

Petri Pölönen, Ph.D

Email: petri.polonen@stjude.org

Address: 262 Danny Thomas Place, Mail Stop 342, USA, Memphis, TN 38105

Twitter: <https://twitter.com/PolonenPetri>

LinkedIn: <https://fi.linkedin.com/in/PetriPolonen>

Github: <https://github.com/ppolonen>

ORCID: <https://orcid.org/0000-0001-6128-9985>

EDUCATION

Ph.D	Doctoral Program for Molecular Medicine, University of Eastern Finland Dissertation: Identification of Targetable Genes across Hematological Malignancies	Mar 2020
M.Sc	Bioinformatics and Biochemistry, University of Eastern Finland Master's thesis: Investigating Nrf2 function in disease using enrichment analysis and top-down systems biology	Aug 2013
ERASMUS B.Sc	Master in Integrated Systems Biology, University of Luxembourg Biosciences, University of Eastern Finland	2011-2012 May 2011

RESEARCH INTERESTS

- Expert in bioinformatics and computational systems biology, specializing in hematology, cancer genomics, immunogenomics, and pan-cancer analysis.
- My long-term vision is to leverage patient samples to systematically profile genomic and epigenomic alterations in leukemia, advancing our understanding of disease biology and facilitating more precise disease classification and risk stratification.
- First author in six publications in high-impact journals.
- Author in 33 publications, H-index 20.

RESEARCH EXPERIENCE

Post-Doctoral Fellow

St. Jude Children's Research Hospital

10/2020-present

Mentor: Charles G. Mullighan, David T. Teachey

- Analysis of over 1300 WGS/WES/WTs T-ALL patient samples published in *Nature*¹ and review in *Blood*²⁶.
- Leading role: managing raw data, data statistical analysis and interpretation. Coordinated all collaborative analysis efforts, created figures, and wrote the manuscript.
- Used long-read sequencing, H3K27ac HiChIP, ATACseq, single-cell RNA/ATACseq on leukemia patient samples to investigate functional effects of non-coding alterations, such as enhancer hijacking by somatic alterations.
- Presented award-winning research at the European Hematology Association (EHA), American Society of Hematology (ASH), and Children's Oncology Group (COG) congresses.
- Authored several collaborative research papers on leukemia genomics^{7,10-18}.
- Received training in long-read sequencing analysis and presented at the "Long-Read Sequencing Workshop 2024" at the Jackson Laboratory.
- Participated in workshops: mentoring, grant writing, communication, research ethics.

Post-Doctoral Fellow

A.I. Virtanen Institute for Molecular Sciences

May-Sep 2020

Mentor: Anna-Liisa Levonen

- Used multi-omics pan-cancer analysis approaches to investigate the *NFE2L2/NRF2* transcription factor. This work resulted in two first/co-first author publications^{5,6}.

- Supervised Ph.D student Jouni Härkönen, teaching multi-omics and immunogenomic analysis. I'm currently his Ph.D advisor.

Doctoral Student

2013-2020

University of Eastern Finland

Mentor: Merja Heinäniemi

- Analyzed transcriptomic data from over 10000 patients from 36 hematological malignancies. This work also included analysis of 2000 samples with multi-omic data.
- This work resulted in three high impact co-first author publications²⁻⁴ and several collaborative publications¹⁹⁻²⁹
- Presented my work at EHA and ASH congress, Recomb and several national symposiums.
- Young Researcher Award on Ph.D thesis work

Visiting Doctoral Student, City of Hope, Duarte, California, USA

2018

Funder: Saastamoinen Foundation, 3-month visit

Mentor: Markus Müschen

- Collaboration with the Müschen lab, this work resulted in collaborative hi-impact publication¹⁹

Visiting Doctoral Student, Karolinska Institutet, Stockholm, Sweden

2016

Funder: ERASMUS+, 2-month visit

Mentor: Olle Sangfelt

- Collaboration with the Sangfelt lab, this work resulted in collaborative hi-impact publication²¹

Visiting Doctoral Student, Institute for Systems Biology, Seattle, USA

2014

Funder: Doctoral Program for Molecular Medicine, 1-month visit

Mentor: Ilya Shmulevich

- Learning pan cancer multiomic analysis using TCGA data. This visit formed the backbone for my analysis of TCGA data and contributed to several publications^{5,6}.

Project scientist

2013-2014

University of Eastern Finland

EU funded project - BIOS Development of Bioinformatics expertise and education

Mentor: Jussi Paananen

- Part of a team of bioinformatics professionals dedicated to advancing bioinformatics at the University.
- Primary responsibilities included teaching and organizing bioinformatics courses.

TEACHING AND MENTORING EXPERIENCE

At The University of Eastern Finland

Doctoral thesis mentor, Jouni Härkönen

2021-present

B.Sc thesis mentor, Laura Mäenpää

2016

▪ Current position: Manager, Bioinformatics Engineering at Blueprint Genetics

2015

M.Sc thesis mentor, Krista Kokki

▪ Current position: Postdoc at the Institute for Molecular Medicine Finland

At University of Eastern Finland

Assistant Teacher: Genome Wide Bioinformatics, Deep sequencing data analysis I&II

2013-2020

- Held two lectures on cancer genomics and gene set enrichment analysis and organized two practical workshops and several tutoring sessions annually.

At The University of Luxembourg

Assistant Teacher: Top-down systems biology

2016

- Master students were working on their bioinformatics projects as teams.

- Provided guidance and helped student download, process and analyze data for their projects.

Other workshops, Organizer, Assistant Teacher:

NordBioMedNet International summer school 2014-2015

- Organizer of a bioinformatics challenge in which students spent an afternoon working in teams to integrate multi-omics data in problem-based learning settings.

Leukemia workshop, Karolinska Institutet 2016

- 80 participants, Research Staff

EU-funded GEF4 scientific symposium at University of Eastern Finland 2014

- 200 participants, Research Staff, PhD students, master students

FELLOWSHIPS, AWARDS AND HONORS

Computational Biology Training in Hematology award (CBTH) 2023

Issued by EHA/EBI/EMBL

- Participated in a rigorous year-long mentoring program designed to build successful careers in hematology research, which included workshops in Cambridge, UK, and at the EHA Congress.
- Funding value 12500 EUR

Best of ASH talk, ASH2022 Congress 2022

Issued by American Society for Hematology

Pölönen P, Elsayed A, Di Giacomo D, et al. Comprehensive Genome Characterization of Childhood T-ALL Links Oncogene Activation Mechanism and Subtypes to Prognosis. Blood. 2022;140(Supplement 1):1727-1729.

Best Abstract Award, Presidential Symposium talk, EHA2022 Congress 2022

Issued by European Hematology Association

Pölönen P, Elsayed A, Montefiori L, et al. S102: Comprehensive Genome Characterization Reveals New Subtypes and Mechanisms of Oncogene Deregulation In Childhood T-ALL. HemaSphere. 2022;6.

Top3 Talk at the 9th Annual Postdoctoral Symposium 2022

Issued by St. Jude Comprehensive Cancer Center

Young Researcher Award on Ph.D thesis work 2020

Issued by University of Eastern Finland

Best Talk Award, Doctoral Symposium 2017, 2015

Issued by Doctoral Program for Molecular Medicine, University of Eastern Finland

RESEARCH GRANTS & FUNDING

Young investigator award; 180000\$ 2025-2028

Funder: Alex Lemonade Stand

Personal grant; 60000€ 2015-2017

Funder: Doctoral Program for Molecular Medicine

Personal grant; 5000€ 2018

Funder: Paavo Koistinen foundation

Personal grant; 6000€ 2017

Funder: Väre foundation

PROFESSIONAL AFFILIATIONS

American Association for Cancer Research	2025-present
American Society for Hematology	2015-present
European Hematology Association	2015-present

PROFESSIONAL SERVICE AND MEDIA

Invited speaker EHA, European Hematology Association	2025
Invited lecture National ALL symposium for hematologists and pediatricians, Helsinki, Finland	2024
Reviewer (8 papers): Blood (1) Leukemia (5) Cancer gene therapy (1) Cell Reports Medicine (1)	2021-
Media: EHA: Genome characterization of T-ALL patients (VJHemOnc)	2022

PUBLICATIONS

Online: [Google Scholar - Citations](#)

First author (6):

1. Pölönen, P., Di Giacomo, D., Seffernick, A. E., Elsayed, A., Kimura, S., Benini, F., Montefiori, L. E., Wood, B. L., Xu, J., Chen, C., Cheng, Z., Newman, H., Myers, J., Iacobucci, I., Li, E., Sussman, J., Hedges, D., Hui, Y., Diorio, C., Uppuluri, L., Frank, D., Fan, Y., Chang, Y., Meshinchi, S., Ries, R., Shraim, R., Li, A., Bernt, K. M., Devidas, M., Winter, S. S., Dunsmore, K. P., Inaba, H., Carroll, W. L., Ramirez, N. C., Phillips, A. H., Kriwacki, R. W., Yang, J. J., Vincent, T. L., Zhao, Y., Ghate, P. S., Wang, J., Reilly, C., Zhou, X., Sanders, M. A., Takita, J., Kato, M., Takasugi, N., Chang, B. H., Press, R. D., Loh, M., Rampersaud, E., Raetz, E., Hunger, S. P., Tan, K., Chang, T.-C., Wu, G., Pounds, S. B., Mullighan, C. G. & Teachey, D. T. The genomic basis of childhood T-lineage acute lymphoblastic leukaemia. *Nature* (2024). <https://doi.org/10.1038/s41586-024-07807-0> (IF, 64.8)
2. Dufva, O.*, Pölönen, P.*, Brück, O., Keränen, M. A. I., Klievink, J., Mehtonen, J., Huuhtanen, J., Kumar, A., Malani, D., Siitonen, S., Kankainen, M., Ghimire, B., Lahtela, J., Mattila, P., Vähä-Koskela, M., Wennerberg, K., Granberg, K., Leivonen, S. K., Meriranta, L., Heckman, C., Leppä, S., Nykter, M., Lohi, O., Heinäniemi, M. & Mustjoki, S. Immunogenomic Landscape of Hematological Malignancies. *Cancer Cell* **38**, 380-399.e313 (2020). <https://doi.org/10.1016/j.ccell.2020.06.002> (IF, 50.3)
3. Pölönen, P.*, Mehtonen, J.*, Lin, J., Liuksiala, T., Häyrynen, S., Teppo, S., Mäkinen, A., Kumar, A., Malani, D., Pohjolainen, V., Porkka, K., Heckman, C. A., May, P., Hautamäki, V., Granberg, K. J., Lohi, O., Nykter, M. & Heinäniemi, M. Hemap: An Interactive Online Resource for Characterizing Molecular Phenotypes across Hematologic Malignancies. *Cancer Res* **79**, 2466-2479 (2019). <https://doi.org/10.1158/0008-5472.Can-18-2970> (IF, 12.7)
4. Mehtonen, J.*, Pölönen, P.*, Häyrynen, S., Dufva, O., Lin, J., Liuksiala, T., Granberg, K., Lohi, O., Hautamäki, V., Nykter, M. & Heinäniemi, M. Data-driven characterization of molecular phenotypes across heterogeneous sample collections. *Nucleic Acids Res* **47**, e76 (2019). <https://doi.org/10.1093/nar/gkz281> (IF, 14.9)
5. Härkönen, J.*, Pölönen, P.*, Deen, A. J., Selvarajan, I., Teppo, H. R., Dimova, E. Y., Kietzmann, T., Ahtiainen, M., Väyrynen, J. P., Väyrynen, S. A., Elomaa, H., Tynkkynen, N., Eklund, T., Kuopio, T., Talvitie, E. M., Taimen, P., Kallajoki, M., Kaikkonen, M. U., Heinäniemi, M. & Levonen, A. L. A pan-cancer analysis shows immunoevasive characteristics in NRF2 hyperactive squamous malignancies. *Redox Biol* **61**, 102644 (2023). <https://doi.org/10.1016/j.redox.2023.102644> (IF, 11.8)
6. Pölönen, P., Jawahar Deen, A., Leinonen, H. M., Jyrkkänen, H. K., Kuosmanen, S., Mononen, M., Jain, A., Tuomainen, T., Pasonen-Seppänen, S., Hartikainen, J. M., Mannermaa, A., Nykter, M., Tavi, P., Johansen,

T., Heinäniemi, M. & Levonen, A. L. Nrf2 and SQSTM1/p62 jointly contribute to mesenchymal transition and invasion in glioblastoma. *Oncogene* **38**, 7473-7490 (2019). <https://doi.org/10.1038/s41388-019-0956-6> (IF, 8.75)

*Equal contribution

Second author (3):

7. Montefiori, L. E.* , Bendig, S.* , Gu, Z.* , Chen, X.* , Pölönen, P., Ma, X., Murison, A., Zeng, A., Garcia-Prat, L., Dickerson, K., Iacobucci, I., Abdelhamed, S., Hiltenbrand, R., Mead, P. E., Mehr, C. M., Xu, B., Cheng, Z., Chang, T. C., Westover, T., Ma, J., Stengel, A., Kimura, S., Qu, C., Valentine, M. B., Rashkovan, M., Luger, S., Litzow, M. R., Rowe, J. M., den Boer, M. L., Wang, V., Yin, J., Kornblau, S. M., Hunger, S. P., Loh, M. L., Pui, C. H., Yang, W., Crews, K. R., Roberts, K. G., Yang, J. J., Relling, M. V., Evans, W. E., Stock, W., Paietta, E. M., Ferrando, A. A., Zhang, J., Kern, W., Haferlach, T., Wu, G., Dick, J. E., Kico, J. M., Haferlach, C. & Mullighan, C. G. Enhancer Hijacking Drives Oncogenic BCL11B Expression in Lineage-Ambiguous Stem Cell Leukemia. *Cancer Discov* **11**, 2846-2867 (2021). <https://doi.org/10.1158/2159-8290.Cd-21-0145> (IF, 39.4)
8. Bouvy-Liivrand, M.* , Hernández de Sande, A.* , Pölönen, P., Mehtonen, J., Vuorenmaa, T., Niskanen, H., Sinkkonen, L., Kaikkonen, M. U. & Heinäniemi, M. Analysis of primary microRNA loci from nascent transcriptomes reveals regulatory domains governed by chromatin architecture. *Nucleic Acids Res* **45**, 9837-9849 (2017). <https://doi.org/10.1093/nar/gkx680> (IF, 14.9)
9. Brummer, O., Pölönen, P., Mustjoki, S. & Brück, O. Computational textural mapping harmonises sampling variation and reveals multidimensional histopathological fingerprints. *Br J Cancer* **129**, 683-695 (2023). <https://doi.org/10.1038/s41416-023-02329-4> (IF, 9.0)

*equal contribution

Collaborative Research (19):

10. Newman, H., Lee, S. H. R., Pölönen, P., Shraim, R., Li, Y., Liu, H., Aplenc, R., Bandyopadhyay, S., Chen, C., Devidas, M., Diorio, C., Dunsmore, K., Elghawy, O., Elhachimi, A., Fuller, T., Gupta, S., Hall, J., Hughes, A. D., Hunger, S. P., Loh, M. L., Martinez, Z., McCoy, M. F., Mullen, C. G., Pounds, S. B., Raetz, E., Seffernick, A. E., Shi, G., Sussman, J., Tan, K., Uppuluri, L., Vincent, T. L., Wang'ondou, R., Winestone, L. E., Winter, S. S., Wood, B. L., Wu, G., Xu, J., Yang, W., Mullighan, C. G., Yang, J. J., Bona, K. & Teachey, D. T. Impact of Genetic Ancestry on Genomics and Survival Outcomes in T-cell Acute Lymphoblastic Leukemia. *Blood Cancer Discovery* (2025). <https://doi.org/10.1158/2643-3230.Bcd-25-0049>
11. Chen, C., Xu, J., Sussman, J. H., Vincent, T. L., Tumulty, J. S., Yoshimura, S., Alikarami, F., Yu, W., Ding, Y.-Y., Chen, C.-H., Li, E. Y., Yang, A., Qin, X., Bandyopadhyay, S., Peng, J. J., Pölönen, P., Newman, H., Wood, B., Hu, J., Shraim, R., Hughes, A. D., Diorio, C., Uppuluri, L., Shi, G., Ryan, T., Fuller, T., Loh, M. L., Raetz, E. A., Hunger, S. P., Pounds, S. B., Mullighan, C. G., Frank, D., Yang, J. J., Bernt, K. M., Teachey, D. T. & Tan, K. Single-cell panleukemia signatures of HSPC-like blasts predict drug response and clinical outcome. *Blood* (2025). <https://doi.org/10.1182/blood.2024027270>
12. Xu, J., Chen, C., Sussman, J. H., Yoshimura, S., Vincent, T., Pölönen, P., Hu, J., Bandyopadhyay, S., Elghawy, O., Yu, W., Tumulty, J., Chen, C.-h., Li, E. Y., Diorio, C., Shraim, R., Newman, H., Uppuluri, L., Li, A., Chen, G. M., Wu, D. W., Ding, Y.-y., Xu, J. A., Karanfilovski, D., Lim, T., Hsu, M., Thadi, A., Ahn, K. J., Wu, C.-Y., Peng, J., Sun, Y., Wang, A., Mehta, R., Frank, D., Meyer, L., Loh, M. L., Raetz, E. A., Chen, Z., Wood, B. L., Devidas, M., Dunsmore, K. P., Winter, S. S., Chang, T.-C., Wu, G., Pounds, S. B., Zhang, N. R., Carroll, W., Hunger, S. P., Bernt, K., Yang, J. J., Mullighan, C. G., Tan, K. & Teachey, D. T. A multiomic atlas identifies a treatment-resistant, bone marrow progenitor-like cell population in T cell acute lymphoblastic leukemia. *Nature Cancer* **6**, 102-122 (2025). <https://doi.org/10.1038/s43018-024-00863-5> (IF 23.5)
13. Xu, J., Sussman, J. H., Yang, A., Yoshimura, S., Hu, J., Chen, C., Vincent, T. L., Bandyopadhyay, S., Li, E. Y., Lim, T. L., Elghawy, O., Barsouk, A., Karanfilovski, D., Wald, S. L., Chen, G. M., Wu, D. W., Newman, H., Li, A., Sun, Y., Chen, C.-H., Bernt, K. M., Wood, B. L., Winter, S. S., Dunsmore, K. P., Raetz, E. A., Devidas, M., Pounds, S. B., Loh, M. L., Hunger, S. P., Chiang, M., Diorio, C., Giacomo, D. D., Pölönen, P., Mullighan, C. G., Yang, J. J., Tan, K. & Teachey, D. T. STAT1-mediated interferon signatures associate with preclinical JAK-inhibitor sensitivity in T-cell acute lymphoblastic leukemia. *Blood* (2025). <https://doi.org/10.1182/blood.2025028566>
14. Kimura, S., Park, C. S., Montefiori, L. E., Iacobucci, I., Pölönen, P., Gao, Q., Arnold, E. D., Attarbaschi, A., Brown, A., Buldini, B., Caldwell, K. J., Chang, Y., Chen, C., Cheng, C., Cheng, Z., Choi, J., Conter, V.,

- Crews, K. R., de Groot-Kruseman, H. A., Deguchi, T., Eguchi, M., Muhle, H. E., Elitzur, S., Escherich, G., Freeman, B. B., Gu, Z., Han, K., Horibe, K., Imamura, T., Jeha, S., Kato, M., Chiew, K. H., Khan, T., Kicinski, M., Kohrer, S., Kornblau, S. M., Kotecha, R. S., Li, C.-K., Liu, Y.-C., Locatelli, F., Luger, S. M., Paietta, E. M., Manabe, A., Marquart, H. V., Masetti, R., Maybury, M., Mazilier, P., Meijerink, J. P. P., Mitchell, S., Miyamura, T., Moore, A. S., Oshima, K., Pawinska-Wasikowska, K., Pieters, R., Prater, M. S., Pruett-Miller, S. M., Pui, C.-H., Qu, C., Reiterova, M., Reyes, N., Roberts, K. G., Rowe, J. M., Sato, A., Schmiegelow, K., Schrappe, M., Shen, S., Skoczen, S., Spinelli, O., Stary, J., Svaton, M., Takagi, M., Takita, J., Tang, Y., Teachey, D. T., Thomas, P. G., Tomizawa, D., Trka, J., Varotto, E., Vincent, T. L., Yang, J. J., Yeoh, A. E., Zhou, Y., Zimmermann, M., Inaba, H. & Mullighan, C. G. Biologic and clinical analysis of childhood gamma delta T-ALL identifies LMO2/STAG2 rearrangements as extremely high-risk. *Cancer Discovery* (2024). <https://doi.org/10.1158/2159-8290.Cd-23-1452> (IF, 39.4)
15. Wang, Q., Boccalatte, F., Xu, J., Gambi, G., Nadorp, B., Akter, F., Mullin, C., Melnick, A. F., Choe, E., McCarter, A. C., Jerome, N. A., Chen, S., Lin, K., Khan, S., Kodgule, R., Sussman, J. H., Pölönen, P., Rodriguez-Hernaez, J., Narang, S., Avrampou, K., King, B., Tsigirgos, A., Ryan, R. J. H., Mullighan, C. G., Teachey, D. T., Tan, K., Aifantis, I. & Chiang, M. Y. Native stem cell transcriptional circuits define cardinal features of high-risk leukemia. *Journal of Experimental Medicine* 222 (2025). <https://doi.org/10.1084/jem.20231349> (IF, 15.3)
 16. Gower, M., Li, X., Aguilar-Navarro, A. G., Lin, B., Fernandez, M., Edun, G., Nader, M., Rondeau, V., Arruda, A., Tierens, A., Eames Seffernick, A., Pölönen, P., Durocher, J., Wagenblast, E., Yang, L., Lee, H. S., Mullighan, C. G., Teachey, D., Rashkovan, M., Tremblay, C. S., Herranz, D., Itkin, T., Loghavi, S., Dick, J. E., Schwartz, G., Perusini, M. A., Sibai, H., Hitzler, J., Gruber, T. A., Minden, M., Jones, C. L., Dolgalev, I., Jahangiri, S. & Tikhonova, A. N. An inflammatory state defines a high-risk T-lineage acute lymphoblastic leukemia subgroup. *Science Translational Medicine* 17, eadr2012 (2025). <https://doi.org/doi:10.1126/scitranslmed.adr2012> (IF 15.8)
 17. Paolino, J., Dimitrov, B., Apsel Winger, B., Sandoval-Perez, A., Rangarajan, A. V., Ocasio-Martinez, N., Tsai, H. K., Li, Y., Robichaud, A. L., Khalid, D., Hatton, C., Gillani, R., Polonen, P., Dilig, A., Gotti, G., Kavanagh, J., Adhav, A. A., Gow, S., Tsai, J., Li, Y. D., Ebert, B. L., Van Allen, E. M., Bledsoe, J., Kim, A. S., Tasian, S. K., Cooper, S. L., Cooper, T. M., Hijjiya, N., Sulis, M. L., Shukla, N. N., Magee, J. A., Mullighan, C. G., Burke, M. J., Luskin, M. R., Mar, B. G., Jacobson, M. P., Harris, M. H., Stegmaier, K., Place, A. E. & Pikman, Y. Integration of Genomic Sequencing Drives Therapeutic Targeting of PDGFRA in T-Cell Acute Lymphoblastic Leukemia/Lymphoblastic Lymphoma. *Clinical Cancer Research* 29, 4613-4626 (2023). <https://doi.org/10.1158/1078-0432.Ccr-22-2562> (IF 10.4)
 18. Ryan, S. L., Peden, J. F., Kingsbury, Z., Schwab, C. J., James, T., Polonen, P., Mijuskovic, M., Becq, J., Yim, R., Cranston, R. E., Hedges, D. J., Roberts, K. G., Mullighan, C. G., Vora, A., Russell, L. J., Bain, R., Moorman, A. V., Bentley, D. R., Harrison, C. J. & Ross, M. T. Whole genome sequencing provides comprehensive genetic testing in childhood B-cell acute lymphoblastic leukaemia. *Leukemia* 37, 518-528 (2023). <https://doi.org/10.1038/s41375-022-01806-8> (IF, 11.4)
 19. Chan, L. N., Murakami, M. A., Robinson, M. E., Caeser, R., Sadras, T., Lee, J., Cosgun, K. N., Kume, K., Khairnar, V., Xiao, G., Ahmed, M. A., Aghania, E., Deb, G., Hurtz, C., Shojaee, S., Hong, C., Pölönen, P., Nix, M. A., Chen, Z., Chen, C. W., Chen, J., Vogt, A., Heinäniemi, M., Lohi, O., Wiita, A. P., Izraeli, S., Geng, H., Weinstock, D. M. & Müschen, M. Signalling input from divergent pathways subverts B cell transformation. *Nature* 583, 845-851 (2020). <https://doi.org/10.1038/s41586-020-2513-4> (IF, 64.8)
 20. Dufva, O., Gandolfi, S., Huuhtanen, J., Dashevsky, O., Duàn, H., Saeed, K., Klievink, J., Nygren, P., Bouhlal, J., Lahtela, J., Näättänen, A., Ghimire, B. R., Hannunen, T., Ellonen, P., Lähteenmäki, H., Rumm, P., Theodoropoulos, J., Laajala, E., Härkönen, J., Pölönen, P., Heinäniemi, M., Hollmén, M., Yamano, S., Shirasaki, R., Barbie, D. A., Roth, J. A., Romee, R., Sheffer, M., Lähdesmäki, H., Lee, D. A., De Matos Simoes, R., Kankainen, M., Mitsiades, C. S. & Mustjoki, S. Single-cell functional genomics reveals determinants of sensitivity and resistance to natural killer cells in blood cancers. *Immunity* 56, 2816-2835.e2813 (2023). <https://doi.org/10.1016/j.immuni.2023.11.008> (IF, 43.47)
 21. Malyukova, A., Lahnalampi, M., Falqués-Costa, T., Pölönen, P., Sipola, M., Mehtonen, J., Teppo, S., Akopyan, K., Viiliainen, J., Lohi, O., Hagström-Andersson, A. K., Heinäniemi, M. & Sangfelt, O. Sequential drug treatment targeting cell cycle and cell fate regulatory programs blocks non-genetic cancer evolution in acute lymphoblastic leukemia. *Genome Biol* 25, 143 (2024). <https://doi.org/10.1186/s13059-024-03260-4> (IF, 10.1)
 22. Kuusanmäki, H., Dufva, O., Vähä-Koskela, M., Leppä, A. M., Huuhtanen, J., Vanttinen, I., Nygren, P., Klievink, J., Bouhlal, J., Pölönen, P., Zhang, Q., Adnan-Awad, S., Mancebo-Pérez, C., Saad, J., Miettinen,

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REFERENCES

Charles G. Mullighan
Post-doctoral research mentor
Email: charles.mullighan@stjude.org

David T. Teachey
Post-doctoral research mentor
Email: teacheyd@chop.edu

Merja Heinäniemi
Ph.D research mentor, teaching mentor
Email: merja.heinaniemi@uef.fi