

Adamová, Sabina	Presenter: Skaláková, Patricie; Adamová, Sabina	
Deciphering genomic complexity in chronic lymphocytic leukemia using nanopore sequencing		42
Aitken, Stuart	Presenter: Brown, Matthew	
Deciphering the role of RNA-chromatin interactions in Glioblastoma		43
Andrianova, Maria	Presenter: Chamorro González, Rocío	
Unraveling the impact of age and chemotherapy in the clonal dynamics of blood by ultradeep error-corrected sequencing		44
Avi-Guy, Yoav		
Detecting the early events of cancer development using spatiotemporally-resolved hair follicles - longitudinal tracking in-vivo by repeated hair waxing		45
Abstract cancelled		46
Bage, Saloni		
STK35 family kinases: a novel kinase emerging as a new prognostic biomarker in breast cancer		47
Berton, Lucrezia		
Chemotherapy reshapes the evolutionary trajectories of breast cancer		48
Biswal, Smruti Sudha		
Engineering mammalian design loci to decipher chromosomal instability driven prostate cancers using synthetic genomics		49
Blanco, Raquel		
Sex and smoking influence selection of somatic mutations in human bladder		50
Bochalís, Eleftherios		
Pan-cancer analysis reveals how non-B DNA structures drive distinct mutational processes		51

Bonthuis, Ine		
Paired gene regulatory network analysis reveals suppression of interferon signaling in metastatic breast cancer		52
Brown, Kevin M.	Presenter: Zhang, Tongwu	
A thiopurine-like mutagenic process defines TGCT subtypes		53
Burn, Aidan		
Genome-wide mapping of LINE-1 elements and their methylation states through targeted long-read sequencing		54
Cernovská, Karolína		
Linking structural rearrangements to transcriptional dysregulation in CLL via Micro-C		55
Chaves-Urbano, Blas		
Engineering chromosomal instability via BRCA1/2 knockout in vitro		56
Chen, Bingjie	Presenter: Lu, Bingxin	
BDDTree: Birth Death Dormant Tree for reconstructing spatial somatic evolution using methylation clock data		57
Cheng, Wen-Chih	Presenter: Sudarshan, Anirudh	
Identity chemical and genetic approaches to enhance translation of LINE-1 encoded ORF2p for cancer therapeutics		58
Cheng, Yixiao		
Single-cell multi-omics reveal evolutionary trajectories and intra-tumor heterogeneity in malignant peripheral nerve sheath tumors		59
Andrades Delgado, Álvaro		
Single-cell multi-omic exploration of complex karyotype acute myeloid leukemia progression		60
Cools, Ruben		
Decoding the evolution and heterogeneity of peripheral T-cell lymphoma		61

Das, Sunetra	
Comparative genomic analysis uncovers contrasting molecular profiles of canine and human thyroid carcinomas	62
de Jong, Daphne	Presenter: Ylstra, Bauke
Oncogenesis of enteropathy-associated T-cell lymphoma: extensive parallel clonal evolution and its clinical consequences	63
Detremmerie, Louis	
Whole-body donors as a resource for large-scale genomic analysis of metastatic cancer	64
Dove, Olivia	
Unravelling the influence of risk factors in the genomic evolution of clear cell renal cell carcinoma	65
Drzewiecki, Marcin	
Ultrasensitive profiling of the TSC1 mutation landscape in the TSC skin tumors	66
Eberth, Sonja	
DSMZCellDive: an open source for browsing and analyzing high-throughput data from cancer cell lines with the example of breast cancer models	67
Farag, Roula	
Uncovering the landscape of chromosomal instability in pediatric solid tumors	68
Figuerola, Elisabet	
The genomic landscape of the tumors of a patient with Xeroderma Pigmentosum with an exceptional response to immunotherapy	69
Forsyth, Robert	
Comprehensive multimodal profiling to advance sarcoma precision oncology and clinical care	70
Fortuna, Alexander	
Leveraging linked-reads to predict extrachromosomal DNA in advanced prostate cancer	71

Fullin, Jonas	Presenter: Zielinska, Karolina	
Genomic and transcriptomic insights into the pathogenesis of therapy-related acute myeloid leukemia from TP53-mutant clonal hematopoiesis		72
Gandini, Francesca		
Multi-omics approaches in CLL vs MBL		73
Garcia Dutton, Natalia		
Characterizing the genetic and epigenetic landscape of high grade serous ovarian cancer		74
Gastaldello, Filippo		
HapScoreDB: enabling functional interpretation of haplotype-resolved coding variants using protein language models in cancer		75
Giulii, Edoardo		
A benchmark of DNA methylation deconvolution methods for tumoral fraction estimation in cfDNA using DecoNFlow		76
Grases, Daniela		
Towards clinical-grade spatial transcriptomics in cancer: a cross-platform benchmark and practical framework		77
Harbers, Luuk		
Long-read single-cell genome, transcriptome and open chromatin profiling links genotype to phenotypes		78
Hayes, James		
Reconstructing clonal dynamics using persistent DNA damage		79
Heidemann, Sophie		
IL-1-producing proinflammatory macrophages alter the mesothelial cell architecture in ovarian cancer metastases		80
Hoogstoel, Sofie		
Clonal and tumoral spatial interdependency in cutaneous squamous cell carcinoma		81

Huskova, Hana	
Distinct mutational signature outcomes of activation-induced cytidine deaminase activity	82
Ickes, Christian	
Unraveling molecular determinants from single-cell RNAseq data of melanoma-infiltrating NK cells to identify melanoma specific therapeutic targets	83
Imschoot, Renske	
Tracking epigenetic plasticity in circulating tumor-derived DNA to monitor tumor progression in triple-negative breast cancer patients	84
Ito, Yu	
Scarpia: An unified approach for detecting accurate allele-specific copy number alteration in cancer genomes across short- and long-read sequencing data	85
Jackson, Oscar	
Tracking melanoma persister cells through minimal residual disease	86
Jeong, Jinsil	
Colorectal serrated polyps exhibit monoclonal architecture and delayed growth kinetics	87
John, Evit	
Driver mutations shape clonal evolution and spatial growth in intrahepatic cholangiocarcinoma	88
Kanwal, Sehrish	
Characterising the mutational landscape and recurrent somatic drivers to uncover therapeutic vulnerabilities in pancreatic cancer progression	90
Kašťánková, Nikola	
Circulating histone signatures in biofluids: toward a non-invasive diagnostic tool for pediatric brain tumors	89

Kaufmann, Tom	
The interplay of mechanism and selection in shaping cancer copy number landscapes	91
Abstract cancelled	92
Klonowska, Katarzyna	
TSC angiofibroma and ungual fibroma have different mutation signatures, with recurrent mutations in KMT2C	93
Knight, Will	
Laser capture microdissection in cancer research	94
Kortendick, Leo	Presenter: Nagel, Stefan
Identification of novel leukemogenic oncogenes via copy number alterations in cell lines	95
Krishna, Rashi	
Identification of drug response biomarkers in uterine leiomyosarcoma	96
Daniela Pavlicenco	
Identifying metastatic endometrial cancer cells through clonal tracking cancelled	97
Kutkina, Anastasiia	
Harvesting and characterization of functional and disease variants from scientific literature using machine learning	98
Lambrechts, Laurens	
Multiomic long-reads for clinical genomics in hematologic cancer: pilot using Fiber-Seq	99
Lara-Gonzalez, Luis	Presenter: Goode, David
Modelling clonal sweep dynamics links tumour fitness to clinical outcomes in solid cancers	100
Lee, Jaejun	
Multi-feature predictive modeling of novel cancer predisposition genes using pan-cancer data	101

Lefèbvre, Maxime	
Decoupled mutation rate quantification of each parental genome in vivo	102
Lembo, Giovanni	
Chromatin-compartment based stratification of prostate cancer patients	103
Leventhal, Matthew	
How many rearrangements can be acquired on a single chromosome in one event?	104
Li, Sen	
Delineating genome instability dynamics in breast cancer by time-course single-cell copy number profiling	105
Lim, Che Kang	
Integrative long-read dna and rna sequencing uncovers isoform landscapes and structural variations in nasopharyngeal carcinoma	106
Liu, Lingchen	
Investigating the role of structural variants and methylation in lung cancer through long-read sequencing	107
Luijts, Tom	
Predicting TP53 mutations from spatial transcriptomics data using a graph neural network	108
Lynch, Andrew	
Clonal evolutionary reconstruction of complex genome rearrangements and focal amplifications in undifferentiated sarcomas	109
Maljanen, Katri	
Modeling effects of the epigenome on somatic variant formation	110
Mateos, Raul	
Splicing junction-based classifier for abnormal KEAP1-NRF2 system activation detection	111

Mazza, Fabio		
Common EXO5 haplotypes impact its protein structure and dynamics, modulating genomic instability and progression in cancer patients		112
McCullough, Marcel	Presenter: Poti, Adam	
Redefining the mutation spectrum at STRs reveals multi-dimensional MMR deficiency phenotypes in cell line models and tumors		113
Monge, Claudia		
Chronic hepatitis b virus infection and xenobiotics exposure interactions at the crossroads of early hepatocellular carcinoma onset		114
Mortvanski, Natasa		
Unravelling of the immunogenomic factors influencing cancers of unknown primary (CUPs)		115
Naeem, Maryam		
Dysregulated expression of cell cycle regulators cdc20, plk1, bub1, cdc45, cdca5 in pancreatic ductal adenocarcinoma		116
Naeem, Maryam	Presenter: Sultan, Aneesa	
Classical protein tyrosine phosphatases as prognostic markers in pancreatic ductal adenocarcinoma		117
Nam, Chang Hyun		
Epigenomic evolution during tumorigenesis in colorectal cancer		118
Nayak, Akshatha	Presenter: Georgakopoulos-Soares, Ilias	
The cumulative impact of passenger mutations on cancer development		119
Ögren, Linnéa		
The influence of genomic contexts on deamination kinetics in UV-exposed DNA		120
Pappaert, Eden		
Defining the complete mutant clonal landscape of head and neck epithelia		121

Park, Hansol		
Comprehensive whole-genome characterization of ALK-rearranged non-small cell lung cancer	122	
Parmentier, Mathieu		
Subtyping xeroderma pigmentosum in tanzania through blood whole-exome sequencing	123	
Patel, Aamena		
A multiomic approach to classifying head and neck tumours	124	
Patil, Srishti		
Somatic evolution in early-onset and advanced colorectal cancer	125	
Pavlova, Sarka		
Genomic context of mutant TP53 clone dynamics under targeted therapy in chronic lymphocytic leukemia	126	
Pellegrini, Stefano	Presenter: Muñios, Ferran	
The structural makeup of missense drivers of somatic clonal selection	127	
Pereira, Ana Rafaela	Presenter: Sussuchi, Luciane	
Genomic profiling of brazilian gastrointestinal stromal tumours using whole-exome sequencing	128	
Pirrie, Scott		
Regional Alteration Signatures: An NMF based approach to characterise regional copy number patterns in whole genome sequenced tumours.	129	
Popp, Ferdinand		
Large-scale telomere maintenance mechanism profiling from routine sequencing data: applications in pediatric precision oncology across tissue and liquid biopsy samples	130	
Puchal-Batriu, marti	Presenter: Muñoz Torres, Pau Marc	
Tronco: a machine learning approach to predict oncogenic translocations	131	

Ritzel, Christoph		
Bridging genome and transcriptome: inferring tumor-specific gene fusions from structural variants		132
Rocha Iraizos, Ana Lucia		
Integrative genomic and transcriptomic Profiling reveals molecular features of post-transplant lymphomas		133
Roerink, Sophie		
Towards CUPPA3.0: a machine-learning classifier for predicting tumor of origin for Cancer of Unknown Primary (CUPs)		134
Romero Arias, J. Roberto	Presenter: Ramirez-Santiago, Guillermo	
Spatial patterns that promote angiogenesis		135
Rosendahl-Huber, Axel		
Estimating the number of mutated cells in human tissues		136
Ruzickova, Lucie		
Long-read sequencing uncovers chromoplectic origin of cryptic CIC-DUX4 fusion through divergent D4Z4 arrays		137
Sakamoto, Yoshitaka		
Detecting somatic mutations in cancer genomes based on personalized reference genome		138
Schiller, Alice		
Early initiation of small intestine neuroendocrine tumors		139
Schlotmann, Balthasar		
The effect of germline predispositions to somatic alterations in prostate cancer		140
Schoppe, Laura		
CRISPR-Cas9 screening to identify ecDNA gene dependencies		141
Sherwood, Kitty		
Genomic instability and complex structural events drive the evolution of malignant pleural mesothelioma		142

Stein, Alexander		
Mathematical modelling predicts selective sweeps to be restricted to very the early stages of tumour growth	143	
Steketee, Mischa	Presenter: Kim, Yongsoo	
Statescope deconvolution reveals the prognostic value of rare cell types in pancreatic ductal AdenoCarcinoma	144	
Stikker, Bernard		
Implementing rapid nanopore methylation profiling and AI classification of adult CNS tumors for routine clinical diagnostics	145	
Stránská, Kamila		
Dynamics of multiclonal expansions in chronic lymphocytic leukemia	146	
Streck, Adam		
CNSistent integration and feature extraction from somatic copy number profiles	147	
Suurenbroek, Lianne		
UV-induced mutations accumulate during early clonal expansion in aneuploid subtypes of pediatric B-cell precursor acute lymphoblastic leukemia	148	
Svozilova, Hana		
Dissecting cellular and molecular features of concurrent lymphoid and myeloid malignancies	149	
Taušová, Kristýna	Presenter: Plevová, Karla	
Principles of TP53 mutagenesis and selection in chronic lymphocytic leukemia	150	
Thompson, Joe Sneath		
Predicting chemotherapy resistance in paediatric osteosarcoma using chromosomal instability signatures	151	
Tiso, Francesca		
Unraveling the origin and development of mucinous ovarian cancer	152	

Trombitas, Tamas	Presenter: De Preter, Katleen	
Improved diagnosis of patients with CUPs using a liquid biopsy assay for DNA methylation-based fingerprinting		153
Turner, Serafina		
Towards de novo phased genome assembly of cancer genomes		154
van Belzen, Ianthe		
Mechanisms underpinning cancer genome complexity, oncogene amplification and ecDNA formation		155
Verhasselt, Amber		
Improved cytogenomic diagnosis in lymphoma through long-read sequencing		156
Villaman, Camilo	Presenter: Espinosa-Parrilla, Yolanda	
Circular RNAs as key gene regulators in cancers from the gastrointestinal tract identified through an integrative genomic approach		157
Vlaicu, Ioana-Antonia		
Integrating methylation and copy number aberrations across a pan cancer database for subtype prediction		158
Walter, Wencke		
SEMA6A::FEM1C, a genomic rearrangement-independent fusion strongly associated with BCR::ABL1 and BCR::ABL1-like B-ALL		159
Wei Ni, Yew		
Characterisation of C6orf15 as a marker for epithelial-mesenchymal transition and lymph node metastasis in colorectal cancer		160
Wong, Wan Chun Ashley		
Spatial DNA sequencing reveals clonal distribution and identifies metastatic clones in prostate cancer archival samples		161
Yu, Tianzhi		
The genomic landscape of juvenile granulosa cell tumours of the ovary		162

Yurchenko, Andrey		
Large-scale characterisation of intratumoral heterogeneity in HR+/HER2– breast cancer at single-cell resolution		163
Zhang, Jia		
Dissecting somatic structural variants in oesophageal cancer using long-read sequencing and SSVanalyser		164
Zilionis, Rapolas	Presenter: Pupelis, Linas	
A scalable platform for single-cell co-profiling of the transcriptome and genotype		165
Zilionis, Rapolas	Presenter: Weren, Robbert	
Next-generation karyotyping: WGA-free single-cell CNV profiling		166