

LABORATORY OF

GENOMICS AND BIOINFORMATICS

Bioinformatics, functional genomics, cancer microenvironment, ancient mtDNA, endogenous retroviruses

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Activity of our laboratory is based on advanced applications of genomics, transcriptomics and bioinformatics, the most vigorously developing disciplines of contemporary life sciences. Since 2017, we have been equipped with the Illumina NextSeq next-generation sequencer, which replaced outdated microarray technology. From 2019, we have been using single cell transcriptomics and epigenomics technology [10x Genomics]. As a part of our know-how, we develop sophisticated bioinformatical tools and pipelines to analyse produced data sets as well as those available in public databases. We use all these high-throughput and bioinformatic tools to conduct our own scientific projects, for long term collaborations with our colleagues and clinicians, and to support other scientific groups at the Institute.

Cancer transcriptomics. We have been involved in a long term-project focused on head and neck squamous cell carcinoma and skin cancers. We focus on tumour microenvironment and interactions between cancer associated fibroblasts and tumour cells. Recently, we have published a summary of this collaborative work [1]. We have collected a large data set of patient samples [>100 patients] and cancer associated fibroblasts that are being analysed in the recently awarded project Centre for Tumor Ecology supported by the Operational Programme Research, Development and Education.

Bioinformatics and databases, genomics. The laboratory forms the local node of the Pan-European ELIXIR bioinformatics research infrastructure. We curate and maintain the database of mitochondrial sequences coming from the ancient DNA samples AmtDB [2] and the database of human endogenous retroviruses HERVd. In collaboration with the

Laboratory of Viral and Cellular Genetics, we study endogeneous retroviruses also in other species [3]. In collaboration with other groups of the Institute, members of the Laboratory became involved in functional genomics research of several models of malignant and immune diseases [4,5].

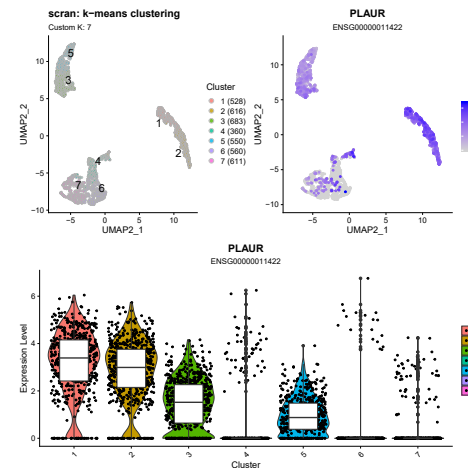


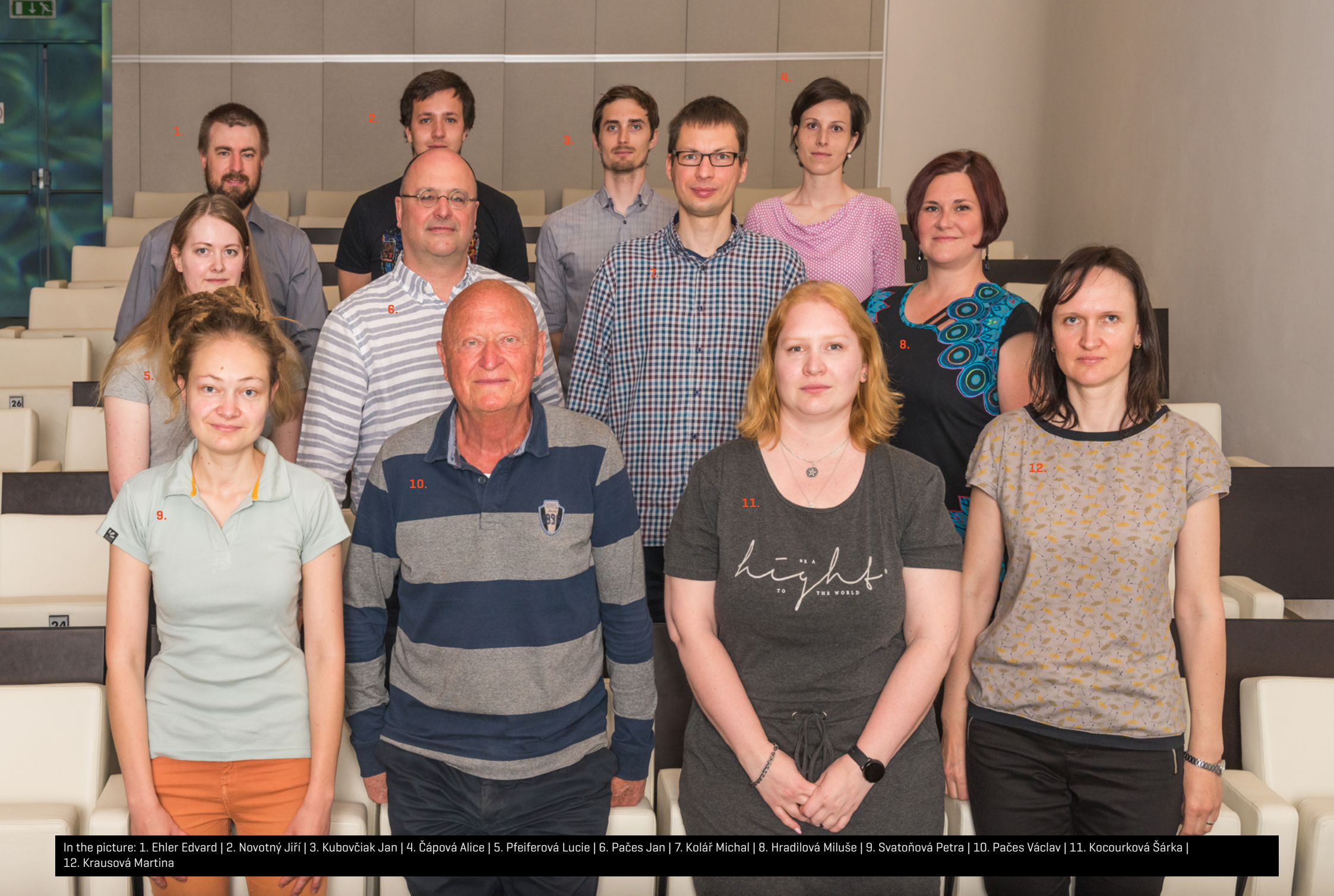
Figure 1. Clustering of single-cell transcriptomic data with emphasized expression of the marker gene PLAUR.



Figure 2. Example output from the AmtDB search engine (A) and visualization of the results on a map (B).

Selected publications:

1. Plzák J, Bouček J, Bandúrová V, Kolář M, Hradilová M, Szabo P, Lacina L, Chovanec M, Smetana, K Jr. (2019) The head and neck squamous cell carcinoma microenvironment as a potential target for cancer therapy. *Cancers* **11**(4):440 [https://doi.org/10.3390/cancers11040440]
2. Ehler E, Novotný J, Juras A, Chylenski M, Moravčík O, Pačes J (2019) AmtDB: a database of ancient human mitochondrial genomes. *Nucleic Acids Res* **47**(D1):D29-D32. [https://academic.oup.com/nar/article/47/D1/D29/5106144]
3. Farkašová H, Hron T, Pačes J, Hulva P, Benda P, Gifford RJ, Elleder D (2017) Discovery of an endogenous Deltaretrovirus in the genome of long-fingered bats (Chiroptera: Miniopteridae). *Proc Natl Acad Sci U S A* **114**(12):3145-3150.
4. Yamano T, Dobeš J, Vobořil M, Steinert M, Brabec T, Ziętara N, Dobešová M, Ohnmacht C, Laan M, Peterson P, Benes V, Sedláček R, Hanayama R, Kolář M, Klein L, Filipp D (2019) Aire-expressing ILC3-like cells in the lymph node display potent APC features. *J Exp Med* **216**(5):1027-1037.
5. Horázná M, Janečková L, Švec J, Babošová O, Hřčkulák D, Vojtěchová M, Galušková K, Šloncová E, Kolář M, Strnad H, Kořínek V (2019) Mx1 loss suppresses formation of the ectopic crypts developed in the Apc-deficient small intestinal epithelium. *Sci Rep* **9**(1):1629.



In the picture: 1. Ehler Edvard | 2. Novotný Jiří | 3. Kubovčiak Jan | 4. Čáповá Alice | 5. Pfeiferová Lucie | 6. Pačes Jan | 7. Kolář Michal | 8. Hradilová Miluše | 9. Svatoňová Petra | 10. Pačes Václav | 11. Kocourková Šárka | 12. Krausová Martina