 2017).

25. Ransey, E., Björkbom, A., Lelyveld, V., Biecek, P., **Pantano, L.,** Szostak, J. & Sliz, P. Comparative analysis of LIN28-RNA binding sites identified at single nucleotide resolution. *RNA Biology* (2017).

26. Ransey, E., Bjorkbom, A., Lelyveld, V. S., Biecek, P., **Pantano, L.,** Szostak, J. W. & Sliz, P. Comparative analysis of LIN28-RNA binding sites identified at single nucleotide resolution. *RNA biology* **14,** 1756–1765 (2017).

27. Steinbaugh, M. J., **Pantano, L.,** Kirchner, R. D., Barrera, V., Chapman, B. A., Piper, M. E., Mistry, M., Khetani, R. S., Rutherford, K. D., Hofmann, O., Hutchinson, J. N. & Ho Sui, S. bcbioRNASeq: R package for bcbio RNA-seq analysis. *F1000Research* **6,** 1976 (Nov. 2017).

28. Bailey, P., Chang, D. K., Nones, K., *et al.* Genomic analyses identify molecular subtypes of pancreatic cancer. *Nature* **531,** 47–52 (2016).

29. Bailey, P., Chang, D. K., Nones, K., Johns, A. L., Patch, A.-M., Gingras, M.-C., Miller, D. K., Christ, A. N., Bruxner, T. J., Quinn, M. C., *et al.* Genomic analyses identify molecular subtypes of pancreatic cancer. *Nature* **531,** 47–52 (2016).

30. **Pantano, L.,** Friedlander, M. R., Escaramis, G., Lizano, E., Pallares-Albanell, J., Ferrer, I., Estivill, X. & Marti, E. Specific small-RNA signatures in the amygdala at premotor and motor stages of Parkinson's disease revealed by deep sequencing analysis. *Bioinformatics (Oxford, England)* (Nov. 2015).

31. **Pantano, L.,** Jodar, M., Bak, M., Ballesca, J. L., Tommerup, N., Oliva, R. & Vavouri, T. The small RNA content of human sperm reveals pseudogene-derived piRNAs complementary to protein-coding genes. *RNA (New York, N.Y.)* **21,** 1085–95 (June 2015).

32. Puig, M., Castellano, D., **Pantano, L.,** Giner-Delgado, C., Izquierdo, D., Gayà-Vidal, M., Lucas-Lledó, J. I., Esko, T., Terao, C., Matsuda, F. & Cáceres, M. Functional Impact and Evolution of a Novel Human Polymorphic Inversion That Disrupts a Gene and Creates a Fusion Transcript. *PLoS Genetics* **11** (2015).

33. Martínez-Fundichely, A., Casillas, S., Egea, R., Ràmia, M., Barbadilla, A., **Pantano, L.,** Puig, M. & Cáceres, M. InvFEST, a database integrating information of polymorphic inversions in the human genome. *Nucleic Acids Research* **42** (2014).

34. Meijer, H. A., Smith, E. M., Bushell, M., *et al.* Regulation of miRNA strand selection: follow the leader? *Biochemical Society transactions* **42,** 1135–40 (2014).

35. Öst, A., Lempradl, A., Casas, E., Weigert, M., Tiko, T., Deniz, M., **Pantano, L.,** Boenisch, U., Itskov, P. M., Stoeckius, M., Ruf, M., Rajewsky, N., Reuter, G., Iovino, N., Ribeiro, C., Alenius, M., Heyne, S., Vavouri, T. & Pospisilik, J. A. Paternal Diet Defines Offspring Chromatin State and Intergenerational Obesity. *Cell* **159,** 1352–1364 (Dec. 2014).

36. Llorens, F., Bañez-Coronel, M., **Pantano, L.,** del Río, J. A., Ferrer, I., Estivill, X. & Martí, E. A highly expressed miR-101 isomiR is a functional silencing small RNA. *BMC genomics* **14,** 104 (Jan. 2013).

37. Llorens, F., Hummel, M., **Pantano, L.,** Pastor, X., Vivancos, A., Castillo, E., Mattlin, H., Ferrer, A., Ingham, M., Noguera, M., Kofler, R., Dohm, J. C., Pluvinet, R., Bayés, M., Himmelbauer, H., del Rio, J. A., Martí, E. & Sumoy, L. Microarray and deep sequencing cross-platform analysis of the mirRNome and isomiR variation in response to epidermal growth factor. *BMC genomics* **14,** 371 (Jan. 2013).

38. Bañez-Coronel, M., Porta, S., Kagerbauer, B., Mateu-Huertas, E., **Pantano, L.,** Ferrer, I., Guzmán, M., Estivill, X. & Martí, E. A Pathogenic Mechanism in Huntington's Disease Involves Small CAG-Repeated RNAs with Neurotoxic Activity. *PLoS genetics* **8** (ed Pearson, C. E.) e1002481 (Feb. 2012).

39. **Pantano, L.,** Estivill, X. & Martí, E. A non-biased framework for the annotation and classification of the non-miRNA small RNA transcriptome. *Bioinformatics (Oxford, England)* **27,** 3202–3 (Nov. 2011).

40. Martí, E., **Pantano, L.,** Bañez-Coronel, M., Llorens, F., Miñones-Moyano, E., Porta, S., Sumoy, L., Ferrer, I. & Estivill, X. A myriad of miRNA variants in control and Huntington's disease brain regions detected by massively parallel sequencing. *Nucleic Acids Research* **38,** 7219–7235 (2010).

41. **Pantano, L.,** Estivill, X. & Martí, E. SeqBuster, a bioinformatic tool for the processing and analysis of small RNAs datasets, reveals ubiquitous miRNA modifications in human embryonic cells. *Nucleic Acids Research* **38,** e34 (2010).

42. Armengol, L., Villatoro, S., González, J. R., **Pantano, L.,** García-Aragonés, M., Rabionet, R., Cáceres, M. & Estivill, X. Identification of Copy Number Variants Defining Genomic Differences among Major Human Groups. *PLoS ONE* **4** (ed Bauchet, M.) 13 (2009).

43. Varas, F., Stadtfeld, M., De Andres-Aguayo, L., Maherali, N., di Tullio, A., **Pantano, L.,** Notredame, C., Hochedlinger, K. & Graf, T. Fibroblast-derived induced pluripotent stem cells show no common retroviral vector insertions. *Stem cells (Dayton, Ohio)* **27,** 300–6 (Feb. 2009).

44. **Pantano, L.,** Armengol, L., Villatoro, S. & Estivill, X. ProSeeK: A web server for MLPA probe design. *BMC Genomics* **9,** 573 (2008).

45. Grynberg, P., Abeel, T., Lopes, P., Macintyre, G. & **Pantano, L.** Highlights from the Third International Society for Computational Biology Student Council Symposium at the Fifteenth Annual International Conference on Intelligent Systems for Molecular Biology. *BMC Bioinformatics* **12** (2007).

46. Khaja, R., Zhang, J., MacDonald, J. R., He, Y., Joseph-George, A. M., Wei, J., Rafiq, M. A., Qian, C., Shago, M., **Pantano, L.,** Aburatani, H., Jones, K., Redon, R., Hurles, M., Armengol, L., Estivill, X., Mural, R. J., Lee, C., Scherer, S. W. & Feuk, L. Genome assembly comparison identifies structural variants in the human genome. *Nature Genetics* **38,** 1413–1418 (2006).