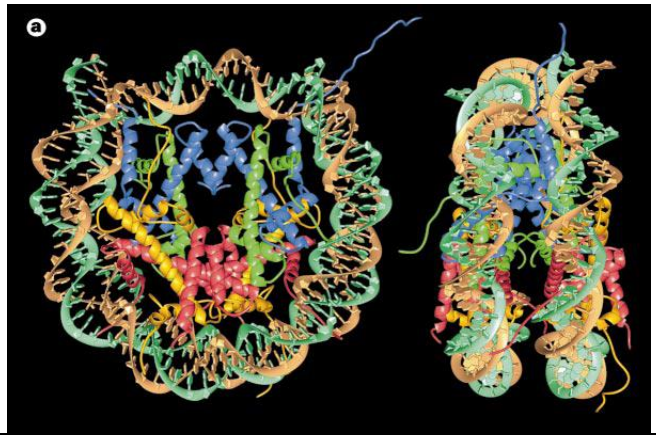
BIOD19 Epigenetics in Health and Disease

Winter 2021

Professor: Dr. Patrick McGowan; **TA:** Mouly Rahman



A lecture/seminar/discussion class on the emerging field of environmental epigenetics. Course will cover basic epigenetic mechanisms, methods in epigenetic research, epigenetic control of gene function, and the role of epigenetics in normal development and human disease.

Environmental epigenetics is a new field of study focusing on mitotically or meiotically heritable changes in gene regulation caused by *environmental factors*. There is evidence that epigenetic changes can occur through diet, toxicants (xenobiotics) and social factors (e.g. parental care). This course will focus on the environmental epigenetic mechanisms that impact human health and disease.

Office hours:

Prof. McGowan: TBD
Mouly Rahman (TA): TBD.

Course email address: epigeneticsD19@gmail.com

Queries are usually answered within 24 business hours.

Lectures: Fridays 10AM-12PM and On-Demand

A course schedule for lectures and presentations is below but is subject to change.

- Weeks 1-2: Prof. McGowan's lectures on **(1)** foundation topics in environmental epigenetics, **(2)** foundations part 2; how to read/present a research article,
- Week 3: Recap of core principles/methods. How to write a minireview
- Weeks 4-11: Student seminars on research articles.
- Week 12: Minireview of research article due.

Course Calendar:

Week	Date	Activity	Topic	Due (10 am of Date, unless otherwise stated)
1	Jan 15	Lecture 1	Foundation topics in environmental epigenetics	
2	Jan 22	Lecture 2	Foundations part 2; how to read/present a research article	Seminar presentation article top 3 choices (via course email)
3	Jan 29	Lecture 3	Recap of core principles/methods. How to write a minireview	Minireview topic (via Quercus)
4	Feb 5	Seminar A	Groups 1-3	Minireview title + Abstract (via Quercus)
5	Feb 12	Seminar B	Groups 4-6	Quiz 1 Seminar A Discussion Part 1 (for Group 7-9)
6	Feb 19	Reading Week		
7	Feb 26	Seminar C	Groups 7-9	Minireview Intro + References (via Quercus) Seminar B Discussion Part 1 (for Group 10-12)
8	March 5	Seminar D	Groups 10-12	Quiz 2 Seminar C Discussion Part 1 (for Group 13-15)
9	March 12	Seminar E	Groups 13-15	Seminar D Discussion Part 1 (for Group 16-18)
10	March 19	Seminar F	Groups 16-18	Quiz 3 Seminar E Discussion Part 1 (for Group 1, 19, 20)
11	March 26	Seminar G	Groups 19-20	Seminar F Discussion Part 1 (for Group 2-4)
12	April 9	-	-	Minireview (10 am April 9 via Quercus) Seminar G Discussion Part 1 (for Group 5,6) Seminar Discussion Part 2 (all groups)

Textbook: There is NO textbook for this class. Prof. McGowan's power point presentations and journal articles will be supplied on Quercus.

Exams: There are NO exams in this class.

Grading scheme overview:

Quizzes (3x5%)	15%
Seminar Presentation	40%
Seminar Discussion	10%
Minireview	35%
	100%

Quizzes: Three quizzes, consisting of questions addressing one of the articles presented in the class. You will be required to answer questions about the background, methods used, results and conclusions of the paper. The specific paper used for the questions is Prof. McGowan's choice, and you will have one week to complete the quiz. Each quiz will contribute to 5% of your final grade (total **15%**).

Seminar Presentation: Seminar presentations will be conducted in groups of two students and will be based on research articles chosen by Prof. McGowan in the **Article List** at the end of this document (or you can suggest an article). One person from each group will need to e-mail their group's top 3 articles of choice to the course e-mail, and we will respond with which article you will be presenting on. In the e-mail, include in the subject line 'Seminar Presentation Topic – Group #', and within the body of the e-mail include the Group number, names of the students, and the top three articles (and whether any of these are NOT from the **Article List**). Each group will then prepare and record a presentation (30 mins maximum) on the research article in PowerPoint format. Seminars will be graded based on length, clarity, style and delivery, use of visual aids (concise text, high resolution figures), and content (provide sufficient background information, correctly identify the hypothesis, methodology and significance of the research and critically evaluate results, conclusions, limitations and future research). Your presentation must be submitted to the course site on Quercus by 10am on the Friday of your presentation as indicated in the Course Calendar. The seminar will contribute to **40%** of your final grade.

Seminar Discussion: An important part of your mark in this class is based on contribution to the critical evaluation of the presentations. You will be graded based on your critical analysis and understanding of the article presented, in addition to your ability to retrieve and interpret relevant primary research to formulate a question and answer.

Seminar Discussion Part 1: Each Group will have a separate discussion thread on Quercus. Within the thread, students from other groups will individually ask one question about the article presented and include an answer for their own question along with two peer-reviewed primary papers (not in the **Article List**) as sources to back up their own supposition. For example, Groups 1-3 will be presenting on Feb 5. Afterwards, each student within Groups 7-9 will ask one question within the thread of **either** Group 1, 2, or 3 by the due date indicated on

the Course Calendar (roughly 1 week after the presentation). There is a limit of **two questions permitted within each thread**. This mark contributes to **5%** of the final grade.

Seminar Discussion Part 2: Each group will respond to their favourite question asked within their thread by including their own insights and two different peer-reviewed primary papers (not already referenced by others in their thread and not in the **Article List**) as sources to back up their claim. This group mark contributes to **5%** of each student's final grade.

Minireview:

Overview: You and your partner will complete a summary/analysis of a topic in environmental epigenetics. This could stem from the article that you will present, but it could also be on another topic (note: must at least be related to a foundation review). Choose your topic by week 3 of class **(10AM Jan 23rd)**. Your Title and Abstract (200-250 words) must be submitted by **10AM Feb 5th**. The first full paragraph of your introduction (5-6 sentences) and a list of 10 references must be submitted by **10AM Feb 26th**. Submit the final document by the final week of class (**10AM, Apr 9th**). See the **Minireview Guidelines** section below for detailed instructions. The minireview contributes **35%** to your final grade.

Minireview Guidelines: A minireview is a concise, focused summary of the literature related to a question of current interest in environmental epigenetics. Scientists may read minireviews to quickly get up to speed on a particular topic that may not be their area of specialty. Sometimes minireviews also raise questions or suggest new hypotheses or attempt to reconcile conflicting data that has recently been published. Writing a minireview is a good way to organize your thoughts and summarize the knowledge you have obtained about a particular topic that you have acquired from reading the literature and thinking and discussing with others and is a good exercise in scientific writing.

Example description of a minireview (from the Journal of Biological Chemistry):

"The goal of the Minireviews is to provide a concise summary of a particular field in a manner understandable to [scientists] working in any area."

The sections of your minireview will be as follows:

Title page (not numbered). The title page includes a clear, concise **title** that is comprehensible to all readers with the purpose of quickly identifying the focus of the reported work. Also include your **name, student number, course (BioD19), prof, TA and date**.

Body of the minireview (10 pages double spaced). Start with a **Brief Abstract (200-250 words)**: Summarize what the minireview is about as concisely as possible in an introductory paragraph. Provide necessary background/context for the reader. Should indicate why the chosen topic is important and timely. **Body of the review:** This section should contain the most relevant aspects and achievements in the reviewed scientific area. The review itself should not be an assembly of detailed information but present a summary of critically selected and evaluated literature, which should reflect the most important findings. It may be subdivided with short, informative headings.

References: You will be obliged to perform literature searches and to cite **original research**

articles. Aim for about 20 references, at least 15 of which are **primary research articles**. Include a reference list at the end in one of the following styles: American Psychological Association (APA), Vancouver, Nature, and PLoS.

Additional guidelines: Submit your minireview double-spaced, with pages numbered, using 12 point font (Arial), 2 cm margins. The maximum length for the minireview is 10 pages including any Figures you make yourself and EXCLUDING the references. Endnote or Mendeley (free) are useful programs for generating a reference list.

Foundation Reviews (Optional reading for background information):

Jirtle RL, Skinner MK. Environmental epigenomics and disease susceptibility. Nature Reviews Genetics. 2007 Apr;8(4):253-62. PubMed PMID: 17363974.

Fagiolini, M., Jensen, C. L. & Champagne, F. A. Epigenetic influences on brain development and plasticity. Current Opinion in Neurobiology 19, 207–212 (2009).

Petronis A. Epigenetics as a unifying principle in the aetiology of complex traits and diseases. Nature. 2010 Jun 10;465(7299):721-7. PubMed PMID: 20535201.

Youngson NA, Whitelaw E. Transgenerational epigenetic effects. Annual Reviews in Genomics and Human Genetics 2008;9:233-57. PubMed PMID: 18767965.

Epigenetics, Second Edition. 2015. Eds. CD Allis, M Caparros, T Jenuwein, D Reinberg. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York.

AccessAbility statement:

Students with diverse learning styles and needs are welcome in this course. In particular, if you have a disability/health consideration that may require accommodations, please feel free to approach me and/or the AccessAbility Services Office as soon as possible. AccessAbility Services staff (located in Rm SW302, Science Wing) are available by appointment to assess specific needs, provide referrals and arrange appropriate accommodations 416-287-7560 or email ability@utsc.utoronto.ca. The sooner you let us know your needs the quicker we can assist you in achieving your learning goals in this course.

Academic Integrity:

The University treats cases of cheating and plagiarism very seriously. The University of Toronto's Code of Behaviour on Academic Matters (http://www.governingcouncil.utoronto.ca/policies/behaveac.htm) outlines the behaviours that constitute academic dishonesty and the processes for addressing academic offences.
Potential offences in papers and assignments include using someone else's ideas or words without appropriate acknowledgement, submitting your own work in more than one course without the permission of the instructor, making up sources or facts, obtaining or providing unauthorized assistance on any assignment.

Intellectual Property:

Recording or photographing any aspect of this course without prior approval of all involved and written approval from the instructor is not permitted.

Resources for Academic English:

Academic English is nobody's mother-tongue. Every student is expected to achieve a high level of Academic English to cope with the demands of their courses. The English Language Development Centre supports all students in developing better Academic English and critical thinking skills needed in academic and professional communication. Make use of the personalized support in academic writing skills development and Communication Café sessions to enhance your ability to do better in the various components of this course. Details and sign-up information available at http://www.utsc.utoronto.ca/eld/

Article List:

Articles to present for the seminars will be assigned on a first-come first-served basis.
Send an email with your top 3 choices to: epigeneticsD19@gmail.com
YOU CAN ALSO SUGGEST AN ARTICLE not in the list below.
Deadline: **Friday January 22, 2021**. After the deadline, an article will be assigned to you.

Nutrition:

1. Lillycrop KA, Slater-Jefferies JL, Hanson MA, Godfrey KM, Jackson AA, Burdge GC. Induction of altered epigenetic regulation of the hepatic glucocorticoid receptor in the offspring of rats fed a protein-restricted diet during pregnancy suggests that reduced DNA methyltransferase-1 expression is involved in impaired DNA methylation and changes in histone modifications. Br J Nutr 2007;97:1064–1073. [PubMed: 17433129]
   Illustrates the impact of methyl donors in the maternal diet on offspring DNA methylation and histone acetylation patterns, providing an important link between nutrition and gene regulation.

2. Weaver, I. C. et al. Reversal of maternal programming of stress responses in adult offspring through methyl supplementation: altering epigenetic marking later in life. J. Neurosci. 25, 11045–11054 (2005).
   Describes the role of methyl donors in altering epigenetic programming of the stress response and behaviours in adult rats.

3. Dunn GA, Bale TL. Maternal high-fat diet effects on third-generation female body size via the paternal lineage. Endocrinology. 2011 Jun;152(6):2228-36. Epub 2011 Mar 29. PubMed PMID: 21447631; PubMed Central PMCID: PMC3100614.
   This study implicates environmental influences on developmental regulation of growth and body size as the result of broad programming events at imprinted loci.

4. Kucharski R, Maleszka J, Foret S, Maleszka R. 2008. Nutritional control of reproductive status in honeybees via DNA methylation. Science 319: 1827–1830.
   Early life nutrition induces epigenetic changes that determine whether a honeybee will become a queen or worker bee.

5. Gao Y, Han Z, Li Q, Wu Y, Shi X, Ai Z, Du J, Li W, Guo Z, Zhang Y. Vitamin C-induced pluripotent state in mouse embryonic stem cells by modulating microRNA expression. FEBS J. 2014 Dec 9. doi: 10.1111/febs.13173.

Examines the effects of vitamin C on the epigenetic machinery, including micro RNA expression, in embryonic stem cells.

6. Dominguez-Salas P, Moore SE, Baker MS, Bergen AW, Cox SE, Dyer RA, Fulford AJ, Guan Y, Laritsky E, Silver MJ, Swan GE, Zeisel SH, Innis SM, Waterland RA, Prentice AM, Hennig BJ. Maternal nutrition at conception modulates DNA methylation of human metastable epialleles. Nat Commun. 2014 Apr 29;5:3746.
   Study of seasonal variations in methyl-donor nutrient intake of mothers in rural Gambia around the time of conception and their influence on 13 plasma biomarkers and DNA methylation.

7. Chastain LG, Franklin T, Gangisetty O, Cabrera MA, Mukherjee S, Shrivastava P, Jabbar S, Sarkar DP. Early life alcohol exposure primers hypothalamic microglia to later-life hypersensitivity to immune stress: possible epigenetic mechanism. Neuropsychopharmacology. 2019 Jan, 44:1579-1588.
   This study examines the effects of early life alcohol exposure on gene expression and histone acetylation of inflammatory genes in microglia.

Xenobiotics and infection:

8. Anway MD, Leathers C, Skinner MK. Endocrine disruptor vinclozolin induced epigenetic transgenerational adult-onset disease. Endocrinology. 2006 Dec;147(12):5515-23.
   Demonstrates the ability of an endocrine disruptor to induce an epigenetic transgenerational disease phenotype for four generations.

9. Dolinoy DC, Huang D, Jirtle RL. 2007. Maternal nutrient supplementation counteracts bisphenol A-induced DNA hypomethylation in early development. Proc Natl Acad Sci USA 104:13056–13061.
   Shows that early developmental exposure to an environmental toxin can change offspring phenotype by stably altering the epigenome, an effect that can be counter-acted by maternal dietary supplements.

10. Wu J, Basha MR, Brock B, Cox DP, Cardozo-Pelaez F, McPherson CA, Harry J, Rice DC, Maloney B, Chen D, Lahiri DK, Zawia NH. Alzheimer's disease (AD)-like pathology in aged monkeys after infantile exposure to environmental metal lead (Pb): evidence for a developmental origin and environmental link for AD. J Neurosci. 2008 Jan 2;28(1):3-9.
    This study in primates finds that early exposure to lead (Pb) results in decreased DNA methyltransferase activity in the brain 23 years later.

11. Chen, R., Xia, L., Tu, K., Duan, M., Kukurba, K., Li-Pook-Than, J., Xie, D. and Snyder, M., 2018. Longitudinal personal DNA methylome dynamics in a human with a chronic condition. *Nature medicine*, *24*(12), p.1930.
    DNA methylome and transcriptome changes in a single individual were profiled over 36 months. Methylome changes were associated with infrequent blood glucose level alterations that rose to diabetic levels, whereas the transcriptome underwent dynamic changes during events such as viral infections.

Stress:

12. Weaver, I. C. G. et al. Epigenetic programming by maternal behavior. Nature Neurosci. 7, 847–854 (2004).
    Describes the role of maternal care in epigenetic programming of the stress response

and behaviours in rats.

13. Franklin TB, Russig H, Weiss IC, Graff J, Linder N, Michalon A, et al. Epigenetic transmission of the impact of early stress across generations. Biol Psychiatry 2010; 68:408-15.
These findings highlight the negative impact of early stress on behavioral responses across generations and on the regulation of DNA methylation in the germline.

14. Rodgers, A. B., Morgan, C. P., Leu, N. A., & Bale, T. L. (2015). Transgenerational epigenetic programming via sperm microRNA recapitulates effects of paternal stress. *Proceedings of the National Academy of Sciences*, *112*(44), 13699-13704.
In this study, through zygote microinjection of nine specific sperm miRs previously identified in a paternal stress mouse model, the authors demonstrate that sperm miRs function to reduce maternal mRNA stores in early zygotes, ultimately reprogramming gene expression in the offspring hypothalamus and recapitulating the offspring stress dysregulation phenotype.

15. Roth TL, Lubin FD, Funk AJ, Sweatt JD. Lasting Epigenetic Influence of Early-Life Adversity on the BDNF Gene. Biol Psychiatry. 2009.
Study of the transgenerational impact of exposure to maternal abuse in infancy and the role of differential methylation of a growth factor gene in the prefrontal cortex in mediating these effects.

16. Murgatroyd C, Patchev AV, Wu Y, Micale V, Bockmühl Y, Fischer D, Holsboer F, Wotjak CT, Almeida OFX, Spengler D (2009) Dynamic DNA methylation programs persistent adverse effects of early-life stress. Nat Neurosci 12:1559–1566.
Shows that early life stress can dynamically control DNA methylation in neurons to generate stable changes in gene expression and phenotypic alterations that are frequent features in depression.

17. Cao-Lei L, Massart R, Suderman MJ, Machnes Z, Elgbeili G, Laplante DP, Szyf M, King S. DNA methylation signatures triggered by prenatal maternal stress exposure to a natural disaster: Project Ice Storm. PLoS One. 2014 Sep 19;9(9):e107653.
Study of effects of the 1998 Quebec Ice Storm on methylation in T-cells and saliva of children in utero at the time.

18. J, Farinelli M, Mirante O, Steiner G, Gapp K, Coiret G, Ebeling M, Duran-Pacheco G, Iniguez AL, Manuella F, Moreau J-L, Mansuy IM. Pathalogical brain plasticity and cognition in the offspring of males subjected to postnatal traumatic stress. Mol Psychiatry. 2015 May 20(5):621-31.
This study suggests that postnatal traumatic stress in males can affect brain plasticity and cognition in their adult offspring through epigenetic alterations in the germline.

Learning and Memory/Addiction:

19. Fischer A, Sananbenesi F, Wang X, Dobbin M, Tsai LH. Recovery of learning and memory is associated with chromatin remodelling. Nature 2007;447:178–182. [PubMed: 17468743]
Rodent study showing that environmental enrichment increases histone acetylation in the hippocampus. Histone deacetylase inhibitors induce increased spatial memory in a neurodegenerative disorder mouse model.

20. Lubin FD, Roth TL, Sweatt JD. Epigenetic regulation of BDNF gene transcription in the consolidation of fear memory. J Neurosci 2008;28:10576–10586. [PubMed: 18923034]

Illustrates the dynamic changes to DNA methylation which occur during the process of learning and the critical role of these modifications in the consolidation of memory.

21. Guan JS, Haggarty SJ, Giacometti E, Dannenberg JH, Joseph N, Gao J, Nieland TJ, Zhou Y, Wang X, Mazitschek R, et al. HDAC2 negatively regulates memory formation and synaptic plasticity. Nature 2009;459:55–60. [PubMed: 19424149]
Study in mice examining the particular histone deacetylase target through which histone deacetylase inhibitors exert enhancements in synaptic plasticity and memory. The authors illustrate the importance of levels of this enzyme in mediating cognitive enhancement.

22. Vassoler FM, White SL, Schmidt HD, Sadri-Vakili G, Pierce RC Epigenetic inheritance of a cocaine-resistance phenotype. Nat Neurosci. 2013 Jan;16(1):42-7. doi: 10.1038/nn.3280. Epub 2012 Dec 16. [PMID: 23242310]
In a case of sex-linked epigenetic inheritance, paternal cocaine use results in a heritable increase in cortical *Bdnf* gene expression that confers a cocaine-resistant phenotype in male, but not female, progeny.

23. Dias BG, Ressler KJ. Parental olfactory experience influences behavior and neural structure in subsequent generations. Nat Neurosci. 2014 Jan;17(1):89-96.
This study shows that when mice are taught to fear an odor, both their offspring and the next generation are born fearing it. The gene for an olfactory receptor activated by the odor is specifically demethylated in the germ line and the olfactory circuits for detecting the odor are enhanced.

24. Wang H, Duclot F, Liu Y, Wang Z, Kabbaj M. Histone deacetylase inhibitors facilitate partner preference formation in female prairie voles. Nat Neurosci 2013; 16: 919-24.
Examines the epigenetics of pair bond formation in the monogamous prairie vole, and uses a pharmacological method to alter epigenetic status and partner preference.

25. Zovkic IB, Paulukaitis BS, Day JJ, Etikala DM, Sweatt JD. Histone H2A.Z subunit exchange controls consolidation of recent and remote memory. Nature. 2014 Nov 27;515(7528):582-6. doi: 10.1038/nature13707.
Examines the role of histone variant exchange in memory in a mouse model.

<u>Human Transgenerational/Health and Disease:</u>

26. Tobi EW, Goeman JJ, Monajemi R, Gu H, Putter H, Zhang Y, Slieker RC, Stok AP, Thijssen PE, Müller F, van Zwet EW, Bock C, Meissner A, Lumey LH, Eline Slagboom P, Heijmans BT. DNA methylation signatures link prenatal famine exposure to growth and metabolism. Nat Commun. 2014 Nov 26;5:5592.
A genome-scale analysis of differential DNA methylation in whole blood after periconceptional exposure to famine during the Dutch Hunger Winter of World War II.

<u>Human Development/Health and Disease:</u>

27. Kaminsky, Z. A. et al. DNA methylation profiles in monozygotic and dizygotic twins. Nature Genet. 41, 240–245 (2009).
A study of genome-wide epigenetic differences among twins.

28. Fraga MF, Ballestar E, Paz MF, Ropero S, Setien F, Ballestar ML, Heine-Suner D, Cigudosa JC, Urioste M, Benitez J, et al. 2005. Epigenetic differences arise during the lifetime of monozygotic twins. Proc Natl Acad Sci 102: 10604– 10609.

This study examined the global and locus-specific differences in DNA methylation and histone acetylation of a large cohort of monozygotic twins. They find that, compared to differences in the early years of life, older monozygous twins exhibit greater differences in their overall content and genomic distribution of 5-methylcytosine DNA and histone acetylation, affecting their gene-expression portrait.

29. Katari S, Turan N, Bibikova M, et al. DNA methylation and gene expression differences in children conceived in vitro or in vivo. Hum Mol Genet 2009;18:3769–78.
This study examined DNA methylation at more than 700 genes in placenta and cord blood and measured gene expression levels of a subset of genes that differed in methylation levels between children conceived in vitro versus in vivo.

30. Lam LL, Emberly E, Fraser HB, Neumann SM, Chen E, Miller GE, Kobor MS. Factors underlying variable DNA methylation in a human community cohort. Proc Natl Acad Sci U S A. 2012 Oct 16;109 Suppl 2:17253-60. doi: 10.1073/pnas.1121249109. Epub 2012 Oct 8.
Genome-wide epigenetic study of the contributions of stress and other factors in early life to epigenetic variability in humans stratified by socio-economic position.

31. Borghol N, Suderman M, McArdle W, Racine A, Hallett M, Pembrey M, Hertzman C, Power C, Szyf M. Associations with early-life socio-economic position in adult DNA methylation. Int J Epidemiol. 2012 Feb;41(1):62-74.
Study reporting that adult blood DNA methylation profiles show more associations with childhood socio-economic position than adult socio-economic position.

32. Petropoulos, S., Edsgärd, D., Reinius, B., Deng, Q., Panula, S. P., Codeluppi, S., ... & Lanner, F. (2016). Single-Cell RNA-Seq Reveals Lineage and X Chromosome Dynamics in Human Preimplantation Embryos. *Cell*, *165*(4), 1012-1026.
Study of human pre-implantation embryo development at single cell resolution, revealing that the lineage path in the human embryo is distinct from that in the mouse.

<u>Mental health (humans):</u>

33. Oberlander TF, Weinberg J, Papsdorf M, Grunau R, Misri S, Devlin AM. Prenatal exposure to maternal depression, neonatal methylation of human glucocorticoid receptor gene (NR3C1) and infant cortisol stress responses. Epigenetics. 2008 Mar-Apr;3(2):97-106. PubMed PMID: 18536531.
This study examined relationships between prenatal exposure to maternal mood and the methylation status of the human glucocorticoid receptor gene in newborns and HPA stress reactivity at age three months.

34. Davies MN, Krause L, Bell JT, Gao F, Ward KJ, Wu H, Lu H, Liu Y, Tsai PC, Collier DA, Murphy T, Dempster E, Mill J; UK Brain Expression Consortium, Battle A, Mostafavi S, Zhu X, Henders A, Byrne E, Wray NR, Martin NG, Spector TD, Wang J. Hypermethylation in the ZBTB20 gene is associated with major depressive disorder. Genome Biol. 2014 Apr 2;15(4):R56. doi: 10.1186/gb-2014-15-4-r56.
Reports that altered methylation profiles affecting the hippocampus are associated with major depressive disorder and shows the potential of the epigenetic twin model in neuro-psychiatric disease.

35. Lunnon K, Smith R, Hannon E, De Jager PL, Srivastava G, Volta M, Troakes C, Al-Sarraj S, Burrage J, Macdonald R, Condliffe D, Harries LW, Katsel P, Haroutunian V, Kaminsky Z, Joachim C, Powell J, Lovestone S, Bennett DA, Schalkwyk LC, Mill J. Methylomic profiling

implicates cortical deregulation of ANK1 in Alzheimer's disease. Nat Neurosci. 2014 Sep;17(9):1164-70.
The first epigenome-wide association study of AD employing a sequential replication design across multiple tissues.

36. Mehta D, Klengel T, Conneely KN, Smith AK, Altmann A, Pace TW, Rex-Haffner M, Loeschner A, Gonik M, Mercer KB, Bradley B, Müller-Myhsok B, Ressler KJ, Binder EB. Childhood maltreatment is associated with distinct genomic and epigenetic profiles in posttraumatic stress disorder. Proc Natl Acad Sci U S A. 2013 May 14;110(20):8302-7.
Study of the interaction between childhood maltreatment and PTSD, examining genome-wide gene expression and epigenetic signatures.

37. McGowan PO, Sasaki A, D'Alessio AC, Dymov S, Labonte B, Szyf M, Turecki G, Meaney MJ. Epigenetic regulation of the glucocorticoid receptor in human brain associates with childhood abuse. Nat Neurosci 2009; 12: 342-8.
This study shows epigenetic alterations of a stress-sensitive gene in the brains of suicide victims in association with early life abuse or neglect.

Genetic, tissue-specific, and intergenerational sources of epigenetic variation:

38. Horvath S. DNA methylation age of human tissues and cell types. Genome Biol 2013; 14: R115.
Uses computational methods and DNA methylation microarray data to examine DNA methylation status as a predictor of chronological age in a variety of tissues.

39. Orozco LD, Rubbi L, Martin LJ, Fang F, Hormozdiari F, Che N, Smith AD, Lusis AJ, Pellegrini M. Intergenerational genomic DNA methylation patterns in mouse hybrid strains. Genome Biol. 2014 Apr 30;15(5):R68.
Concludes that the majority of DNA methylation differences among individuals are associated with genetic differences, and a much smaller proportion of these epigenetic differences are due to sex, imprinting or stochastic intergenerational effects.

40. Heijmans, B. T., Kremer, D., Tobi, E. W., Boomsma, D. I. & Slagboom, P. E. Heritable rather than age-related environmental and stochastic factors dominate variation in DNA methylation of the human IGF2/H19 locus. Hum. Mol. Genet. 16, 547–554 (2007).
This study investigated the contribution of heritable influences and the combined effect of environmental and stochastic factors to variation in DNA methylation of the IGF2/H19 locus.

41. Reinius LE, Acevedo N, Joerink M, Pershagen G, Dahlen S-E, Greco D, Soderhall C, Scheynius A, Kere J. Differential DNA methylation in purified human blood cells: Implications for cell lineage and studies on disease susceptibility. PLoS ONE 2012; 7: e41361.
Addresses the tissue-specific nature of epigenetic modifications by examining methylation profiles in subsets of peripheral blood cells, which are commonly used in human clinical investigations.

42. Flanagan, J. M. et al. Intra- and interindividual epigenetic variation in human germ cells. Am. J. Hum. Genet. 79, 67–84 (2006).
This study provides evidence for significant epigenetic variability in human germ cells, which warrants further research to determine whether such epigenetic patterns can be efficiently transmitted across generations and what impact inherited epigenetic individuality may have on phenotypic outcomes in health and disease.

43. Radford EJ, Ito M, Shi H, Corish JA, Yamazawa K, Isganaitis E, Seisenberger S, Hore TA, Reik W, Erkek S, Peters AH, Patti ME, Ferguson-Smith AC. In utero effects. In utero undernourishment perturbs the adult sperm methylome and intergenerational metabolism. Science. 2014 Aug 15;345(6198):1255903.
Reports that prenatal undernutrition can compromise male germline epigenetic reprogramming and thus permanently alter DNA methylation in the sperm of adult offspring at regions resistant to zygotic reprogramming. However, persistence of altered DNA methylation into late-gestation somatic tissues of the subsequent generation is not observed.