

CURRICULUM VITAE
The Johns Hopkins University School of Medicine

Luigi Marchionni, M.D. Ph.D.

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DEMOGRAPHIC AND PERSONAL INFORMATION

Current Appointments

- July 2009-present Core Faculty Member and co-Director – Center for Computational Genomics,
Johns Hopkins University School of Medicine, Baltimore, MD, USA
- January 2018-present Associate Professor of Oncology – Cancer Biology Program
Johns Hopkins University School of Medicine Baltimore, MD, USA

Personal Data

The Sidney Kimmel Comprehensive Cancer Center
Johns Hopkins University School of Medicine
CRB2, Room 1M52
1550 Orleans Street,
Baltimore, MD, 21231 USA

Phone: 410 502 8179
Mobile: 410 227 5113
E-mail: marchion@jhu.edu
URL: <http://luigimarchionni.org>

Education and Training

- July 16, 1998 M.D, Summa cum Laude
School of Medicine, University of Turin, Italy
Dissertation in Human Genetics: The role of Histocompatibility HLA-B27 molecule in the pathogenesis of seronegative spondyloarthropathies.
Advisor: Prof. E. Sergio Curtoni
Licensed for medical practice in Italy in 1999
- July 5, 2004 Ph.D., Structural and Functional Genomics
International School of Advanced Studies (SISSA), Trieste, Italy
Dissertation title: Comprehensive gene expression data exploration in ovarian cancer uncovers molecular signatures related to cell plasticity and involving fibroblast growth factor.
Advisor: Prof. Antonino Cattaneo, SISSA, Trieste, Italy
External Advisor: Prof. Marcelo Magnusco, Rockefeller University, New York, USA
- August 2004 Post-doctoral fellowship – Interuniversity Consortium for Biotechnologies
June 2005 National Laboratory (LNCIB), Trieste, Italy
During my fellowship at LNCIB I have continued my work on the analysis of gene expression profiles in human cancer and laboratory models.
- September 2005 Post-doctoral fellowship – Oncology Biostatistics
June 2007 Johns Hopkins School of Medicine, Baltimore, MD, USA
During my post-doctoral fellowship, I developed novel computational and visualization approaches for high dimensional genomic data analysis and integration.

Professional Experience

- 1993 - 1998 Research internship – Transplant Immunology, S. Giovanni Battista Hospital, Turin, Italy
- Molecular typing techniques of the human MHC system, and HLA-B27 molecular analysis in seronegative spondyloarthropathies.
- 1999 - 2001 Visiting researcher – RIKEN Genome Science Laboratory, Tsukuba, Japan
- Gene expression profiling analysis of Wnt signaling by cDNA microarrays.
- Participation to the first three FANTOM projects for the annotation of the mouse transcriptome.
- 1999 - 2000 Research fellowship – FIRC Institute of Molecular Oncology (IFOM), Milan, Italy
- Set up of the cDNA microarray facility operating at IFOM, in the framework of the first Italian Cancer Research Association (AIRC) project for nanotechnology applications to cancer research.
- 1999 - 2005 Research fellowship – LNCIB, Trieste, Italy
- Set up and coordination of the cDNA microarray Unit and gene expression profiling analyses for the following research projects:
1. Analysis of serous ovarian cancer gene expression profiles in collaboration with the National Cancer Institute (INT, Milan, Italy).
2. European Integrated Project, Translational and Functional Onco-Genomics (TRANSFOG): from cancer-oriented genomic screenings to new diagnostic tools and improved cancer treatments.
3. Development of innovative technologies for gene expression analysis and genotyping in collaboration with ST-Microelectronics (Catania, Italy).
4. Italian Integrated Project for Oncology: Validation of DNA microarray based cancer classification, research funded by the Italian Ministry of Education, Universities, and Research (MIUR) and the Italian National Research Council (CNR).
- 2007 - 2010 Instructor – Cancer Biology Program, Johns Hopkins School of Medicine, Baltimore, MD, USA
- Development of innovative approaches to gene expression profiling and integration based on pathway and gene set analysis.
- Evaluation of the impact of gene expression based prognostic assays on the outcome and treatment choice of women diagnosed with early stage breast cancer.
- 2010 - 2017 Assistant Professor – Cancer Biology Program, Johns Hopkins School of Medicine, Baltimore, MD, USA
- Same as above.

PUBLICATIONS

Original Research

1. Kawai J, Shinagawa A, Shibata K, Yoshino M, Itoh M, Ishii Y, Arakawa T, Hara A, Fukunishi Y, Konno H, Adachi J, Fukuda S, Aizawa K, Izawa M, Nishi K, Kiyosawa H, Kondo S, Yamanaka I, Saito T, Okazaki Y, Gojobori T, Bono H, Kasukawa T, Saito R, Kadota K, Matsuda H, Ashburner M, Batalov S, Casavant T, Fleischmann W, Gaasterland T, Gissi C, King B, Kochiwa H, Kuehl P, Lewis S, Matsuo Y, Nikaido I, Pesole G, Quackenbush J, Schriml LM, Staubli F, Suzuki R, Tomita M, Wagner L, Washio T, Sakai K, Okido T, Furuno M, Aono H, Baldarelli R, Barsh G, Blake J, Boffelli D, Bojunga N, Carninci P, de Bonaldo MF, Brownstein MJ, Bult C, Fletcher C, Fujita M, Gariboldi M, Gustincich S, Hill D, Hofmann M, Hume DA, Kamiya M, Lee NH, Lyons P, **Marchionni L**, Mashima J, Mazzarelli J, Mombaerts P, Nordone P, Ring B, Ringwald M, Rodriguez I, Sakamoto N, Sasaki H, Sato K, Schönbach C, Seya T, Shibata Y, Storch KF, Suzuki H, Toyo-oka K, Wang KH, Weitz C, Whittaker C, Wilming L, Wynshaw-Boris A, Yoshida K, Hasegawa Y, Kawaji H, Kohtsuki S, Hayashizaki Y. Functional annotation of a full-length mouse cDNA collection. *Nature*. 2001; 409(6821):685-90, PMID: 11217851
 - *As a member of the FANTOM consortium, I was directly involved in the FANTOM1 project by actively participating to the annotation of mouse transcripts sequenced during the project. I also participated to the FANTOM1 meeting in Tsukuba, Japan, being involved in the manuscript planning and writing.*
2. Okazaki Y, Furuno M, Kasukawa T, Adachi J, Bono H, Kondo S, Nikaido I, Osato N, Saito R, Suzuki H, Yamanaka I, Kiyosawa H, Yagi K, Tomaru Y, Hasegawa Y, Nogami A, Schönbach C, Gojobori T, Baldarelli R, Hill DP, Bult C, Hume DA, Quackenbush J, Schriml LM, Kanapin A, Matsuda H, Batalov S, Beisel KW, Blake JA, Bradt D, Brusica V,

- Chothia C, Corbani LE, Cousins S, Dalla E, Dragani TA, Fletcher CF, Forrest A, Frazer KS, Gaasterland T, Gariboldi M, Gissi C, Godzik A, Gough J, Grimmond S, Gustincich S, Hirokawa N, Jackson IJ, Jarvis ED, Kanai A, Kawaji H, Kawasaki Y, Kedzierski RM, King BL, Konagaya A, Kurochkin IV, Lee Y, Lenhard B, Lyons PA, Maglott DR, Maltais L, **Marchionni L**, McKenzie L, Miki H, Nagashima T, Numata K, Okido T, Pavan WJ, Pertea G, Pesole G, Petrovsky N, Pillai R, Pontius JU, Qi D, Ramachandran S, Ravasi T, Reed JC, Reed DJ, Reid J, Ring BZ, Ringwald M, Sandelin A, Schneider C, Semple CA, Setou M, Shimada K, Sultana R, Takenaka Y, Taylor MS, Teasdale RD, Tomita M, Verardo R, Wagner L, Wahlestedt C, Wang Y, Watanabe Y, Wells C, Wilming LG, Wynshaw-Boris A, Yanagisawa M, Yang I, Yang L, Yuan Z, Zavolan M, Zhu Y, Zimmer A, Carninci P, Hayatsu N, Hirozane-Kishikawa T, Konno H, Nakamura M, Sakazume N, Sato K, Shiraki T, Waki K, Kawai J, Aizawa K, Arakawa T, Fukuda S, Hara A, Hashizume W, Imotani K, Ishii Y, Itoh M, Kagawa I, Miyazaki A, Sakai K, Sasaki D, Shibata K, Shinagawa A, Yasunishi A, Yoshino M, Waterston R, Lander ES, Rogers J, Birney E, Hayashizaki Y. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. *Nature*. 2002; 420(6915):563-73, PMID: 12466851
- *As a member of the FANTOM consortium, I was directly involved in the FANTOM2 project by actively participating to the annotation of mouse transcripts sequenced during the project. I also participated to the FANTOM2 meeting in Tsukuba, Japan, being involved in the manuscript planning and writing.*
- Dalla E, Verardo R, Lazarević D, **Marchionni L**, Reid JF, Bahar N, Klarić E, Marcuzzi G, Marzio R, Belgrano A, Licastro D, Schneider C. LNCIB human full-length cDNAs collection: towards a better comprehension of the human transcriptome. *Comptes Rendus Biologies*. 2003; 326(10-11):967-70, PMID: 14744102
 - *As a member of the Structural Genomics unit at LNCIB, I collaborated to the cloning, sequencing, and annotation procedures of the full-length cDNA libraries being produced at LNCIB.*
 - Monte M, Benetti R, Collavin L, **Marchionni L**, Del Sal G, Schneider C. hGTSE-1 expression stimulates cytoplasmic localization of p53. *The Journal of Biological Chemistry*. 2004; 279(12):11744-52, PMID: 14707141
 - *For this research project, I assisted Dr. Monte, at the time my direct supervisor at LNCIB, in performing the molecular biology experiments (Western blotting, cloning, transfection) involved with the characterization of the human homolog of GTSE-1.*
 - De Cecco L*, **Marchionni L***, Gariboldi M, Reid JF, Lagonigro MS, Caramuta S, Ferrario C, Bussani E, Mezzanzanica D, Turatti F, Delia D, Daidone MG, Oggionni M, Bertuletto N, Ditto A, Raspagliesi F, Pilotti S, Pierotti MA, Canevari S, Schneider C. Gene expression profiling of advanced ovarian cancer: characterization of a molecular signature involving fibroblast growth factor 2. *Oncogene*. 2004; 23(49):8171-83, PMID: 15377994
 - ***Equally contributing first author.** *This manuscript is the result of a substantial part of the work I did during my Ph.D. training. For this research project, I have coordinated the setup of the IFOM microarray facility and the preparation of the experimental protocols successfully used by Dr. De Cecco to generate the ovarian cancer gene expression profiles I subsequently characterized in depth. Hence, I have performed all computational analyses contained in the manuscript, comparing our findings with data derived from the public domain. Finally, I wrote most of the manuscript, prepared most of the figures, and I was responsible for the submission and revisions of the paper.*
 - Dalla E, Mignone F, Verardo R, **Marchionni L**, Marzinotto S, Lazarević D, Reid JF, Marzio R, Klarić E, Licastro D, Marcuzzi G, Gambetta R, Pierotti MA, Pesole G, Schneider C. Discovery of 342 putative new genes from the analysis of 5'-end-sequenced full-length-enriched cDNA human transcripts. *Genomics*. 2005; 85(6):739-51, PMID: 15885500
 - *As a member of the Structural Genomics unit at LNCIB, I collaborated to the cloning, sequencing, and annotation procedures of the full-length cDNA libraries being produced at LNCIB.*
 - Carninci P, Kasukawa T, Katayama S, Gough J, Frith MC, Maeda N, Oyama R, Ravasi T, Lenhard B, Wells C, Kodzius R, Shimokawa K, Bajic VB, Brenner SE, Batalov S, Forrest AR, Zavolan M, Davis MJ, Wilming LG, Aidinis V, Allen JE, Ambesi-Impombato A, Apweiler R, Aturaliya RN, Bailey TL, Bansal M, Baxter L, Beisel KW, Bersano T, Bono H, Chalk AM, Chiu KP, Choudhary V, Christoffels A, Clutterbuck DR, Crowe ML, Dalla E, Dalrymple BP, de Bono B, Della Gatta G, di Bernardo D, Down T, Engstrom P, Fagiolini M, Faulkner G, Fletcher CF, Fukushima T, Furuno M, Futaki S, Gariboldi M, Georgii-Hemming P, Gingeras TR, Gojobori T, Green RE, Gustincich S, Harbers M, Hayashi Y, Hensch TK, Hirokawa N, Hill D, Huminiecki L, Iacono M, Ieko K, Iwama A, Ishikawa T, Jakt M, Kanapin A, Katoh M, Kawasaki Y, Kelso J, Kitamura H, Kitano H, Kollias G, Krishnan SP, Kruger A, Kummerfeld SK, Kurochkin IV, Lareau LF, Lazarevic D, Lipovich L, Liu J, Liuni S, McWilliam S, Madan Babu M, Madera M, **Marchionni L**, Matsuda H, Matsuzawa S, Miki H, Mignone F, Miyake S, Morris K, Mottagui-Tabar S, Mulder N, Nakano N, Nakauchi H, Ng P, Nilsson R, Nishiguchi S, Nishikawa S, Nori F, Ohara O, Okazaki Y, Orlando V, Pang KC, Pavan WJ, Pavesi G, Pesole G, Petrovsky N, Piazza S, Reed J, Reid JF, Ring BZ, Ringwald M, Rost B, Ruan Y, Salzberg SL, Sandelin A, Schneider C, Schönbach C, Sekiguchi K, Semple CA, Seno S, Sessa L, Sheng Y, Shibata Y, Shimada H, Shimada K, Silva D, Sinclair B, Sperling S, Stupka E, Sugiura K, Sultana R, Takenaka Y, Taki K, Tammoja K, Tan SL, Tang S, Taylor MS, Tegner J, Teichmann SA, Ueda HR, van Nimwegen E, Verardo R, Wei CL, Yagi K,

- Yamanishi H, Zabarovskiy E, Zhu S, Zimmer A, Hide W, Bult C, Grimmond SM, Teasdale RD, Liu ET, Brusic V, Quackenbush J, Wahlestedt C, Mattick JS, Hume DA, Kai C, Sasaki D, Tomaru Y, Fukuda S, Kanamori-Katayama M, Suzuki M, Aoki J, Arakawa T, Iida J, Imamura K, Itoh M, Kato T, Kawaji H, Kawagashira N, Kawashima T, Kojima M, Kondo S, Konno H, Nakano K, Ninomiya N, Nishio T, Okada M, Plessy C, Shibata K, Shiraki T, Suzuki S, Tagami M, Waki K, Watahiki A, Okamura-Oho Y, Suzuki H, Kawai J, Hayashizaki Y. The transcriptional landscape of the mammalian genome. *Science (New York, N.Y.)*. 2005; 309(5740):1559-63, PMID: 16141072
- *As a member of the FANTOM consortium, I was directly involved in the FANTOM3 project by actively participating to the annotation of transcripts sequenced during the project. Overall, I directly annotated over 4000 transcripts. I also participated to the FANTOM3 meeting in Yokohama, Japan, being involved in the manuscript planning and writing.*
- Schaeffer EM*, **Marchionni L***, Huang Z, Simons B, Blackman A, Yu W, Parmigiani G, Berman DM. Androgen-induced programs for prostate epithelial growth and invasion arise in embryogenesis and are reactivated in cancer. *Oncogene*. 2008; 27(57):7180-91. NIHMSID: NIHMS84639, PMID: 18794802, PMCID: PMC2676849
 - ***Equally contributing first author.** *For this research project, I have performed all computational and bioinformatics analyses necessary to characterize the transcriptional programs orchestrating prostate development during embryogenesis and to identify their reactivation during prostate cancer progression. For this project, I have analyzed our mouse gene expression data together with many additional human datasets available from the public domain, developing novel methods for performing and visualizing an integrated analysis of gene expression across species. Furthermore, my contributions were not limited to data analysis, since I provided intellectual insights instrumental for interpreting our findings and putting them into biological and clinical context. Finally, I wrote part of the manuscript, prepared several figures, and assembled all supplementary material associated with the manuscript.*
 - Daniel VC*, **Marchionni L***, Hierman JS, Rhodes JT, Devereux WL, Rudin CM, Yung R, Parmigiani G, Dorsch M, Peacock CD, Watkins DN. A primary xenograft model of small-cell lung cancer reveals irreversible changes in gene expression imposed by culture in vitro. *Cancer research*. 2009; 69(8):3364-73. NIHMSID: NIHMS97707, PMID: 19351829, PMCID: PMC2821899
 - ***Equally contributing first author.** *For this research project, I have performed all computational and bioinformatics analyses necessary to characterize the transcriptional programs altered in small cell lung cancer cell culture and xenograft models. This analysis revealed that patient derived xenografts directly obtained from tumor biopsies without intervening cell culturing more closely resemble the primary tumors. Also, for this project, I have analyzed our data together with many additional publically available datasets, using the same methods I developed for my previous research on prostate development and cancer. Also in this case, I provided intellectual insights that were instrumental for interpreting our findings and putting them into biological and clinical context. Finally, I wrote part of the manuscript, prepared several figures, and assembled all supplementary material associated with the paper.*
 - He X, **Marchionni L**, Hansel DE, Yu W, Sood A, Yang J, Parmigiani G, Matsui W, Berman DM. Differentiation of a highly tumorigenic basal cell compartment in urothelial carcinoma. *Stem cells (Dayton, Ohio)*. 2009; 27(7):1487-95. NIHMSID: NIHMS236727, PMID: 19544456, PMCID: PMC3060766
 - *For this research project, I have designed the microarray experiment and performed all computational and bioinformatics analyses necessary to characterize the transcriptional programs associated with the bladder cancer basal cell compartment described in the study. I have also helped with the interpretation of the results, wrote part of the manuscript, prepared a figure, and prepared a great part of the supplementary material associated with the manuscript.*
 - Lin X, Afsari B, **Marchionni L**, Cope L, Parmigiani G, Naiman D, Geman D. The ordering of expression among a few genes can provide simple cancer biomarkers and signal BRCA1 mutations. *BMC Bioinformatics*. 2009 Aug 20;10:256. doi:10.1186/1471-2105-10-256. PubMed PMID: 19695104; PubMed Central PMCID: PMC2745389.
 - *For this research project, I have provided all biological insights necessary for interpreting the role of the genes participating in the classifiers discovered for breast cancer. Furthermore, I directly participated in the analyses, preparing the last two figures and writing part of the manuscript.*
 - Kachhap SK, Rosmus N, Collis SJ, Kortenhorst MS, Wissing MD, Hedayati M, Shabbeer S, Mendonca J, Deangelis J, **Marchionni L**, Lin J, Höti N, Nortier JW, DeWeese TL, Hammers H, Carducci MA. Downregulation of homologous recombination DNA repair genes by HDAC inhibition in prostate cancer is mediated through the E2F1 transcription factor. *PloS one*. 2010; 5(6):e11208, PMID: 20585447, PMCID: PMC2887841
 - *For this research project, I have performed the Analysis of Functional Annotation – preparing the relative figure – which was used for identifying the downregulation of homologous recombination DNA repair genes mediated by HDAC inhibition in prostate cancer cells. Furthermore, I directly participated in interpreting the results and writing the manuscript.*
 - Seeber LM, Zweemer RP, **Marchionni L**, Massuger LF, Smit VT, van Baal WM, Verheijen RH, van Diest PJ. Methylation profiles of endometrioid and serous endometrial cancers. *Endocrine-related cancer*. 2010; 17(3):663-73, PMID: 20488783
 - *For this study, I have helped with bioinformatics and statistical analysis of methylation and survival data. Furthermore, I directly participated in preparing the figures, interpreting the results, and writing the manuscript.*

14. Noonan K, **Marchionni L**, Anderson J, Pardoll D, Roodman GD, Borrello I. A novel role of IL-17-producing lymphocytes in mediating lytic bone disease in multiple myeloma. *Blood*. 2010; 116(18):3554-63, PMID: 20664052, PMCID: PMC4017298
 - *For this study, I have helped with statistical analysis of ELISA and clinico-pathological data, directly participating in preparing the figures, interpreting the results, and writing the manuscript.*
15. Schreck KC, Taylor P, **Marchionni L**, Gopalakrishnan V, Bar EE, Gaiano N, Eberhart CG. The Notch target Hes1 directly modulates Gli1 expression and Hedgehog signaling: a potential mechanism of therapeutic resistance. *Clinical cancer research*. 2010; 16(24):6060-70. NIHMSID: NIHMS247142, PMID: 21169257, PMCID: PMC3059501
 - *For this study, I have helped with all bioinformatics and statistical analyses performed, including the identification, through microarray analysis, of the genes and pathways modulated by Notch signaling. I have also participated in preparing the figures, interpreting the results, and writing the manuscript.*
16. Ross AE, **Marchionni L**, Phillips TM, Miller RM, Hurley PJ, Simons BW, Salmasi AH, Schaeffer AJ, Gearhart JP, Schaeffer EM. Molecular effects of genistein on male urethral development. *The Journal of urology*. 2011; 185(5):1894-8, PMID: 21421236
 - *For this study, I have performed all bioinformatics and statistical analyses, which were instrumental for the identification of the genes and pathways modulated by genistein during urethral development, I have also participated in preparing the figures, interpreting the results, and writing the manuscript.*
17. Liu H, Kim Y, Sharkis S, **Marchionni L**, Jang YY. In vivo liver regeneration potential of human induced pluripotent stem cells from diverse origins. *Science translational medicine*. 2011; 3(82):82ra39. NIHMSID: NIHMS358406, PMID: 21562231, PMCID: PMC3305909
 - *For this study, I have performed all bioinformatics and statistical analyses used to identify the molecular processes and signaling pathways modulated by DNA methylation in human induced pluripotent stem cells. I have also participated in preparing the figures, interpreting the results, writing the manuscript, and I have assembled the supplementary material associated with the manuscript.*
18. Ling S, Chang X, Schultz L, Lee TK, Chaux A, **Marchionni L**, Netto GJ, Sidransky D, Berman DM. An EGFR-ERK-SOX9 signaling cascade links urothelial development and regeneration to cancer. *Cancer research*. 2011; 71(11):3812-21. NIHMSID: NIHMS283473, PMID: 21512138, PMCID: PMC3107391
 - *For this study, I have performed all bioinformatics and statistical analyses used to characterize the signaling pathways associated with bladder development, regeneration, and cancer. I have also participated in preparing the figures, interpreting the results, and writing the manuscript.*
19. Cesselli D, Beltrami AP, D'Aurizio F, Marcon P, Bergamin N, Toffoletto B, Pandolfi M, Puppato E, Marino L, Signore S, Livi U, Verardo R, Piazza S, **Marchionni L**, Fiorini C, Schneider C, Hosoda T, Rota M, Kajstura J, Anversa P, Beltrami CA, Leri A. Effects of age and heart failure on human cardiac stem cell function. *The American journal of pathology*. 2011; 179(1):349-66, PMID: 21703415, PMCID: PMC3175070
 - *For this study, I have assisted with statistical analyses.*
20. Ross AE, Emadi A, **Marchionni L**, Hurley PJ, Simons BW, Schaeffer EM, Vuica-Ross M. Dimeric naphthoquinones, a novel class of compounds with prostate cancer cytotoxicity. *BJU international*. 2011; 108(3):447-54. NIHMSID: NIHMS403303, PMID: 21176082, PMCID: PMC3700341
 - *For this study, I have assisted with statistical analyses and figures preparation.*
21. Ross AE, **Marchionni L**, Vuica-Ross M, Cheadle C, Fan J, Berman DM, Schaeffer EM. Gene expression pathways of high grade localized prostate cancer. *The Prostate*. 2011; 71(14):1568-77, PMID: 21360566
 - *For this research project, I have performed all computational and bioinformatics analyses necessary to characterize the transcriptional programs associated with lethal prostate cancer in the epithelial compartment. In particular, I was directly involved in designing the study and I directly performed the analysis of differential gene expression, I have identified the most important signaling pathways distinguishing lethal from indolent cancers, and I have compared the profiles obtained in our research with previously published studies. Also in this case, I provided intellectual insights that were instrumental for interpreting our findings and putting them into biological and clinical context. Finally, I wrote a great part of the manuscript, prepared all figures and tables, and assembled all supplementary material associated with the paper. I was surprised and disappointed that I was not listed as equally contributing first author despite my request.*
22. Tyekucheva S, **Marchionni L**, Karchin R, Pammigiani G. Integrating diverse genomic data using gene sets. *Genome biology*. 2011; 12(10):R105, PMID: 22018358, PMCID: PMC3333775
 - *For this study, I have provided all biological insights necessary for interpreting the results obtained from gene set enrichment analysis. Furthermore, I have directly analyzed TCGA data, preparing several figures, and writing part of the manuscript. Finally, I also wrote most of the R code used in the study, which is now part of the RTopper R package I have released through Bioconductor.*

23. Benassi B, Flavin R, **Marchionni L**, Zanata S, Pan Y, Chowdhury D, Marani M, Strano S, Muti P, Blandino G, Loda M. MYC is activated by USP2a-mediated modulation of microRNAs in prostate cancer. *Cancer discovery*. 2012; 2(3):236-47. NIHMSID: NIHMS379659, PMID: 22585994, PMCID: PMC3523361
 - *For this study, I have performed all computational and bioinformatics analyses necessary to characterize the transcriptional programs modulated by USP2a and the associated microRNAs in prostate cancer. I have also analyzed the associated gene expression data together with many additional human datasets available from the public domain. My contributions were not limited to data analysis, since I also provided intellectual insights instrumental for interpreting our findings and putting them into biological and clinical context. Finally, I wrote part of the manuscript, prepared two figures, and assembled all supplementary material.*
24. Huang TC, Sahasrabudde NA, Kim MS, Getnet D, Yang Y, Peterson JM, Ghosh B, Chaerkady R, Leach SD, **Marchionni L**, Wong GW, Pandey A. Regulation of lipid metabolism by Dicer revealed through SILAC mice. *Journal of proteome research*. 2012; 11(4):2193-205. NIHMSID: NIHMS360335, PMID: 22313051, PMCID: PMC3612551
 - *For this study, I have assisted with statistical analyses and figure preparation, and I have also mentored Drs. Huang and Getnet, teaching them how to analyze "omics" data using R.*
25. Huang Z, Hurley PJ, Simons BW, **Marchionni L**, Berman DM, Ross AE, Schaeffer EM. Sox9 is required for prostate development and prostate cancer initiation. *Oncotarget*. 2012; 3(6):651-63, PMID: 22761195, PMCID: PMC3442290
 - *For this study, I have assisted with statistical analyses.*
26. Kornegoor R, Moelans CB, Verschuur-Maes AH, Hogenes MC, de Bruin PC, Oudejans JJ, **Marchionni L**, van Diest PJ. Oncogene amplification in male breast cancer: analysis by multiplex ligation-dependent probe amplification. *Breast cancer research and treatment*. 2012; 135(1):49-58, PMID: 22527098, PMCID: PMC3413821
 - *For this study, I have helped with bioinformatics and statistical analysis of copy number data and survival data. Furthermore, I directly participated in preparing the figures, interpreting the results, and writing the manuscript.*
27. Hurley PJ, **Marchionni L**, Simons BW, Ross AE, Peskoe SB, Miller RM, Erho N, Vergara IA, Ghadessi M, Huang Z, Gurel B, Park BH, Davicioni E, Jenkins RB, Platz EA, Berman DM, Schaeffer EM. Secreted protein, acidic and rich in cysteine-like 1 (SPARCL1) is down regulated in aggressive prostate cancers and is prognostic for poor clinical outcome. *Proceedings of the National Academy of Sciences of the United States of America*. 2012; 109(37):14977-82, PMID: 22927397, PMCID: PMC3443123
 - *For this study, I have performed bioinformatics analyses, assessing expression levels of several genes across different prostate cancer phenotypes using public domain data, preparing several figures, interpreting the results, and writing part of the manuscript.*
28. Simons BW, Hurley PJ, Huang Z, Ross AE, Miller R, **Marchionni L**, Berman DM, Schaeffer EM. Wnt signaling through beta-catenin is required for prostate lineage specification. *Developmental biology*. 2012; 371(2):246-55. NIHMSID: NIHMS404765, PMID: 22960283, PMCID: PMC3472417
 - *For this study, I have assisted with statistical analyses.*
29. Ho CY, Bar E, Giannini C, **Marchionni L**, Karajannis MA, Zagzag D, Gutmann DH, Eberhart CG, Rodriguez FJ. MicroRNA profiling in pediatric pilocytic astrocytoma reveals biologically relevant targets, including PBX3, NFIB, and METAP2. *Neuro-oncology*. 2013; 15(1):69-82, PMID: 23161775, PMCID: PMC3534421
 - *For this study, I performed all bioinformatics and statistical analyses used to derive and integrate microRNA and gene expression profiles associated with pediatric pilocytic astrocytoma. Furthermore, I directly participated in preparing the figures, interpreting the results, and writing the manuscript.*
30. Zinn RL, Gardner EE, Dobromilskaya I, Murphy S, **Marchionni L**, Hann CL, Rudin CM. Combination treatment with ABT-737 and chloroquine in preclinical models of small cell lung cancer. *Molecular cancer*. 2013; 12:16, PMID: 23452820, PMCID: PMC3599053
 - *For this study, I have assisted with statistical analyses and figures preparation.*
31. **Marchionni L**, Afsari B, Geman D, Leek JT. A simple and reproducible breast cancer prognostic test. *BMC genomics*. 2013; 14:336, PMID: 23682826, PMCID: PMC3662649
 - *I have designed the study and performed all analyses included in the paper. I have generated all figures, interpreted all results, wrote the manuscript, and assembled all associated supplementary material, including the experimental data necessary to fully reproduce the analyses. To this end I have released two R packages through Bioconductor: **mammaPrintData** and **seventyGeneData**. This study is a prototypic example of best practices for omics-based cancer classifiers development.*
32. Iglesias-Ussel M, **Marchionni L**, Romerio F. Isolation of microarray-quality RNA from primary human cells after intracellular immunostaining and fluorescence-activated cell sorting. *Journal of immunological methods*. 2013; 391(1-2):22-30. NIHMSID: NIHMS454380, PMID: 23434645, PMCID: PMC3627819
 - *For this study, I performed all bioinformatics and statistical analyses used to compare gene expression data from RT-PCR and microarray analysis, starting from RNA obtained from fixed cells after fluorescence-activated cell sorting. Furthermore, I directly participated in preparing the figures, interpreting the results, and writing the manuscript.*

33. Zinn RL, Gardner EE, **Marchionni L**, Murphy SC, Dobromilskaya I, Hann CL, Rudin CM. ERK phosphorylation is predictive of resistance to IGF-1R inhibition in small cell lung cancer. *Molecular cancer therapeutics*. 2013; 12(6):1131-9. NIHMSID: NIHMS457979, PMID: 23515613, PMCID: PMC3681842
- *For this study, I have assisted with statistical analyses and figures preparation.*
34. Iglesias-Ussel M, Vandergeeten C, **Marchionni L**, Chomont N, Romerio F. High levels of CD2 expression identify HIV-1 latently infected resting memory CD4+ T cells in virally suppressed subjects. *Journal of virology*. 2013; 87(16):9148-58, PMID: 23760244, PMCID: PMC3754042
- *For this study, I have participated in designing the experiments, and I performed all bioinformatics and statistical analyses used to analyze gene expression profiles obtained by RT-PCR and microarray analyses of human T-cells latently infected by HIV. I have also performed the characterization of such expression profiles via Analysis of Functional Annotation. Finally, I directly participated in preparing the figures, interpreting the results, and writing the manuscript.*
35. **Kortenhorst MS, Wissing MD, Rodríguez R, Kachhap SK, Jans JJ, Van der Groep P, Verheul HM, Gupta A, Aiyetan PO, van der Wall E, Carducci MA, Van Diest PJ, Marchionni L§.** Analysis of the genomic response of human prostate cancer cells to histone deacetylase inhibitors. *Epigenetics*. 2013; 8(9):907-20, PMID: 23880963, PMCID: PMC3883768
- **§Corresponding author.** *For this research project, I have design the study, performed all computational and bioinformatics analyses necessary to characterize the transcriptional programs modulated by HDAC inhibition in prostate cancer cells. Furthermore, I provided intellectual insights for interpreting our findings and putting them into biological and clinical context, I wrote part of the manuscript, prepared several figures, and assembled all supplementary material associated with the manuscript. Finally, I have co-mentored the junior authors on this manuscript (Drs. Kortenhorst and Wissing).*
36. Rossello FJ, Tothill RW, Britt K, Marini KD, Falzon J, Thomas DM, Peacock CD, **Marchionni L**, Li J, Bennett S, Tantoso E, Brown T, Chan P, Martelotto LG, Watkins DN. Next-generation sequence analysis of cancer xenograft models. *PloS one*. 2013; 8(9):e74432, PMID: 24086345, PMCID: PMC3784448
- *For this study, I have assisted with statistical and computational analyses.*
37. Brait M, Maldonado L, Noordhuis MG, Begum S, Loyo M, Poeta ML, Barbosa A, Fazio VM, Angioli R, Rabitti C, **Marchionni L**, de Graeff P, van der Zee AG, Wisman GB, Sidransky D, Hoque MO. Association of promoter methylation of VGF and PGP9.5 with ovarian cancer progression. *PloS one*. 2013; 8(9):e70878, PMID: 24086249, PMCID: PMC3785492
- *For this study, I have assisted with statistical analyses.*
38. Ferlito M, Wang Q, Fulton WB, Colombani PM, **Marchionni L**, Fox-Talbot K, Paolucci N, Steenbergen C. Hydrogen sulfide [corrected] increases survival during sepsis: protective effect of CHOP inhibition. *Journal of immunology* (Baltimore, Md.: 1950). 2014; 192(4):1806-14. NIHMSID: NIHMS547372, PMID: 24403532, PMCID: PMC3946246
- *For this study, I have assisted with statistical analyses and figures preparation.*
39. Riester M, Werner L, Bellmunt J, Selvarajah S, Guancial EA, Weir BA, Stack EC, Park RS, O'Brien R, Schutz FA, Choueiri TK, Signoretti S, Lloreta J, **Marchionni L**, Gallardo E, Rojo F, Garcia DI, Chekaluk Y, Kwiatkowski DJ, Bochner BH, Hahn WC, Ligon AH, Barletta JA, Loda M, Berman DM, Kantoff PW, Michor F, Rosenberg JE. Integrative analysis of 1q23.3 copy-number gain in metastatic urothelial carcinoma. *Clinical cancer research*. 2014; 20(7):1873-83. NIHMSID: NIHMS562563, PMID: 24486590, PMCID: PMC3975677
- *For this study, I have assisted with statistical and computational analyses.*
40. Munari E*, **Marchionni L***, **Chitre A**, Hayashi M, Martignoni G, Brunelli M, Gobbo S, Argani P, Allaf M, Hoque MO, Netto GJ. Clear cell papillary renal cell carcinoma: micro-RNA expression profiling and comparison with clear cell renal cell carcinoma and papillary renal cell carcinoma. *Human pathology*. 2014; 45(6):1130-8. NIHMSID: NIHMS662126, PMID: 24703100, PMCID: PMC4332813
- ***Equally contributing first author.** *For this research project, I have both directly performed, and supervised Ms. Chitre in performing all computational and bioinformatics analyses necessary to characterize the microRNA expression profiles associated with clear cell papillary renal cell carcinoma. Furthermore, I have provided intellectual insights that were crucial for interpreting our findings and putting them into biological and clinical context. Finally, I wrote part of the manuscript, prepared several figures, and assembled all supplementary material associated with the paper.*
41. Guerrero-Preston R, Michailidi C, **Marchionni L**, Pickering CR, Frederick MJ, Myers JN, Yegnasubramanian S, Hadar T, Noordhuis MG, Zizkova V, Fertig E, Agrawal N, Westra W, Koch W, Califano J, Velculescu VE, Sidransky D. Key tumor suppressor genes inactivated by "greater promoter" methylation and somatic mutations in head and neck cancer. *Epigenetics*. 2014; 9(7):1031-46, PMID: 24786473, PMCID: PMC4143405

- For this study, I have performed the bioinformatics and statistical analyses used to identify the biological processes and signaling pathways associated with promoter methylation and gene mutation in head and neck cancer. Finally, I directly participated in preparing the figures, interpreting the results, writing the manuscript, and assembling the supplemental material.
42. Huang TC, Renuse S, Pinto S, Kumar P, Yang Y, Chaerkady R, Godsey B, Mendell JT, Halushka MK, Civin CI, **Marchionni L**, Pandey A. Identification of miR-145 targets through an integrated omics analysis. *Molecular bioSystems*. 2015; 11(1):197-207. NIHMSID: NIHMS659355, PMID: 25354783, PMCID: PMC4352311
 - **§Co-corresponding last author.** For this research project, I have helped designing the experiments and the analyses, and I have directly supervised Dr. Huang in performing all computational and bioinformatics analyses included in paper. Further, I provided intellectual insights for interpreting our findings and putting them into biological context, and I participated in writing parts of the manuscript.
 43. Tomasetti C, **Marchionni L**, Nowak MA, Parmigiani G, Vogelstein B. Only three driver gene mutations are required for the development of lung and colorectal cancers. *Proceedings of the National Academy of Sciences of the United States of America*. 2015; 112(1):118-23, PMID: 25535351, PMCID: PMC4291633
 - For this study, I have assisted with the design of the study, data analysis, and manuscript and figures preparation.
 44. Afsari B, Fertig EJ, Geman D, **Marchionni L**. switchBox: an R package for k-Top Scoring Pairs classifier development. *Bioinformatics (Oxford, England)*. 2015; 31(2):273-4, PMID: 25262153, PMCID: PMC4287945
 - **§Corresponding author.** I have designed and lead the study, supervising Dr. Afsari in performing the analysis, implementing the switchBox R package, preparing the figures, and writing the manuscript. Furthermore, I wrote part of the code included in the package.
 45. Brandt WD, Schreck KC, Bar EE, Taylor I, **Marchionni L**, Raabe E, Eberhart CG, Rodriguez FJ. Notch signaling activation in pediatric low-grade astrocytoma. *Journal of neuropathology and experimental neurology*. 2015; 74(2):121-31. NIHMSID: NIHMS642970, PMID: 25575134, PMCID: PMC4357229
 - For this study, I have assisted with bioinformatics and statistical analyses.
 46. Lim Y, Gondek L, Li L, Wang Q, Ma H, Chang E, Huso DL, Foerster S, **Marchionni L**, McGovern K, Watkins DN, Peacock CD, Levis M, Smith BD, Merchant AA, Small D, Matsui W. Integration of Hedgehog and mutant FLT3 signaling in myeloid leukemia. *Science translational medicine*. 2015; 7(291):291ra96. NIHMSID: NIHMS733757, PMID: 26062848, PMCID: PMC4644635
 - For this study, I have helped with bioinformatics and statistical analyses, participating in figures preparation and manuscript writing.
 47. Carvalho FL, **Marchionni L**, Gupta A, Kummangal BA, Schaeffer EM, Ross AE, Berman DM. HES6 promotes prostate cancer aggressiveness independently of Notch signalling. *Journal of cellular and molecular medicine*. 2015; 19(7):1624-36, PMID: 25864518, PMCID: PMC4511360
 - For this study, I have helped with bioinformatics and statistical analyses, supervising Dr. Gupta, and participating in figures preparation and manuscript writing.
 48. Baras AS, Gandhi N, Munari E, Faraj S, Shultz L, **Marchionni L**, Schoenberg M, Hahn N, Hoque MO, Berman D, Bivalacqua TJ, Netto G. Identification and Validation of Protein Biomarkers of Response to Neoadjuvant Platinum Chemotherapy in Muscle Invasive Urothelial Carcinoma. *PloS one*. 2015; 10(7):e0131245, PMID: 26230923, PMCID: PMC4521868
 - For this study, I have helped with bioinformatics and statistical analyses, participating in figures preparation and manuscript writing.
 49. Izumchenko E, Chang X, Brait M, Fertig E, Kagohara LT, Bedi A, **Marchionni L**, Agrawal N, Ravi R, Jones S, Hoque MO, Westra WH, Sidransky D. Targeted sequencing reveals clonal genetic changes in the progression of early lung neoplasms and paired circulating DNA. *Nature communications*. 2015; 6:8258. NIHMSID: NIHMS713162, PMID: 26374070, PMCID: PMC4595648
 - For this study, I have helped with bioinformatics and statistical analyses, participating in figures preparation and manuscript writing.
 50. Ramirez-Correa GA, Ma J, Slawson C, Zeidan Q, Lugo-Fagundo NS, Xu M, Shen X, Gao WD, Caceres V, Chakir K, DeVine L, Cole RN, **Marchionni L**, Paolucci N, Hart GW, Murphy AM. Removal of Abnormal Myofilament O-GlcNAcylation Restores Ca²⁺ Sensitivity in Diabetic Cardiac Muscle. *Diabetes*. 2015; 64(10):3573-87, PMID: 26109417, PMCID: PMC4587639
 - For this study, I have helped with bioinformatics and statistical analyses, participating in figures preparation and manuscript writing.
 51. Romano A, Parrinello NL, Consoli ML, **Marchionni L**, Forte S, Conticello C, Pompa A, Corso A, Milone G, Di Raimondo F, Borrello I. Neutrophil to lymphocyte ratio (NLR) improves the risk assessment of ISS staging in newly diagnosed MM patients treated upfront with novel agents. *Annals of hematology*. 2015; 94(11):1875-83. NIHMSID: NIHMS737797, PMID: 26223359, PMCID: PMC4695982
 - For this study, I have helped with bioinformatics and statistical analyses, participating in figures preparation and manuscript writing.

52. Mitchell CJ, **Getnet D**, Kim MS, Manda SS, Kumar P, Huang TC, Pinto SM, Nirujogi RS, Iwasaki M, Shaw PG, Wu X, Zhong J, Chaerkady R, Marimuthu A, Muthusamy B, Sahasrabudde NA, Raju R, Bowman C, Danilova L, Cutler J, Kelkar DS, Drake CG, Prasad TS, **Marchionni L**, Murakami PN, Scott AF, Shi L, Thierry-Mieg J, Thierry-Mieg D, Irizarry R, Cope L, Ishihama Y, Wang C, Gowda H, Pandey A. A multi-omic analysis of human naïve CD4⁺ T cells. *BMC systems biology*. 2015; 9:75, PMID: 26542228, PMCID: PMC4636073
- *For this study, I have helped with bioinformatics and statistical analyses, supervising Dr. Getnet, participating in figures preparation and manuscript writing.*
53. Ross AE, Johnson MH, Yousefi K, Davicioni E, Netto GJ, **Marchionni L**, Fedor HL, Glavaris S, Choerung V, Buerki C, Erho N, Lam LL, Humphreys EB, Faraj S, Bezerra SM, Han M, Partin AW, Trock BJ, Schaeffer EM. Tissue-based Genomics Augments Post-prostatectomy Risk Stratification in a Natural History Cohort of Intermediate- and High-Risk Men. *European urology*. 2016; 69(1):157-65, PMID: 26058959
- *For this study, I have helped with bioinformatics and statistical analyses, participating in figures preparation and manuscript writing.*
54. Hurley PJ, Sundi D, Shinder B, Simons BW, Hughes RM, Miller RM, Benzon B, Faraj SF, Netto GJ, Vergara IA, Erho N, Davicioni E, Karnes RJ, Yan G, Ewing C, Isaacs SD, Berman DM, Rider JR, Jordahl KM, Mucci LA, Huang J, An SS, Park BH, Isaacs WB, **Marchionni L**, Ross AE, Schaeffer EM. Germline Variants in Asporin Vary by Race, Modulate the Tumor Microenvironment, and Are Differentially Associated with Metastatic Prostate Cancer. *Clinical cancer research*. 2016; 22(2):448-58. NIHMSID: NIHMS729650, PMID: 26446945, PMCID: PMC4715968
- *For this study, I have helped with bioinformatics and statistical analyses, participating in figures preparation and manuscript writing.*
55. Kahlert UD, Cheng M, Koch K, **Marchionni L**, Fan X, Raabe EH, Maciaczyk J, Glunde K, Eberhart CG. Alterations in cellular metabolome after pharmacological inhibition of Notch in glioblastoma cells. *International journal of cancer*. 2016; 138(5):1246-55. NIHMSID: NIHMS759533, PMID: 26422827, PMCID: PMC4772139
- *For this study, I have helped with bioinformatics and statistical analyses, participating in figures preparation and manuscript writing.*
56. Rettig EM, Talbot CC Jr, Sausen M, Jones S, Bishop JA, Wood LD, Tokheim C, Niknafs N, Karchin R, Fertig EJ, Wheelan SJ, **Marchionni L**, Considine M, Fakhry C, Papadopoulos N, Kinzler KW, Vogelstein B, Ha PK, Agrawal N. Whole-Genome Sequencing of Salivary Gland Adenoid Cystic Carcinoma. *Cancer prevention research (Philadelphia, Pa.)*. 2016; 9(4):265-74. NIHMSID: NIHMS759794, PMID: 26862087, PMCID: PMC4818686
- *For this study, I have helped with bioinformatics and statistical analyses, participating in figures preparation and manuscript writing.*
57. Christensen-Quick A, Lafferty M, Sun L, **Marchionni L**, DeVico A, Garzino-Demo A. Human Th17 Cells Lack HIV-Inhibitory RNases and Are Highly Permissive to Productive HIV Infection. *Journal of virology*. 2016; 90(17):7833-47, PMID: 27334595, PMCID: PMC4988157
- *For this study, I have performed all bioinformatics and statistical analyses involved with differential gene and pathway analysis, participating in figures preparation and manuscript writing.*
58. Kumar B, Khaleghzadegan S, Mears B, Hatano K, Kudrolli TA, Chowdhury WH, Yeater DB, Ewing CM, Luo J, Isaacs WB, **Marchionni L**, Lupold SE. Identification of miR-30b-3p and miR-30d-5p as direct regulators of androgen receptor signaling in prostate cancer by complementary functional microRNA library screening. *Oncotarget*. 2016; 7(45):72593-72607, PMID: 27683042
- *For this study, I have performed all bioinformatics and statistical analyses to assess the clinical relevance of the identified microRNAs in prostate cancer using public domain datasets. I was further involved with figures preparation and manuscript writing.*
59. Carroll VA, Lafferty MK, **Marchionni L**, Bryant JL, Gallo RC, Garzino-Demo A. Expression of HIV-1 matrix protein p17 and association with B-cell lymphoma in HIV-1 transgenic mice. *Proceedings of the National Academy of Sciences of the United States of America*. 2016; 113(46):13168-13173, PMID: 27799525, PMCID: PMC5135339
- *For this study, I have performed all bioinformatics and statistical analyses involved with differential gene and pathway analyses, participating in figures preparation and manuscript writing.*
60. Lee BJ*, **Marchionni L***, Andrews CE, Norris AL, Nucifora LG, Wu YC, Wright RA, Pevsner J, Ross CA, Margolis RL, Sawa A, Nucifora FC Jr. Analysis of differential gene expression mediated by clozapine in human postmortem brains. *Schizophrenia Research*. 2017 Jul;185:58-66. doi: 10.1016/j.schres.2016.12.017. Epub 2016 Dec 27, PMID: 28038920
- ***Equally contributing first author.** *For this research project, I have directly performed all computational and bioinformatics analyses necessary to characterize the gene expression programs associated with atypical anti-psychotic treatment in human brain, analyzing a large collection of all available public domain data. Furthermore, I have provided intellectual insights that were instrumental for interpreting our findings and putting them into biological and clinical context. Finally, I wrote part of the manuscript, prepared several figures, and helped assembling the supplementary material associated with the paper.*
61. De Robertis M, Loiacono L, Fusilli C, Poeta ML, Mazza T, Sanchez M, **Marchionni L**, Signori E, Lamorte G, Vescovi AL, Garcia-Foncillas J, Fazio VM. Dysregulation of EGFR Pathway in EphA2 Cell Subpopulation Significantly Associates with Poor Prognosis in Colorectal Cancer. *Clinical cancer research*. 2017; 23(1):159-170, PMID: 27401248

- *For this study, I have helped with bioinformatics and statistical analyses, participating in figures preparation and manuscript writing.*
62. Stein-O'Brien GL, Carey JL, Lee WS, Considine M, Favorov AV, Flam E, Guo T, Li S, **Marchionni L**, Sherman T, Sivy S, Gaykalova DA, McKay RD, Ochs MF, Colantuoni C, Fertig EJ. PatternMarkers & GWCoGAPS for novel data-driven biomarkers via whole transcriptome NMF. *Bioinformatics*. 2017 Jun 15;33(12):1892-1894. doi: 10.1093/bioinformatics/btx058, PMID: 28174896
- *For this study, I have helped with bioinformatics and statistical analyses, participating in figures preparation and manuscript writing.*
63. **Marchionni L***§, Hayashi M*, Guida E, Ooki A, Munari E, Jabboure FJ, Dinalankara W, Raza A, Netto GJ, Hoque MO, and Argani P§. MicroRNA expression profiling of Xp11 renal cell carcinoma. *Human pathology*. 2017; 67:18-29. NIHMSID: NIHMS902381, PMID: 28411178, PMCID: PMC5628161
- ***Equally contributing first author** and **§Co-corresponding author**. *For this research project, I have both directly performed, and supervised Dr. Dinalankara in executing all computational and bioinformatics analyses necessary to characterize the microRNA expression profiles associated with Xp11 renal cell carcinoma. Furthermore, I have provided intellectual insights that were instrumental for interpreting our findings and putting them into biological and clinical context. Finally, I wrote the manuscript, prepared most figures, and assembled all supplementary material associated with the paper.*
64. Isella C, Brundu F, Bellomo SE, Galimi F, Zanella E, Porporato R, Petti C, Fiori A, Orzan F, Senetta R, Boccaccio R, Ficarra E, **Marchionni L**, Trusolino L, Medico E, and Bertotti A. Selective analysis of cancer-cell intrinsic transcriptional traits defines novel clinically relevant subtypes of colorectal cancer. *Nature communications*. 2017; 8:15107, PMID: 28561063, PMCID: PMC5499209
- *For this study, I have helped with bioinformatics and statistical analyses, participating in figures preparation and manuscript writing.*
65. Gandy L, Gumm J, Fertig B, Kennish MJ, Chavan S, Thessen A, **Marchionni L**, Xia X, Shankrit S, Fertig EJ. Synthesizer: Expediting synthesis studies from context-free data with natural language processing. *PloS one*. 2017; 12(4):e0175860, PMID: 28437440, PMCID: PMC5402950.
- *For this study, I have helped with bioinformatics and statistical analyses, participating in figures preparation and manuscript writing.*
66. **Marchionni L**§, Netto GJ, Hoque MO, Argani P. MicroRNAs, promising biomarkers in the diagnosis of Xp11 translocation RCC – reply. *Human pathology*. 2017; , PMID: 28811253
- **§Co-corresponding author**. *I have prepared this response letter to the comments to our original article.*
67. Begum A, Ewachiw T, Jung C, Huang A, Norberg KJ, **Marchionni L**, McMillan R, Penchev V, Rajeshkumar NV, Maitra A, Wood L, Wang C, Wolfgang C, DeJesus-Acosta A, Laheru D, Shapiro IM, Padval M, Pachter JA, Weaver DT, Rasheed ZA, Matsui W. The extracellular matrix and focal adhesion kinase signaling regulate cancer stem cell function in pancreatic ductal adenocarcinoma. *PloS one*. 2017; 12(7):e0180181, PMID: 28692661, PMCID: PMC5503247
- *For this study, I have helped with bioinformatics and statistical analyses, participating in figures preparation and manuscript writing.*
68. Ross ER, Hughes RM, Glavaris S, Ghabili K, He P, Anders NM, Harb R, Tosoian JJ, **Marchionni L**, Schaeffer EM, Partin AW, Allaf ME, Bivalacqua TJ, Chapman C, O'Neal T, DeMarzo AM, Hurley PJ, Rudek MA, and Antonarakis ES. Pharmacodynamic and pharmacokinetic neoadjuvant study of hedgehog pathway inhibitor Sonidegib (LDE-225) in men with high-risk localized prostate cancer undergoing prostatectomy. *Oncotarget*. In press (accepted on September 15, 2017)
- *For this study, I was the statistician on the clinical trial, and I have helped with bioinformatics and statistical analyses, participating in figures preparation and manuscript writing.*
69. Guerrero-Preston R, White JR, Godoy-Vitorino F, Rodríguez-Hilario A, Navarro K, González H, Michailidi C, Jedlicka A, Canapp S, Bondy J, Dziedzic A, Mora-Lagos B, Rivera-Alvarez G, Ili-Gangas C, Brebi-Mieville P, Westra W, Koch W, Kang H, **Marchionni L**, Kim Y, and Sidransky D. High-resolution microbiome pro ling uncovers *Fusobacterium nucleatum*, *Lactobacillus gasseri/johnsonii*, and *Lactobacillus vaginalis* associated to oral and oropharyngeal cancer in saliva from HPV positive and HPV negative patients treated with surgery and chemotherapy. *Oncotarget*. In press (accepted on July 12, 2017)
- *For this study, I have helped with bioinformatics and statistical analyses, participating in figures preparation and manuscript writing.*
70. Ooki A, Del Carmen Rodriguez Pena M, **Marchionni L**, Dinalankara W, Begum A, Hahn NM, VandenBussche CJ, Rasheed ZA, Mao S, Netto GJ, Sidransky D, Hoque MO. YAP1 and COX2 Coordinately Regulate Urothelial Cancer Stem-like Cells. *Cancer research*. 2018; 78(1):168-181. NIHMSID: NIHMS919734 PubMed [journal] PMID: 29180467, PMCID: PMC5754245
- *I have both directly performed, and supervised Dr. Dinalankara in executing all computational and bioinformatics analyses, and I have participated in figures preparation and manuscript writing.*

71. Ooki A, Begum A, **Marchionni L**, Vanden-Bussche CJ, Mao S, Kates M, Hoque MO. Arsenic promotes the COX2/PGE2-SOX2 axis to increase the malignant stemness properties of urothelial cells. *International journal of cancer*. 2018; PubMed [journal] PMID: 29396848
 - *For this study, I have helped with bioinformatics and statistical analyses, participating in figures preparation and manuscript writing.*
72. Ravi R, Noonan KA, Pham V, Bedi R, Zhavoronkov A, Ozerov IV, Makarev E, V Artemov A, Wysocki PT, Mehra R, Nimmagadda S, **Marchionni L**, Sidransky D, Borrello IM, Izumchenko E, Bedi A. Bifunctional immune checkpoint-targeted antibody-ligand traps that simultaneously disable TGF β enhance the efficacy of cancer immunotherapy. *Nature communications*. 2018; 9(1):741. PubMed [journal] PMID: 29467463, PMCID: PMC5821872
 - *For this study, I have helped with bioinformatics and statistical analyses, participating in figures preparation and manuscript writing.*
73. Bellazzo A, Di Minin G, Valentino E, Sicari D, Torre D, **Marchionni L**, Serpi F, Stadler MB, Taverna D, Zuccolotto G, Montagner IM, Rosato A, Tonon F, Zennaro C, Agostinis C, Bulla R, Mano M, Del Sal G, Collavin L. Cell-autonomous and cell non-autonomous downregulation of tumor suppressor DAB2IP by microRNA-149-3p promotes aggressiveness of cancer cells. *Cell death and differentiation*. 2018; PubMed [journal] PMID: 29568059
 - *For this study, I have helped with bioinformatics and statistical analyses, participating in figures preparation and manuscript writing.*
74. Dinalankara W, Ke Q, Xu Y, Ji L, Pagane N, Lien A, Matam T, Fertig EJ, Price ND, Younes L, **Marchionni L**, and Geman D \S . Digitizing omics profiles by divergence from a baseline. To appear in PNAS
 - **\S Co-corresponding last author.** *For this research project, I have both directly performed, and supervised Dr. Dinalankara in executing all computational and bioinformatics analyses necessary to develop this innovative method of analysis for omics data. Furthermore, I have provided intellectual insights that were instrumental for interpreting our findings and putting them into biological and clinical context. Finally, I wrote the manuscript, prepared figures, and assembled all supplementary material associated with the paper.*

Review Articles

1. **Marchionni L**, Wilson RF, Wolff AC, Marinopoulos S, Parmigiani G, Bass EB, Goodman SN. Systematic review: gene expression profiling assays in early-stage breast cancer. *Annals of internal medicine*. 2008; 148(5):358-69, PMID: 18252678
 - *For this review article, I have identified from the literature all eligible studies on gene expression based assays available at the time for use in early stage breast cancer (MammaPrint, OncotypeDX, and H/I ratio). I further abstracted and summarized all available evidence from these studies, providing intellectual insights that were instrumental for assessing the analytical validity, clinical validity, and clinical utility of these tests. Finally, I wrote most the manuscript, prepared all figures and tables, and assembled all supplementary material associated with the paper and relative monograph (see below).*
2. Lerner SP, Bajorin DF, Dinney CP, Efstathiou JA, Groshen S, Hahn NM, Hansel D, Kwiatkowski D, O'Donnell M, Rosenberg J, Svatek R, Abrams JS, Al-Ahmadie H, Apolo AB, Bellmunt J, Callahan M, Cha EK, Drake C, Jarow J, Kamat A, Kim W, Knowles M, Mann B, **Marchionni L**, McConkey D, McShane L, Ramirez N, Sharabi A, Sharpe AH, Solit D, Tangen CM, Amiri AT, Van Allen E, West PJ, Witjes JA, Quale DZ. Summary and Recommendations from the National Cancer Institute's Clinical Trials Planning Meeting on Novel Therapeutics for Non-Muscle Invasive Bladder Cancer. *Bladder cancer (Amsterdam, Netherlands)*. 2016; 2(2):165-202, PMID: 27376138, PMCID: PMC4927845
 - *For this review article, I wrote the section on epigenetic mechanisms role in non-muscle invasive bladder cancer clinical management.*

Book Chapters, Monographs

1. **Marchionni L**, Wilson RF, Marinopoulos SS, Wolff AC, Parmigiani G, Bass EB, Goodman SN. Impact of gene expression profiling tests on breast cancer outcomes. *Evid Rep Technol Assess (Full Rep)*. 2007 Dec;(160):1-105. PMID: 18457476, PMCID: PMC4781418.
 - *For this monograph see the activities described above for my review article published in *Annals of Internal Medicine*.*
2. **Marchionni L** and Theodorescu D. "Chapter 18: Molecular Pathogenesis of Bladder Cancer - The Urinary Tract - A Comprehensive Guide to Patient Diagnosis and Management". Editors: Donna E. Hansel, Jesse K. McKenney, Andrew J. Stephenson, and Sam S. Chang. 2012, Springer, New York.
 - *For the preparation of this book chapter, I have retrieve, reviewed, and summarized all the literature available at the time on the molecular underpinnings of bladder cancer, writing the chapter.*
3. Zhong X, **Marchionni L**, Cope L, Iversen ES, Garrett-Mayer ES, Gabrielson E, and Parmigiani G. "Optimized cross-study analysis of microarray-based predictors". Editors: Kim-Anh Do, Zhaohui Steve Qin, and Marina Vannucci. Cambridge University Press.

- For the preparation of this book chapter, I have both directly performed, and supervised Dr. Zhong in doing, all computational and bioinformatics analyses necessary to perform the research described. Furthermore, I participated in writing the manuscript and preparing the figures.

Other Publications – Pre-prints

1. Gandy L, Gumm J, Fertig B, Kennish MJ, Chavan S, Thessen A, **Marchionni L**, Xia X, **Shankrit S**, Fertig EJ. Synthesizer: Expediting synthesis studies from context-free data with natural language processing. bioRxiv: 053629. doi: <http://dx.doi.org/10.1101/053629>
 - For this study, I have helped with bioinformatics and statistical analyses, participating in figures preparation and manuscript writing.
2. Kumar B, Rosenberg AZ, Choi SM, Fox-Talbot K, DeMarzo AM, Nonn L, Brennen WN, **Marchionni L**, Halushka MK, Lupold SE. Cell-type specific expression of oncogenic and tumor suppressive microRNAs in the human prostate and prostate cancer. 2018, biorXiv; doi: <https://doi.org/10.1101/251090>
 - For this study, I have helped with bioinformatics and statistical analyses, participating in figures preparation and manuscript writing.

Other Publications – Software packages

1. Afsari B, Dinalankara W, and **Marchionni L**. Bioconductor R package switchBox: Utilities to train and validate classifiers based on pair switching using the K-Top-Scoring-Pair (KTSP) algorithm. <https://www.bioconductor.org/packages/release/bioc/html/switchBox.html>
2. Gupta A and **Marchionni L**. Bioconductor R package RTopper: Utilities to perform and integrate gene set enrichment results across multiple genomic platforms. <https://www.bioconductor.org/packages/release/bioc/html/RTopper.html>
3. Gupta A and **Marchionni L**. Bioconductor R package matchBox: Utilities to enable comparing ranked vectors of features, merging multiple datasets, removing redundant features, using CAT-plots and Venn diagrams, and computing statistical significance. <https://www.bioconductor.org/packages/release/bioc/html/matchBox.html>
4. **Marchionni L**. Bioconductor R package mammaPrintData: Gene expression data for the two breast cancer cohorts published by van't Veer and Van de Vijver in 2002. <https://www.bioconductor.org/packages/release/data/experiment/html/seventyGeneData.html>
5. **Marchionni L**. Bioconductor R package seventyGeneData: Gene expression data for the two breast cancer cohorts published by van't Veer and Van de Vijver in 2002. <https://www.bioconductor.org/packages/release/data/experiment/html/seventyGeneData.html>

Other Publications – Patents

1. Ross AE, Schaeffer EM and **Marchionni L**. Genes encoding secreted proteins which identify clinically significant prostate cancer. (2017). Publication date: Jan 19, 2017; Publication #: US20170016903 A1

FUNDING

EXTRAMURAL Funding

ACTIVE

R01 CA200859 (Marchionni) NIH - NCI	04/05/2016-03/31/2021 \$285,689/year	2.83 calendar
Project title: Hardwiring Mechanism into Predicting Cancer Phenotypes by Computational Learning. Project goal: To develop mechanistic algorithms for prediction in cancer. Role: Principal investigator		
PC150699 (Marchionni - Lotan) DoD - PCRP - 2015 IDA	01/10/2016-09/30/2019 \$750,000	3.0 calendar
Project title: Developing a PTEN-ERG Signature to Improve Molecular Risk Stratification in Prostate Cancer. Project goal: To identify the molecular underpinnings of PTEN-ERG interaction in prostate cancer. Role: Principal investigator		
(Marchionni) NIH R21 AI124776-01	04/01/2017-03/31/2018 \$43,573	1.2 calendar

Sub-contract from University of Maryland (Romerio)

Project title: PrimeFlow RNA for detection of latently-infected CD4+ T cells.

Project goal: To develop a PrimeFlow RNA-based assay for the detection, enumeration, and phenotypic characterization of HIV-1 latently infected cells in clinical samples.

Role: Sub-contract PI

P30 CA006973 (Nelson) 05/07/2012-04/30/2017 0.96 calendar
NIH - NCI \$141,400

Regional Oncology Research Center

Project Goal: Bioinformatics Core: To provide bioinformatics support to investigators in the Cancer Center.

Role: Bioinformatician and Biostatistician

Regional Oncology Research Center \$185,425 0.6 calendar

Project Goal: Microarray Core: To provide statistical support to the Cancer Center microarray core.

Role: Bioinformatician

U01CA196390 - (De Marzo - Pienta) 09/10/2015-08/31/2020 1.2 calendar
NCI – NIH \$6,090 (salary only)

Project title: Multidisciplinary Integrative Genomic Approach to Distinguish Lethal from Indolent Prostate Cancer in Men of European and African Ancestry

Project goal: To characterize “multi-omics” profiles in selected population of prostate cancer men.

Role: Co-investigator

(Sidransky - Hoque) 03/01/2016-02/28/2021 1.14 calendar
NIH - NCI – PQ1 \$499,900

Project title: Identification and characterization of genetic alterations for the progression of pre-neoplastic lung lesions by using novel PDx models and deep sequencing.

Project goal: To develop PDX models of early lung lesions for comprehensively identifying molecular markers for lung cancer clinical management.

Role: Co-investigator

(Sidransky - Hoque) 07/01/2016-06/20/2021 0.48 calendar
NIH - NCI – PQ5 \$250,000

Project title: Exploring whole mitochondrial genome of screen detected pre-neoplastic lung lesions by novel approaches.

Project goal: To obtain a clear understanding of changes in mitochondrial DNA (mtDNA) along the pathway of lung adenocarcinoma pathogenesis. Results from this proposal will provide new insight in the mechanisms of genesis of pre-neoplastic lesions and its progression.

Role: Co-investigator

(Lupold) 07/01/2017-06/30/2020 0.59 calendar
DoD - PCRP IDA - PC160669 \$375,000

Project title: Tissue-specific alternative polyadenylation events as biomarkers for prostate cancer.

Project goal: The goals of this project are to identify and study alternatively polyadenylated prostate specific transcripts as potential biomarkers for active surveillance.

Role: Co-investigator

(Hurley) 09/01/2017-08/31/2022 0.36 calendar
NIH - NCI – 1R01CA211695-01A1 \$250,000/year

Project title: Regulation of Metastatic Development by Heritable Variants in the Tumor Microenvironment.

Project goal: To determine the contribution of ASPN to local tumor growth and metastatic development in autochthonous animal models.

Role: Co-investigator

Completed

R01 GM083084 (Marchionni)

Sub-Contract – Dana Farber Cancer Institute - Irizarry (PI)

NIH 09/01/2013-08/31/2016 0.6 calendar

Project title: Preprocessing and Analysis Tools for Contemporary Microarrays

Project goal: To develop the next generation of preprocessing and analysis tools with an emphasis on translational applications.

Role: Co-investigator

R21-CA164613-02 (Marchionni)

Sub-Contract – Dana Farber Cancer Institute – Rosenberg (PI)

NIH 12/01/2011-11/30/2013 0.6 calendar

Project Title: Evaluation of a novel urothelial cancer biomarker of lethality

Project goal: To validate a novel biomarker based on copy number variation for urothelial cancer.

Role: Co-investigator

PC141474 (Tomlins and Lotan) 07/01/2015-06/30/2018 0.6 calendar

DoD - PCRP \$261,456

Project title: Comprehensive Molecular Profiling of African-American Prostate Cancer to Inform on Prognosis and Disease Biology

Project goal: To assess prostate cancer gene expression signatures and other molecular alterations in African American men.

Role: Co-Investigator

(Lotan) 09/30/2013-09/29/2016 0.6 calendar

DOD - PCRP-IDA \$75,000

Molecular Profiling of Intraductal Carcinoma of the Prostate

Project goal: To ascertain the molecular profile (at DNA and RNA level) of intraductal prostate carcinoma.

Role: Co-investigator

R01 CA163594 (Sidransky) 07/01/2012-04/30/2017 0.6 calendar

NIH \$237,315/year

Discovery and Characterization of methylation Markers

Project goal: Identify common epigenetic alterations in bladder tumor evolution to help us understand their impact on UCC development, role in cancer progression and biological role in drug resistance.

Role: Co-investigator

(Ha) 09/01/2012-08/31/2015 1.53 calendar

NIH \$250,000

Project title: Integrated pathway analysis of altered driver genes in adenoid cystic carcinoma

Projects goal: to utilize the newest array-based technologies and an integrated pathway-based analysis to identify relevant driver genes in adenoid cystic carcinoma tumorigenesis.

Role: Co-investigator

(Hurley) 09/01/2012-08/31/2015 1.53 calendar

PCRP-CDMRP/DoD \$5,385 (salary only)

Project title: ASPN, a Novel Inhibitor of TGF-beta and a Putative Biomarker for Aggressive Prostate Cancer

Project goal: The major goals of this project are to study the inhibitory role of Asporin on TGF-beta signaling in aggressive prostate cancer, evaluating its role as lethality and progression biomarker.

Role: Co-investigator

(Hoque) 07/01/2011-06/30/2014 0.6 calendar

FAMRI

Project Title: Tobacco Induced Epigenetic Alterations in COPD.

Projects Goal: to identify molecular marker related to smoking and COPD

Role: Co-investigator

(Schaeffer) 10/01/2011-09/30/2014 0.6 calendar

DOD-PCRP Idea Award

Project Title: RNASEH2A - a Putative “Non-Oncogene Addiction” Gene Target and Marker for Radio-sensitivity in High Risk Prostate Cancer

Role: Co-investigator

1R21AI084711-01 (Marchionni) 07/01/2009-06/31/2011 1.2 calendar

Sub-Contract - University of Maryland/NIH - Romerio (PI)

Project title: A New Insight into HIV-1 Latency Through a Novel in Vitro System.
Projects Goal: To Determine the determinant of HIV latency using an innovative in vitro system
Role: Co-investigator

R25HG005955 (Wheelan) 09/22/2010-07/31/2013 1.2 calendar
R25 - PAR-09-245 – NHGRI – NIH
Project title: Gaining Skills and Collaborating Through Interdisciplinary Education.
Role: Co-investigator

904112 (Rudin) 07/01/2006-06/30/2013 1.2 calendar
Burroughs Wellcome Foundation
Projects Goal: To develop novel therapies and treatment approaches in lung cancer.
Role: Co-Investigator

R01MH083738 (Zandi) 12/01/2009-11/30/2012 1.2 calendar
NIH
Project title: METAMOODICS: Meta-analyses and Bioinformatics Display of Mood Disorders Genetics.
Projects goal: to establish a genomic data base on mood disorders with the related analytical tools.
Role: Co-investigator

R01 DK072000 (Berman) 07/01/2006-4/30/2011 1.2 calendar
NIH - NIDDK
Project Title: Hedgehog signaling links bladder injury and cancer.
Project Goal: To define molecular events involving the Hedgehog pathway in bladder cancer.
Role: Co-Investigator

290020018 (Goodman/Bass) 10/01/2006-06/30/2007 1.2 calendar
Task Order for the AHRQ
Project Title: Impact of Gene Expression Profiling Tests on Breast Cancer Outcomes
Project Goal: Asses the use of gene expression based assays on breast cancer outcomes.
Role: Co-Investigator

P50 CA058236 (Nelson/Berman) 9/30/1992-3/31/2008 1.2 calendar
NIH - NCI
Project Title: SPORE in Prostate Cancer

DMS0342111 (Parmigiani) 10/1/2004-12/30/2009 6.0 calendar
NSF
Project Title: Multi-Study Genomic Data Analysis
Project Goal: To develop novel data analysis tools for comparison and integration of genomic information across studies, across measurement technologies and across biological systems.

1U54RR023561-01A1 (Ford) 9/17/2007-05/31/2009 0.6 calendar
NIH - NCRR
Project Title: Institute for Clinical and Translational Research, CTSA. Project: Integrated Discovery of Biomarkers and Prognostic Molecular Profiles
Project Goal: To develop biomarkers through the integration of public domain gene expression data.
Role: Co-Investigator

1R21CA135877 (Karchin) 09/09/2008-08/31/2010 0.6 calendar
NIH - NCI
Project Title: Tools for Large-Scale Analysis of Driver Pathways
Projects Goal: To establish methods to integrate across genomic data types (i.e, gene expression, SNPs, etc)
Role: Co-Investigator

3UL1RR025005-03S2 (Ford) 01/01/2009-09/08/2011 1.2 calendar
NIH
Project Title: Genomic Supplement to the Institute for Clinical and Translational Research (ICTR).
Project goal: To foster translational research and expedite the translation of discoveries from bench to clinic.
Role: Co-investigator

R21CA158898 (Leach) 04/10/2011-03/31/2013 1.2 calendar
NIH - NCI
Pilot studies in Pancreatic Cancer
Project Title: "High resolution and single cell analyses of PanIN initiation and progression"
Project goal: To reconstruct the molecular mechanisms involved in pancreatic cancer initiation.
Role: Co-investigator

INTRAMURAL Funding

Completed

O'Brien (pilot project) 10/01/09-07/31/10 0.0 calendar
O'Brien Urology Research Center (NIDDK)
Project Title: Benign Prostatic Hyperplasia Genomic Encyclopedia: analysis and validation of novel and established cellular pathways.
Projects Goal: To establish an encyclopedia of genomic responses in Benign Prostatic Hyperplasia (BPH).
Role: Principal Investigator

Johns Hopkins (Schaeffer) 07/1/07-2006/30/2009 1.2 calendar
Patrick C. Walsh Foundation
Project Title: The Role of Sox9 in Fibroblast Growth Factor Signaling and Prostate Cancer.
Project Goal: To decipher the role of the Fibroblast Growth Factor Signaling and Sox9 in Prostate Cancer.
Role: Co-Investigator

90039865 (Eberhart) 08/01/09 – 07/31/12 0.6 calendar
James S. McDonnell Foundation
Project title: Notch and Hedgehog Signaling in Glioblastoma.
Projects Goal: To understand Notch and Hedgehog pathways as therapeutic targets in malignant gliomas.
Role: Co-investigator

(Marchionni) 7/1/12 – 6/31/13 0.0 calendar
Safeway Foundation – Breast Cancer SPORE
Pilot Project
Project Title: Implementation of simple genomic based predictors for breast cancer clinical management
Role: Principal investigator

CLINICAL ACTIVITIES

I do not currently have clinical responsibilities.

Certifications and Memberships

2004 - present Member of the Italian Medical Board, (01/23/2004, Trieste chapter, Italy, identification: 3753)
2009 – present American Association for Cancer Research, Active Member
2016 – present American Association for the Advancement of Science, Active Member

EDUCATIONAL ACTIVITIES

Educational Focus

I think of teaching, both in the classroom and out, as a core component of a faculty career. To date, the instructional experiences I have been afforded have been fulfilling. I have enjoyed my interactions with students, and found that teaching is also beneficial to my research. I am convinced that there is no better way to learn something than to learn to teach it, since I believe one must be clear and structured to be able to pass on his knowledge to the students. Teaching is the perfect opportunity to settle down a fuzzy theory, and the clarification it creates is always beneficial.

Teaching

Classroom instruction

- 1999 Human Genetics – non-tenured lecturer
Undergraduate program, School of Nursing, University of Turin, Italy
- 2000 Human Genetics – non-tenured lecturer
Undergraduate program, Biotechnology Sciences, School of Medicine, University of Trieste, Italy
- 2004-05 Computational Biology – non-tenured lecturer
Undergraduate program, Biotechnology Sciences, School of Medicine, University of Udine, Italy
- 2004-05 Molecular Investigation Techniques – non-tenured lecturer
Human Genetics Graduate School, School of Medicine, University of Trieste, Italy
- 2005 Bioinformatics – non-tenured lecturer
Structural and Functional Genomics PhD Program at SISSA, Trieste, Italy
- 2009-11 Basic Computing with R
Center for Computational Genomics at Johns Hopkins, Baltimore, MD
- 2010-15 Gene Expression Analysis with R
Center for Computational Genomics at Johns Hopkins, Baltimore, MD
- 2012-16 Bioinformatics
Johns Hopkins University School of Medicine, Baltimore, MD
- 2012-16 ME:510.707 - Statistics & Data Analysis Using R
Johns Hopkins University School of Medicine, Baltimore, MD

Workshops /seminars

- 2014 Bioinformatics Course
Workshop for the Center for Bioinformatics Analysis for Genomics (CABGen)
Institute of Molecular Genetics (IGM), Italian National Research Council (CNR), Pavia, Italy
- 2011-17 Practical Genomics: From Biology to Biostatistics
Workshop for the Center for Computational Genomics at Johns Hopkins, Baltimore, MD
- June 2010 Lecturer on Statistical Genomics
Summer School on Modern Methods in Epidemiology and Biostatistics (www.biostat.epi.org)
Castello Brandolini Colombaro, Cison di Valmarino, Treviso, Italy

Mentoring

Undergraduates Mentees

- 2004 Co-supervisor (with Prof. Claudio Schneider) of Nabil Bahar, Graduate candidate
Chemistry and Pharmaceutical Technologies Program, University of Trieste, Italy
Dissertation topics: "cDNA microarray protocols optimization"
- 2003 Co-supervisor (with Prof. Alberto Policriti) of Silvia Carlino, Graduate candidate
Informatics Program, University of Udine, Italy.
Dissertation topics: "MATS, an integrated database for microarray data"

Elective Internships

Roohan Jhan, Vikas Sud, Abbas Naqvi, Sabeeh Baig, Gurcan Gunaydin, Anurag Chahal, and Akshay Sood

Pre-doctoral Advisees /Mentees

Apurva Chitre, Anuj Gupta, Tai-Chung Huang, Derese Getnet, Shambavhi Sankrit, Nitesh Turaga, John Poirier, Nichole Pagane, Annie Lien, Qian Qe, Eddie Luidi Imada, and Tejasvi Matam

Post-doctoral Advisees /Mentees

Paul O. Aiyetan, Wikum Dinalankara, Diego Fernando Sánchez Martínez, and Aleksei Stupnikov

Thesis committees

2016 - Present	PhD Thesis Committee of Heather Wick, PhD candidate Johns Hopkins University School of Medicine, Baltimore, MD
2016 - Present	PhD Thesis Committee of Roo Steinberg, PhD candidate Johns Hopkins University School of Medicine, Baltimore, MD
2014 - 2017	PhD Thesis Committee of Bracha Avigdor Erlanger, PhD candidate Johns Hopkins University School of Medicine, Baltimore, MD
2014 – 2016	PhD Thesis Committee of Prasad Patil, PhD candidate Johns Hopkins University, School of Public Health, Baltimore, MD
2013 – 2016	PhD Thesis Committee of Sean Soonweng Cho, PhD candidate Johns Hopkins University School of Medicine, Baltimore, MD
2012	PhD Thesis Committee of John Poirier, PhD candidate Johns Hopkins University School of Medicine, Baltimore, MD
2010	PhD Thesis Committee of Marco Carone, PhD candidate Johns Hopkins University, School of Public Health, Baltimore, MD
2010	PhD Thesis Committee of Silvano Piazza, PhD candidate International School for Advanced Studies (SISSA/ISAS), Trieste, Italy
2009	PhD Thesis Committee of Mady Kortenhorst, PhD candidate Utrecht University, Utrecht, The Netherlands

RESEARCH ACTIVITIES

I have extensive experience in the analysis and interpretation of genomic and genetic data. My current research focuses on knowledge integration across different genomic data types, on the development of novel classification algorithms for cancer prognostication and therapy selection, and on the integration of genomic-based predictors into current clinical management of cancer patients. Given my background in medicine, cancer research, and systems biology, I have a unique research perspective, and I have the drive, determination, and creativity to make a difference.

SYSTEM INNOVATION AND QUALITY IMPROVEMENT ACTIVITIES

Not Applicable

ORGANIZATIONAL ACTIVITIES

Institutional Administrative Appointments

2009 - present	Core Faculty Member and Skills Development Director January Center for Computational Genomics, Johns Hopkins University, Baltimore, MD, USA
2010 - present	Resident and Faculty recruitment selection committees Participation to committees for faculty recruitments and resident selection in the Oncology and Pathology Departments

Editorial Activities

Journal peer review activities

Peer reviewer for New England Journal of Medicine, Nature Medicine, Nature Communications, Cancer Discovery, Cancer Research, Annals of Internal Medicine, Clinical Cancer Research, Cancer Research, Current Molecular Medicine, Oncogene, BMC Cancer, Cancer Genetics, Cancer Investigation, Frontiers in Systems Physiology, PLoS ONE,

Bioinformatics, Breast Cancer Research Treatment, Journal of Urology, JNCI, The Prostate, Scientific Reports, Nucleic Acids Research, and BMC Bioinformatics

Advisory Committees, Review Groups/Study Sections

2010	Bankhead-Coley Cancer Research Program, Florida Department of Health
2010	DOD-CDMRP Prostate Cancer Research Program
2010	Davidson Institute for Talent Development Fellowships
2010	DOD-CDMRP Breast Cancer Research Program
2013	Medical Research Council (MRC), Swindon, United Kingdom
2015	Canadian Breast Cancer Foundation, Toronto, Ontario, Canada
2017	NCI Special Emphasis Panel – Emerging Questions in Cancer Systems Biology (ZCA1 SRB-C(J2)
2017	NCI Special Emphasis Panel – Emerging Questions in Cancer Systems Biology (ZRG1 GGG-B 02)
2018	DOD-CDMRP Kidney Cancer Research Program

Professional Societies

2004 - present	Member of the Italian Medical Board
2009 - present	American Association for Cancer Research, Active Member
2016 - present	American Association for The Advancement of Science, Active Member
2016 - present	Advisory Board Member, Intercultura/AFS, Italy

Consultantship

2007 - 2008	Bekton Dickinson Differential gene expression analysis and classification methods.
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RECOGNITION

Awards, Honors

1999 - 2000	FIRC Fellowship, Institute of Molecular Oncology IFOM, Milan, Italy
2000 - 2005	LNCIB Fellowship, Interuniversity Consortium for Biotechnologies, National Laboratory, Trieste, Italy
1999 - 2006	FANTOM Consortium member (RIKEN Genome Science Laboratory, Yokohama Institute, Japan)
2009	Selected for the 2009 AACR Cancer Biostatistics Workshop - "Developing Targeted Agents"
2013 - 2014	Helen Masenhimer Fellowship, Cleveland Foundation New Investigator Research Award (INIRA)
2016 - present	FANTOM Consortium member (RIKEN Genome Science Laboratory, Yokohama Institute, Japan)

Invited Talks

Luigi Marchionni. "cDNA Microarray protocols optimization". 1st Italian Workshop on DNA microarray technology. LITA, Milan, Italy, 2001

Luigi Marchionni. "Gene Expression analysis by cDNA microarray in cancer research". Lecture for the Biology Ph.D. program, University of Udine, Italy, 2002.

Luigi Marchionni. "Data sets and computational tools for transcriptional profiling". Genomics workshop for the SISSA Ph.D. course in Structural and Functional Genomics, Trieste, Italy, 2002.

Luigi Marchionni. "Gene expression profiling analysis in cancer reveals relevant biological processes and pathways". 1st Advanced Course on Molecular Biology and Genetics of Cancer, University of Trieste, Italy, 2003.

Luigi Marchionni. "The transcriptional program of the developing prostate". First Annual Young Investigator

Symposium on Genomics and Bioinformatics. Baltimore, Johns Hopkins Medical Institution. September 25, 2007.

Luigi Marchionni. “Genomic responses to tobacco smoke: A new shared research resource. Analysis of effects on immune activation and function”. Environmental Health Sciences Retreat - Johns Hopkins Bloomberg School of Public Health. Baltimore, January 11, 2008.

Luigi Marchionni. "The prostate cancer transcriptome: dissection by Gleason Grade". International Center for Genetic Engineering and Biotechnology (ICGEB); Trieste, Italy; Thursday, October 21, 2010.

Luigi Marchionni. “Gene Expression Pathways of High Grade Localized Prostate Cancer”. 4th Multi-Institutional Prostate Cancer Program Retreat. Fort Lauderdale, FL, USA, March 21-23, 2011

Luigi Marchionni. “A Hitchhiker’s Guide to Biomarker Genomics – Learning swim in a sea of data”. Hosted by David Berman and Victor Tron. Queens’ University, Kingston, Ontario, Canada, January 8, 2014.

Luigi Marchionni. “Statistics and Analysis of Gene Expression Data”. Anne Arundel Medical Center, The Breast Center of the DeCesaris Cancer Institute, Annapolis, Maryland, USA, February 7, 2014.

Luigi Marchionni. “Identifying targets through genome scale epigenetic analysis”. Clinical Trials Planning Meetings (CTPM) NCI Workshop – Session I: Key Genetic Targets and Relevant Pathways for Intervention in Bladder Cancer: “Novel Therapeutics for Non-Muscle Invasive Bladder Cancer”. NIH Campus, Rockville, MD, March 26, 2015.

Luigi Marchionni. “A Hitchhiker’s Guide to Biomarker Genomics – Learning swim in a sea of data”. Keynote Lecturer – Annual Retreat of The Johns Hopkins National Heart Lung and Blood Institute (NHLBI) Innovative Proteomics Center. Baltimore, MD, April 17, 2015

Luigi Marchionni. “Statistical strategies for optimizing classification by biomarkers”. 2015 Canadian Cancer Research Conference – Session A2: Biomarkers from idea to implementation. Montreal, Quebec, Canada, November 8, 2015.

Luigi Marchionni. “A Hitchhiker’s Guide to Biomarker Genomics – Learning swim in a sea of data”. Johns Hopkins School of Medicine – Pathology Grand Rounds. Baltimore, March 21, 2016.

Luigi Marchionni. “A Hitchhiker’s Guide to Biomarker Genomics – Learning swim in a sea of data”. Candiolo Cancer Institute – University of Turin, Italy, July 1st, 2016.

Luigi Marchionni. “The restaurant at the end of the “omics” universe – What to order and what not...”. 10th Annual Symposium on Genomics and Bioinformatics. Baltimore, Johns Hopkins Medical Institution. October 13, 2016.

Luigi Marchionni. “Decoding Tumor Infiltrating Lymphocyte Expression and Function Across Solid Tumors”. EMBL-EBI Industry Programme Workshop – Computational Immuno-Oncology. Cambridge, MA, October 26, 2016.

Luigi Marchionni. “Hardwiring Biological Mechanisms into Computational Learning of Cancer Phenotypes”. Dana Farber Cancer Institute, Harvard Medical School, Boston, MA, February 16, 2017.

Luigi Marchionni. “Loss of HLA-A in acute myeloid leukemia transmitted by the donor to liver and kidney graft recipients”. 32nd European Immunogenetics and Histocompatibility Conference - Plenary Session - Best Abstract Section Podium Presentation, Venice, Italy, May 9-12, 2018.

OTHER PROFESSIONAL ACCOMPLISHMENTS

Posters

Marchionni L, Modena V, Roggero R, Curtoni ES. “The polymorphism of HLA-B27 and the seronegative spondyloarthropathies in the Italian population”. 13th European Histocompatibility Conference; Crete, Greece, 1999. European Federation for Immunogenetics.

Alessi E, Cuce G, **Marchionni L,** Reid JF, Rizzotto GG, Schneider C and Zivillica F, “Fully automated microarray image analysis”. MGED3 (Microarray Gene Expression Databases), Stanford University, CA, USA, 2001.

De Cecco L, **Marchionni L,** Gariboldi M, Reid JF, Lagonigro S, Caramuta S, Ferrario C, Bussani E, Canevari S, Daidone MG, Pilotti S, Raspagliesi F, Ditto A, Delia D, Schneider C and Pierotti MA. “Microarray technology for gene expression profiling in ovarian cancer: correlation with clinical features”. Oncogenomics, Dublin, Ireland, 2002.

Mezzanzanica D, Gariboldi M, Pilotti S, Fabbi M, Ferrini S, Barbareschi M, **Marchionni L,** Schneider C, Pierotti MA and Canevari S. “IgCAMs in ovarian cancer progression: contribute of cDNA and tissue arrays in their identification and validation”. 3rd International Conference on “Tumor microenvironment: progression, therapy and prevention”, Prague, Czech Republic, 2004.

Marchionni L and C Schneider. "Biological Processes and Signal ling Pathways involved in Ovarian Carcinoma". 8th Annual Armenise-Harvard Foundation Symposium on Cancer Biology and Genomics. Siena, Italy, 2004.

Kortenhorst MSQ, **Marchionni L**, Zahurak ML, Shabbeer S, Kachhap SK, Parmigiani G. "Gene set enrichment analysis of prostate cancer cells to study histone deacetylase inhibitor resistance". AACR Annual Meeting. Los Angeles, CA. April 14 -18, 2007.

Marchionni L, Schaffer EM and Berman DM. "Prostate Cancer Genomic Encyclopedia: generation and validation of a new shared research resource". Prostate Cancer Research Day. The Sidney Kimmel Cancer Center and the Departments of Oncology, Pathology and Urology. Johns Hopkins Medical Institution. Baltimore, MD. February 9, 2008.

Kortenhorst MSQ, Rodriguez R, van der Groep P, **Marchionni L**, Chowdhury WH, Jans J, van Diest PJ "Deregulation of MHC-1 protein expression in human prostate cancer and in vitro re-expression after chronic histone deacetylase inhibitor treatment in prostate cancer cells". AACR Annual Meeting. San Diego, CA. April 12 -16, 2008.

Kachhap SK, Collis SJ, Kortenhorst MSQ, Shabbeer S, **Marchionni L**, Lin J, DeWeese T, Carducci M. "Involvement of E2F1 in down-regulation of homologous recombination repair genes upon histone deacetylase inhibition in prostate cancer." AACR Annual Meeting 2009, Denver, CO. April 18-22, 2009.

Marchionni L, Daniel V, Hierman J, Rhodes J, Devereux W, Rudin C, Yung R, Dorsch M, Parmigiani G, Peacock C and Watkins N. "A primary xenograft model of small cell lung cancer reveals irreversible changes in gene expression imposed by culture in-vitro." AACR Annual Meeting 2009, Denver, CO. April 18-22, 2009.

Shizhang L, Xiaofei C, Thomas L, **Marchionni L**, Netto G, Sidransky D, Berman DM. "EGFR induction of SOX9 is required in a cellular migration program induced by urothelial injury and maintained in cancer". AACR Annual Meeting. Washington, DC. April 17 -21, 2010.

Marini A, Parvez K, **Marchionni L**, and Romerio F. "Modeling HIV-1 Latency in vitro". 12th Annual International Meeting of the Institute of Human Virology; October 4-8, 2010

Rigamonti D, Batra S, Kapoor S, Carson K, Shuck J, Kharkhar S, Gandhi R, Jackson J, Wemmer J, Terezakis S, Shokek O, Kleinberg L, **Marchionni L** "A call for a better definition of success and failure in radiosurgery for Vestibular Schwannomas (VS)". ISRS Paris, France on May 8-12, 2011.

Iglesias-Ussel M, **Marchionni L**, Romerio F. "Complete transcriptome analysis of latently infected CD4 (+) T cells." XIX International AIDS Conference, July 22-27 2012, Washington DC, USA.

Fu C, Gerber S, Van Den Berg S, Steenwinkel F, Kant H, Moriarty W, Keizman D, **Marchionni L**, Carducci M, and Netto G. "Epithelial mesenchymal transition: A mechanism of resistance to VEGF pathway inhibition in genitourinary cancers." Cancer Res. American Association for Cancer Research; 2012;72(8 Supplement):1913–3.

Iglesias-Ussel M, **Marchionni L**, Krishnan S, Romerio F. E4 Modeling HIV-1 Latency In Vitro. JAIDS Journal of Acquired Immune Deficiency Syndromes. LWW; 2012;59:83.

Iglesias-Ussel M, Vandergeeten C, **Marchionni L**, Chomont N, and Romerio F. "High levels of CD2 expression identify HIV-1 latently infected resting memory CD4+ T cells in virally suppressed subjects". 20th Conference on Retroviruses and Opportunistic Infections, Atlanta, GA, March 3-6, 2013.

Kim JJ, Labots M, **Marchionni L**, Begum S, Meijer GA, Verheul HMW, Carducci MA, Hammers HJ, Allaf M, Netto GJ, Hoque MO. "Genome-wide methylation profiling to identify potential epigenetic biomarkers associated with response to sunitinib in metastatic renal cell cancer patients". 2013 ASCO Annual Meeting, Chicago, IL, May 31 - June 4, 2013

Afsari B, Fertig EJ, Younes L, Geman D, and **Marchionni L**. "Hardwiring Mechanism into Predicting Cancer Phenotypes by Computational Learning." AACR Annual Meeting 2014, San Diego, CA. April 5-9, 2014.

Carvalho FL, **Marchionni L**, Gupta A, Ross AE, Ahamad B, Schaeffer EM, et al. 847 HES6 promotes prostate cancer aggressiveness and is independent of Notch signaling. European Urology Supplements. 2014;1(13):e847.

Mullane P, Duan Y, Benzon B, Simons B, Hurley P, Huang Z, **Marchionni L**, Vergara IS, Alshalalfa M, and Davicioni E. "An expression-guided screen for small molecules targeting aggressive prostate cancer." ASCO Annual Meeting Proceedings. 2014;32(15_suppl):e16081.

Robertis MD, Bandrés E, Poeta ML, Loiacono L, Lamorte G, Sanchez M, **Marchionni L**, Diodoro MG, Pescarmona E, and Vescovi AL. "Phase specific microRNA deregulation of oncogenesis and stemness in a mouse model of sporadic CRC." Cancer Res. American Association for Cancer Research; 2014;74(19 Supplement):1465–5.

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