

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

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

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

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Divergent mutational processes distinguish hypoxic and normoxic tumours

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The non-catalytic role of DNA polymerase epsilon in replication initiation in human cells

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Pathway and network analysis of more than 2500 whole cancer genomes

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

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