David Christopher Johnson

Curriculum Vitae

e-mail: davecj23@gmail.com
https://github.com/dcjohnson23
https://linkedin.com/in/david-johnson-ab90033b/
dcjohnson23.github.io
https://orcid.org/0000-0003-0887-3343
https://scholar.google.co.uk/citations?user=yidb_JkAAAAJ&hl=en

Summary

- Experienced researcher with extensive experience comprising:
  - Bioinformatics pipelines and analyses of large -omics datasets.
  - Clinical-trial-grade longitudinal analysis of clinical outcome data and relevant statistical methods.
  - Wet-laboratory methods including genomics, multi-omics and cell biology.
- Self-driven and readily able to work independently; experienced in managing junior laboratory and analytical staff.
- Seeking opportunities to apply this highly unique breadth of scientific expertise to exciting translational studies, and/or data analytic projects in the genomics and health care sector.

Employment History

Aug 2004-Jan 2019: **Myeloma Group. Molecular Pathology, Institute of Cancer Research, London.**
Senior Scientific Officer: from Sep 2011.
Higher Scientific Officer: Aug 2004-Aug 2011.

Jan 1998-Aug 2004: **The Wellcome Trust Sanger Institute, Cambridge**
Advanced Research Assistant**,** Sub-cloning group: Jan 2002-Aug 2004.
Research Assistant**,** Sub-cloning group: Jan 1998-Dec 2001.

Education / Qualifications

2006-10: PhD **-** Pharmacogenetics in Multiple Myeloma, Institute of Cancer Research, London.
1994-97: Biotechnology BSc. (Hons) at Imperial College, London.

Key Skills

- **Analyst of genomic data,** including:
  - Analysis of SNP association with aetiology, drug related outcomes in over 4000 patients.[6, 9-12]
  - Integrated genomics analysis (combining constitutional and somatic variation, High-throughput sequencing, copy number, expression (eQTL) and DNA methylation (meQTL) with drug related outcomes (>600-2000 patients), in R and Python. [1-12]
  - Genomic annotation of association results with experimental sequencing tracks and integration public domain data sources. [1-12]
- **Bioinformatics analyst,** including extensive experience in:
  - R, Bash, Python, SQL and working experience of Julia.
  - High performance computing platforms. Linux and Colab/Kaggle.

- Version control through use of Git.
- Machine learning algorithms with experience in unsupervised and supervised learning, regression analyses and classification algorithms, dimension reduction techniques such as PCA, MDS and TSNE. [1,8]
- Advanced linear (ridge regression, lasso, elastic net) and non-linear regression/classification techniques (e.g. KNN, random and random forest) using R and python packages.[1,2,18]

- **Longitudinal analysis of clinical trials data,** including extensive experience in:
  - Interpretation and presentation of multi-centre phase III clinical trial data including adaptive and maintenance arms. [1-2, 6-8]
  - Meta-analysis of trial-based clinical end point data and combining data from multi-country real world datasets or cancer registries. [1-12]
  - Integration of translational data with clinical endpoints. [1-12]
  - Statistical analyses in SPSS, R and Python. [1-12]
  - Generation of publication ready clinical trials analyses for JCO, Nature Comms, Leukemia. [1-12]
  - Application of relevant statistical techniques include sample size/power calculation, cox regression, multi-variable analysis, ROC modelling, landmark analysis, C-stats and Bayesian methods.
  - Collection of clinical trial data, data cleaning, HTA.
  - Development of trials protocols, and REC approvals.

- **Academic and laboratory management and leadership** including:
  - Management of purchasing and large acquisitions in a medium sized laboratory with annual budget £0.8-1.5M.
  - Training of junior staff in laboratory and bioinformatics techniques, protocols and SOPs.
  - Ph.D. supervision.[2,4,5]
  - Management of complex collaborations across internal, domestic and international groups.
  - Peer review for: American Society of Hematology (ASH) annual meeting abstract evaluator (**2016**). European Research Council (ERC) grant referee (**2018**).
  - Extensive oral/poster conference presentations.
  - Career mentorship through ICR scientific officer association.
  - Roles on Health and safety and genetic modification committees.

- **Extensive experience in wet-lab molecular biology laboratory** [1-12, 32, 47-55]**,** including:
  - Sample/batch processing, data generation.
  - QC assessment for genomics platforms.
  - Arrays workflows for SNP,[6, 9-12] copy number,[1,2,4] gene expression,[1, 5, 8, 15] and methylation.[1, 8]
  - High throughput sequencing.[1,3, 26, 28]

Key Research Grants obtained

I have co-developed >£20 million of successful grants by which the work of our team has been supported, including:

- Leukaemia and lymphoma research program grant (Co-applicant) - £15 million (**2006-10**)
- Bank on a Cure Consortium by International Myeloma Foundation (Co-applicant) - £1.8 million. (**2004-2010**)
- Myeloma UK program grant - Origins section - £4.2 million. (**2011-18**)

Key manuscripts (*Authors contributed equally to the work, for additional publications see appendix 2)

Author of 56 original research publications, including 10 first/final author position.

H-Index: 34 (as of Jan 19) i10-index: 49 (as of Aug 19).

1. Johnson DC, Shah V, Sherbourne A, Ellis S, Price A, Owen R**,** et al. DNA methylation profiling of multiple myeloma trial patients implicates MEIS2 as a determinant of response to immunomodulatory therapy. Submitted 2019.

2. V.Shah, **Johnson DC** Sherbourne A, Ellis S, Albridge FM, Howard-Reeves FM, et al. Sub-clonal TP53 copy number is associated with prognosis in multiple myeloma, **Blood. 2018** Oct 2.

3. Johnson DC, Lenive O, Mitchell J, Jackson G, Owen R, Drayson M et al. Neutral tumor evolution in myeloma is associated with poor prognosis. **Blood, 2017** Oct 5;130 (14):1639-1643.

4. Li N, **Johnson DC**, Weinhold N, Kimber S, Dobbins SE, Mitchell JS, et al. Genetic Predisposition to Multiple Myeloma at 5q15 Is Mediated by an ELL2 Enhancer Polymorphism. **Cell Rep. 2017** Sep 12;20(11):2556-2564.

5. Li N, **Johnson DC**, Weinhold N, Studd JB, Orlando G, Mirabella F, et al. Multiple myeloma risk variant at 7p15.3 creates an IRF4-binding site and interferes with CDCA7L expression. **Nat Commun. 2016**.

6. Johnson DC, Weinhold N, Mitchell JS, Chen B, Kaiser M, Begum DB et al. Genome-wide association study identifies variation at 6q25.1 associated with survival in multiple myeloma. **Nat Commun. 2016** Jan 8; 7:10290.

7. Johnson DC, Weinhold N, Mitchell J, Chen B, Stephens OW, Försti A, et al. Genetic factors influencing the risk of multiple myeloma bone disease. **Leukemia. 2016** Apr;30 (4):883-8.

8. Kaiser MF, **Johnson DC**, Wu P, Walker BA, Brioli A, Mirabella F, et al. Global methylation analysis identifies prognostically important epigenetically inactivated tumor suppressor genes in multiple myeloma. **Blood. 2013** Jul 11;122(2):219-26.

9. Weinhold N***, Johnson DC***, Chubb D, Chen B, Försti A, Hosking FJ, et al. The CCND1 c.870G>A polymorphism is a risk factor for t(11;14) (q13;q32) multiple myeloma. **Nat Genet. 2013** May;45(5):522-525.

10. Broderick P*****, Chubb D***, Johnson DC***, Weinhold N, Försti A, Lloyd A, et al. Common variation at 3p22.1 and 7p15.3 influences multiple myeloma risk. **Nat Genet. 2011** Nov 27;44(1):58-61.

11. Johnson DC, Corthals SL, Walker BA, Ross FM, Gregory WM, Dickens NJ, et al. Genetic factors underlying the risk of thalidomide-related neuropathy in patients with multiple myeloma. **J Clin Oncol. 2011** Mar 1;29(7):797-804.

12. Johnson DC, Corthals S, Ramos C, Hoering A, Cocks K, Dickens NJ, et al, Genetic associations with thalidomide mediated venous thrombotic events in myeloma identified using targeted genotyping. **Blood. 2008** Dec 15;112(13):4924-34.

Key International Spoken Presentations

- International Myeloma Workshop (**2017**).
- ASH Annual Meetings (**2016, 2009, 2006, 2005**).
- Annual Congress of EHA (**2014**).

Appendix 1
Additional Technical Skills and training

Data analytics:

- Strong Microsoft Office skills (Word, Excel, Access, PowerPoint and Visio)
- Image editing tools and processes utilizing GIMP2 and photoshop.
- Project tracking and management with MS project, Podio and Freedcamp.
- Registered Azure and AWS user.
- Collaborative working through Slack, Asana and Git/Jupyter notebooks.
- Keen twitter follower of health care luminaires and advocates
- Utilise bioRxiv to follow emerging research and technologies.

2011-2019:

- Sequencing data: QC, ENCODE processing pipelines, Bedtools, UCSC utilities, MutSigCV, Galaxy, Mutational Signatures, MEDIPS, GVIZ.[1,3,26,28]
- Mendelian Randomisation.
- Admixture analyses.
- Methylation array data: QC, normalisation, summation and functional/factor annotation.
- Expression array data: QC, normalisation, CoMBAT, Consensus clustering and Limma.
- SNP association studies: Imputation, GTOOL, SNPTEST, META and PLINK 2.0.
- Modelling/Machine learning: Regression, KNN, random forest, Lasso. Ridge regression - R; Pandas, NumPy, Matplotlib, scikit-learn, pomegranate, hmmlearn - Python.[1,2,3,6]
- Optical mapping - BioNano restriction genomic mapping.
- Custom sequencing panel design, amplicon and pull down.
- Laboratory management, equipment acquisition and Agresso purchasing.
- Good Clinical Practice (GCP) training course.
- Experience in sequence variant interpretation packages/databases e.g. Mutation Taster, PolyPhen2, SIFT and Splice Predictors.

2004-2011:

- SNP association studies: PLINK 1.7, Rstudio, Haploview, pathway analysis.[6-7,9-12]
- Clinical trial demographics QC - bone disease, drug related neuropathy and thrombosis.
- Real-time PCR and primer design.
- Affymetrix expression, mapping and genotyping workflows. Custom SNP array design.[6-7,9-12]
- Cat 2 cell culture.
- Accredited training for personnel working under the Animals - modules 1-4.
- Experience with pathway and network analyses including: DAVID, GSEA, WebGestalt GSAT, GeneGO MetaCore and Ingenuity Pathways.

1998-2004:

- YAC or whole/partial chromosome DNA isolation using rotational PGFE and CHEF.
- Restriction digest analysis in BAC, Cosmid and YAC clones. Cell culture.
- YACture (a YAC based “Gapture”) and Vetorette capture (a PCR based gap capture protocol)
- YAC transfer to window strains. YAC transfer to fosmids. Southern blotting and Sub-cloning.
- DNA sequencing with 377 and 3700.
- Techniques/information exchange - the Genome Centre, Washington University, St. Louis.

Appendix 2
Additional authored manuscripts

13. Transcriptome-wide association study of multiple myeloma identifies candidate susceptibility genes. Went M, Kinnersley B, Sud A, Johnson DC, Weinhold N, Försti A, van Duin M, Orlando G, Mitchell JS, Kuiper R, Walker BA, Gregory WM, Hoffmann P, Jackson GH, Nöthen MM, da Silva Filho MI, Thomsen H, Broyl A, Davies FE, Thorsteinsdottir U, Hansson M, Kaiser M, Sonneveld P, Goldschmidt H, Stefansson K, Hemminki K, Nilsson B, Morgan GJ, Houlston RS. Hum Genomics. 2019 Aug 20;13(1):37. doi: 10.1186/s40246-019-0231-5. PMID: 31429796

14. Regions of homozygosity as risk factors for multiple myeloma. Went M, Sud A, Li N, Johnson DC, Mitchell JS, Kaiser M, Houlston RS. Annals of human genetics. 2019.

15. Clonal evolution in myeloma: the impact of maintenance lenalidomide and depth of response on the genetics and sub-clonal structure of relapsed disease in uniformly treated patients. Jones JR, Weinhold N, Ashby C, Walker BA, Wardell C, Pawlyn C, Rasche L, Melchor L, Cairns DA, Gregory WM, Johnson D, Ellis S, Sherborne AL, Cook G, Kaiser MF, Drayson MT, Owen RG, Jackson GH, Davies FE, Greaves M, Morgan GJ. Haematologica. 2019.

16. The coordinated action of VCP/p97 and GCN2 regulates cancer cell metabolism and proteostasis during nutrient limitation Parzych K, Saavedra-García P, Valbuena GN, Al-Sadah HA, Robinson ME, Penfold L, Kuzeva DM, Ruiz-Tellez A, Loaiza S, Holzmann V, Caputo V, Johnson DC, Kaiser MF, Karadimitris A, Lam EWF, Chevet E, Feldhahn Ni, Keun HC, Auner HW, Oncogene, 1, 2019.

17. The genomic landscape of plasma cells in systemic light chain amyloidosis. Boyle EM, Ashby C, Wardell CP, Rowczenio D, Sachchithanantham S, Wang Y, Johnson SK, Bauer MA, Weinhold N, Kaiser MF, Johnson DC, Jones JR, Pawlyn C, Proszek P, Schinke C, Facon T, Dumontet C, Davies FE, Morgan GJ, Walker BA, Wechalekar AD. Blood 132 (26), 2775-2777.

18. Genetic correlation between multiple myeloma and chronic lymphocytic leukaemia provides evidence for shared aetiology. Went M, Sud A, Speedy H, Sunter NJ, Försti A, Law PJ, Johnson DC, Mirabella F, Holroyd A, Li N, Orlando G, Weinhold N, Duin MV, Chen B, Mitchell JS, Mansouri L, Juliusson G, Smedby KE, Jayne S, Majid A, Dearden C, Allsup DJ, Bailey JR, Pratt G, Pepper C, Fegan C, Rosenquist R, Kuiper R, Stephens OW, Bertsch U, Broderick P, Einsele H, Gregory WM, Hillengass J, Hoffmann P, Jackson GH, Jöckel KH, Nickel J, Nöthen MM, da-Silva-Filho MI, Thomsen H, Walker BA, Broyl A, Davies FE, Hansson M, Goldschmidt H, Dyer MJS, Kaiser M, Sonneveld P, Morgan GJ, Hemminki K, Nilsson B, Catovsky D, Allan JM, Houlston RS. Blood cancer journal 9 (1), 2019.

19. Prediction of outcome in newly diagnosed myeloma: a meta-analysis of the molecular profiles of 1905 trial patients. Shah V, Sherborne AL, Walker BA, Johnson DC, Boyle EM, Ellis S, Begum DB, Proszek PZ, Jones JR, Pawlyn C, Savola S, Jenner MW, Drayson MT, Owen RG, Houlston RS, Cairns DA, Gregory WM, Cook G, Davies FE, Jackson GH, Morgan GJ, Kaiser MF. Leukemia. 2018 Jan;32(1):102-110. PMID: 28584253.

20. Identification of multiple risk loci and regulatory mechanisms influencing susceptibility to multiple myeloma. Went M, Sud A, Försti A, Halvarsson BM, Weinhold N, Kimber S, van Duin M, Thorleifsson G, Holroyd A, Johnson DC, Li N, Orlando G, Law PJ, Ali M, Chen B, Mitchell JS, Gudbjartsson DF, Kuiper R, Stephens OW, Bertsch U, Broderick P, Campo C, Bandapalli OR, Einsele H, Gregory WA, Gullberg U, Hillengass J, Hoffmann P, Jackson GH, Jöckel KH, Johnsson E, Kristinsson SY, Mellqvist UH, Nahi H, Easton D, Pharoah P, Dunning A, Peto J, Canzian F, Swerdlow A, Eeles RA, Kote-Jarai Z, Muir K, Pashayan N, Nickel J, Nöthen MM, Rafnar T, Ross FM,

da Silva Filho MI, Thomsen H, Turesson I, Vangsted A, Andersen NF, Waage A, Walker BA, Wihlborg AK, Broyl A, Davies FE, Thorsteinsdottir U, Langer C, Hansson M, Goldschmidt H, Kaiser M, Sonneveld P, Stefansson K, Morgan GJ, Hemminki K, Nilsson B, Houlston RS; PRACTICAL consortium. Nat Commun. 2018 Sep 13;9(1):3707. PMID: 30213928

21. A multiple myeloma classification system that associates normal B-cell subset phenotypes with prognosis. Bødker JS, Brøndum RF, Schmitz A, Schönherz AA, Jespersen DS, Sønderkær M, Vesteghem C, Due H, Nørgaard CH, Perez-Andres M, Samur MK, Davies F, Walker B, Pawlyn C, Kaiser M, Johnson DC, Bertsch U, Broyl A, Duin MV, Shah R, Johansen P, Nørgaard MA, Samworth RJ, Sonneveld P, Goldschmidt H, Morgan GJ, Orfao A, Munshi N, Johnson HE, El-Galaly T, Dybkær K, Bøgsted M. Blood advances. 2:18, 2400-2411.2018

22. Assessing the effect of obesity-related traits on multiple myeloma using a Mendelian randomisation approach. Went M, Sud A, Law PJ, Johnson DC, Weinhold N, Försti A, van Duin M, Mitchell JS, Chen B, Kuiper R, Stephens OW, Bertsch U, Campo C, Einsele H, Gregory WM, Henrion M, Hillengass J, Hoffmann P, Jackson GH, Lenive O, Nickel J, Nöthen MM, da Silva Filho MI, Thomsen H, Walker BA, Broyl A, Davies FE, Langer C, Hansson M, Kaiser M, Sonneveld P, Goldschmidt H, Hemminki K, Nilsson B, Morgan GJ, Houlston RS. Blood Cancer J. 2017 Jun 16;7(6):e573. PMID: 28622301.

23. Search for rare protein altering variants influencing susceptibility to multiple myeloma. Scales M, Chubb D, Dobbins SE, Johnson DC, Li N, Sternberg MJ, Weinhold N, Stein C, Jackson G, Davies FE, Walker BA, Wardell CP, Houlston RS, Morgan GJ. Oncotarget. 2017 May 30;8(22):36203-36210. PMID: 28404951.

24. Genome-wide association analysis of chronic lymphocytic leukaemia, Hodgkin lymphoma and multiple myeloma identifies pleiotropic risk loci. Law PJ, Sud A, Mitchell JS, Henrion M, Orlando G, Lenive O, Broderick P, Speedy HE, Johnson DC, Kaiser M, Weinhold N, Cooke R, Sunter NJ, Jackson GH, Summerfield G, Harris RJ, Pettitt AR, Allsup DJ, Carmichael J, Bailey JR, Pratt G, Rahman T, Pepper C, Fegan C, von Strandmann EP, Engert A, Försti A, Chen B, Filho MI, Thomsen H, Hoffmann P, Noethen MM, Eisele L, Jöckel KH, Allan JM, Swerdlow AJ, Goldschmidt H, Catovsky D, Morgan GJ, Hemminki K, Houlston RS. Sci Rep. 2017 Jan 23;7:41071. PMID: 28112199.

25. The Spectrum and Clinical Impact of Epigenetic Modifier Mutations in Myeloma. Pawlyn C, Kaiser MF, Heuck C, Melchor L, Wardell CP, Murison A, Chavan SS, Johnson DC, Begum DB, Dahir NM, Proszek PZ, Cairns DA, Boyle EM, Jones JR, Cook G, Drayson MT, Owen RG, Gregory WM, Jackson GH, Barlogie B, Davies FE, Walker BA, Morgan GJ. Clin Cancer Res. 2016 Dec 1;22(23):5783-5794. Epub 2016 May 27. PMID: 27235425.

26. Genome-wide association study identifies multiple susceptibility loci for multiple myeloma. Mitchell JS, Li N, Weinhold N, Försti A, Ali M, van Duin M, Thorleifsson G, Johnson DC, Chen B, Halvarsson BM, Gudbjartsson DF, Kuiper R, Stephens OW, Bertsch U, Broderick P, Campo C, Einsele H, Gregory WA, Gullberg U, Henrion M, Hillengass J, Hoffmann P, Jackson GH, Johnsson E, Jöud M, Kristinsson SY, Lenhoff S, Lenive O, Mellqvist UH, Migliorini G, Nahi H, Nelander S, Nickel J, Nöthen MM, Rafnar T, Ross FM, da Silva Filho MI, Swaminathan B, Thomsen H, Turesson I, Vangsted A, Vogel U, Waage A, Walker BA, Wihlborg AK, Broyl A, Davies FE, Thorsteinsdottir U, Langer C, Hansson M, Kaiser M, Sonneveld P, Stefansson K, Morgan GJ, Goldschmidt H, Hemminki K, Nilsson B, Houlston RS. Nat Commun. 2016 Jul 1;7:12050. PMID: 27363682.

27. Mutational Spectrum, Copy Number Changes, and Outcome: Results of a Sequencing Study of Patients With Newly Diagnosed Myeloma. Walker BA, Boyle EM, Wardell CP, Murison A, Begum DB, Dahir NM, Proszek PZ, Johnson DC, Kaiser MF, Melchor L, Aronson LI, Scales M, Pawlyn C, Mirabella F, Jones JR, Brioli A, Mikulasova A, Cairns DA, Gregory WM, Quartilho A, Drayson MT, Russell N, Cook G, Jackson GH, Leleu X, Davies FE, Morgan GJ. J Clin Oncol. 2015 Nov 20;33(33):3911-20. Epub 2015 Aug 17. PMID: 26282654.

28. Implementation of genome-wide complex trait analysis to quantify the heritability in multiple myeloma. Mitchell JS, Johnson DC, Litchfield K, Broderick P, Weinhold N, Davies FE, Gregory WA, Jackson GH, Kaiser M, Morgan GJ, Houlston RS. Sci Rep. 2015 Jul 24;5:12473. PMID: 26208354.

29. APOBEC family mutational signatures are associated with poor prognosis translocations in multiple myeloma. Walker BA, Wardell CP, Murison A, Boyle EM, Begum DB, Dahir NM, Proszek PZ, Melchor L, Pawlyn C, Kaiser MF, Johnson DC, Qiang YW, Jones JR, Cairns DA, Gregory WM, Owen RG, Cook G, Drayson MT, Jackson GH, Davies FE, Morgan GJ. Nat Commun. 2015 Apr 23;6:6997. PMID: 25904160.

30. A gene expression-based predictor for high risk myeloma treated with intensive therapy and autologous stem cell rescue. Wu P, Walker BA, Broyl A, Kaiser M, Johnson DC, Kuiper R, van Duin M, Gregory WM, Davies FE, Brewer D, Hose D, Sonneveld P, Morgan GJ. Leuk Lymphoma. 2015 Mar;56(3):594-601. PMID: 24913504.

31. Translocations at 8q24 juxtapose MYC with genes that harbor superenhancers resulting in overexpression and poor prognosis in myeloma patients. Walker BA, Wardell CP, Brioli A, Boyle E, Kaiser MF, Begum DB, Dahir NB, Johnson DC, Ross FM, Davies FE, Morgan GJ. Blood Cancer J. 2014 Mar 14;4:e191. PMID: 24632883.

32. Single-cell genetic analysis reveals the composition of initiating clones and phylogenetic patterns of branching and parallel evolution in myeloma. Melchor L, Brioli A, Wardell CP, Murison A, Potter NE, Kaiser MF, Fryer RA, Johnson DC, Begum DB, Hulkki Wilson S, Vijayaraghavan G, Titley I, Cavo M, Davies FE, Walker BA, Morgan GJ. Leukemia. 2014 Aug;28(8):1705-15. PMID: 24480973.

33. Inherited genetic susceptibility to monoclonal gammopathy of unknown significance. Weinhold N*, Johnson DC*, Rawstron AC, Försti A, Doughty C, Vijayakrishnan J, Broderick P, Dahir NB, Begum DB, Hosking FJ, Yong K, Walker BA, Hoffmann P, Mühleisen TW, Langer C, Dörner E, Jöckel KH, Eisele L, Nöthen MM, Hose D, Davies FE, Goldschmidt H, Morgan GJ, Hemminki K, Houlston RS. Blood. 2014 Apr 17;123(16):2513-7; quiz 2593. PMID: 24449210.

34. Inherited genetic susceptibility to multiple myeloma. Morgan GJ, Johnson DC, Weinhold N, Goldschmidt H, Landgren O, Lynch HT, Hemminki K, Houlston RS. Leukemia. 2014 Mar;28(3):518-24. PMID: 24247655

35. Common variation at 3q26.2, 6p21.33, 17p11.2 and 22q13.1 influences multiple myeloma risk. Chubb D, Weinhold N, Broderick P, Chen B, Johnson DC, Försti A, Vijayakrishnan J, Migliorini G, Dobbins SE, Holroyd A, Hose D, Walker BA, Davies FE, Gregory WA, Jackson GH, Irving JA, Pratt G, Fegan C, Fenton JA, Neben K, Hoffmann P, Nöthen MM, Mühleisen TW, Eisele L, Ross FM, Straka C, Einsele H, Langer C, Dörner E, Allan JM, Jauch A, Morgan GJ, Hemminki K, Houlston RS, Goldschmidt H. Nat Genet. 2013 Oct;45(10):1221-1225.PMID: 23955597.

36. Intraclonal heterogeneity is a critical early event in the development of myeloma and precedes the development of clinical symptoms. Walker BA, Wardell CP, Melchor L, Brioli A, Johnson DC, Kaiser MF, Mirabella F, Lopez-Corral L, Humphray S, Murray L, Ross M, Bentley D, Gutiérrez NC, Garcia-Sanz R, San Miguel J, Davies FE, Gonzalez D, Morgan GJ. Leukemia. 2014 Feb;28(2):384-390. PMID: 23817176.

37. Improved risk stratification in myeloma using a microRNA-based classifier. Wu P, Agnelli L, Walker BA, Todoerti K, Lionetti M, Johnson DC, Kaiser M, Mirabella F, Wardell C, Gregory WM, Davies FE, Brewer D, Neri A, Morgan GJ. Br J Haematol. 2013 Aug;162(3):348-59. PMID: 23718138.

38. MMSET is the key molecular target in t(4;14) myeloma. Mirabella F, Wu P, Wardell CP, Kaiser MF, Walker BA, Johnson DC, Morgan GJ. Blood Cancer J. 2013 May 3;3:e114. PMID: 23645128.

39. Characterization of IGH locus breakpoints in multiple myeloma indicates a subset of translocations appear to occur in pregerminal center B cells. Walker BA, Wardell CP, Johnson DC, Kaiser MF, Begum DB, Dahir NB, Ross FM, Davies FE, Gonzalez D, Morgan GJ. Blood. 2013 Apr 25;121(17):3413-9. PMID: 23435460.

40. Intraclonal heterogeneity and distinct molecular mechanisms characterize the development of t(4;14) and t(11;14) myeloma. Walker BA, Wardell CP, Melchor L, Hulkki S, Potter NE, Johnson DC, Fenwick K, Kozarewa I, Gonzalez D, Lord CJ, Ashworth A, Davies FE, Morgan GJ. Blood. 2012 Aug 2;120(5):1077-86. PMID: 22573403.

41. Genetic factors underlying the risk of bortezomib induced peripheral neuropathy in multiple myeloma patients. Corthals SL, Kuiper R, Johnson DC, Sonneveld P, Hajek R, van der Holt B, Magrangeas F, Goldschmidt H, Morgan GJ, Avet-Loiseau H. Haematologica. 2011 Nov;96(11):1728-32. PMID: 21791469.

42. A compendium of myeloma-associated chromosomal copy number abnormalities and their prognostic value. Walker BA, Leone PE, Chiecchio L, Dickens NJ, Jenner MW, Boyd KD, Johnson DC, Gonzalez D, Dagrada GP, Protheroe RK, Konn ZJ, Stockley DM, Gregory WM, Davies FE, Ross FM, Morgan GJ. Blood. 2010 Oct 14;116(15):e56-65. PMID: 20616218.

43. XBP1s levels are implicated in the biology and outcome of myeloma mediating different clinical outcomes to thalidomide-based treatments. Bagratuni T, Wu P, Gonzalez de Castro D, Davenport EL, Dickens NJ, Walker BA, Boyd K, Johnson DC, Gregory W, Morgan GJ, Davies FE. Blood. 2010 Jul 15;116(2):250-3. PMID: 20421453.

44. Homozygous deletion mapping in myeloma samples identifies genes and an expression signature relevant to pathogenesis and outcome. Dickens NJ, Walker BA, Leone PE, Johnson DC, Brito JL, Zeisig A, Jenner MW, Boyd KD, Gonzalez D, Gregory WM, Ross FM, Davies FE, Morgan GJ. Clin Cancer Res. 2010 Mar 15;16(6):1856-64. PMID: 20215539.

45. Deletions of CDKN2C in multiple myeloma: biological and clinical implications. Leone PE, Walker BA, Jenner MW, Chiecchio L, Dagrada G, Protheroe RK, Johnson DC, Dickens NJ, Brito JL, Else M, Gonzalez D, Ross FM, Chen-Kiang S, Davies FE, Morgan GJ. Clin Cancer Res. 2008 Oct 1;14(19):6033-41. PMID: 18829482.

46. Gene mapping and expression analysis of 16q loss of heterozygosity identifies WWOX and CYLD as being important in determining clinical outcome in multiple myeloma. Jenner MW, Leone PE, Walker BA, Ross FM, Johnson DC, Gonzalez D, Chiecchio L, Dachs Cabanas E, Dagrada GP, Nightingale M, Protheroe RK, Stockley D, Else M, Dickens NJ, Cross NC, Davies FE, Morgan GJ. Blood. 2007 Nov 1;110(9):3291-300. PMID: 17609426.

47. Integration of global SNP-based mapping and expression arrays reveals key regions, mechanisms, and genes important in the pathogenesis of multiple myeloma. Walker BA, Leone PE, Jenner MW, Li C, Gonzalez D, Johnson DC, Ross FM, Davies FE, Morgan GJ. Blood. 2006 Sep 1;108(5):1733-43. PMID: 16705090.

48. The DNA sequence and biological annotation of human chromosome 1. Gregory SG, Barlow KF, McLay KE, Kaul R, Swarbreck D, Dunham A*, et al. Nature* 2006 May 18; **441**(7091)**:** 315-321.

49. The DNA sequence of the human X chromosome.Ross MT, Grafham DV, Coffey AJ, Scherer S, McLay K, Muzny D*, et al. Nature* 2005 Mar 17; **434**(7031)**:** 325-337.

50. The genome of the social amoeba Dictyostelium discoideum. Eichinger L, Pachebat JA, Glockner G, Rajandream MA, Sucgang R, Berriman M*, et al. Nature* 2005 May 5; **435**(7038)**:** 43-57.

51. The genome of the African trypanosome Trypanosoma brucei.Berriman M, Ghedin E, Hertz-Fowler C, Blandin G, Renauld H, Bartholomeu DC*, et al. Science* 2005 Jul 15; **309**(5733)**:** 416-422.

52. Humphray SJ, Oliver K, Hunt AR, Plumb RW, Loveland JE, Howe KL*, et al.* DNA sequence and analysis of human chromosome 9. *Nature* 2004 May 27; **429**(6990)**:** 369-374.

53. Dunham A, Matthews LH, Burton J, Ashurst JL, Howe KL, Ashcroft KJ*, et al.* The DNA sequence and analysis of human chromosome 13. *Nature* 2004 Apr 1; **428**(6982)**:** 522-528.

54. Deloukas P, Earthrowl ME, Grafham DV, Rubenfield M, French L, Steward CA*, et al.* The DNA sequence and comparative analysis of human chromosome 10. *Nature* 2004 May 27; **429**(6990)**:** 375-381.

55. Hall N, Pain A, Berriman M, Churcher C, Harris B, Harris D*, et al.* Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13. *Nature* 2002 Oct 3; **419**(6906)**:** 527-531.

56. Deloukas P, Matthews LH, Ashurst J, Burton J, Gilbert JG, Jones M*, et al.* The DNA sequence and comparative analysis of human chromosome 20. *Nature* 2001 Dec 20-27; **414**(6866)**:** 865-871.