FULL NAME: Michael T Hallett	
POSITION TITLE: Professor, Department of Biology, Centre for Structural and Functional Genomics	
INSTITUTION: Concordia University	
FULL ADDRESS: 7141 Rue Sherbrooke Ouest, Rm 120.07, Montreal, Quebec, Canada, H4B 1R6	
TELEPHONE: +1-514-848-2424 ex 2296	EMAIL: Michael.Hallett@concordia.ca
WEB-ADDRESS: http://www.bci.mcgill.ca	

ACADEMIC BACKGROUND			
Degree Type	*MM/YY*	*Discipline/Field/Specialty*	*Institution & Country*
Post-doctorate	**07/00**	**Computational Biology**	**Swiss Federal Institute of Technology (ETH)**
Doctorate	**06/96**	**Computer Science**	**University of Victoria, Canada**
Bachelor's	**06/92**	**Computer Science**	**Queen's University, Canada**

WORK EXPERIENCE			
Position, Organization	*Department/Division*	*Start Date*	*End Date*
Full Professor, CRC Tier 1, Concordia University	**Biology**	**01/2017**	**-**
Adjunct Professor, McGill University	**Computer Science/Biochemistry**	**06/2017**	**-**
Full Member, Centre for Structural and Functional Genomics	**Concordia University**	**01/2017**	**-**
Associate Professor, McGill University	**School of Computer Science**	**2006**	**2017**
Associate Member, McGill University	**Biochemistry**	**2003**	**2017**
Associate Member, McGill University	**Goodman Cancer Centre**	**2011**	**2015**
Full Member, McGill University	**Goodman Cancer Centre**	**2009**	**2011**
Visiting Scientist, German Cancer Research Centre	**German Cancer Research Centre**	**2007**	**2008**
Director, McGill University	**Centre for Bioinformatics**	**2006**	**2012**
Interim Director, McGill University	**Centre for Bioinformatics**	**2000**	**2006**
Assistant Professor, McGill University	**School of Computer Science**	**2000**	**2006**
Oberassistant, Swiss Federal Institute of Technology	**Computer Science**	**1998**	**2000**

Honours & Awards

2017 Canadian Research Chair Tier 1, Algorithmic Bioinformatics
2008 Alexander von Humboldt Fellow, Germany

Personal Statement

My lab has a long-standing interest in the development of bioinformatics/systems biology methodology for breast cancer with over 40 publications in the area. Of relevance to this proposal, one of our main focuses has been on the development of gene set predictors. Gene set predictors use, for example, mRNA levels for a (small) set of genes in a multivariate fashion to classify or stratify patients relative to a clinical end-point eg prognosis or benefit from a therapy. The majority of predictors in breast cancer (eg. Oncotype DX, MammaPrint and Prosignia) have focused on predicting whether an estrogen receptor positive breast tumors should receive chemotherapy in addition to Tamoxifen, or whether the Tamoxifen alone would suffice. Our projects have taken gene set predictors in new and novel bioinformatic directions. As one example, we attempted to predict the likely site of metastases (eg bone, liver, kidney, brain) from an expression profile of the primary tumor. For some cites such as bone, there are drugs that can inhibit colonization. If we know patient is at high risk for a specific type of metastasis, then she can be given the prophylactic treatment (this area of work has received 1883 citations).

Several of my most significant research contributions stem from my breast cancer project funded by Genome Quebec. Of relevance to this proposal, this project sequenced the DNA and RNA for a sizeable cohort (n=500 invasive breast cancers). We then compared 110 previously reported prognostic set predictors in the literature led to a concept we call *inherent prognostic difficulty* (Tofigh et al. (2014) Cell Reports). Essentially, we observe that the prognosis of some

patients are very easy to predict, while other patients appear very difficult), using molecular profiles from the primary tumor at time of diagnosis. In other words, almost every reported prognostic gene set predictor (which poll a wide range of cancer hallmarks) correctly estimates the easy patients, but none of the existing prognostic signatures is capable of predicting outcome for the difficult cases.

Our lab has also introduced new approaches for patient subtyping that address some of the "real world" clinical constraints associated with personalized medicine. In research settings, we typically have access to a large cohort of profiled samples. Using this cohort, we have the "luxury" of classifying patient subtype using comparative analysis. Essentially, approaches in the literature estimate the subtype of a new sample as the subtype of the sample's closest neighbor in the cohort. In clinical applications, a tumor must often be examined "in isolation" without recourse to relativistic approaches. We presented an approach entitled AIMS (Paquet and Hallett 2014 Journal of the National Cancer Institute) that accurately assessed subtype in an absolute manner, only looking at the target sample and without the use of a comparative group. The manuscript was the subject of two editorials (Staaf, Ringner, JNCI and Kim JY, Kim S-I, Paik S (2015) JAMA Oncology) underscoring perhaps their promise of clinical utility. A second article predicts activation of all molecular pathways in an analogous absolute (AIPS) recently appeared in Breast Cancer Research. We also recently introduced our framework entitled BreSAT (Breast Signatures Analysis Tool). The mathematics and computational framework (based on linear orders and extremal probability) was supported by my previous NSERC Discovery grant. To date, the tool has been used in 14 manuscripts with our collaborators including a Science article, a Nature Methods article and four PNAS articles.

Also of relevance to this proposal, we have a history of developing predictors for early, pre-invasive forms of breast cancer in collaboration with the famous Oslo group led by Sorlie and Borressen-Dale, and now this propoal with E Rakovitch at Sunnybrooke. In 2010, we published a manuscript (Muggerud et al.) that studies ductal carcinoma in situ (DCIS), a non-obligate precursor to invasive breast cancer that affects approximately one in five women. However, only a small fraction (estimated at less than ½) will ever progress to a life-threatening form of the disease. Unfortunately we currently have no means of differentiating between the DCIS that are likely to progress, and those that are likely to remain indolent. Therefore, an enormous number of women are being over-treated, sometimes with mastectomy. In Muggerud et al. (2012) and a follow up manuscript Lesurf et al. (2015), we identified a set of genes that could differentiate between those instances of ductal carcinoma in situ (DCIS) that are likely to progress to an invasive form of the disease from those likely to remain indolent. This work has served as a stepping-stone to projects with Norway, Sweden and now Toronto with larger cohorts of DCIS patients to explore clinically relevant signatures that ablate over-treatment of this disease.

Additional Activities and Contributions

With respect to international leadership, I am one of three founding members of the Computational Cancer workshop, a satellite of RECOMB (Research on Computational Molecular Biology; http://www.recomb.org). This bi-annual meeting was the first to focus specifically on the use of computational biology to study cancer. I have been a co-organizer of large conferences including RECOMB '01 in Montreal, and several smaller bioinformatics workshops. I have organized 17 workshops at McGill's Bellairs research station in Barbados, covering a wide range of topics from fundamental computational biology to cancer immunology http://www.bci.mgill.ca/home/barbados. Nationally, I have served on several CIHR steering committees related to new programs (2010), priority reviews (2012) and the recent funding reforms (2014). I served on the program committees of the Canadian Society for Biochemistry and Molecular Cell Biology in 2008 and the Canadian Cancer Research Conference in 2013. In the latter conference, I designed and chaired the first systems biology session in this venue that attracts both clinical and molecular oncologists. I have also served on the steering committee to build a national centre of excellence for bioinformatics (CBIN), and as an advisor to training programs in systems biology/bioinformatics at the University of Ottawa (Regulomics program 2006) and Universite de Montreal (Robert Cedegren program 2008). Lastly, I supported (co-applicant or collaborator) almost 200 individual research grants to various agencies by different researchers at McGill. As the director of the McGill Centre for Bioinformatics, I helped hire five professors in this area, and developed intellectual support services for many groups spread across the Faculty of Medicine and the MUHC hospitals.

Over the past 18 years, I have maintained an inter-disciplinary lab with 10-15 researchers who have backgrounds in either the quantitative or life sciences. Five of the 11 research associates/postdocs are now professors at universities (Nebraska, Ottawa, Laval, Bristol, McGill). The lab has also produced 10 PhDs, of which two are now professors in bioinformatics (Sherbrooke, USC), one is completing his postdoctoral training, six have found positions as senior bioinformatic scientists at major research institutes or companies (Sage Bionetworks Inc, Hutchinson Cancer Centre, Princess Margaret Hospital, Sequenta Inc., Google). Of the 20 MSc students, 11 have now received their Ph.d. (9 in bioinformatics), and three have bioinformatic related jobs. I have consistently supported two undergraduate students per year in his lab with typically summer research projects. Every one of the 12 since 2012 has gone on to graduate or medical school.

The highly inter-disciplinary nature of the research group presents many challenges for training. My goal is to form students who are true researchers in a particular area of biology but for whom bioinformatics is their primary assay. I have developed and taught various types of graduate courses in bioinformatics and systems biology including two advanced courses within the School of Computer Science but also courses geared towards undergraduate students in the life sciences. In 2003, I created a graduate program in Bioinformatics at McGill that spanned three faculties and 11 departments involving quantitative, life science and clinical researchers. I was the principle applicant for, and directed, the CIHR-STIHR funded systems biology training program at McGill entitled Integrative Approaches to Human Health ($1.7M over 5 years). The program offered many *de novo* training events including workshops, courses, roundtables, retreats, and student-run symposia to help in cross-training and supported 44 Ph.D.

I have been an active reviewer for most federal granting agencies including NSERC (Biosciences as panel member and reviewer for the Discovery and Chair programs), CFI, Genome Canada and CRC. For the CIHR, I have served on four different panels as a member including Genomics (6 years). I also chaired the Genomics committee for two years and I continue to serve as a virtual chair in the reformed system. I contributed to many of the provincial agencies throughout Canada (eg FRSQ, Michael Smith Foundation, Alberta Heritage Fund) and served as a member on some panels (eg Ontario Genomics Research Council). I also served as a committee member on cancer panels for the Canadian Cancer Research Initiative (CCSRI) and Prostate Canada and served as a reviewer for other non-profit agencies such as the Terry Fox Research Initiative and Quebec Breast Cancer Foundation.

<u>Service on panels for granting agencies (last 5 years)</u>

2010, 11, 13, 18	Ontario Genomics Research Council
2017	Prostate Canada
2012-2014	Canadian Cancer Society Research Institute, Gene Regulation
2012-2016	Canadian Institute of Health Research (CIHR) Genomics, Chair
2011-2012	Terry Fox Cancer Research Society, Panel Member
2014-2018	CIHR, Foundation Grants Competition, Virtual Chair.
2002-2018	8 additional CIHR panels

Research Support

<u>Awarded</u>

Computational infrastructure for transcriptional signature networks,
2017/11 - 2018/11 Canada Foundation for Innovation (CFI), Equipment Grant (37083)
Principal Applicant. Total Funding - 250,000

Algorithmic bioinformatics: Transcriptional signature networks
2017/11 - 2024/10 Canada Research Chairs (CRC) Tier 1, Operating Grant
Principal Applicant. Total Funding - 900,000

DCIS-Precise: A Genomics-Driven Model for Predicting DCIS Response to Radiation,
2018/4 - 2022/3 Canadian Institutes of Health Research (CIHR) Operating Grant
Principal Applicant. Total Funding - 1,350,000
Co-applicants: Anne Martel; Lawrence Paszat; Lincoln Stein; Rinku Sutradhar; Sharon Nofech-Mozes; Tim Whelan;

Torsten Nielsen; Vanessa Dumeaux.

Completed

Interactions between the tumor-microenvironment and the systemic response of breast cancer patients
2014/8 - 2017/7 Canadian Cancer Society Research Institute (CCSRI) Innovation 2014
Total Funding - 199,860
Co-principal applicant: Vanessa Dumeaux

Signature Analysis Tools for the Life Sciences
2011/4 - 2016/3 NSERC Discovery
Principal Applicant. Total Funding - 200,000

Genetic Analysis of the Breast Tumor Microenvironment,
2012/4 - 2017/3 National Cancer Institute (USA) 2P01CA097189-06
Co-applicant. Total Funding - 7,870,825 (United States dollar) (Hallett 2.5%)
Principal Applicant: Michael Ostrowski

Integrative Approaches to Human Health
2009/4 - 2015/3 Canadian Institutes of Health Research (CIHR) STIHR
Principal Applicant. Total Funding - 1,790,000 (Canadian dollar)
Co-investigator: 40 researchers at McGill

Development of integrated tumor-microenvironmental classifiers for personalized therapy targeting
2012/1 - 2014/12 Québec Consortium for Drug Discovery (CQDM), Operating grant
Co-applicant. Total Funding - 1,312,507 (Canadian dollar)

Principal Investigator: Park, Morag

Next Generation Predictive Signatures for Breast Cancer
2010/7 - 2013/7 Genome Quebec - Genomics Research in Human Health
Principal applicant. Total Funding - 1,449,560 (Canadian dollar) (Hallett 17%)
Portion of Funding Received - 255,000
Co-investigators: Avard, D; Basik, M; Batist, G; Muller, W; Nepveu, A; Park, M; Siegel, P;
Ursini-Siegel, J;
Collaborator: Dumeaux, V

Pre-clinical models and therapeutic targets for metastatic breast disease
2009/4 - 2014/4 National Cancer Institute of Canada (NCIC) Program Project Grant
Co-applicant. Total Funding - 5,153,424 (Hallett 5%)
Co-applicants: Giguere, V; Park, M; Siegel, P;
Principal Investigator: Muller W

List of Publications
(Italics denote students in my lab.)

Busby M, **Hallett MT**, Plante I (2018) The complex subtype-dependent role of Connexin 43 (GIA1) in breast cancer. 19(3). pii: E693. doi: 10.3390/ijms19030693.

Saleh SMI¸ Bertos N, Gruosso T, Gigoux M, Souleimanova M, Zhao H, Omeroglu A, **Hallett M**, Park M (2017) Identification of interacting stromal properties in tripe-negative breast cancer. Cancer Research. 77(17):4673-4683

Dumeaux V, Fjukstad B, Fjosne HE, Frantzen J-O, Muri Holmen M, Rodegerdts E, Schlichting E, Borresen-Dale A-L, Ailo Bongo L, Lund E, **Hallett M** (2017) Interactions between the tumor and blood systemic response of breast cancer patients. PLoS Computational Biology. 13(9):e1005680.

Paquet E, Lesurf R, Tofigh A, Dumeaux V, **Hallett M** (2017) Detecting gene signature activation in breast cancer in an absolute, single patient manner. Breast Cancer Research. doi: 10.1186/s13058-017-0824-7.

Fjukstad B, *Dumeaux V*, Standahl Olsen K, **Hallett M**, Lund E, Bongo L (2017) Building applications for interactive data exploration in systems biology. bioRxiv. doi: https://doi.org/10.1101/141630

Liu H, Dowdle JA, Khurshid S, Sullivan NJ, Bertos N, Rambani K, Mair M, Daniel P, Wheeler E, Tang X, Toth K, Lause M, Harrigan ME, Eiring K, Sullivan C, Sullivan MJ, Chang SW, Srivastava S, Conway JS, Kladney R, McElroy J, Bae S, Lu Y, *Tofigh A*, *Saleh SMI*, Fernandez SA, Parvin JD, Coppola V, Macrae ER, Majumder S, Shapiro CL, Yee LD, Ramaswamy B, **Hallett M**, Ostrowski MC, Park M, Chamberlin HM, Leone G (2017) Discovery of stromal regulatory networks that suppress Ras-sensitive epithelial cell proliferation. Dev Cell. 41(4):392-407.

Lesurf R, Ragle Aure Miriam,Haberg Mork H, Vitelli V, Kleivi K, Lundgren S, Borresen-Dale A-L, Kristensen VN, Warnberg F, **Hallett M**, Sorlie T (2016) Molecular features of subtype-specific progression from ductal carcinoma in situ to invasive breast cancer. Cell Reports. 16(4):1166-79.

Boucher B, *Lee AY*, **Hallett M**, Jenna S (2016) Structural and Functional Characterization of a Caenorhabditis elegans Genetic Interaction Network within Pathways. PLoS Comput Biol. 12(2):e1004738. doi: 10.1371/journal.pcbi.1004738. eCollection 2016 Feb.

Cyr-Depauw C, Northey JJ, Tabariès S, Annis MG, Dong Z, *Cory S*, **Hallett M**, Rennhack JP, Andrechek ER, Siegel PM (2016) Chordin-Like 1 Suppresses Bone Morphogenetic Protein 4-Induced Breast Cancer Cell Migration and Invasion. Mol Cell Biol. 36(10):1509-25.

Boulay PL, Mitchell L, Turpin J, Huot-Marchand JÉ, Lavoie C, Sanguin-Gendreau V, Jones L, Mitra S, *Livingstone JM*, Campbell S, **Hallett M**, Mills GB, Park M, Chodosh L, Strathdee D, Norman JC, Muller WJ (2016) Rab11-FIP1C Is a Critical Negative Regulator in ErbB2-Mediated Mammary Tumor Progression. Cancer Res. 76(9):2662-74.

Turpin J, Ling C, Crosby EJ, Hartman ZC, Simond AM, Chodosh LA, Rennhack JP, Andrechek ER, *Ozcelik J*, **Hallett M**, Mills GB, Cardiff RD, Gray JW, Griffith OL, Muller WJ (2016) The ErbB2ΔEx16 splice variant is a major oncogenic driver in breast cancer that promotes a pro-metastatic tumor microenvironment. Oncogene. 35(47):6053-64.

Jones LM, Broz ML, Ranger JJ, *Ozcelik J*, Ahn R, Zuo D, Ursini-Siegel J, **Hallett M**, Krummel M, Muller MJ (2016) Stat3 establishes an immunosuppressive microenvironment during the early stages of breast carcinogenesis to promote tumor growth and metastasis. Cancer Research 76(6):1416-28.

Siklenka K, Erkek S, Godmann M, Lambrot R, McGraw S, Lafleur C, Cohen T, Xia J, *Suderman M*, **Hallett M**, Trasler J, Peters AH, Kimmins S. (2015) Science 6:350(6261):aab2006.

Paquet E, Cui J, Davidson D, Pietrosemoli N, Hassan HH, Tsofack SP, Maltais A, **Hallett M**, Delorenzi M, Batist G, Aloyz R, Lebel M (2015) A 12-gene signature associated with prognosis and benefit from 5-fluorouracil in colon cancer. *Journal of Pathology – Clinical Research. 1(3):160-172*.

Ali-Khan S, Black L, Palmour N, **Hallett M**, Avard D (2015) Socio-ethical issues in personalized medicine: a systematic review of english language HTAs of gene expression profiling tests for breast cancer prognosis. *International Journal of Technology Assessment in Health Care.* 31(1-2):36-50.

Jones LM, Broz ML, Ranger JJ, *Ozcelik J*, Ahn R, Zuo D, Ursini-Siegel J, **Hallett M**, Krummel M, Muller WJ. (2015) Stats establishes an immunosuppressive microenvironment during the early stages of breast carcinogenesis to promote tumor growth and metastasis. Cancer Res 76(6):1416-28.

Hosein AN, *Livingstone J,* Buchanan M, Reid JF, **Hallett** M, Basik M. (2015) A functional in vitro model of heterotypic interactions reveals a role for interferon-positive carcinoma associated fibroblasts in breast cancer. *BMC Cancer*. Mar 15;15:130.

Massart R, Barnea R, Bar-Ilan Y, *Suderman M*, Meier O, **Hallett M**, Kennedy P, Nestler E, Szyf M, Yadid G (2015) Role of DNA methylation in the nucleus accumbens incubation of cocaine craving. The Journal of Neuroscience. In press.

Nemoda Z, Massart R, Suderman M, **Hallett** M, Li T, Coote M, Cody N, Sun ZS, Soares CN, Turecki G, Steiner M, Szyf M (2015) Maternal depression is associated with DNA methylation changes in cord blood T lymphocytes and adult hippocampi. Translational Psychiatry. 5:e545. doi: 10.1038/tp.2015.32.

Tofigh A, *Suderman M*, *Paquet E*, *Livingstone J*, Bertos N, *Saleh S*, Zhao H, Souleimanova M, *Cory S*, *Lesurf R*, *Shahalizadeh S*, Garcia Lopez N, Riazalhosseini Y, Omeroglu A, Ursini-Siegel J, Park M, Dumeaux V, **Hallett M** (2014) The prognostic ease and difficulty of invasive breast carcinoma. Cell Reports. 9(1), 129–142.

Paquet E and **Hallett M** (2014) Absolute assignment of breast cancer intrinsic molecular subtype. JNCI J Natl Cancer Inst 107:1.

Cheishvili D, Chik F, Li CC, *Bhattacharya B*, *Suderman M*, Arakelian A, **Hallett M**, Rabbani SA, Szyf M. (2014) Synergistic effects of combined DNA methyltransferase inhibition and MBD2 depletion on breast cancer cells; MBD2 depletion blocks 5-aza-2'-deoxycytidine-triggered invasiveness. Carcinogenesis 35(11):2436-46.

Vadnais C, Shooshtarizadeh P, Rajadurai CV, *Lesurf R*, Hulea L, Davoudi S, Cadieux C, **Hallett M**, Park M, Nepveu A. (2014) Autocrine Activation of the Wnt/β-Catenin Pathway by CUX1 and GLIS1 in Breast Cancers. Biol Open. 3(10):937-46.

Hudson J, Ha J, Sabourin V, Ahn R, La Selva R, *Livingstone J*, Podmore L, Knight J, Forrest L, Beauchemin N, **Hallett M**, Park M, Ursini-Siegel J (2014) p66ShcA Promotes Breast Cancer Plasticity by Inducing an Epithelial to Mesenchymal Transition. Molecular and Cellular Biology. 34(19):3689-701.

Stefanska B, Cheishvili D, *Suderman M*, Arakelian A, Huang J, **Hallett M**, Han ZG, Al-Mahtab M, Akbar SM, Khan WA, Raqib R, Tanvir I, Khan HA, Rabbani SA, Szyf M (2014) Genome-wide study of hypomethylated and induced genes in liver cancer patients unravels novel anticancer targets. Clin Cancer Res 20(12):3118-32. PMID: 24763612.

Lai AZ, *Cory S*, Zhao H, Gigoux M, Monast A, Guiot MC, Huang S, *Tofigh A*, Thompson C, Naujokas M, Marcus VA, Bertos N, Sehat B, Perera RM, Bell ES, Page BD, Gunning PT, Ferri LE, **Hallett M**, Park M (2014) Dynamic reprogramming of

signaling upon met inhibition reveals a mechanism of drug resistance in gastric cancer. Sci Signal 7(322):ra38. PMID: 24757178.

Provençal N, *Suderman MJ*, Guillemin C, Vitaro F, Côté SM, **Hallett M**, Tremblay RE, Szyf M (2014) Association of childhood chronic physical aggression with a DNA methylation signature in adult human T cells. PLoS One 9(4):e89839. PMID: 24691403.

Zastepa E, Fitz-Gerald L, **Hallett M**, Antel J.P, Bar-Or A, Baranzini S, Lapierre Y, and Haegert D (2014) Naive CD4 T-cell activation identifies MS patients having rapid transition to progressive MS. Neurology 82(8):681-90. PMID: 24453076.

Guillemin C, Provençal N, *Suderman M*, Côté SM, Vitaro F, **Hallett M**, Tremblay RE, Szyf M (2014) DNA methylation signature of childhood chronic physical aggression in T cells of both men and women. PLoS One 9(1):e86822. PMID: 24475181.

Hudson J, Ha J, Sabourin V, Ahn R, La Selva R, *Livingstone J*, Podmore L, Knight J, Forrest L, Beauchemin N, **Hallett M**, Park M, Ursini-Siegel J (2013) p66ShcA Promotes Breast Cancer Plasticity by Inducing an Epithelial to Mesenchymal Transition. Molecular and Cellular Biology. 34(19):3689-3701.

Stefanska B, *Suderman M*, Machnes Z, *Bhattacharyya B*, **Hallett M**, Szyf M (2013) Transcription onset of genes critical in liver carcinogenesis is epigenetically regulated by methylated DNA binding protein MBD2. Carcinogenesis 34(12):2738-49. PMID:23955541.

Stefanska B, Bouzelmat A, Huang J, *Suderman M,* **Hallett M**, Han ZG, Al-Mahtab M, Sheikh Akbar SFM, Ali Khan W, Raqib R, Szyf M (2013) Discovery and Validation of DNA Hypomethylation Biomarkers for Liver Cancer Using HRM-Specific Probes. PLoS ONE 8(8):e68439. PMID: 23950870.

Lambrot R, Xu C, Saint-Phar S, Chountalos G, Cohen T, Paquet M, *Suderman M*, **Hallett M**, and Kimmins S. (2013) Low paternal dietary folate alters the sperm epigenome and is associated with negative pregnancy outcomes. Nature Communications 4:2889. PMID: 24326934.

Wallace JA, Li F, Balakrishnan S, Cantemir-Stone CZ, Pecot T, Martin C, Kladney RD, Sharma SM, Trimboli AJ, Fernandez SA, Yu L, Rosol TJ, Stromberg PC, *Lesurf R*, **Hallett M,** Park M, Leone G, Ostrowski MC. (2013) Ets2 in tumor fibroblasts promotes angiogenesis in breast cancer. PLoS One 8(8):e71533. PMID: 23977064.

Crudo A, *Suderman M,* Petropoulos S, Moisiadis V, Kostaki A, **Hallett M**, Szyf M, Matthews SG (2013) Effects of Antenatal Synthetic Glucocorticoid on Glucocorticoid Receptor Binding, DNA Methylation and Genome-Wide mRNA Levels in the Fetal Male Hippocampus. Endocrinology 154(11):4170-81. PMID: 24029241.

Provençal N, *Suderman MJ*, Caramaschi D, Wang D, **Hallett M**, et al. (2013) Differential DNA Methylation Regions in Cytokine and Transcription Factor Genomic Loci Associate with Childhood Physical Aggression. PLoS ONE 8(8):e716918(8): e71691. PMID: 23977113.

Ahn R, Sabourin V, Ha JR, *Cory S,* Maric G, Im YK, Hardy WR, Zhao H, Park M, **Hallett M**, Siegel PM, Pawson T, Ursini-Siegel J (2013) The ShcA PTB Domain Functions as a Biological Sensor of Phosphotyrosine Signaling during Breast Cancer Progression. Cancer Research 73(14):4521-32. PMID: 23695548.

Pluquet O, Dejeans N, Bouchecareilh M, Lhomond S, Pineau R, Higa A, Delugin M, Combe C, Loriot S, Cubel G, Dugot-Senant N, Vital A, Loiseau H, *Gosline SJ*, Taouji S, Saltel F, **Hallett M**, Sarkaria JN, Anderson K, Wu W, Rodriguez FJ, Rosenbaum J, Fernandez-Zapico ME, Chevet E (2013) Post-transcriptional regulation of PER1 mRNA underlies the oncogenic function of IREα Cancer Research 73(15):4732-43. PMID: 23752693.

Suderman M, Borghol N, Pappas JJ, McArdle W, Racine A, **Hallett M**, Pembrey ME, Hertzman C, Power C, Szyf M (2013) Epigenomic socioeconomic studies more similar than different. Proc Natl Acad Sci U S A 110(14):E1246. PMID: 23493547.

Schade B, *Lesurf R*, Sanguin-Gendreau V, Bui T, Deblois G, O'Toole SA, Millar EK, Zardawi SJ, Lopez-Knowles E, Sutherland RL, Giguere V, Kahn M, **Hallett M**, Muller WJ (2013) β-catenin signaling is a critical event in ErbB2-mediated mammary tumor progression. Cancer Research 73(14):4474-4487. PMID: 23720052.

Crudo A, *Suderman M*, Moisiadis VG, Petropoulos S, Kostaki A, **Hallett M**, Szyf M, Matthews SG (2013) Glucocorticoid Programming of the Fetal Male Hippocampal Epigenome. Endocrinology 154(3):1168-80. PMID: 23389956.

Knight J, *Lesurf R*, Zhao H, Pinnaduwage D, Davis R, *Saleh S*, Zuo D, Naujokas M, Chughtai N, Herschkowitz J, Prat A, Mulligan A-M, Muller W, Cardiff R, Gregg J, Andrulis I, **Hallett M**, Park M (2013) Met synergizes with p53 loss to induce mammary tumors that possess features of claudin-low breast cancer. Proc Natl Acad Sci U S A 110(14):E1301-10. PMID: 23509284.

Additional Creative outputs

MIxT, Matched Interactions across Tissues. [maintained 2016-] A web-based software platform for the analysis and visualization of cross-tissue comparisons eg between primary tumor, lymph node metastasis, and/or blood based expression profiles. http://mixt-blood-tumor.bci.mcgill.ca/

Stroma 4. [maintained 2016 -] An R package that facilitates subtyping of triple negative breast cancers based on our subtyping scheme (Stroma4) identified in gene expression profiles obtained via laser capture microdissection of the tumor microenvironment. https://github.com/smisaleh/STROMA4

AIPS, Absolute Inference of Patient Signatures. [maintained 2017 -] A R package containing several thousand classifiers that estimate the activation status of different molecular processes and cell types in invasive breast cancers. The classifiers operate in an "absolute" manner and can be applied to single patients without a reference cohort. https://github.com/meoyo/AIPS

AIMS, Absolute Inference of breast cancer Molecular Subtype. [maintained 2014 -] A R package that attempts to mimic PAM50 breast cancer (intrinsic) molecular subtypes using our "absolute" methodology. AIMS allows the subtype of a invasive breast cancer to be determined in isolation without recourse to a reference cohort. http://www.bci.mcgill.ca:8080/AIMS/

BreSect. [maintained 2014 -] Web-bases software that allows for the examination of prognostic gene signatures across a large compendium of gene expression profiles for invasive ductal breast carcinoma. http://www.bci.mcgill.ca/bresect/

BreSAT, Breast Signatures Analysis Tool. [maintained 2013 -] This is a set of R based functions that compute linear orderings of samples based on gene expression signatures, and computes various related statistics. http://www.bci.mcgill.ca/bresat/