Benjamin Jean-Marie Tremblay

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Research Interests

I study how non-coding transcription, chromatin accessibility and transcription-factor regulatory networks shape gene expression during plant developmental transitions and responses to environmental cues. My work integrates genome-wide profiling (ATAC-seq, csRNA-seq, single-cell multi-omics) with targeted molecular genetics and the development of performant open-source software. As an independent researcher I aim to dissect the cis-regulatory logic that governs cell-state transitions in plants, leveraging scalable computational tools I build and release to the community.

Education

Centre for Research in Agricultural Genomics / Autonomous University of Barcelona **Spain**
PhD, Plant Biology and Biotechnology (Cum Laude) *2020–2024*
Supervisor: Dr. Julia I. Qüesta.
Thesis: *Non-coding regulation of transcription during plant development.*
International Doctorate Mention (doctoral work performed partly outside Spain, with external expert endorsement).

University of Waterloo **Canada**
MSc, Biology *2016–2019*
Supervisor: Prof. Barbara A. Moffatt.
Thesis: *Investigating the impact of 5'-methylthioadenosine accumulation in* Arabidopsis thaliana.

University of Waterloo **Canada**
BSc, Honours Biology *2012–2016*
Undergraduate thesis supervisor: Prof. Barbara A. Moffatt.
Thesis: *Altered 5'-methylthioadenosine metabolism affects lipid homeostasis and hormone regulation in* Arabidopsis.

Research Positions

Nobori group, The Sainsbury Laboratory **Norwich, UK**
Postdoctoral Scientist *Aug 2024–present*
Mentor: Dr. Tatsuya Nobori. Single-cell multi-omic profiling of active regulatory elements during plant immunity in *Arabidopsis*.

Team ChromD (Moussa Benhamed), Institute of Plant Sciences Paris-Saclay **Gif-sur-Yvette, France**
International PhD Secondment *Feb–May 2024*
Host: Dr. David Latrasse. Collaborative work on plant chromatin biology and 3D genome regulation.

Epigenetics and Plant Development Group, CRAG **Barcelona, Spain**
PhD Student *Sep 2020–Jul 2024*
Supervisor: Dr. Julia I. Qüesta.

Epigenetics and Plant Development Group, CRAG **Barcelona, Spain**
Research Assistant *Feb–Aug 2020*
Supervisor: Dr. Julia I. Qüesta.

Doxey Lab, University of Waterloo **Canada**
Bioinformatics Research Assistant *Jan 2019–Jun 2020*
Supervisor: Prof. Andrew C. Doxey.

Moffatt Lab, University of Waterloo **Canada**
MSc Student *Jan 2016–Jan 2019*

Hell Lab, Heidelberg University — **Germany**
Ontario/Baden-Württemberg Summer Research Student — *May–Aug 2016*
Supervisor: Dr. Markus Wirtz.

Moffatt Lab, University of Waterloo — **Canada**
Honours Thesis Student — *Jan–Dec 2015*

Fellowships, Scholarships and Awards

BBSRC Early Independence Fellowship
shortlisted lead applicant, invited to the full stage — *2026*

International Doctorate Mention — **Spain**
Autonomous University of Barcelona — *2024*
For doctoral work performed partly outside Spain, with two supporting letters from external experts.

FPI Doctoral Fellowship (EUR 98,250) — **Spain**
Ministry of Economy, Trade and Enterprise — *2020–2024*
Four-year competitive PhD grant under the National Programme for the Promotion of Talent and its Employability.

Dean of Science Award — **Canada**
University of Waterloo — *2019*
Awarded annually to one student per academic unit in the Faculty of Science for outstanding performance and creative research in the MSc programme.

Summer Research Scholarship ($3,500)
Ontario/Baden-Württemberg Summer Research Program — *2016*
Competitive research exchange scholarship for students in Ontario, Canada and Baden-Württemberg, Germany.

President's Entrance Scholarship ($1,000) — **Canada**
University of Waterloo — *2012*

Training

EMBO Lab Leadership for Postdocs — **Norwich, UK**
John Innes Centre — *2025*

Non-coding Genome (11th edition) — **Paris, France**
Institut Curie — *2022*

Network Analysis and Modeling — **Barcelona, Spain**
Centre for Research in Agricultural Genomics — *2022*

Publications

21 peer-reviewed publications (10 first or co-first author, 3 corresponding), 1 book chapter, 1 preprint. Full list on Google Scholar. Author symbols: * co-first author; # co-corresponding author; + corresponding author.

First-author peer-reviewed research articles

1. Ormancey, M.*, **Tremblay, B.J.M.***, Cheng, Y.*, Praat, M., Antoniou-Kourounioti, R.L., Krumbach, J., van Zanten, M., and Qüesta, J.I. (2026). Autumn–winter progression triggers distinct transcriptional programmes in *Arabidopsis thaliana*. *Genome Biology*. doi:10.1186/s13059-026-04289-3
2. **Tremblay, B.J.M.+**, Adeel, S.A., Saechao, M., Dong, Y., Andrianasolo, E., Steele, J.M., Traa, A., Yogadasan, N., Waduwara-Jayabahu, I., Katzenback, B.A., Hell, R., Wirtz, M., and Moffatt, B.A. (2026). Methylthioadenosine-driven rewiring of sulfur assimilation lowers the methyl index and fertility in *Arabidopsis*. *Journal of Experimental Botany* 77, 6209–6223.
3. **Tremblay, B.J.M.**, Santini, C.P., Cheng, Y., Zhang, X., Rosa, S., and Qüesta, J.I. (2024). Interplay between coding and non-coding regulation drives the *Arabidopsis* seed-to-seedling transition. *Nature Communications* 15, 1724.
4. **Tremblay, B.J.M.**, Lobb, B., and Doxey, A.C. (2021). PhyloCorrelate: inferring bacterial gene-gene functional associations through large-scale phylogenetic profiling. *Bioinformatics* 37, 17–22.
5. Mansfield, M.J.*, **Tremblay, B.J.M.***, Zeng, J., Wei, X., Hodgkins, H., Worley, J., Bry, L., Dong, M., and Doxey,

A.C. (2020). Phylogenomics of 8,839 *Clostridioides difficile* genomes reveals recombination-driven evolution and diversification of toxin A and B. *PLOS Pathogens* 16, e1009181.

6. Banerjee, A.*, Doxey, A.C.*, **Tremblay, B.J.M.***, Mansfield, M.J.*, MacKay, K., Subudhi, S., Hirota, J.A., Miller, M.S., McArthur, A.G., Mubareka, S., and Mossman, K. (2020). Predicting the recombination potential of severe acute respiratory syndrome coronavirus 2 and Middle East respiratory syndrome coronavirus. *Journal of General Virology* 101, 1251–1260.

Preprints

7. Cameron, E.S., **Tremblay, B.J.M.**, Yahr, R., Blaxter, M.L., and Finn, R.D. (2026). Transposable element diversification and the evolution of Peltigerales lichen symbionts. *bioRxiv*. doi:10.64898/2026.02.14.705750

Software papers

8. **Tremblay, B.J.M.#**, and Qüesta, J.I.# (2024). quaqc: efficient and quick ATAC-seq quality control and filtering. *Bioinformatics* 40, btae649.
9. **Tremblay, B.J.M.+** (2024). universalmotif: an R package for biological motif analysis. *Journal of Open Source Software* 9, 7012.

Co-author peer-reviewed research articles

10. Cheng, Y., **Tremblay, B.J.M.**, Balanzá, V., Larran, A.S., and Qüesta, J.I. (2025). The transcriptional regulator VAL1 promotes *Arabidopsis* flowering by repressing the organ boundary genes BOP1 and BOP2. *Plant Physiology* 198, kiaf160.
11. Hodgins, H.P., Chen, P., Lobb, B., Wei, X., **Tremblay, B.J.M.**, Mansfield, M.J., Lee, V.C.Y., Lee, P., Coffin, J., Duggan, A.T., Dolphin, A.E., Renaud, G., Dong, M., and Doxey, A.C. (2023). Ancient *Clostridium* DNA and variants of tetanus neurotoxins associated with human archaeological remains. *Nature Communications* 14, 5475.
12. Tian, S., Xiong, X., Zeng, J., Wang, S., **Tremblay, B.J.M.**, Chen, P., Chen, B., Liu, M., Chen, P., Sheng, K., Zeve, D., Qi, W., Breault, D.T., Rodríguez, C., Gerhard, R., Jin, R., Doxey, A.C., and Dong, M. (2022). Identification of TFPI as a receptor reveals recombination-driven receptor switching in *Clostridioides difficile* toxin B variants. *Nature Communications* 13, 6786.
13. Wentz, T.G., **Tremblay, B.J.M.**, Bradshaw, M., Doxey, A.C., Sharma, S.K., Sauer, J.D., and Pellett, S. (2022). Endogenous CRISPR-Cas systems in group I *Clostridium botulinum* and *Clostridium sporogenes* do not directly target the botulinum neurotoxin gene cluster. *Frontiers in Microbiology* 12, 787726.
14. Lobb, B., **Tremblay, B.J.M.**, Moreno-Hagelsieb, G., and Doxey, A.C. (2021). PathFams: statistical detection of pathogen-associated protein domains. *BMC Genomics* 22, 663.
15. Cameron, E.S., Schmidt, P.J., **Tremblay, B.J.M.**, Emelko, M.B., and Müller, K.M. (2021). Enhancing diversity analysis by repeatedly rarefying next generation sequencing data describing microbial communities. *Scientific Reports* 11, 22302.
16. Banerjee, A., El-Sayes, N., Budylowski, P., Jacob, R.A., Richard, D., Maan, H., Aguiar, J.A., Demian, W.L., Baid, K., D'Agostino, M.R., Ang, J.C., Murdza, T., **Tremblay, B.J.M.**, Afkhami, S., Karimzadeh, M., Irving, A.T., Yip, L., Ostrowski, M., Hirota, J.A., Kozak, R., Capellini, T.D., Miller, M.S., Wang, B., Mubareka, S., McGeer, A.J., McArthur, A.G., Doxey, A.C., and Mossman, K. (2021). Experimental and natural evidence of SARS-CoV-2-infection-induced activation of type I interferon responses. *iScience* 24, 102477.
17. Fantauzzi, M.F., Aguiar, J.A., **Tremblay, B.J.M.**, Yanagihara, T., Chandiramohan, A., Revill, S., Hyung, M.R., Carlsten, C., Ask, K., Stämpfli, M., Doxey, A.C., and Hirota, J.A. (2020). Expression of endocannabinoid system components in human airway epithelial cells: impact of sex and chronic respiratory disease status. *ERJ Open Research* 6, 00128-2020.
18. Cao, Q., Aguiar, J.A., **Tremblay, B.J.M.**, Abbas, N., Tiessen, N., Makhdami, N., Revill, S., Cox, G., Ask, K., Doxey, A.C., and Hirota, J.A. (2020). ABCF1 regulates dsDNA-induced immune responses in human airway epithelial cells. *Frontiers in Cellular and Infection Microbiology* 10, 487.
19. Aguiar, J.A., **Tremblay, B.J.M.**, Mansfield, M.J., Woody, O., Lobb, B., Banerjee, A., Chandiramohan, A., Tiessen, N., Dvorkin-Gheva, A., Revill, S., Miller, M.S., Carlsten, C., Organ, L., Joseph, C., John, A., Jenkins, G., Mossman, K., Ask, K., Doxey, A.C., and Hirota, J.A. (2020). Gene expression and in situ protein profiling of candidate SARS-CoV-2 receptors in human airway epithelial cells and lung tissue. *European Respiratory Journal* 56, 2001123.
20. Lobb, B., **Tremblay, B.J.M.**, Moreno-Hagelsieb, G., and Doxey, A.C. (2020). An assessment of genome annotation

coverage across the bacterial tree of life. *Microbial Genomics* 6, e000341.

Reviews and book chapters

21. **Tremblay, B.J.M.**, and Qüesta, J.I. (2026). Identification of accessible transcription factor binding sites during the seed-to-seedling transition. In: Franco-Zorrilla, J.M., Martín-Pizarro, C. (eds) *Plant Transcription Factors. Methods in Molecular Biology* 2985, 51–62. Humana, New York, NY.
22. **Tremblay, B.J.M.**, and Qüesta, J.I. (2025). Non-coding and epigenetic mechanisms in the regulation of seed germination in *Arabidopsis thaliana*. *Journal of Experimental Botany* 76, 2455–2467.
23. **Tremblay, B.J.M.**, and Qüesta, J.I. (2023). Mechanisms of epigenetic regulation of transcription by lncRNAs in plants. *IUBMB Life* 75, 427–439.

Editorial features

- **Tremblay, B.J.M.** (2026). A link to the past: the *Bangia* genome connects an ancient body plan to modern stress biology. *Plant Physiology*, kiag830.
- **Tremblay, B.J.M.** (2026). Two genes, one switch: a bidirectional promoter strategy for inducible plant immunity. *Plant Physiology* 201, kiag243.
- **Tremblay, B.J.M.** (2026). Position matters: light repatterns m6A to tune anthocyanin accumulation in roses. *Plant Physiology* 200, kiag125.

Software Tools and Databases

- **universalmotif**: R/C++ package for the analysis and manipulation of biological sequence motifs, with Rust and Python versions. Over 150,000 downloads from Bioconductor and Bioconda since 2018. Sole maintainer. (Tremblay, 2024) https://bioconductor.org/packages/universalmotif
- **quaqc**: fast quality control and filtering of ATAC-seq data, written in C with scalability in mind; companion R package **quaqcr** on CRAN. (Tremblay# & Qüesta#, 2024) https://github.com/bjmt/quaqc
- **csRNAseq_pipeline**: Snakemake pipeline (Bash/Python/R) for capped-small RNA-seq data, from raw FASTQ files to analysed transcription start sites. (Nobori Lab) https://github.com/noborilab/csRNAseq_pipeline
- **bfqutils**: high-performance C toolkit for trimming, merging and analysis of FASTQ files. (Nobori Lab) https://github.com/noborilab/bfqutils
- **tssUtils**: R package for the analysis of TSS sequencing data. (Nobori Lab) https://github.com/noborilab/tssUtils
- **bam2td**: builds HOMER tag directories directly from SAM, BAM or CRAM files (C). (Nobori Lab) https://github.com/noborilab/bam2td
- **TAIR12 blacklist**: problematic high-signal regions of the TAIR12 *Arabidopsis* assembly for filtering ATAC-seq and ChIP-seq data. (Tremblay & Nobori, 2026) doi:10.5281/zenodo.20084760
- **yamtk**: high-performance C toolkit for genome-scale transcription factor binding site scanning and enrichment. https://github.com/bjmt/yamtk
- **bwtk**: C toolkit for converting, merging, subsetting and transforming bigWig and bedGraph files. https://github.com/bjmt/bwtk
- **msaviz**: R package for visualising large multiple sequence alignments. https://github.com/bjmt/msaviz
- **PhyloCorrelate** and **phylocorrpkg**: functional predictions from phylogenetically co-occurring gene and protein families, as a web database and a stand-alone R package. (Tremblay et al., 2021) https://phylocorrelate.uwaterloo.ca
- **DiffBase**: online database of *C. difficile* toxins. (Mansfield*, Tremblay* et al., 2020) https://diffbase.uwaterloo.ca
- **PathFams**: online database of pathogen-association predictions for protein families. (Lobb et al., 2021) https://pathfams.uwaterloo.ca
- **mirlyn** (co-author): R package implementing amplicon library size normalisation strategies for diversity analysis. (Cameron et al., 2021) https://github.com/escamero/mirlyn

Invited Talks and Oral Presentations

- **Tremblay, B.J.M.**, Pai, H., and Nobori, T. (2026). Resolving the cell state-specific regulatory logic of plant immunity with single-nucleus multiome profiling. Norwich single-cell and spatial symposium, Earlham Institute, Norwich, UK.
- **Tremblay, B.J.M.**, Pai, H., and Nobori, T. (2026). The regulatory dynamics of pattern-triggered immunity at single-cell resolution. TSL internal seminar, The Sainsbury Laboratory, Norwich, UK.
- **Tremblay, B.J.M.**, Pai, H., Nobori, T., He, X., Latrasse, D., Benhamed, M., and Qüesta, J.I. (2026). Identification of *Arabidopsis* transcriptional enhancers during development. EpiPlant2026, Nantes Université, Nantes, France.
- **Tremblay, B.J.M.**, Santini, C.P., Cheng, Y., Zhang, X., Rosa, S., and Qüesta, J.I. (2024). Control of germination by chromatin accessibility and non-coding transcription. 8th European Workshop on Plant Chromatin, Barcelona, Spain.
- **Tremblay, B.J.M.**, Santini, C.P., Cheng, Y., Zhang, X., Rosa, S., and Qüesta, J.I. (2023). The hidden noncoding transcriptome of germinating seeds in *Arabidopsis*. CRAG internal seminar, Barcelona, Spain.
- **Tremblay, B.J.M.**, and Qüesta, J.I. (2023). Genome-wide DNA accessibility dynamics during germination. CRAG Retreat: Plant Development and Signal Transduction, Barcelona, Spain.
- **Tremblay, B.J.M.**, and Qüesta, J.I. (2022). The regulatory landscape of transcription during the seed-to-seedling transition. EpiPlant2022, Banyuls-sur-Mer, France.
- **Tremblay, B.J.M.**, and Qüesta, J.I. (2022). Bidirectional promoter activity during early *Arabidopsis* development. CRAG Retreat: Plant Development and Signal Transduction, Barcelona, Spain.
- **Tremblay, B.J.M.** (2021). Large-scale analyses of biological sequence motifs with the universalmotif package. BioC2021: Where Software and Biology Connect (virtual).
- **Tremblay, B.J.M.**, and Qüesta, J.I. (2020). Investigating the role of lncRNAs in the seed-to-seedling transition. CRAG Retreat: Plant Development and Signal Transduction, Barcelona, Spain.
- **Tremblay, B.J.M.**, Wirtz, M., Hell, R., and Moffatt, B.A. (2018). Effects of transgenerational spermidine-restoration of fertility in 5'-methylthioadenosine nucleosidase deficient plants. Canadian Society of Plant Biologists Eastern Regional Meeting, London, Canada.
- **Tremblay, B.J.M.**, Wirtz, M., Hell, R., and Moffatt, B.A. (2018). Elucidating the impact of methylthioadenosine nucleosidase deficiency on the transcriptome and metabolite profile in *Arabidopsis*. University of Waterloo Biology Graduate Symposium, Waterloo, Canada.
- **Tremblay, B.J.M.**, Steele, J., Wirtz, M., Hell, R., and Moffatt, B.A. (2018). Determining the impact of methylthioadenosine nucleosidase deficiency in *Arabidopsis*. University of Waterloo Cell and Molecular Research interest group, Waterloo, Canada.
- **Tremblay, B.J.M.**, Waduwara-Jayabahu, I., Sakakibara, H., Saechao, M., and Moffatt, B.A. (2015). Altered MTA metabolism affects lipid homeostasis and vascular development. Canadian Society of Plant Biologists Eastern Regional Meeting, Toronto, Canada.

Poster Presentations

- **Tremblay, B.J.M.**, Pai, H., and Nobori, T. (2026). Cell-state-specific cis-regulatory logic of pattern-triggered immunity with csRNA-seq and snMultiome. Plant Biology, Ottawa, Canada. doi:10.5281/zenodo.21476601
- **Tremblay, B.J.M.**, Pai, H., and Nobori, T. (2025). Profiling active regulatory elements during immunity in *Arabidopsis*. 35th International Conference on Arabidopsis Research, Ghent, Belgium. doi:10.5281/zenodo.21476383
- **Tremblay, B.J.M.**, Santini, C.P., Cheng, Y., Zhang, X., Rosa, S., and Qüesta, J.I. (2023). Genome-wide non-coding regulation in the *Arabidopsis* seed-to-seedling transition. Symposium "Signaling through Chromatin: From Molecules to Ecosystems", Grenoble, France.
- **Tremblay, B.J.M.**, and Qüesta, J.I. (2023). Genome-wide non-coding transcription dynamics during the seed-to-seedling transition. At the Forefront of Plant Research Conference, Barcelona, Spain.
- **Tremblay, B.J.M.**, and Qüesta, J.I. (2022). The regulatory landscape of transcription during the seed-to-seedling transition. Non-Coding Genome course, 11th edition, Institut Curie, Paris, France.
- **Tremblay, B.J.M.**, Saechao, M., Steele, J.M., Adeel, S.A., Dong, Y., Wirtz, M., Hell, R., and Moffatt, B.A. (2019). Methylthioadenosine accumulation in *Arabidopsis* leads to reprogramming of sulfur assimilation. Mechanisms in Plant Development Conference, Olean, New York, USA.

- **Tremblay, B.J.M.**, Saechao, M., Steele, J.M., Wirtz, M., Dong, Y., Hell, R., and Moffatt, B.A. (2018). Multi-generational spermidine restoration of methylthioadenosine nucleosidase deficiency-induced fertility in *Arabidopsis*. 29th International Conference on Arabidopsis Research, Turku, Finland.
- **Tremblay, B.J.M.**, Saechao, M., Waduwara-Jayabahu, I., Sakakibara, H., and Moffatt, B.A. (2016). Reduced MTA metabolism affects thermospermine regulation of auxin and lipid pathways. 22nd International Conference on Plant Growth Substances, Toronto, Canada.

Mentoring and Student Supervision

Revocatus Byanyuma-Bahitwa — **Nobori group, The Sainsbury Laboratory, UK**
PhD rotation student mentor — *2026*

Vidyashree Shivakumaraswamy — **Nobori group, The Sainsbury Laboratory, UK**
Predoctoral intern mentor — *2024–2025*

Cristina P. Santini — **Qüesta Lab, CRAG, Spain**
MSc thesis co-supervisor — *2022–2023*
Thesis: *Characterization of antisense long non-coding RNAs underlying* Arabidopsis *germination and early seedling development.*

Saeer Adeel — **Moffatt Lab, University of Waterloo, Canada**
Honours thesis mentor — *2018–2019*

John Steele — **Moffatt Lab, University of Waterloo, Canada**
Honours thesis mentor — *2016–2017*

Teaching Experience

Lecturer (graduate level) — **Spain**
Autonomous University of Barcelona — *Jan 2023*
MO58139: Molecular basis of plant development and responses to the environment (Week 2: Embryo development, germination and dormancy; Week 6: Epigenetics in development).

Laboratory Teaching Assistant (undergraduate level) — **Canada**
University of Waterloo — *2014–2018*
BIOL 120: Introduction to plant structure and function; BIOL 130L: Cell biology; BIOL 323: Plant physiology; BIOL 325: Flowering plants; BIOL 428: Plant molecular genetics.

Tutorial Teaching Assistant (undergraduate level) — **Canada**
University of Waterloo — *Sep–Dec 2013*
BIOL 309: Molecular biology techniques.

Academic Service and Outreach

Assistant Features Editor
Plant Physiology — *2026–2028*

American Society of Plant Biologists (ASPB)
Member — *2026–present*

British Society for Plant Pathology (BSPP)
Member — *2026–present*

Ad hoc peer reviewer
ongoing
The Plant Cell, *BMC Bioinformatics*, *BMC Genomics*, *BMC Plant Biology*, *Genome Biology*, *Plant Direct*, *Bioinformatics Advances*, *PeerJ*.

European Researchers' Night (volunteer) — **Barcelona, Spain**
CosmoCaixa — *Sep 2021*
Public engagement with elementary school-age children on why we study the model plant *Arabidopsis thaliana*.

Biology Graduate Symposium (judge) — **Canada**
University of Waterloo — *Apr 2019*

Science Open House (volunteer) — **Canada**
University of Waterloo — *2015–2017*
Guided elementary school-age children through plant-themed teaching stations.