

ABCA4 locus as a model for complex genetics in monogenic diseases = ABCA4 lookus kui monogeensete haiguste kompleksse geneetika mudel

Zernant, Jana 2019 <https://digi.lib.ttu.ee/i/?12387>

Analyses of non-coding somatic drivers in 2,658 cancer whole genomes

Rheinbay, Esther; Nielsen, Morten Muhl; Abascal, Federico; Wala, Jeremiah A.; Shapira, Ofer; Tiao, Grace; Hornshøj, Henrik; Hess, Julian M.; Juul, Randi Istrup; **Uusküla-Reimand, Liis** Nature 2020 / 10 p. : ill <https://doi.org/10.1038/s41586-020-1965-x> [Journal metrics](#) [at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

ASK1, a SKP1 homolog, is required for nuclear reorganization, presynaptic homolog juxtaposition and the proper distribution of cohesin during meiosis in Arabidopsis

Zhao, Dazhong; Yang, Xiaohui; Quan, Li; **Timofejeva, Ljudmilla** Plant molecular biology 2006 / 1/2, p. 99-110 https://www.researchgate.net/publication/6890651_ASK1_a_SKP1_homolog_is_required_for_nuclear_reorganization_presynaptic_homolog_juxtaposition_and_the_proper_distribution_of_cohesin_during_meiosis_in_Arabidopsis

Author Correction: A deep learning system accurately classifies primary and metastatic cancers using passenger mutation patterns (Nature Communications, (2020), 11, 1, (728), 10.1038/s41467-019-13825-8)

Jiao, Wei; Atwal, Gurmit; Polak, Paz; Karlic, Rosa; Cuppen, Edwin; Al-Shahrour, Fatima; Bailey, Peter J.; Biankin, Andrew V.; Boutros, Paul C.; **Uusküla-Reimand, Liis** Nature Communications 2022 / Art. 7573 <https://doi.org/10.1038/s41467-022-32329-6> [Journal metrics](#) [at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

Author Correction: Divergent mutational processes distinguish hypoxic and normoxic tumours (Nature Communications, (2020), 11, 1, (737), 10.1038/s41467-019-14052-x)

Bhandari, Vinayak; Li, Constance H.; Bristow, Robert G.; Boutros, Paul C.; Aaltonen, Lauri A.; Abascal, Federico; Abeshouse, Adam; Aburatani, Hiroyuki; Adams, David J.; **Uusküla-Reimand, Liis** Nature Communications 2022 / Art. nr. 7569 <https://doi.org/10.1038/s41467-022-32339-4> [Journal metrics](#) [at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

Author Correction: High-coverage whole-genome analysis of 1220 cancers reveals hundreds of genes deregulated by rearrangement-mediated cis-regulatory alterations (Nature Communications, (2020), 11, 1, (736), 10.1038/s41467-019-13885-w)

Zhang, Yiqun; Chen, Fengju; Fonseca, Nuno A.; He, Yao; Fujita, Masashi; Nakagawa, Hidewaki; Zhang, Zemin; Brazma, Alvis; Amin, Samirkumar B.; **Uusküla-Reimand, Liis** Nature Communications 2022 / Art. nr. 7572 <https://doi.org/10.1038/s41467-022-32333-w> [Journal metrics](#) [at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

Author Correction: Pathway and network analysis of more than 2500 whole cancer genomes (Nature Communications, (2020), 11, 1, (729), 10.1038/s41467-020-14367-0)

Reyna, Matthew A.; Haan, David; Paczkowska, Marta; Verbeke, Lieven P. C.; Vazquez, Miguel; Kahraman, Abdullah; Pulido-Tamayo, Sergio; Barenboim, Jonathan; Wadi, Lina; **Uusküla-Reimand, Liis** Nature Communications 2022 / Art. nr. 7566 <https://doi.org/10.1038/s41467-022-32334-9> [Journal metrics](#) [at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

Author Correction: Reconstructing evolutionary trajectories of mutation signature activities in cancer using TrackSig (Nature Communications, (2020), 11, 1, (731), 10.1038/s41467-020-14352-7)

Rubanov, Yulia; Shi, Ruian; Harrigan, Caitlin F.; Li, Roujia; Wintersinger, Jeff; Sahin, Nil; Deshwar, Amit G.; Dentre, Stefan C.; Leshchiner, Ignaty; **Uusküla-Reimand, Liis** Nature Communications 2022 / Art. nr. 7567 <https://doi.org/10.1038/s41467-022-32336-7> [Journal metrics](#) [at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

Author Correction: Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples (Nature Communications, (2020), 11, 1, (4748), 10.1038/s41467-020-18151-y)

Bailey, Matthew H.; Meyerson, William U.; Dursi, Lewis Jonathan; Wang, Liang-Bo; Dong, Guanlan; Liang, Wen-Wei; Weerasinghe, Amila; Li, Shantao; Li, Yize; **Uusküla-Reimand, Liis** Nature Communications 2020 / Art. nr. 6232 <https://doi.org/10.1038/s41467-020-20128-w> [Journal metrics](#) [at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

Candidate cancer driver mutations in distal regulatory elements and long-range chromatin interaction networks

Zhu, Helen; **Uusküla-Reimand, Liis**; Isaev, Keren; Wadi, Lina; Alizada, Azad; Shuai, Shimin; Huang, Vincent; Aduloso-Nwaobasi, Dike; Paczkowska, Marta; Abd-Rabbo, Diala; Ocsenas, Oliver; Liang, Minggao; Thompson, J. Drew; Li, Yao; Ruan, Luyao; Krassowski, Michal; Dzeladze, Irakli; Simpson, Jared T.; Lupien, Mathieu; Stein, Lincoln D.; Boutros, Paul C.; Wilson, Michael D.; Reimand, Jüri Molecular Cell 2020 / p. 1307-1321.e10 <https://doi.org/10.1016/j.molcel.2019.12.027> [Journal metrics](#) [at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

Characterization of novel anther mutants in maize

Moon, Jihyun; **Timofejeva, Ljudmilla**; Lee, Sidae 53rd Annual Maize Genetics Conference Abstracts : St. Charles, Illinois, USA, March 17-20, 2011 2011 / p. P096

Combined burden and functional impact tests for cancer driver discovery using DriverPower

Shuai, Shimin; Abascal, Federico; Amin, Samirkumar B.; Bader, Gary D.; Bandopadhyay, Pratiti; Barenboim, Jonathan; Beroukhim, Rameen; Bertl, Johanna; Boroevich, Keith A.; **Uusküla-Reimand, Liis** Nature Communications 2020 / art. 734 <https://doi.org/10.1038/s41467-019-13929-1> [Journal metrics](#) [at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing

Cortés-Ciriano, Isidro; Lee, Jake June-Koo; Xi, Ruibin; Jain, Dhawal; Jung, Youngsook Lucy; Yang, Lixing; Gordenin, Dmitry; Klimczak, Leszek J.; **Uusküla-Reimand, Liis** Nature Genetics 2020 / p. 331-341 <https://doi.org/10.1038/s41588-019-0576-7> [Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

Comprehensive molecular characterization of mitochondrial genomes in human cancers

Yuan, Yuan; Ju, Young Seok; Kim, Youngwook; Li, Jun; Wang, Yumeng; Yoon, Christopher J.; Yang, Yang; Martincorena, Inigo; Creighton, Chad J.; **Uusküla-Reimand, Liis** Nature Genetics 2020 / p. 342 - 352 <https://doi.org/10.1038/s41588-019-0557-x> [Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

CRISPR/Cas-mediated plant genome editing : outstanding challenges a decade after implementation

Cardi, Teodoro; Murovec, Jana; Bakhsh, Allah; Boniecka, Justyna; Brueggemann, Tobias; Bull, Simon E.; Eeckhaut, Tom; Fladung, Matthias; Galovic, Vladislava; Linkiewicz, Anna; Lukan, Tjaša; Mafra, Isabel; Michalski, Krzysztof; Kavas, Musa; Nicolai, Alessandro; Nowakowska, Justyna; Sagi, Laszlo; **Sarmiento Guerin, Maria Cecilia**; Yildirim, Kubilay; Zlatkovic, Milica; Hensel, Goetz; Van Laere, Katrijn Trends in plant science 2023 <https://doi.org/10.1016/j.tplants.2023.05.012>

A deep learning system accurately classifies primary and metastatic cancers using passenger mutation patterns

Jiao, Wei; Atwal, Gurnit; Polak, Paz; Karlic, Rosa; Cuppen, Edwin; Al-Shahrour, Fatima; Bailey, Peter J.; Biankin, Andrew V.; Boutros, Paul C.; **Uusküla-Reimand, Liis** Nature Communications 2020 / art. 728, 12 p. : ill <https://doi.org/10.1038/s41467-019-13825-8> [Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

Differential patterns of cross-reactive antibody response against SARS-CoV-2 spike protein detected for chronically ill and healthy COVID-19 naïve individuals

Jaago, Mariliis; Rähni, Annika; Pupina, Nadezda; **Sadam, Helle**; **Tuvikene, Jürgen**; **Avarlaid, Annela**; Planken, Anu; Planken, Margus; Haring, Liina; Vasar, Eero; Bacevic, Miljana; Lambert, France; Kalso, Eija; Pussinen, Pirkko; Tienari, Pentti J.; Vaheri, Antti; Lindholm, Dan; **Timmusk, Tõnis**; Ghaemmaghami, Amir M.; Palm, Kaia Scientific reports 2022 / art. 16817 : ill <https://doi.org/10.1038/s41598-022-20849-6> [Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

Divergent mutational processes distinguish hypoxic and normoxic tumours

Bhandari, Vinayak; Li, Constance H.; Bristow, Robert G.; Boutros, Paul C.; Aaltonen, Lauri A.; Abascal, Federico; Abeshouse, Adam; Aburatani, Hiroyuki; Adams, David J.; Uusküla-Reimand, Liis Nature Communications 2020 / art. 737, 10 p. : ill <https://doi.org/10.1038/s41467-019-14052-x> [Article at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

DNA chip for mutation analysis

Metspalu, A.; Shumaker, J.M. BIOBALT '96 : Biotechnology in Estonia, Latvia and Lithuania : International Workshop, 19-20 April, 1996, Tartu, Estonia : abstract book 1996 / p. 27

Functions of the basic helix-loop-helix transcription factor TCF4 in health and disease = Aluselise heeliks-ling-heeliks transkriptsioonifaktori TCF4 funktsioonid ja seosed haigustega

Sepp, Mari 2012

Gravitropic response of arabidopsis inflorescence stems in myosin mutant plants [Online resource]

Talts, Kristiina; Ojangu, Eve-Ly; Ilau, Birger; Truve, Erkki; Paves, Heiti Environmental adaptation : from molecules to the planet : the Estonian Centre of Excellence in Environmental Adaptation ENVIRON. Final conference : October 1-3, 2015, Dorpat Conference Centre, Tartu, Estonia : abstract book 2015 / p. 57-58 http://environ.emu.ee/userfiles/environ/Abstract_Book_ENVIRON%20final%20conference%202015.pdf

High-coverage whole-genome analysis of 1220 cancers reveals hundreds of genes deregulated by rearrangement-mediated cis-regulatory alterations

Zhang, Yiqun; Chen, Fengju; Fonseca, Nuno A.; He, Yao; Fujita, Masashi; Nakagawa, Hidewaki; Zhang, Zemin; Brazma, Alvis; Amin, Samirkumar B.; **Uusküla-Reimand, Liis** Nature Communications 2020 / Art. nr. 736 <https://doi.org/10.1038/s41467-019-13885-w> [Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

Integrative pathway enrichment analysis of multivariate omics data

Paczkowska, Marta; Barenboim, Jonathan; Sintupisut, Nardnisa; Fox, Natalie S.; Zhu, Helen; Abd-Rabbo, Diala; Mee, Miles W.; Boutros, Paul C.; Abascal, Federico; **Uusküla-Reimand, Liis** Nature Communications 2020 / Art. nr. 735 <https://doi.org/10.1038/s41467-019-13983-9> [Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

Introducing Pitt-Hopkins syndrome-associated mutations of TCF4 to Drosophila daughterless

Tamberg, Laura; Sepp, Mari; Timmusk, Tõnis; Palgi, Mari Biology open 2015 / p. 1762-1771 : ill <http://dx.doi.org/10.1242/bio.014696>

Introducing Pitt-Hopkins Syndrome-associated mutations of TCF4 to Drosophila daughterless : [conference paper]

Palgi, Mari; Tamberg, Laura; Timmusk, Tõnis VI Baltic Genetics Congress : September 30 - October 3, 2015, Institute of Molecular and Cell Biology, Tartu, Estonia : book of abstracts 2015 / 1 p

Is the maize ortholog of the yeast Pch2 (Pachytene checkpoint 2) involved in meiotic surveillance?

Timofejeva, Ljudmilla; Golubovskaya, Inna; **Relvik, Tõnis**; Pawlowski, W.; **Truve, Erkki** EMBO Meiosis Conference 2015 : St Catherine's College, Oxford, UK 2015 / p. 183

The landscape of viral associations in human cancers

Zapatka, Marc; Borozan, Ivan; Brewer, Daniel S.; Iskar, Murat; Grundhoff, Adam; Alawi, Malik; Desai, Nikita; Sülthmann, Holger; Moch, Holger; Cooper, Colin S.; **Uusküla-Reimand, Liis** Nature Genetics 2020 / p. 320 - 330 <https://doi.org/10.1038/s41588-019-0558-9>
[Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

Lynch syndrome mutations shared by the Baltic States and Poland

Dymerska, D.; **Kelve, Merike** Clinical genetics 2014 / p. 190-193 : ill

Maize meiosis and collection of meiotic mutants

Golubovskaja, Inna; Wang, Rachel; **Timofejeva, Ljudmilla**; Cande, Zac 51st Maize Genetics Conference : March 12-15, 2009, St.Charles, Illinois, USA 2009 / p. 34

Maize meiotic mutants with improper or non-homologous synapsis due to problems in pairing or synaptonemal complex formation

Golubovskaya, Inna; Wang, Rachel; **Timofejeva, Ljudmilla**; Cande, W.Zacheus Journal of experimental botany 2011 / p. 1533-1544 : ill <https://pubmed.ncbi.nlm.nih.gov/20926553/>

Molecular characterization of basic helix-loop-helix transcription factor TCF4 : from expression to function = Aluselise heeliks-ling-heeliks transkriptsiooniteguri TCF4 ekspressiooni ja funktsiooni kirjeldamine

Sirp, Alex 2023 <https://doi.org/10.23658/taltech.25/2023> <https://digikogu.taltech.ee/et/Item/67e0b91f-4c35-4eeb-ae4-5da8e859ae6e>
https://www.ester.ee/record=b5567490*est

Mutations for testing hardware and correcting design errors

Hantson, Hanno Info- ja kommunikatsioonitehnoloogia doktorikooli IKTDK viienda aastakonverentsi artiklite kogumik : 25.-26. novembril 2011, Nelijärve 2011 / p. 105-108 : ill

New maize mutants defective in anther development

Timofejeva, Ljudmilla; Lee, Sidae; Harper, Lisa; **Golubovskaja, Inna**; Wang, Rachel; Vasudevan, Srividya; Walbot, Virginia; Cande, Zac 51st Maize Genetics Conference : March 12-15, 2009, St.Charles, Illinois, USA 2009 / p. 93

Pan-cancer analysis of whole genomes

Campbell, Peter J.; Getz, Gad; Korbel, Jan O.; Stuart, Joshua M.; Jennings, Jennifer L.; Stein, Lincoln D.; Perry, Marc D.; Nahal-Bose, Hardeep K.; Ouellette, B. F. Francis; **Uusküla-Reimand, Liis** Nature 2020 / 12 p. : ill <https://doi.org/10.1038/s41586-020-1969-6> [Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

Partial deletion of TCF4 in three generation family with nonsyndromic intellectual disability, without features of Pitt-Hopkins syndrome

Kharbanda, Mira; **Kannike, Kaja**; Lampe, Anne; Berg, Jonathan; **Timmusk, Tõnis**; **Sepp, Mari** European journal of medical genetics 2016 / p. 310-314 : ill <http://dx.doi.org/10.1016/j.ejmg.2016.04.003>

Pathway and network analysis of more than 2500 whole cancer genomes

Reyna, Matthew A.; Haan, David; Paczkowska, Marta; Verbeke, Lieven P. C.; Vazquez, Miguel; Kahraman, Abdullah; Pulido-Tamayo, Sergio; Barenboim, Jonathan; Wadi, Lina; Dhingra, Priyanka; **Uusküla-Reimand, Liis** Nature Communications 2020 / art. 729 <https://doi.org/10.1038/s41467-020-14367-0> [Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

Pärmimutatsioonid muudavad veini paremaks : [Toidu- ja Fermentatsioonitehnoloogia Arenduskeskuse teadlaste katseprotsessist]

Aru, Erik Mente et Manu 2013 / lk. 10 : fot https://www.ester.ee/record=b1242496*est

Reconstructing evolutionary trajectories of mutation signature activities in cancer using TrackSig

Rubanova, Yulia; Shi, Ruian; Harrigan, Caitlin F.; Li, Roujia; Wintersinger, Jeff; Sahin, Nil; Deshwar, Amit G.; Dentre, Stefan C.; Leshchiner, Ignaty; **Uusküla-Reimand, Liis** Nature Communications 2020 / Art. nr. 731 <https://doi.org/10.1038/s41467-020-14352-7>
[Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples

Bailey, Matthew H.; Meyerson, William U.; Dursi, Lewis Jonathan; Wang, Liang-Bo; Dong, Guanlan; Liang, Wen-Wei; Weerasinghe, Amila; Li, Shantao; Kelso, Sean; **Vijay Raghavan, Krishnaswamy** Nature Communications 2020 / Art. nr. 4748 <https://doi.org/10.1038/s41467-020-18151-y> [Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

Sex differences in oncogenic mutational processes

Li, Constance H.; Prokopec, Stephenie D.; Sun, Ren X.; Yousif, Fouad; Schmitz, Nathaniel; Al-Shahrour, Fatima; Atwal, Gurnit; Bailey, Peter J.; Biankin, Andrew V.; **Uusküla-Reimand, Liis** Nature Communications 2020 / Art. nr. 4330 <https://doi.org/10.1038/s41467-020->

Uudne diagnostikameetod määrab ära päriliku rinnavähiriski : [TTÜ Vähiuuringute Tehnoloogia Arenduskeskuse teadustööst]

Lõhmus, Alo Postimees 2008 / 1. aug., lk. 4-5 <https://www.postimees.ee/23910/uudne-diagnostikameetod-maarab-ara-pariliku-rinnavahiriski>