

Selected Publications from 2020

The Centre for Genomics Research has contributed to project design, method development/optimisation, data generation or analysis for the following publications:

- Arnold, D., Cawley, A., Darby, A.C., Falciani, F., Grimshaw, S.G., Hawkins, S.S., Hoptroff, M., MacGuire-Flanagan, A., Mayes, A.E., Murphy, B. and Paterson, S., 2020. 16282 Community relationships in the dry skin microbiome. *Journal of the American Academy of Dermatology*, 83(6), p.AB59.
- Pulford, C.V., Perez-Sepulveda, B.M., Canals, R., Bevington, J.A., Bengtsson, R.J., Wenner, N., Rodwell, E.V., Kumwenda, B., Zhu, X., Bennett, R.J. and Stenhouse, G.E., 2020. Stepwise evolution of Salmonella Typhimurium ST313 causing bloodstream infection in Africa. *Nature Microbiology*, pp.1-12.
- Pulford, C.V., Perez-Sepulveda, B.M., Canals, R., Bevington, J.A., Bengtsson, R.J., Wenner, N., Rodwell, E.V., Kumwenda, B., Zhu, X., Bennett, R.J. and Stenhouse, G.E., 2020. Stepwise evolution of Salmonella Typhimurium ST313 causing bloodstream infection in Africa. *Nature Microbiology*, pp.1-12.
- Moore, S.C., Penrice-Randall, R., Alruwaili, M., Randle, N., Armstrong, S., Hartley, C., Haldenby, S., Dong, X., Alrezaihi, A., Almsaud, M. and Bentley, E., 2020. Amplicon-Based Detection and Sequencing of SARS-CoV-2 in Nasopharyngeal Swabs from Patients With COVID-19 and Identification of Deletions in the Viral Genome That Encode Proteins Involved in Interferon Antagonism. *Viruses*, 12(10), p.1164.
- Roberts, K.E., Meaden, S., Sharpe, S., Kay, S., Doyle, T., Wilson, D., Bartlett, L.J., Paterson, S. and Boots, M., 2020. Resource quality determines the evolution of resistance and its genetic basis. *Molecular Ecology*.
- Padfield, D., Vujakovic, A., Paterson, S., Griffiths, R., Buckling, A. and Hesse, E., 2020. Evolution of diversity explains the impact of pre-adaptation of a focal species on the structure of a natural microbial community. *The ISME Journal*, 14(11), pp.2877-2889.
- Hardwick, Kayla M., Gladys Bosibori Bichang'a, Andnet Bayleyegn Abteu, Ryan Musumba Awori, Leah Cepko, Lorna Jemosop Chebon-Bore, Alistair Darby et al. Comprehensive transcriptome of the maize stalk borer, *Busseola fusca*, from multiple tissue types, developmental stages, and parasitoid wasp exposures. *Genome Biology and Evolution* (2020).
- Houte, S.V., Padfield, D., Gomez, P., Lujan, A.M., Brockhurst, M.A., Paterson, S. and Buckling, A., 2020. Compost spatial heterogeneity promotes evolutionary diversification of a Bacterium. *Journal of Evolutionary Biology*.



- Moore, S.C., Penrice-Randall, R., Alruwaili, M., Randle, N., Armstrong, S., Hartley, C., Haldenby, S., Dong, X., Alrezaihi, A., Almsaud, M. and Bentley, E., 2020. Amplicon-Based Detection and Sequencing of SARS-CoV-2 in Nasopharyngeal Swabs from Patients With COVID-19 and Identification of Deletions in the Viral Genome That Encode Proteins Involved in Interferon Antagonism. *Viruses*, 12(10), p.1164.
- Wanelik, K.M., Begon, M., Arriero, E., Bradley, J.E., Friberg, I.M., Jackson, J.A., Taylor, C.H. and Paterson, S., 2020. Transcriptome-wide analysis reveals different categories of response to a standardised immune challenge in a wild rodent. *Scientific Reports*, 10(1), pp.1-11.
- Mulindwa, J., Noyes, H., Ilboudo, H., Pagani, L., Nyangiri, O., Kimuda, M.P., Ahouty, B., Asina, O.F., Ofon, E., Kamoto, K. and Kabore, J.W., 2020. High Levels of Genetic Diversity within Nilo-Saharan Populations: Implications for Human Adaptation. *The American Journal of Human Genetics*.
- Asina, O.F., Noyes, H., Bucheton, B., Ilboudo, H., MacLeod, A. and Ngoyi, D.M., 2020. SNPs in IL4 and IFNG show no protective associations with human African trypanosomiasis in the Democratic Republic of the Congo: a case-control study. *AAS Open Research*, 3(35), p.35.
- Pongchaikul, P., Santanirand, P., Antonyuk, S., Winstanley, C. and Darby, A.C., 2020. AcGI1, a novel genomic island carrying antibiotic resistance integron In687 in multidrug resistant *Achromobacter xylosoxidans* in a teaching hospital in Thailand. *FEMS Microbiology Letters*, 367(14), p.fnaa109.
- Buttimer, C., Lynch, C., Hendrix, H., Neve, H., Noben, J.P., Lavigne, R. and Coffey, A., 2020. Isolation and Characterization of Pectobacterium Phage vB_PatM_CB7: New Insights into the Genus Certrevirus. *Antibiotics*, 9(6), p.352.
- Khoo, J.J., Kurtti, T., Husin, N.A., Beliavskaia, A., Lim, F.S., Zulkifli, M.M.S., Al-Khafaji, A., Hartley, C., Darby, A., Hughes, G. and AbuBakar, S., 2020. Isolation and Propagation of Laboratory Strains and a Novel Flea-Derived Field Strain of Wolbachia in Tick Cell Lines.
- Zhu, W., Liu, X., Hughes, M., de Crécy-Lagard, V. and Richards, N.G., 2020. Whole-Genome Sequence of *Streptomyces kaniharaensis* Shomura and Niida SF-557. *Microbiology Resource Announcements*, 9(14).
- Nyangiri, O.A., Noyes, H., Mulindwa, J., Ilboudo, H., Kabore, J.W., Ahouty, B., Koffi, M., Asina, O.F., Mumba, D., Ofon, E. and Simo, G., 2020. Copy number variation in human genomes from three major ethno-linguistic groups in Africa. *BMC genomics*, 21, pp.1-15.
- Thornton, S., Coupland, S.E., Olohan, L., Sibbring, J.S., Kenny, J.G., Hertz-Fowler, C., Liu, X., Haldenby, S., Heimann, H., Hussain, R. and Kipling, N., 2020. Targeted next-generation sequencing of 117 routine clinical samples provides further insights into the molecular landscape of uveal melanoma. *Cancers*, 12(4), p.1039.

- van de Wijgert, J.H., Verwijs, M.C., Agaba, S.K., Bronowski, C., Mwambarangwe, L., Uwineza, M., Lievens, E., Nivoliez, A., Ravel, J. and Darby, A.C., 2020. Intermittent Lactobacilli-containing vaginal probiotic or metronidazole use to prevent bacterial vaginosis recurrence: a pilot study incorporating microscopy and sequencing. *Scientific reports*, 10(1), pp.1-15.
- Copple, I.M., den Hollander, W., Callegaro, G., Mutter, F.E., Maggs, J.L., Schofield, A.L., Rainbow, L., Fang, Y., Sutherland, J.J., Ellis, E.C. and Ingelman-Sundberg, M., 2019. Characterisation of the NRF2 transcriptional network and its response to chemical insult in primary human hepatocytes: implications for prediction of drug-induced liver injury. *Archives of toxicology*, 93(2), pp.385-399.
- Culbert, N.J., Kaiser, M., Venter, N., Vreysen, M.J., Gilles, J.R. and Bouyer, J., 2020. A standardised method of marking male mosquitoes with fluorescent dust. *Parasites & Vectors*, 13, pp.1-11.
- Lilley, T.M., Wilson, I.W., Field, K.A., Reeder, D.M., Vodzak, M.E., Turner, G.G., Kurta, A., Blomberg, A.S., Hoff, S., Herzog, C.J. and Sewall, B.J., 2020. Genome-wide changes in genetic diversity in a population of *Myotis lucifugus* affected by white-nose syndrome. *G3: Genes, Genomes, Genetics*, 10(6), pp.2007-2020.
- Husnik, F., Hypsa, V. and Darby, A., 2020. Insect—symbiont gene expression in the midgut bacteriocytes of a blood-sucking parasite. *Genome Biology and Evolution*, 12(4), pp.429-442.
- Ward, C.M., Aumann, R.A., Whitehead, M.A., Nikolouli, K., Leveque, G., Gouvi, G., Fung, E., Reiling, S.J., Djambazian, H.H.V., Hughes, M.A. and Whiteford, S., 2020. White pupae genes in the Tephritids *Ceratitis capitata*, *Bactrocera dorsalis* and *Zeugodacus cucurbitae*: a story of parallel mutations. *bioRxiv*.
- Zhu, W., Liu, X., Hughes, M., de Crécy-Lagard, V. and Richards, N.G., 2020. Whole-Genome Sequence of *Streptomyces kaniharaensis* Shomura and Niida SF-557. *Microbiology Resource Announcements*, 9(14).
- Acha-Sagredo, A., Uko, B., Pantazi, P., Bediaga, N.G., Moschandrea, C., Rainbow, L., Marcus, M.W., Davies, M.P., Field, J.K. and Liloglou, T., 2020. Long non-coding RNA dysregulation is a frequent event in non-small cell lung carcinoma pathogenesis. *British Journal of Cancer*, pp.1-9.
- Haldenby, S., Bronowski, C., Nelson, C., Kenny, J., Martinez-Rodriguez, C., Chaudhuri, R., Williams, N.J., Forbes, K., Strachan, N.J., Pulman, J. and Winstanley, I.N., 2020. Increasing prevalence of a fluoroquinolone resistance mutation amongst *Campylobacter jejuni* isolates from four human infectious intestinal disease studies in the United Kingdom. *PLoS One*, 15(1), p.e0227535.

- Blow, F., Gioti, A., Goodhead, I.B., Kalyva, M., Kampouraki, A., Vontas, J. and Darby, A.C., 2020. Functional genomics of a symbiotic community: shared traits in the olive fruit fly gut microbiota. *Genome biology and evolution*, 12(2), pp.3778-3791.
- Culbert, N.J., Somda, N.S.B., Hamidou, M., Soma, D.D., Caravantes, S., Wallner, T., Wadaka, M., Yamada, H. and Bouyer, J., 2020. A rapid quality control test to foster the development of the sterile insect technique against *Anopheles arabiensis*. *Malaria journal*, 19(1), pp.1-10.
- Lloyd, K.A., Parsons, B.N., Burkitt, M.D., Moore, A.R., Papoutsopoulou, S., Boyce, M., Duckworth, C.A., Exarchou, K., Howes, N., Rainbow, L. and Fang, Y., 2020. Netazepide Inhibits Expression of Pappalysin 2 in Type 1 Gastric Neuroendocrine Tumors. *Cellular and Molecular Gastroenterology and Hepatology*.
- Liu, Q., Lei, J., Darby, A.C. and Kadowaki, T., 2020. Trypanosomatid parasite dynamically changes the transcriptome during infection and modifies honey bee physiology. *Communications Biology*, 3(1), pp.1-8.
- Lees, E.A., Carrol, E.D., Ellaby, N.A., Roberts, P., Corless, C.E., Lenzi, L., Darby, A., O'Brien, S.J., Cunliffe, N.A., Turner, M.A. and Miyajima, F., 2020. Characterization of Circulating *Clostridium difficile* Strains, Host Response and Intestinal Microbiome in Hospitalized Children With Diarrhea. *The Pediatric Infectious Disease Journal*, 39(3), pp.221-228.
- Van de Wijgert Janneke, H.H.M., Verwijs, M.C., Agaba, S.K., Christina, B., Lambert, M., Mireille, U., Elke, L., Adrien, N., Ravel, J. and Darby, A.C., 2020. Intermittent Lactobacilli-containing Vaginal Probiotic or Metronidazole Use to Prevent Bacterial Vaginosis Recurrence: A Pilot Study Incorporating Microscopy and Sequencing. *Scientific Reports (Nature Publisher Group)*, 10(1).
- Verwijs, M.C., Agaba, S.K., Darby, A.C. and van de Wijgert, J.H., 2020. Impact of oral metronidazole treatment on the vaginal microbiota and correlates of treatment failure. *American journal of obstetrics and gynecology*, 222(2), pp.157-e1.
- Goodhead, I., Blow, F., Brownridge, P., Hughes, M., Kenny, J., Krishna, R., McLean, L., Pongchaikul, P., Beynon, R. and Darby, A.C., 2020. Large-scale and significant expression from pseudogenes in *Sodalis glossinidius*—a facultative bacterial endosymbiont. *Microbial Genomics*, p.mgen000285.
- Van De Wijgert, J.H., Gill, A.C., Chikandiwa, A., Verwijs, M.C., Kelly, H.A., Omar, T., Delany-Moretlwe, S., Segondy, M., Francis, S., Darby, A.C. and Mayaud, P., 2020. Human papillomavirus infection and cervical dysplasia in HIV-positive women: potential role of the vaginal microbiota. *Aids*, 34(1), pp.115-125.

The Centre for Genomics Research has generated data and/or analysis for the following publications:

- Choudhury, A., Aron, S., Botigué, L.R., Sengupta, D., Botha, G., Bensellak, T., Wells, G., Kumuthini, J., Shriner, D., Fakim, Y.J. and Ghoorah, A.W., 2020. High-depth African genomes inform human migration and health. *Nature*, 586(7831), pp.741-748.
- Roberts, K.E., Meaden, S., Sharpe, S., Kay, S., Doyle, T., Wilson, D., Bartlett, L.J., Paterson, S. and Boots, M., 2020. Resource quality determines the evolution of resistance and its genetic basis. *Molecular Ecology*.
- Padfield, D., Vujakovic, A., Paterson, S., Griffiths, R., Buckling, A. and Hesse, E., 2020. Evolution of diversity explains the impact of pre-adaptation of a focal species on the structure of a natural microbial community. *The ISME Journal*, 14(11), pp.2877-2889.
- Hardwick, K.M., Bichang'a, G.B., Abteu, A.B., Awori, R.M., Cepko, L., Chebon-Bore, L.J., Darby, A., deVries, J.D., Filée, J., Fuad, M. and Gachara, G., 2020. Comprehensive transcriptome of the maize stalk borer, *Busseola fusca*, from multiple tissue types, developmental stages, and parasitoid wasp exposures. *Genome Biology and Evolution*.
- Houte, S.V., Padfield, D., Gomez, P., Lujan, A.M., Brockhurst, M.A., Paterson, S. and Buckling, A., 2020. Compost spatial heterogeneity promotes evolutionary diversification of a Bacterium. *Journal of Evolutionary Biology*.
- Suligoy, C.M., Díaz, R.E., Gehrke, A.K., Ring, N., Yebra, G., Alves, J., Gómez, M.I., Wendler, S., Fitzgerald, J.R., Tuchscher, L. and Löffler, B., 2020. Acapsular *Staphylococcus aureus* with a non-functional agr regains capsule expression after passage through the bloodstream in a bacteremia mouse model. *Scientific Reports*, 10(1), pp.1-12.
- Brettell, L.E., Schroeder, D.C. and Martin, S.J., 2020. RNAseq of Deformed Wing Virus and Other Honey Bee-Associated Viruses in Eight Insect Taxa with or without Varroa Infestation. *Viruses*, 12(11), p.1229.
- George, P.B., Coelho, K.P., Creer, S., Lebron, I., Robinson, D.A. and Jones, D.L., 2020. Decoupled richness of generalist anaerobes and sulphate-reducing bacteria is driven by pH across land uses in temperate soils. *European Journal of Soil Science*.
- Doonan, J.M., Broberg, M., Denman, S. and McDonald, J.E., 2020. Host–microbiota–insect interactions drive emergent virulence in a complex tree disease. *Proceedings of the Royal Society B*, 287(1933), p.20200956.
- Sevillano, M., Dai, Z., Calus, S., Bautista-de los Santos, Q.M., Eren, A.M., van der Wielen, P.W., Ijaz, U.Z. and Pinto, A.J., 2020. Differential prevalence and host-association of antimicrobial resistance traits in disinfected and non-disinfected drinking water systems. *Science of The Total Environment*, p.141451.

- Nair, R.R., Tibbit, C., Thompson, D., McLeod, R., Nakhuda, A., Simon, M.M., Baloh, R.H., Fisher, E.M., Isaacs, A.M. and Cunningham, T.J., 2020. Sizing, stabilising, and cloning repeat-expansions for gene targeting constructs. *Methods*.
- Weedall, G.D., Riveron, J.M., Hearn, J., Irving, H., Kamdem, C., Fouet, C., White, B.J. and Wondji, C.S., 2020. An Africa-wide genomic evolution of insecticide resistance in the malaria vector *Anopheles funestus* involves selective sweeps, copy number variations, gene conversion and transposons. *PLoS Genetics*, 16(6).
- Kelly, L.J., Plumb, W.J., Carey, D.W., Mason, M.E., Cooper, E.D., Crowther, W., Whittemore, A.T., Rossiter, S.J., Koch, J.L. and Buggs, R.J., 2020. Convergent molecular evolution among ash species resistant to the emerald ash borer. *Nature Ecology & Evolution*, pp.1-13.
- Street, C., Street, A. and Liverpool, A.S., Kinobead Profiling Reveals Reprogramming of B-cell Receptor Signaling in Response to Therapy Within Primary Chronic Lymphocytic Leukemia Cells. *bioRxiv*.
- Becher, H., Brown, M.R., Powell, G., Metherell, C., Riddiford, N.J. and Twyford, A.D., 2020 Maintenance of species differences in closely related tetraploid parasitic *Euphrasia* (Orobanchaceae) on an isolated island. *bioRxiv*.
- Abdelhamed, H., Ramachandran, R., Narayanan, L., Ozdemir, O., Cooper, A., Olivier, A.K., Karsi, A. and Lawrence, M.L., 2020. Contributions of a LysR transcriptional regulator to *Listeria monocytogenes* virulence and identification of its regulons. *Journal of Bacteriology*, 202(10).
- Orkin, J.D., Montague, M.J., Tejada-Martinez, D., de Manuel, M., del Campo, J., Di Fiore, A., Fontseré, C., Hodgson, J.A., Janiak, M.C., Kuderna, L.F. and Lizano, E., 2020. Selection and local adaptation in capuchin monkeys revealed through fluorescence-activated cell sorting of feces (fecalFACS). *bioRxiv*
- Brearley, F.Q., 2020. Sequence data describing the fungal community in a tropical quartzite soil. *Data in Brief*, p.105112.
- Ndhlovu, V., Kiran, A., Sloan, D.J., Mandala, W., Nliwasa, M., Everett, D.B., Mwapasa, M., Kontogianni, K., Kamdolozi, M., Corbett, E.L. and Caws, M.,. Understanding the diversity of DNA methylation in *Mycobacterium tuberculosis*. *bioRxiv 2020*.
- Avelar, R.A., Ortega, J.G., Tacutu, R., Tyler, E.J., Bennett, D., Binetti, P., Budovsky, A., Chatsirisupachai, K., Johnson, E., Murray, A. and Shields, S., 2020. A multidimensional systems biology analysis of cellular senescence in aging and disease. *Genome Biology*, 21, pp.1-22.
- Geoghegan, I.A., Stratford, M., Bromley, M., Archer, D.B. and Avery, S.V., 2020. Weak Acid Resistance A (WarA), a novel transcription factor required for regulation of weak-acid resistance and spore-spore heterogeneity in *Aspergillus niger*. *mSphere*, 5(1).

- Weedall, G.D., Riveron, J.M., Hearn, J., Irving, H., Kamdem, C., Fouet, C., White, B.J. and Wondji, C.S., 2020. An Africa-wide genomic evolution of insecticide resistance in the malaria vector *Anopheles funestus* involves selective sweeps, copy number variations, gene conversion and transposons. *PLoS Genetics*, 16(6), p.e1008822.
- Barrera, L.N., Evans, A., Lane, B., Brumskill, S., Oldfield, F.E., Campbell, F., Andrews, T., Lu, Z., Perez-Mancera, P.A., Liloglou, T. and Ashworth, M., 2020. Fibroblasts from distinct pancreatic pathologies exhibit disease-specific properties. *Cancer Research*.
- Brunsdon, H. and Isaacs, H.V., 2020. A comparative analysis of fibroblast growth factor receptor signalling during *Xenopus* development. *Biology of the Cell*.
- Richards-Rios, P., Fothergill, J., Bernardeau, M. and Wigley, P., 2020. Development of the Ileal Microbiota in Three Broiler Breeds. *Frontiers in veterinary science*, 7, p.17.
- Ferrari, R.C., Bittencourt, P.P., Rodrigues, M.A., Moreno-Villena, J.J., Alves, F.R., Gastaldi, V.D., Boxall, S.F., Dever, L.V., Demarco, D., Andrade, S.C. and Edwards, E.J., 2020. C4 and crassulacean acid metabolism within a single leaf: deciphering key components behind a rare photosynthetic adaptation. *New Phytologist*, 225(4), pp.1699-1714.
- Dey, N.S., Senarathna, S., Somaratne, V., Madarasinghe, N., Seneviratne, B., Reis, L.C., Moulik, S., Walrad, P., Chatterjee, M., Goto, H. and Wickremasinghe, R., 2020. Reduced expression of PD-L1 and IDO1 characterises early response to antimonial therapy in cutaneous leishmaniasis patients. *bioRxiv*.
- Llewellyn, C.A., Airs, R.L., Farnham, G. and Greig, C., 2020. Synthesis, Regulation and Degradation of Carotenoids Under Low Level UV-B Radiation in the Filamentous Cyanobacterium *Chlorogloeopsis fritschii* PCC 6912. *Frontiers in microbiology*, 11, p.163
- Kamgang, B., Wilson-Bahun, T.A., Yougang, A.P., Lenga, A. and Wondji, C.S., 2020. Contrasting resistance patterns to type I and II pyrethroids in two major arbovirus vectors *Aedes aegypti* and *Aedes albopictus* in the Republic of the Congo, Central Africa. *Infectious Diseases of Poverty*, 9(1), pp.1-10.
- Wilding, C.S., Fletcher, N., Smith, E.K., Prentis, P., Weedall, G.D. and Stewart, Z., 2020. The genome of the sea anemone *Actinia equina* (L.): Meiotic toolkit genes and the question of sexual reproduction. *Marine Genomics*, p.100753.
- Cazares, A., Moore, M.P., Hall, J.P., Wright, L.L., Grimes, M., Emond-Rhéault, J.G., Pongchaikul, P., Santanirand, P., Levesque, R.C., Fothergill, J.L. and Winstanley, C., 2020. A megaplasmid family driving dissemination of multidrug resistance in *Pseudomonas*. *Nature Communications*, 11(1), pp.1-13.

- Chevallereau, A., Meaden, S., Fradet, O., Landsberger, M., Maestri, A., Biswas, A., Gandon, S., van Houte, S. and Westra, E.R., 2020. Exploitation of the cooperative behaviors of anti-CRISPR phages. *Cell host & microbe*, 27(2), pp.189-198.
- Dai, Z., Sevillano-Rivera, M.C., Calus, S.T., Bautista-de los Santos, Q.M., Eren, A.M., van der Wielen, P.W., Ijaz, U.Z. and Pinto, A.J., 2020. Disinfection exhibits systematic impacts on the drinking water microbiome. *Microbiome*, 8(1), pp.1-19.
- Czaja, W., Bensasson, D., Ahn, H.W., Garfinkel, D.J. and Bergman, C.M., 2020. Evolution of Ty1 copy number control in yeast by horizontal transfer and recombination. *PLoS Genetics*, 16(2), p.e1008632.
- Richards-Rios, P., Leeming, G., Fothergill, J., Bernardeau, M. and Wigley, P., 2020. Topical application of adult cecal contents to eggs transplants spore-forming microbiota but not other members of the microbiota to chicks. *Applied and Environmental Microbiology*, 86(5).
- McAteer, P.G., Trego, A.C., Thorn, C., Mahony, T., Abram, F. and O'Flaherty, V., 2020. Reactor configuration influences microbial community structure during high-rate, low-temperature anaerobic treatment of dairy wastewater. *Bioresource Technology*, p.123221.
- Macey, M.C., Pratscher, J., Crombie, A.T. and Murrell, J.C., 2020. Impact of plants on the diversity and activity of methylotrophs in soil. *Microbiome*, 8(1), pp.1-17.
- Arrowsmith, S., Fang, Y. and Sharp, A., 2020. Comparison of the myometrial transcriptome from singleton and twin pregnancies by RNA-Seq. *Plos one*, 15(1), p.e0227882.
- Geoghegan, I.A., Stratford, M., Bromley, M., Archer, D.B. and Avery, S.V., 2020. Weak Acid Resistance A (WarA), a novel transcription factor required for regulation of weak-acid resistance and spore-spore heterogeneity in Aspergillus niger. *mSphere*, 5(1).
- Martinez, D.T., de Magalhaes, J.P. and Opazo, J.C., 2020. Positive selection and fast turnover rate in tumor suppressor genes reveal how cetaceans resist cancer. *bioRxiv*.
- Parker, M.T., Knop, K., Sherwood, A.V., Schurch, N.J., Mackinnon, K., Gould, P.D., Hall, A.J., Barton, G.J. and Simpson, G.G., 2020. Nanopore direct RNA sequencing maps the complexity of Arabidopsis mRNA processing and m6A modification. *eLife*, 9.
- Monnin, D., Jackson, R., Kiers, E.T., Bunker, M., Ellers, J. and Henry, L.M., 2020. Parallel evolution in the integration of a co-obligate aphid symbiosis. *bioRxiv*