Abbasi, Ammal
Detecting homologous recombination deficiency from exome sequenced breast and ovarian cancers 43

Abdullaev, Eldar
Presenter: Tiso, Francesca; Abdullaev, Eldar
Commonly mutated driver genes in primary mucinous ovarian carcinoma 44

Acedo-Terrades, Ariadna
Transcriptomic landscape of muscle-invasive bladder cancer before and after neoadjuvant chemotherapy treatment 45

Adamová, Sabina
Presenter: Stránská, Kamila
Application of long-read sequencing in chronic lymphocytic leukemia cases with complex karyotype 46

Adhikari, Swagata
Remodeling of extracellular matrix by chromatin regulator UBR7 in Triple-negative breast cancer: insight into chemoresistance 47

Aguilar, Mario
EAGLE: Predicting and evaluating per-nucleotide mutation susceptibility 48

Aguilar, Mario
Presenter: Poetsch, Anna
Genetic encoding of per nucleotide single base substitution probabilities for individual patients 49

Ahmed Nur, Hashim
TREX1 and TREX2 as therapeutic targets to enhance cisplatin-induced cell death 50

Ahrenfeldt, Johanne
Indication of immune protection against cancer in obese younger men 51

Aitken, Sarah
Rerunning tumour evolution reveals germline influences on mutagenesis and cancer susceptibility 52
Aitken, Stuart
Transposable elements are hotspots for copy number breakpoints in high grade serous ovarian cancer 53

Alexander, Diana
The deep subclonal landscape of clear cell renal cell carcinoma 54

Alghamdi, Rana
Claudin genes: prognostic and diagnostic significance in colon cancer via integrated bioinformatics 55

Alvarez, Miguel M
Contrasts of local mutation rates elucidate DNA repair deficiencies 56

Andersen, Laura
Plasma cell-free DNA profiling for deciphering cellular origins and immune competence in cancer patients 57

Anderson, Craig
Using lesion segregation to infer multiple mutagen exposures in cancer 58

Andrianova, Maria
Estimation of minimum required number of drivers and their fitness from genealogy of cell divisions in cancer 60

Arnedo-Pac, Claudia
Hotspot propensity across mutational processes 61

Baird, Tarrion
GS-TCGA: Gene set-based analysis of the cancer genome atlas 62

Baker, Toby
The development of mutational processes in primary and metastatic cancers 63
Bendixsen, Devin
**Charting the mutational landscape of triple negative breast cancer tumours during treatment** 64

Benedetto, Sarah
**Evolutionary Dynamics of Oligodendrogliomas** 65

Besedina, Elizaveta
**Copy number losses of oncogenes and gains of tumor suppressor genes generate common driver events of human cancer** 66

Blanco, Raquel
**Deciphering the molecular signatures of cancer promotion through the analysis of normal tissues** 67

Boll, Lilian Marie
**Unveiling biomarkers to improved response prediction to immune checkpoint inhibitors in advanced bladder cancer** 68

Bowes, Amy
**Profiling the genomic landscape of giant cancer cells in undifferentiated pleomorphic sarcomas: Hopeful monsters or an evolutionary dead end?** 69

Calvet, Ferriol
**Effect of cancer risk factors on the clonal structure of normal tissues** 70

Cao, Xueqi
**Aberrant transcriptome analysis of 3,760 hematologic malignancies reveals LRP1B as hairy cell leukemia variant biomarker** 71

Cast, Oliver
**Multi-species reference free transcriptomic immune estimation with ConsensusTME** 72

Castresana Aguirre, Miguel
**Differential oncogenic pathway expression within cell cycle phases when comparing breast cancer subgroups at a single-cell level** 73
<table>
<thead>
<tr>
<th>Title</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>Resolving chromatin organization in chronic lymphocytic leukemia</td>
<td>74</td>
</tr>
<tr>
<td>Mutational signatures of ethanol and acetaldehyde in oral cancer: an experimental modelling approach</td>
<td>75</td>
</tr>
<tr>
<td>RNAi and chemogenomic screens to identify novel modulators of the nonsense-mediated decay pathway</td>
<td>76</td>
</tr>
<tr>
<td>MHC class II genotypes are independent predictors of anti-PD1 immunotherapy response in melanoma</td>
<td>77</td>
</tr>
<tr>
<td>Decoding the evolution and heterogeneity of Peripheral T-cell Lymphoma through deep multiomic sequencing</td>
<td>78</td>
</tr>
<tr>
<td>Disentangling the chromatin accessibility landscape of Multiple Myeloma patients identified the transcription factor NRF1 a key driver for neoplastic development and progression</td>
<td>79</td>
</tr>
<tr>
<td>Impaired formation of a stable RPA/RNaseH1 complex in senescent cells leads to uncontrolled processing of R-loops and unsuccessful DNA repair</td>
<td>80</td>
</tr>
<tr>
<td>Deciphering mechanisms of T-ALL relapse on a single cell multi-omic level</td>
<td>81</td>
</tr>
<tr>
<td>Germline genetics correlates with aberrant signaling pathways in cancer</td>
<td>82</td>
</tr>
<tr>
<td>Phylogenetic analysis shows genetic bottlenecks in embryogenesis</td>
<td>83</td>
</tr>
</tbody>
</table>
Draškovic, Tina
LIFR-AS1 promoter methylation as a potential diagnostic biomarker differentiating colorectal cancer and colorectal liver metastases from other adenocarcinomas

Elrick, Hillary
SAVANA: a computational method to characterise structural variation in human cancer genomes using long-read sequencing

Espejo Valle-Inclán, Jose
Evolutionary trajectories of complex genome rearrangements in cancer

Espinosa, Marta
The translation of non-canonical ORFs is associated with the generation of neoantigens in hepatocellular carcinoma

Fernández-Sanromán, Ángel
The evolution of chromosomal instability in prostate cancer

Fito, Bruno
Prevalence, causes and impact of TP53-loss phenocopying events in human tumors

Fong, Vernon
Defining the Involvement of the Perivascular Niche in Brain Tumour Metastases

Gabre, Jonatan
Preclinical exploration of the DNA Damage Response pathway using the interactive neuroblastoma cell line explorer CLEaN

Gallardo, María
Epigenetic and transcriptomic signatures to predict response to immune checkpoint inhibition in NSCLC

Gao, Miaomiao
Evolutionary trajectories and mechanisms of colorectal peritoneal metastasis formation
Ghosh, Avantika  
Presenter: Diederichs, Sven  
*Global analysis uncovers frequent loss of tumor suppressor proteins by stop-loss mutations*  
94

Godfrey, Laura  
*Clonal expansion and adaptive DNA methylation-based epigenetic plasticity underlie resistance to oncogenic pathway inhibition in pancreatic cancer*  
95

Govada, Pravallika  
*Landscape of differentiation induced oncogenesis regulated by pseudogenes: a study of gastrointestinal tract*  
96

Gu, Andrea  
*Whole-genome CRISPR-Cas9 screens reveal genetic dependencies in NRAS-mutant melanoma cell lines*  
97

Harbers, Luuk  
*High clonal diversity and spatial genetic admixture in early prostate cancer and surrounding normal tissue*  
98

Harvey, Luke  
CANCELLED  
99

Hazelwood, Emma  
*Integrating large-scale genomic and transcriptomic datasets to identify colorectal cancer susceptibility genes with therapeutic potential*  
100

Helminen, Laura  
*Chromatin accessibility and pioneer factor FOXA1 shape glucocorticoid receptor action in prostate cancer*  
101

Höfer, Thomas  
*Optimal hematopoietic stem cell dynamics suppress the selection of leukemic mutations*  
102

Hohenleitner, Maximilian  
*Identification of genes diverging metastasis in the intestinal type of gastric cancer*  
103
Hoogstoel, Sofie
The potential of whole-body donors in studying mutant clones in normal tissues 104

Hoppe, Sascha Presenter: Hillmer, Axel
Molecular adaption to radio-chemotherapy in esophageal adenocarcinoma and influence of BRCA2 function 105

Hörsch, Franziska
Clonal hematopoiesis through dysfunction of the Fanconi anemia DNA repair pathway 106

Jokinen, Vilja
RNA-sequencing reveals a subset of uterine leiomyomas with FGFR1 and FGFR2 mutations 107

Juul, Randi Istrup
Exploring changes in protein levels in plasma before and after cystectomy in patients with bladder cancer 108

Kadam, Aditee
Detection, characterization, and prevention of MMEJ deletions 109

Kalyva, Maria
Elucidating the clonal evolutionary dynamics of hypermutated tumors using single-cell whole-genome sequencing 110

Kaufmann, Tom
Inferring copy number signatures from distinct evolutionary events 111

Kazachkova, Mariya
Evolutionary analysis reveals independent clonal populations in single Barrett’s esophagus biopsies 112

Khalil, Ahmed
Signatures of conditional selection in cancer whole-genome sequences identify chemotherapy resistance genes 113

Khare, Sanika Presenter: Danielski, Katharina
Enhanced single cell DNA methylation analysis using combinatorial sequencing 114
Kisakol, Batuhan
An atlas of CMS in colorectal cancers at spatial single-cell resolution 115

Kjær, Asbjørn
T cell receptor repertoire diversity and blood T cell fraction is associated with outcome in bladder cancer 116

Kongprajug, Akechai
Regulation of Brachyury gene expression in breast cancer 117

Kranas, Hanna
Genome segmentation by DNA damage repair dynamics 118

Lang, Franziska
Identification of neoantigen candidates from splicing in human tumor cell lines 119

Lee, Nathan
Longitudinal tracking of acute myeloid leukemia clonal evolution after allogeneic hematopoietic cell transplantation 120

Lefèbvre, Maxime
Studying differences in mutability between parental sets of chromosomes 121

Leppä, Aino-Maija
Single-cell dissection of CK-AMLs characterizes targetable disease-driving leukemic stem cell clones 122

Leppä, Aino-Maija
Longitudinal assessment of NPM1-mutated acute myeloid leukemia patient samples reveals novel insights into targeting therapy-resistant leukemic stem cells 123

Livingston, Bryn
Investigating the function of the recurrent TBR1 G275C mutation in group 4 medulloblastoma 124
Love, Marian
**Multi-dimensional DPClust is a valuable strategy for analysing the clonal/subclonal relationship between multiple WGS LCM samples.**

Lu, Zhaolian
Presenter: Hu, Zheng
**Single-cell lineage mapping of IBD or FAP-associated colorectal tumorigenesis**

Luhari, Laura
**Genetic alterations as independent prognostic factors to predict organ-specific metastases of lung cancer**

Luhari, Laura
**Genetic alterations as independent prognostic factors to predict the type of recurrence of lung cancer**

Luijts, Tom
**Predicting TP53 mutations from spatial transcriptomics data using graph neural networks**

Mäkinen, Netta
**Genomic and transcriptomic analyses of small intestinal neuroendocrine tumors**

Margaux, Gras
**The importance of somatic reference materials for precision medicine.**

Martin, Samantha
**Genomic characterisation of mismatch repair deficient colorectal cancer: tumours from Lynch syndrome patients show extreme resemblance with sporadic cases**

Mayoh, Chelsea
**Expanding the utility of transcriptome analysis in high-risk childhood precision oncology**

McClellan, Michael
**Polymerase Error Rate sequencing (PER-seq); a novel method for detection of DNA polymerase errors in single molecules**
McCullough, Marcel
Combinatorial gene editing to model genetic interactions in DNA repair deficiencies

McNamara, Megan
Circulating cell-free methylated DNA reveals tissue-specific, cellular damage from radiation treatment

Mensah, Nana
Revealing aberrant DNA methylation in SINETs through pure-methylome analysis with an EC-like cell line

Mitchell, Jonathan
Clinical application of tumour in normal contamination assessment from whole genome sequencing data

Mukherjee, Nivedita
Factors shaping biallelic mutation frequencies of tumour suppressor genes

Neumaier, Jennifer
Using Machine Learning to tackle tumor heterogeneity

Nicholson, Michael
Quantifying the mechanics of transcription coupled repair

Oitaben, Ana
Genomic profiling for predicting ICI response in lung and bladder tumors

Paassen, Irene
SMARCB1 loss activates patient-specific distal MYC enhancers that drive malignant rhabdoid tumor growth

Pablo-Fontecha, Veronica
Chromosome instability and aneuploidy tolerance influence single-cell fate upon replication stress

Parmentier, Mathieu
Subtyping Xeroderma Pigmentosum in Tanzania through blood whole-exome sequencing
<table>
<thead>
<tr>
<th>Name</th>
<th>Title</th>
</tr>
</thead>
<tbody>
<tr>
<td>Paterson, Chay</td>
<td>Evolution on graphs and the transition to cancer</td>
</tr>
<tr>
<td>Pellegrini, Stefano</td>
<td>Structure-based models to identify driver genes and mutations</td>
</tr>
<tr>
<td>Pensch, Raphaela</td>
<td>Comparative analysis of non-coding constraint mutations in canine and human osteosarcoma</td>
</tr>
<tr>
<td>Pham, My</td>
<td>A comprehensive survey of somatic mutations in normal human cells</td>
</tr>
<tr>
<td>Poon, Yeuk Pin Gladys</td>
<td>Clonal evolution preceding cancer revealed using single-cell DNA sequencing and computational modelling</td>
</tr>
<tr>
<td>Przybilla, Moritz</td>
<td>DNA damage in alveolar stem cells mirrors long-term lung cancer risk in smokers</td>
</tr>
<tr>
<td>Purohit, Krishna</td>
<td>YAP/TAZ activation predicts clinical outcomes in mesothelioma and is conserved in in vitro model of driver mutations</td>
</tr>
<tr>
<td>Rabenius, Adelina</td>
<td>Deciphering drug-induced transcriptional responses in cancer cells</td>
</tr>
<tr>
<td>Räisänen, Maritta</td>
<td>Chromatin state annotation to unravel epigenetic changes in tumorigenesis with uterine leiomyoma as a model</td>
</tr>
<tr>
<td>Rajamani, Anantharamanan</td>
<td>Deciphering whole genome doubling and temporal mutational dynamics in mouse models of pancreatic ductal adenocarcinoma (mPDAC)</td>
</tr>
<tr>
<td>Ramis Zaldívar, Joan Enric</td>
<td>In Silico Saturation Mutagenesis to Identify Clonal Hematopoiesis Driver Mutations</td>
</tr>
</tbody>
</table>
EMBL Conference: Cancer Genomics

Ramnarayanan, Sunandini
Experimental and statistical evidence for fitness-altering tumour mutations acting via long non-protein-coding RNAs

Reigl, Tomas
CLLue: Searching for connections among clinical, biological, and molecular features in the dataset of leukemia patients

Reigl, Tomáš
Web-based bioinformatic tool LYNX: lymphoid next-generation sequencing data analysis and visualization in hematological malignancies

Rodriguez Fos, Elias
Mutational topography reflects clinical neuroblastoma heterogeneity

Romero Arias, J. Roberto
A mathematical model for pancreatic cancer during intraepithelial neoplasia*

Rosendahl-Huber, Axel
Estimating mutation risks conferred by mutational processes in cancer genomes

Rueda, Bertha
Exploring the exome of lung adenocarcinoma in Mexican patients and some insights about worldwide discrepancies in its treatment

Ryan, Kevin
Identification of potential neoantigens in cancer-associated fibroblasts isolated from breast cancer patients

Sanabria, Melissa
GROVER: Building a Language Model of the Human Genome

Sanghvvi, Rashesh
Clonal dynamics of TP53 mutations in male germline cells and the implications for cancer predisposition in offspring
Sauer, Carolin
Application of Nanopore sequencing for liquid biopsy analysis in children with cancer 167

Sax, Irmi
Challenges of Tumour-only variant calling from Amplicon-based sequencing 168

Scandino, Riccardo
Rapid and data-driven generation of synthetic NGS Cancer Datasets with SYNGEN 169

Segueni, Julie
DNA methylation changes cause pervasive reorganization of CTCF binding and 3D genome structure in breast cancer cells 170

Selway-Claire, Hugh
In silico testing of hypotheses for the effect of smoking on somatic evolution in the healthy human lung 171

Siaw, Joachim Tetteh
RUVBL1 and RUVBL2 as novel druggable DNA damage response regulators in the N-Myc regulatory network in neuroblastoma 172

Sibai, Mustafa
Unraveling the spatial architecture of Cancer Hallmarks 173

Singh, Minu
Identification of Genomic and Transcriptomic Aberrations of Clinical and Biological Relevance in Pediatric T-ALL: Data from a Tertiary Care Centre of India 174

Sipilä, Lauri
Genome-wide somatic mutation analysis of formalin-fixed paraffin-embedded sinonasal adenocarcinomas 175

Smits, Kim
Presenter: Zavadil, Jiri
Identification of a mutational signature of dietary acrylamide in renal cancer genomes 176

Spinou, Anastasia
Inference of pathway functional interactions in pediatric cancer 177
EMBL Conference: Cancer Genomics

Streck, Adam  
Presenter: Duncan, Cody  
Quantifying Fitness Effects of Structural Variants with SimChA  

Sulo, Päivi  
Nanopore sequencing reveals structural features of somatic and germline retrotransposon insertions  

Svozilova, Hana  
Enhanced in vitro culture of leukemic cells: insights from collagen scaffolds and carboxymethyl cellulose-polyethylene glycol gel  

Taher, Dalil  
Measuring the interplay between chromosomal instability and whole-genome doubling in human cancer  

Taira, Aurora  
Epigenetics meets metabolomics: studying the link between methylation and metabolism in BRAF mutated colorectal cancer  

Teague, Jonathan  
An Update: COSMIC - Catalogue Of Somatic Mutations in Cancer  

Tolotto, Vanessa  
HDAC4 targeting in FBXW7 mutated CRC re-sensitizes cells to Oxaliplatin treatment  

Tomkova, Marketa  
Epigenome-instructed pan-cancer discovery of non-coding cancer drivers  

Torra I Benach, Maria  
Clonal Evolution Trajectories of Mature and Immature Teratomas  

Trinh, Mi  
Stepwise transcriptional progression of myeloid leukaemia associated with Down syndrome  

Trinh, Mi  
Stepwise transcriptional progression of myeloid leukaemia associated with Down syndrome
van Belzen, Ianthe
**Complex structural variation is prevalent and highly pathogenic in pediatric solid tumors**

Vázquez, Sergio
**Effect of bladder cancer subtypes on response to immunotherapy**

Verburg, Jan
**Accurate comparison of insertion and deletion mutation rates using sequence composition correction with novel sequence ambiguity scoring**

Viana-Errasti, Julen
**Optimizing POLE and POLD1 variant interpretation: gene-specific classification guidelines and in vitro system for functional assessment**

Vlaicu, Ioana-Antonia
**A pan-cancer copy number profile database from published array-based studies**

Volakhava, Anastasiya
**“Hide and seek” Retroelement Activity in Hematological Malignancies**

von Berg, Joanna
**The Dutch childhood cancer genome project: characterizing tumor drivers**

Vorberg, Tim
**Extrachromosomal DNA promotes drug resistance in pancreatic ductal adenocarcinoma cells**

Waise, Sara
**Profiling the complex rearrangement architecture of sarcoma**

Wang, Evan
**Genomic analysis of WNT medulloblastoma reveals drivers of monosomy 6**
Wang, Yichen
Mutational processes in tumour-adjacent normal kidneys across countries with varying RCC incidence rates 199

weaver, jamie
Establishing a rapid autopsy program to explore cancer evolution: preliminary experience within the UK regulatory framework 200

Wenger, Anna
Tracing the origin of hepatoblastoma 201

Whitfield, Holly
Differentiation states of paediatric B-cell acute lymphoblastic leukaemia 202

Woodhouse, Laura
Profiling copy number mutational signatures in KRAS mutant non-small cell lung cancer 203

Yang, Ting
Mapping the somatic mutations during the evolutionary transition from oral leukoplakia to oral squamous cell carcinoma 204

Yao, Zhihao
Identifying significant genomic information in cancer through integrating multi-omics datasets 205

Yemelyanenko Lyalenko, Julia
Deciphering FGFR3-TACC3 oncogenic fusions 206

Yong, Hanting
Improved methods of analysis in functional genomics screens: application to screens of tumour microenvironment stress 207

Zhang, Tongwu
mSigPortal: A comprehensive platform for interactive mutational signature analysis in cancer genomics 208

Zuljan, Erika
Analysis of the tumor immune microenvironment in advanced salivary gland cancers 209