Alireza Heravi Moussavi, BSc, MSc, PhD

HIGHLIGHTS OF QUALIFICATIONS

- In-depth bioinformatics and wet-lab skills in:
  - analyzing large-scale genomic and proteomics data
  - molecular and cell biology experiments
  - stem cell research
  - microRNA studies
- Several years of experience on epigenomics studies
- Experience with big data studies
- Statistical analysis and modeling using R and SAS
- Programming skills: R, Python

GOOGLE SCHOLAR CITATIONS REPORT:

https://scholar.google.com/citations?user=DeiW-W0AAAAJ&hl=en

WORK EXPERIENCES

- (2012- present) **Researcher/Computational Biologist**, Genome Sciences Centre. BC Cancer Agency, Vancouver, Canada.

- (2009 - 2011) **Postdoctoral Fellow/Research Associate**. Centre for Translational and Applied Genomics (CTAG) and Department of Molecular Oncology, BC Cancer Agency, Vancouver, Canada.

- (2008 - 2009) **Associate Professor**
  Department of Animal Sciences, Ferdowsi University of Mashhad, Iran

- (2004 - 2008) **Assistant Professor**
  Department of Animal Science, Ferdowsi University of Mashhad, Iran
  - ❖ Carried out seven national field studies, authored or co-authored 20+ peer-reviewed journal papers, graduated 3 PhD and 6 MSc students.

- (2005) **Visiting Scientist**, Department of Clinical Science, Cornell University
  - ❖ Project: Effect of conjugated linoleic acid on prostaglandins production in vitro

- (2005 - 2007) **Head of Department of Animal Science**
  Department of Animal Science, Ferdowsi University of Mashhad, Iran
  - ❖ Established three laboratories.

- (2005 - 2007) **Director of Excellence Centre of Animal Science**
  Department of Animal Science, Ferdowsi University of Mashhad, Iran

- (2002 - 2003) **Visiting fellow**, Department of Animal Science, Cornell University

- (1994 - 2004) **Lecturer**
  Department of Animal Science, Ferdowsi University of Mashhad, Iran

SELECTED PUBLICATIONS IN SCIENTIFIC JOURNALS

Alireza Heravi-Moussavi, M. Bilenky, S. Gakkhar, A. Lorzadeh, A. Carles, J. Parker, C. J. Brown, A. A. Karimuddin, P. T. Phang, M. Raval, W. Xiong, R. Moore, A. Mungall, M. A. Marra, S. JM. Jones, A. Karsan, M. Hirst. 2019. Epigenetic dysregulation in colorectal cancer with CpG island methylator phenotype disturbs differentiation and promotes stem cell-like signature (in preparation).

A. Lorzadeh, C. Hammond, D.J.H.F. Knapp, Q. Cao, F. Wang, **A. Heravi-Moussavi**, M. Wong, M. Bilenky, M. Moksa, Z. Sharafianardakani, P.M. Lavoie, C.J. Eaves, M. Hirst. 2019. Polycomb contraction differentially regulates terminal human hematopoietic differentiation programs (Submitted).

M. Ghaedi, Z. Y. Shen, M. Orangi, I. Martinez-Gonzalez, L. Wei, X. Lu, A. Das, **A. Heravi-Moussavi**, M. A. Marra, A. Bhandoola, and F. Takei. 2020. Single-cell analysis of RORα tracer mouse lung reveals ILC progenitors and effector ILC2 subsets. J Exp Med. 2: 217(3). Doi: 10.1084/jem.20182293.

E. Schneider, N. Pochert, C. Rueß, L. MacPhee, L. Escano, C. Miller, K. Krowiorz, E. Malmberg, **A. Heravi-Moussavi**, A. Lorzadeh, A. Ashouri, S. Grasedieck, N. Sperb, P. Kopparapu, S. Iben, A. Staffas, P. Xiang, R. Rösler, M. Kanduri, E. Larsson, L. Fogelstrand, H. Döhner, K. Doehner, S. Wiese, M. Hirst, R. Keith Humphries, L. Palmqvist, F. Kuchenbauer, and A. Rouhi. 2019. MicroRNA-708 is a novel regulator of the Hoxa9 program in myeloid cells. Leukemia. doi:10.1038/s41375-019-0651-1

E. Schneider, A. Staffas, L. Röhner, E.D. Malmberg, A. Ashouri, K. Krowiorz, N. Pochert, C. Miller, S.Y. Wei, L. Arabanian, C. Buske, H. Döhner, L. Bullinger, L. Fogelstrand, M. Heuser, K. Döhner, P. Xiang, J. Ruschmann, O.I. Petriv, **A. Heravi-Moussavi**, C.L. Hansen, M. Hirst, R.K. Humphries, A. Rouhi, L. Palmqvist, F. Kuchenbauer. MicroRNA-155 is a direct target of Meis1, but not a driver in acute myeloid leukemia. 2018. Haematologica. 103: 246-255.

S. Celia, S. Wiseman, S. Gakkhar, **A. Heravi-Moussavi**, M. Bilenky, A. Carles, T. Sierocinski, A. Tam, E. Zhao, K. Kasaian, R. A. Moore, A. J. Mungall, B. Walker,

T. Thomson, M. A. Marra, M. Hirst, and S. J. M. Jones. 2017. Characterization of the human thyroid epigeome. Journal of Endocrinology. 235: 153-165.

M. Mingay, A. Chaturvedi, M. Bilenky, Q. Cao, L. Jackson, T. Hui, M. Moksa, **A. Heravi-Moussavi**, R. K. Humphries, M. Heuser and M. Hirst. 2017.Vitamin C-induced epigenomic remodelling in IDH1 mutant acute myeloid leukaemia. Leukemia. doi:10.1038/leu.2017.171.

N. Forouzanfar, A. Baranova, S. Milanizadeh, **A. Heravi-Moussavi**, A. Jebelli, M. R. Abbaszadegan. 2017. Novel candidate genes may be possible predisposing factors revealed by whole exome sequencing in familial esophageal squamous cell carcinoma. Tumor Biology. 39: 1-8.

D. Pellacani, M. Bilenky, N. Kannan, **A. Heravi-Moussavi**, D. J.H.F. Knapp, S. Gakkhar, M. Moksa, A. Carles, R. Moore, A. Mungall, M. A. Marra, S. JM Jones, S. Aparicio, M. Hirst, C.J. Eaves. 2016. Analysis of normal human mammary epigenomes reveals cell-specific active enhancer states and associated transcription factor networks. Cell Reports. 17: 2060-2074.

A. Lorzadeh, M. Bilenky, C. Hammond, D. J.H.F. Knapp, L. Li, P. H. Miller, A. Carles, **A. Heravi-Moussavi**, S. Gakkhar, M. Moksa, C. J Eaves, and M. Hirst. 2016. Nucleosome density ChIP-seq identifies distinct chromatin modification signatures associated with MNase accessibility. Cell Reports. 17: 2112-2124.

J. Li, S. L. Woods, S. Healey, J. Beesley, X. Chen, J. S. Lee, H. Sivakumaran, N. Wayte, K. Nones, J. J. Waterfall, J. Pearson, A. Patch, J. Senz, M. Ferreira, P. Kaurah, R. Mackenzie, **A. Heravi-Moussavi**, S. Hansford, T. R.M.Lannagan, A. B. Spurdle, P. T. Simpson, L. da Silva, S. R. Lakhani, A. D. Clouston, M. Bettington, F. Grimpen, R. A. Busuttil, N. DiCostanzo, A. Boussioutas, M. Jeanjean, G. Chong, A. Fabre, S. Olschwang, G. J. Faulkner, E. Bellos, L. Coin, K. Rioux, O. F. Bathe, X. Wen, H. C. Martin, D. W. Neklason, S. R. Davis, R. L. Walker, K. A. Calzone, I. Avital, T. Heller, C. Koh, M. Pineda, U. Rudloff, M. Quezado, P. N. Pichurin, P. J. Hulick, S. M. Weissman, A. Newlin., W. S. Rubinstein, J. E. Sampson, K. Hamman, D. Goldgar, N. Poplawski., K. Phillips, L. Schofield., J. Armstrong, C. Kiraly-Borri., G. K. Suthers., D. G. Huntsman, W. D. Foulkes, F. Carneiro, N. M. Lindor, S. L. Edwards, J. D. French, N. Waddell, P. S. Meltzer, D. L. Worthley, K. A. Schrader and G. Chenevix-Trench. 2016. Point mutations in exon 1B of APC reveal gastric adenocarcinoma and proximal polyposis of the stomach as a familial adenomatous polyposis variant. The American Journal of Human Genetics. 98: 830-842.

H. E. Chun, E. L. Lim, **A. Heravi-Moussavi**, S, Saberi, K. L. Mungall, M. Bilenky, A. Carles, K. Tse, I. Shlafman, K. Zhu, J. Q. Qian, D. L. Palmquist, A. He, W. Long, R. Goya, M. Ng, V. G. LeBlanc, E. Pleasance, N. Thiessen, T. Wong, E. Chuah, Y. Zhao, J. E. Schein, D. S. Gerhard, M. D. Taylor, A. J. Mungall, R. A. Moore, Y. Ma, S. JM Jones, E. J. Perlman, M. Hirst, M. A. Marra. 2016. Genome-Wide Profiles of Extra-cranial Malignant Rhabdoid Tumors Reveal Heterogeneity and Dysregulated Developmental Pathways. Cancer Cell. 29: 394-406.

Roadmap Epigenomics Consortium, A. Kundaje, W. Meuleman, J. Ernst, M. Bilenky, A. Yen, **A. Heravi-Moussavi**, P. Kheradpour, Z. Zhang, J. Wang, M. J. Ziller, V. Amin, J. W. Whitaker, M. D. Schultz, L. D. Ward, A. Sarkar, G. Quon, R. S. Sandstrom, M. L. Eaton, Y. Wu, A. R. Pfenning, X. Wang, M. Claussnitzer, Y. Liu, C. Coarfa, R. A. Harris, N. Shoresh, C. B. Epstein, E. Gjoneska, D. Leung, W. Xie, R. D. Hawkins, R. Lister, C. Hong, P. Gascard, A. J. Mungall, R. Moore, E. Chuah, A. Tam, T. K. Canfield, R. S. Hansen, R. Kaul, P. J. Sabo, M. S. Bansal, A. Carles, J. R. Dixon, K. Farh, S. Feizi, R. Karlic, A. Kim, A. Kulkarni, D. Li, R. Lowdon, G. Elliott, T. R. Mercer, S. J. Neph, V. Onuchic, P. Polak, N. Rajagopal, P. Ray, R. C. Sallari, K. T. Siebenthall, N. A. Sinnott-Armstrong, M. Stevens, R. E. Thurman, J. Wu, B. Zhang, X. Zhou, A. E. Beaudet, L. A. Boyer, P. L. De Jager, P. J. Farnham, S. J. Fisher, D. Haussler, S. JM Jones, W. Li, M. A. Marra, M. T. McManus, S. Sunyaev, J. A. Thomson, T. D. Tlsty, L. Tsai, W. Wang, R. A. Waterland, M. Q. Zhang, L. H. Chadwick, B. E. Bernstein, J. F. Costello, J. R. Ecker, M. Hirst, A. Meissner, A. Milosavljevic, B. Ren, J. A. Stamatoyannopoulos, T. Wang, M. Kellis. 2015. Integration analysis of 111 reference human epigenomes. Nature. 518: 317-330.

P. Gascard, M. Bilenky, M. Sigaroudinia1, J. Zhao, L. Li, A. Carles, A. Delaney, A. Tam, B. Kamoh, S. Cho, M. Griffith, A. Chu, G. Robertson, D. Cheung, I. Li, **A. Heravi-Moussavi**, M. Moksa, M. Mingay, A. Hussainkhel, R. P. Nagarajan, C. Hong, L. Echipare, H. O'Geen, M. J. Hangauer, J. B. Cheng, D. Neel, M. McManus, R. Moore, A. Mungall, E. Ziv, T. Wang, P. J. Farnham, S. JM Jones, M. A. Marra, T. D. Tlsty, J. F. Costello, M. Hirst. 2014. Epigenetic and transcriptional determinants of the human breast. Nature Communications 6, doi: 10.1038/ncomms7351.

H. Younesy, T. Moller, **A. Heravi-Moussavi**, JB. Cheng, JF. Costello, MC. Lorincz, MM. Karimi, SJ. Jones. 2014. ALEA: a toolbox for allele-specific epigenomics analysis. Bioinformatics. 30: 1172-1174.

M. S. Angeliso, W. Yang, J. Senz, A. Wan, Y. Wang, **A. Heravi-Moussavi**, C. Salamanca, S. Maines-Bandiera, D. G. Huntsman, G. B. Morin. 2013. Cancer-associated somatic DICER1 hotspot mutations cause defective miRNA processing and reverse strand expression bias to predominantly mature 3p strands through loss of 5p strand cleavage. J. Pathol. 229:400-409.

A. Heravi-Moussavi, M. S. Anglesio, S.-W. Grace Cheng, J. Senz, W. Yang, L. Prentice, A. Fejes, C. Chow, A. Tone, S. E. Kalloger, N. Hamel, A. Roth, G. Ha, A. N.C. Wan, S. Maines-Bandiera, C. Salamanca, B. Pasini, B. A. Clarke, A. F. Lee, C.-H Lee, C. Zhou, R. H. Young, S. A. Aparicio, P. H.B. Sorensen, M. M.M. Woo, N. Boyd, S. J.M. Jones, M. Hirst, M. A. Marra, B. Gilks, S. P. Shah, W. D. Foulkes, G. B. Morin, D. G. Huntsman. 2012. Recurrent somatic DICER1 mutations in non-epithelial ovarian cancers. N Engl J Med. 366:234-242

S. P. Shah, A. Roth, R. Goya, A. Oloumi, G. Ha, Y. Zhao, G. Turashvili, J. Ding, K. Tse, G. Haffari, A. Bashashati, L. Prentice, J. Khattra, A. Burleigh, D. Yap, V. Bernard, A. McPherson, K. Shumansky, A. Crisan, R. Giuliany, **A. Heravi-Moussavi**, J. Rosner, D. Lai, I. Birol, R. Varhol, A. Tam, N. Dhalla, T. Zeng, K. Ma, S. Chan, M. Griffith, A. Moradian, S.-W. G. Cheng, G. Morin, P. Watson, K. Gelmon, S. Chia, S.- F. Chin, C. N. Curtis, O. Rueda, P. Pharoah, S. Damaraju, J. Mackey, K. Hoon, T. Harkins, V. Tadigotla, M. Sigaroudinia, P. Gascard, T. Tlsty, J. Costello, I. M. Meyer, C. J. Eaves, S. Jones, D. Huntsman, M. Hirst, C. Caldas, M. A. Marra, S. Aparicio. 2012. Mutational landscapes of primary triple negative breast cancers reveal individual heterogeneity but distinct patterns of somatic mutation. Nature. 486: 395-399.

K.A. Schrader*, **A. Heravi-Moussavi***, P. J. Waters, J. Senz, J. Whelan, G. Ha, P. Eydoux, T. Nielsen, B. Gallagher, A. Oloumi, N. Boyd, B. A. Fernandez, T. L. Young, S. J. Jones, M. Hirst, S. P. Shah, M. A. Marra, J. Green, D. G. Huntsman. 2011. Using next-generation sequencing for the diagnosis of rare disorders: a family with retinitis pigmentosa and skeletal abnormalities. J Pathol. 225:12-8 (*: co-first author)

A. McPherson, F. Hormozdiari, A. Zayed, J. Senz, R. Giuliany, M. Sun, N. Melnyk, M. Pacheco, M. Grith, **A. Heravi Moussavi**, M. Marra, T. Nielsen, C. Sahinalp, D. Huntsman, and S. Shah. 2010. deFuse: an algorithm for gene fusion discovery in tumor RNA-Seq data. PLoS Comput Biol. 7(5):e1001138

M. K. McConechy, M. S. Anglesio, S. E. Kalloger, W. Yang, J. Senz, C. Chow, **A. Heravi-Moussavi**, G. B. Morin, A. M. Mes-Masson; Australian Ovarian Cancer Study Group, M. S. Carey, J. N. McAlpine, J. S. Kwon, L. M. Prentice, N. Boyd, S.

P. Shah, C. B. Gilks, D. G. Huntsman. 2011. Subtype-specific mutation of PPP2R1A in endometrial and ovarian carcinomas. J Pathol. 223:567-73

K. C. Wiegand, S. P. Shah, O. M. Al-Agha, Y. Zhao, K. Tse, T. Zeng, J Senz, M. K. McConechy, M. S. Anglesio, S. E. Kalloger, W. Yang, **A. Heravi-Moussavi**, R. Giuliany, C. Chow, J. Fee, A. Zayed, L. Prentice, N. Melnyk, G. Turashvili, A. D. Delaney, J. Madore, S. Yip, A. W. McPherson, G. Ha, L. Bell, S. Fereday, A. Tam, L. Galletta, P. N. Tonin, D. Provencher, D. Miller, S. J. Jones, R. A. Moore, G. B. Morin, A. Oloumi, N. Boyd, S. A. Aparicio, IeM. Shih, A. M. Mes-Masson, D. D. Bowtell, M. Hirst, B. Gilks, M. A. Marra, D. G. Huntsman. 2010. ARID1A mutations in endometriosis-associated ovarian carcinomas. N Engl J Med. 363:1532-43.

K. A. Schrader, B Gorbatcheva, J. Senz, **A. Heravi-Moussavi**, N. Melnyk, C. Salamanca, S. Maines-Bandiera, S. Cooke, P. Leung, J. D. Brenton, C. B. Gilks, J. Monahan, and D. G. Huntsman. 2009. The Specificity of the FOXL2 c.402C>G Somatic Mutation: A Survey of Solid Tumors. PLoS ONE 4 (11): e7988. doi: 10. 1371/ journal.pone.0007988