

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

Rheinbay, Esther; Nielsen, Morten Muhligh; 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](#)

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: Analyses of non-coding somatic drivers in 2,658 cancer whole genomes (Nature, (2020), 578, 7793, (102-111), 10.1038/s41586-020-1965-x)

Rheinbay, Esther; Nielsen, Morten Muhligh; Abascal, Federico; Wala, Jeremiah A.; Shapira, Ofer; Tiao, Grace; Hornshøj, Henrik; Hess, Julian M.; Juul, Randi Istrup; Lin, Ziao; Feuerbach, Lars; Sabarinathan, Radhakrishnan; **Uusküla-Reimand, Liis** Nature 2023 / p. E40 <https://doi.org/10.1038/s41586-022-05599-9> [Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

Author Correction: Butler enables rapid cloud-based analysis of thousands of human genomes (Nature Biotechnology, (2020), 38, 3, (288-292), 10.1038/s41587-019-0360-3)

Yakneen, Sergei; Waszak, Sebastian M.; Aminou, Brice; Bartolome, Javier; Boroevich, Keith A.; Boyce, Rich; Brooks, Angela N.; Buchanan, Alex; Buchhalter, Ivo; Butler, Adam P.; Byrne, Niall J.; Cafferkey, Andy; **Uusküla-Reimand, Liis** Author Correction: Butler enables rapid cloud-based analysis of thousands of human genomes (Nature Biotechnology, (2020), 38, 3, (288-292), 10.1038/s41587-019-0360-3) 2023 / p. 577 <https://doi.org/10.1038/s41587-022-01554-1> [Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

Author Correction: Combined burden and functional impact tests for cancer driver discovery using DriverPower (Nature Communications, (2020), 11, 1, (734), 10.1038/s41467-019-13929-1)

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 2022 / art. 7571 <https://doi.org/10.1038/s41467-022-32343-8> [Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

Author Correction: Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing (Nature Genetics, (2020), 52, 3, (331-341), 10.1038/s41588-019-0576-7)

Cortés-Ciriano, Isidro; Lee, Jake June-Koo; Xi, Ruibin; Jain, Dhawal; Jung, Youngsook Lucy; Yang, Lixing; Gordenin, Dmitry A.; Klimczak, Leszek J.; Zhang, Cheng-Zhong; Pellman, David S.; Akdemir, Kadir Caner; Alvarez, Eva Garcia; **Uusküla-Reimand, Liis** Nature Genetics 2023 / p. 1076 <https://doi.org/10.1038/s41588-023-01315-z> [Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

Author Correction: Comprehensive molecular characterization of mitochondrial genomes in human cancers (Nature Genetics, (2020), 52, 3, (342-352), 10.1038/s41588-019-0557-x)

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Yuan, Yuan; Ju, Young Seok; Kim, Youngwook; Li, Jun; Wang, Yumeng; Yoon, Christopher J.; Yang, Yang; Martincorena, Inigo; Creighton, Chad J.; Weinstein, John N.; Xu, Yanxun; Han, Leng; **Uusküla-Reimand, Liis** Nature Genetics 2023 / p. 1078 <https://doi.org/10.1038/s41588-023-01317-x> [Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

Author Correction: Disruption of chromatin folding domains by somatic genomic rearrangements in human cancer (Nature Genetics, (2020), 52, 3, (294-305), 10.1038/s41588-019-0564-y)

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Author Correction: Genomic footprints of activated telomere maintenance mechanisms in cancer (Nature Communications, (2020), 11, 1, (733), 10.1038/s41467-019-13824-9)

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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)

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Author Correction: Inferring structural variant cancer cell fraction (Nature Communications, (2020), 11, 1, (730), 10.1038/s41467-020-14351-8)

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Author Correction: Integrative pathway enrichment analysis of multivariate omics data (Nature Communications, (2020), 11, 1, (735), 10.1038/s41467-019-13983-9)

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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)

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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)

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Author Correction: The landscape of viral associations in human cancers (Nature Genetics, (2020), 52, 3, (320-330), 10.1038/s41588-019-0558-9)

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Cancer LncRNA Census reveals evidence for deep functional conservation of long noncoding RNAs in tumorigenesis

Carlevaro-Fita, Joan; Lanzós, Andrés; Feuerbach, Lars; Hong, Chen; Mas-Ponte, David; Pedersen, Jakob Skou; Abascal, Federico; Amin, Samirkumar B.; Johnson, Rory; **Uusküla-Reimand, Liis** Communications Biology 2020 / Art. nr. 56

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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

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

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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

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

Disruption of chromatin folding domains by somatic genomic rearrangements in human cancer

Akdemir, Kadir Caner; Le, Victoria T.; Chandran, Sahaana; Li, Yilong; Verhaak, Roel G.W.; Beroukhim, Rameen; Campbell, Peter J.; Chin, Lynda; Dixon, Jesse R.; Futreal, Phillip Andrew; **Uusküla-Reimand, Liis** Nature Genetics 2020 / p. 294 - 305

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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

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Gene expression profiling of puberty-associated genes reveals abundant tissue and sex-specific changes across postnatal development

Hou, Huayun; **Uusküla-Reimand, Liis**; Makarem, Maisam; Corre, Christina; Saleh, Shems; Metcalf, Ariane; Goldenberg, Anna; Palmert, Mark R.; Wilson, Michael D. Human molecular genetics 2017 / p. 3585-3599 : ill <https://doi.org/10.1093/hmg/ddx246> Journal metrics at Scopus Article at Scopus Journal metrics at WOS Article at WOS

Genomic footprints of activated telomere maintenance mechanisms in cancer

Sieverling, Lina; Hong, Chen; Koser, Sandra D.; Ginsbach, Philip; Kleinheinz, Kortine; Hutter, Barbara; Braun, Delia M.; Cortés-Ciriano, Isidro; Xi, Ruibin; **Uusküla-Reimand, Liis** Nature Communications 2020 / art. 733, 13 p. ill <https://doi.org/10.1038/s41467-019-13824-9> Journal metrics at Scopus Article at Scopus Journal metrics at WOS Article at WOS

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>
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Inferring structural variant cancer cell fraction

Cmero, Marek; Yuan, Ke; Ong, Cheng Soon; Schröder, Jan; Adams, David J.; Anur, Pavana; Beroukhi, Rameen; Boutros, Paul C.; Bowtell, David D. L.; **Uusküla-Reimand, Liis** Nature Communications 2020 / Art. nr. 730 <https://doi.org/10.1038/s41467-020-14351-8>
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Integrative pathway enrichment analysis of multivariate omics data

Paczowska, 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>
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Lambert, Jean-Philippe; Picaud, Sarah; Fujisawa, Takao; **Uusküla-Reimand, Liis** Molecular cell 2019 / p. 621-638.e17 : ill <https://doi.org/10.1016/j.molcel.2018.11.006>
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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>
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Pan-cancer analysis of whole genomes

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Pathway and network analysis of more than 2500 whole cancer genomes

Reyna, Matthew A.; Haan, David; Paczowska, 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>
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Reconstructing evolutionary trajectories of mutation signature activities in cancer using TrackSig

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 2020 / Art. nr. 731 <https://doi.org/10.1038/s41467-020-14352-7>
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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/s41467-020-17359-2>
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Topoisomerase II beta interacts with cohesin and CTCF at topological domain borders

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