

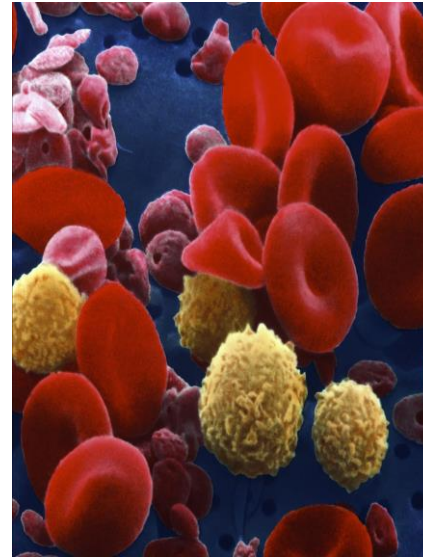
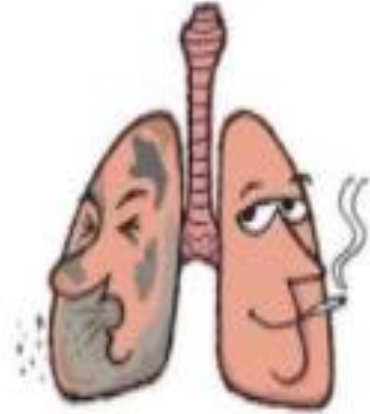
*Non coding RNAs high
throughput sequencing data to
classify human blood cell
types and lung tumor samples.*

Natasha Jorge

34th TBI Winterseminar in Bled

13rd Annual Meeting of the Bompfünowerer Consortium

Non coding RNAs high throughput sequencing data to classify human blood cell types and lung tumor samples.



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 PLOS ONE

RESEARCH ARTICLE

snRNA and piRNA expression levels
modified by tobacco use in women with lung
adenocarcinoma

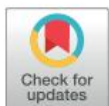
Natasha Andressa Nogueira Jorge¹, Gabriel Wajnberg¹, Carlos Gil Ferreira², Benilton de Sa Carvalho³, Fabio Passetti^{1*}

¹ Laboratory of Functional Genomics and Bioinformatics, Oswaldo Cruz Institute, Fundação Oswaldo Cruz, Rio de Janeiro, RJ, Brazil, ² D'or Institute for Research and Education, Rio de Janeiro, RJ, Brazil, ³ Department of Statistics, State University of Campinas, Campinas, SP, Brazil

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Abstract

BLUEPRINT
epigenome



RESEARCH ARTICLE

snoRNA and piRNA expression levels modified by tobacco use in women with lung adenocarcinoma

Natasha Andressa Nogueira Jorge¹, Gabriel Wajnberg¹, Carlos Gil Ferreira², Benilton de Sa Carvalho³, Fabio Passetti^{1*}

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Abstract

snoRNA and piRNA expression levels modified by tobacco use in women with lung adenocarcinoma

OPEN ACCESS Freely available online



A High-Dimensional, Deep-Sequencing Study of Lung Adenocarcinoma in Female Never-Smokers

Sang Cheol Kim^{1*}, Yeonjoo Jung^{2,3*}, Jinah Park^{1*}, Sooyoung Cho^{2,3*}, Chaehwa Seo^{1*}, Jaesang Kim^{2,3*}, Pora Kim^{2,3}, Jehwan Park¹, Jihae Seo^{1,2,3}, Jiwoong Kim¹, Seongjin Park¹, Insu Jang¹, Namshin Kim¹, Jin Ok Yang¹, Byungwook Lee¹, Kyoohyoung Rho¹, Yeonhwa Jung^{2,3}, Juhee Keum^{2,3}, Jinseon Lee⁴, Junggho Han⁵, Sangeun Kang⁴, Sujin Bae⁴, So-Jung Choi⁴, Sujin Kim⁶, Jong-Eun Lee⁶, Wankyu Kim^{2,3}, Jhngook Kim^{4,7*}, Sanghyuk Lee^{1,2,3*}



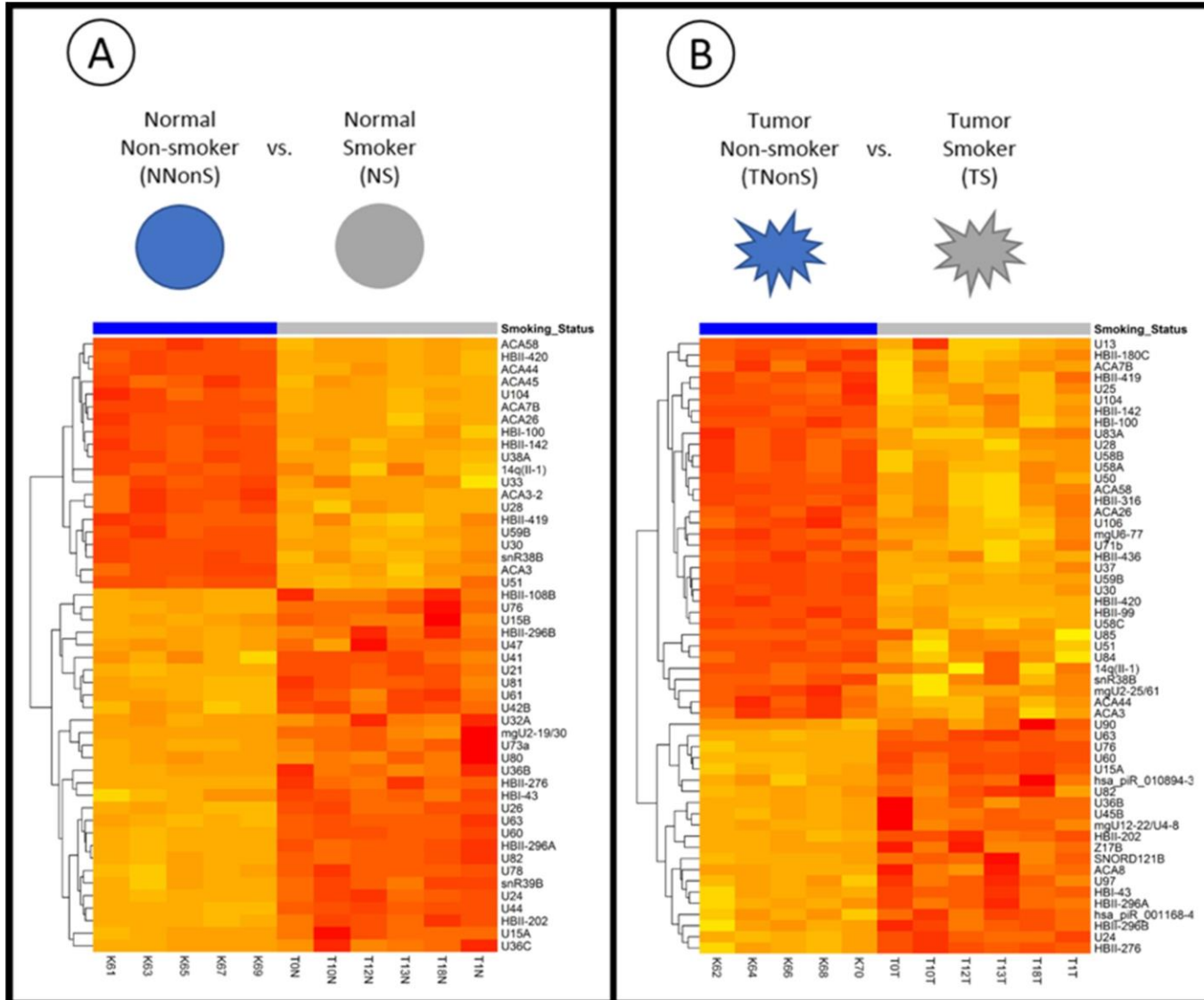
THE CANCER GENOME ATLAS

National Cancer Institute

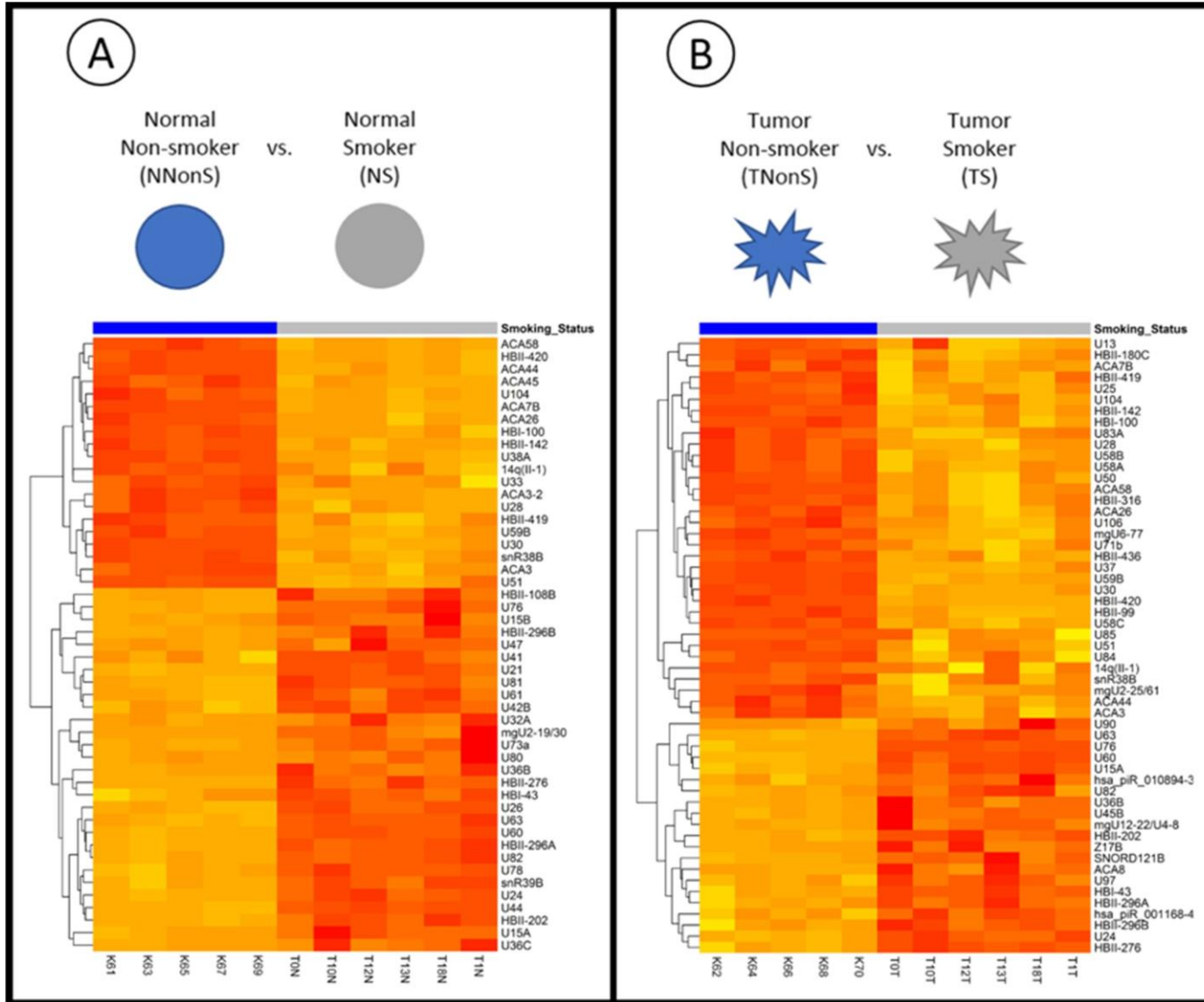
National Human Genome Research Institute



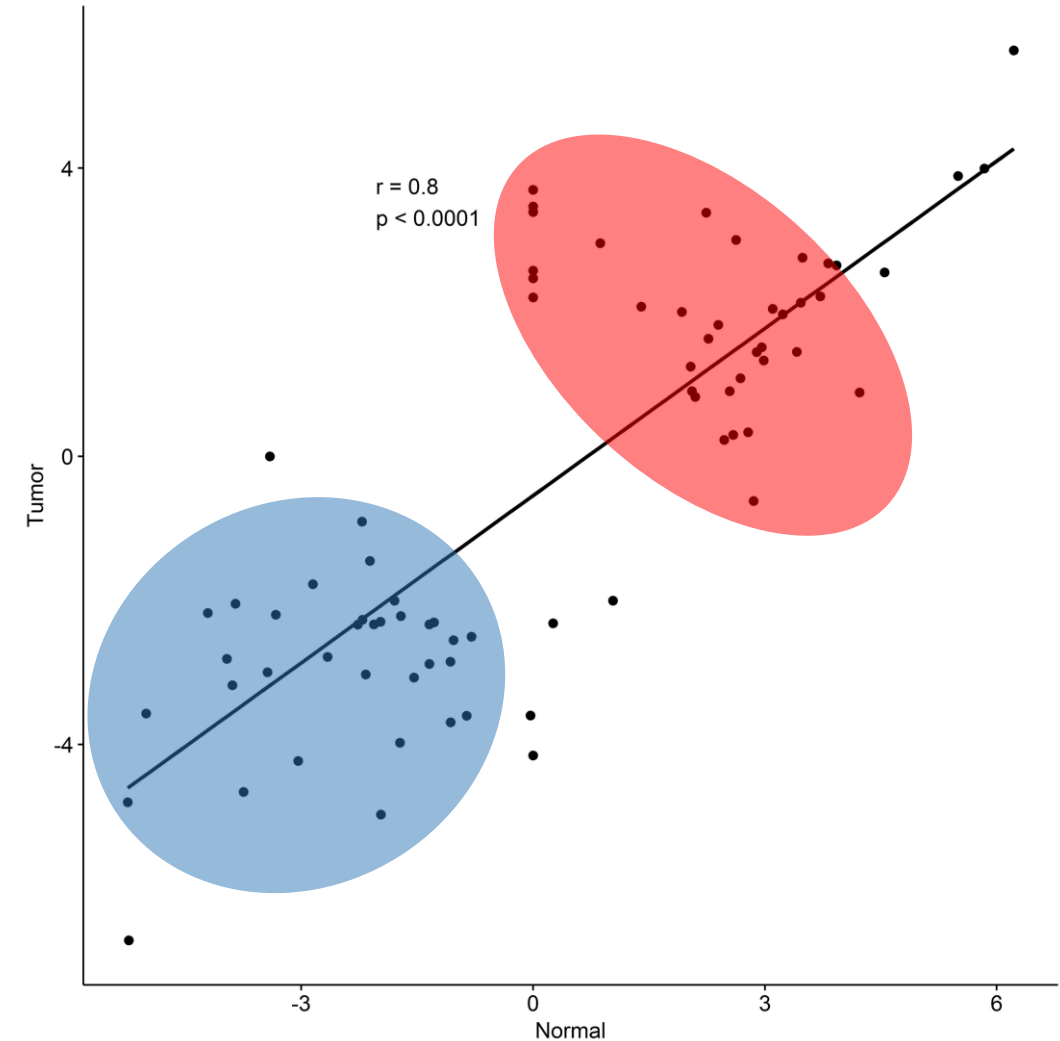
snoRNA and piRNA expression levels modified by tobacco use in women with lung adenocarcinoma



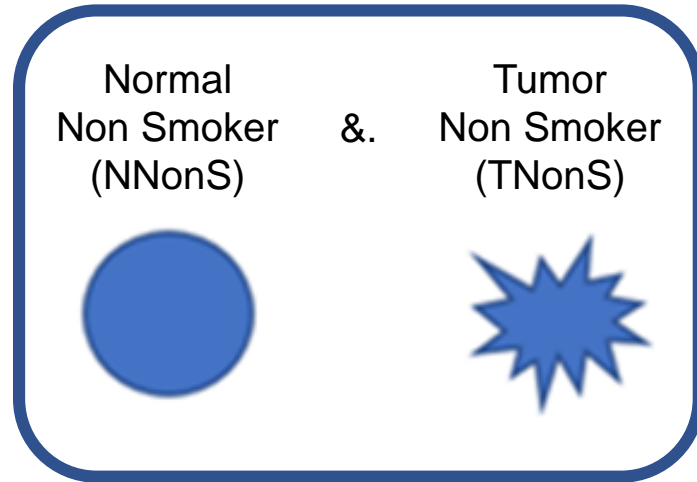
snoRNA and piRNA expression levels modified by tobacco use in women with lung adenocarcinoma



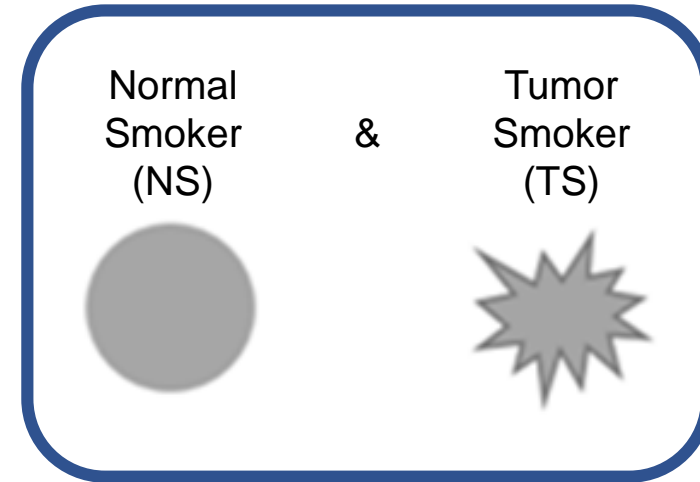
28 genes in common



snoRNA and piRNA expression levels modified by tobacco use in women with lung adenocarcinoma



179 constitutive genes



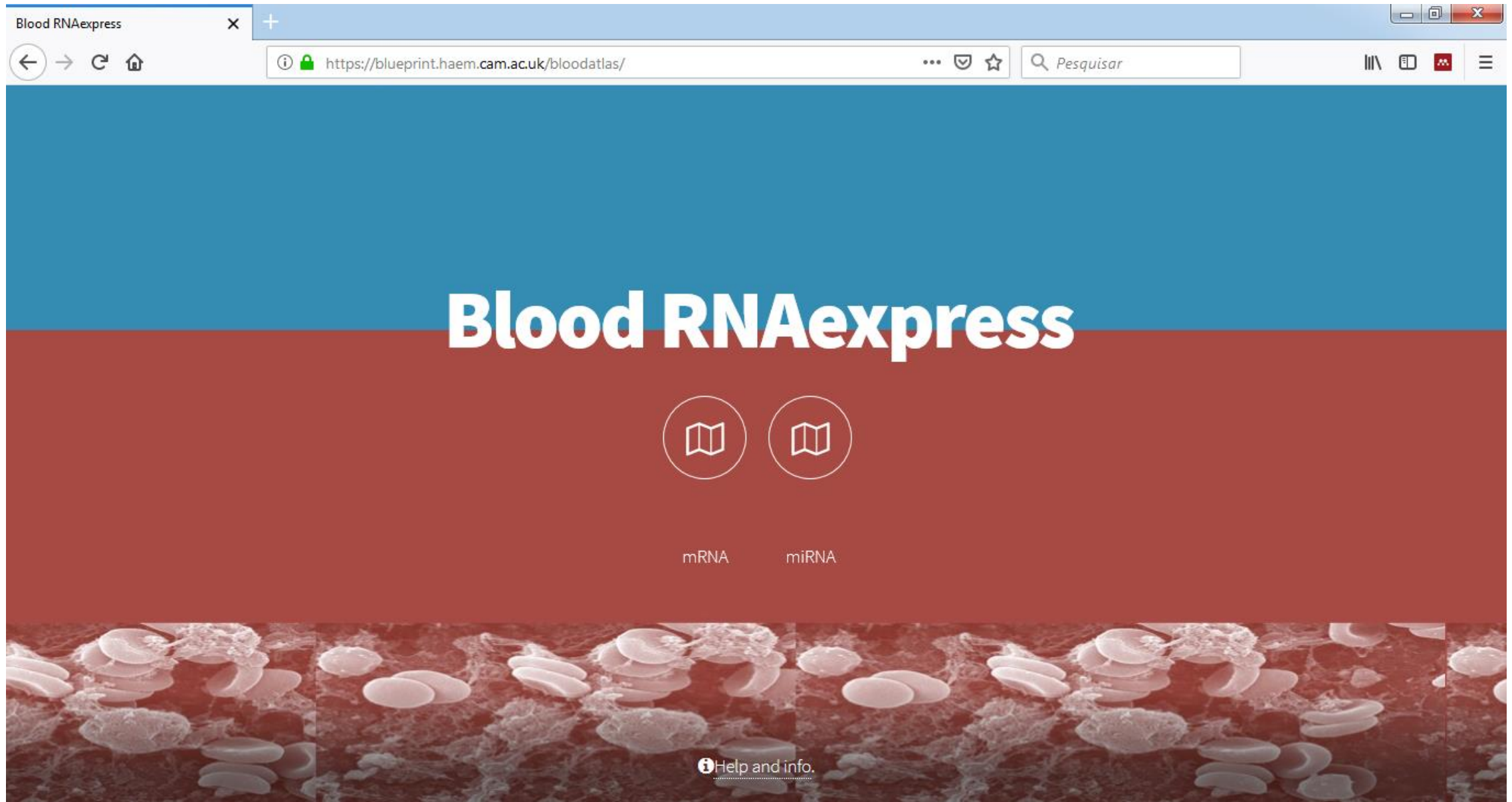
33 constitutive genes

(all in common with non smokers)

snoRNA and piRNA expression levels modified by tobacco use in women with lung adenocarcinoma

- DE snoRNA and piRNA between smokers and non-smokers
- Set of constitutive snoRNA between smoker and non-smokers
- Improve diagnosis and treatment

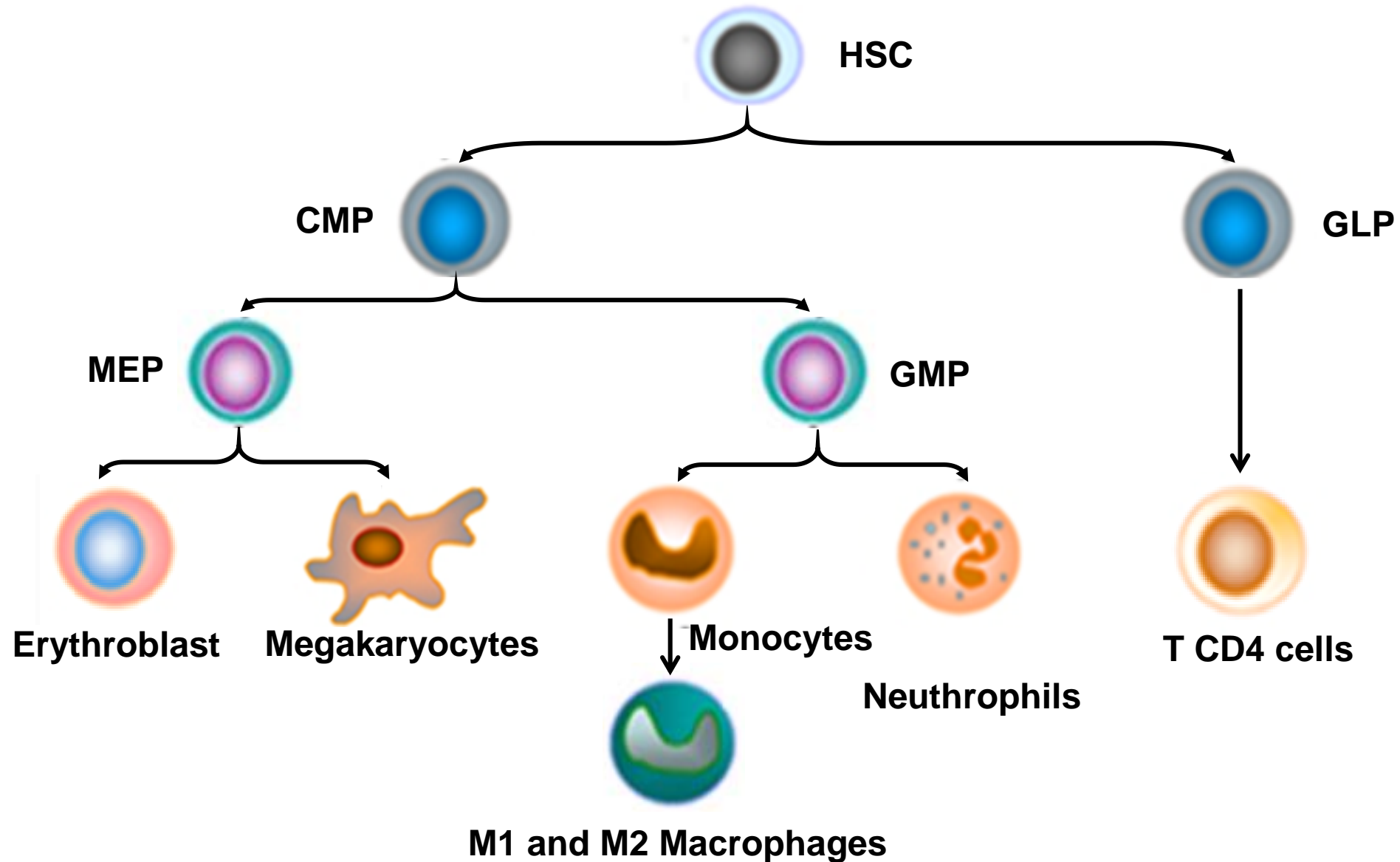
The BLUEPRINT atlas of mature hematopoietic cells transcriptomes.



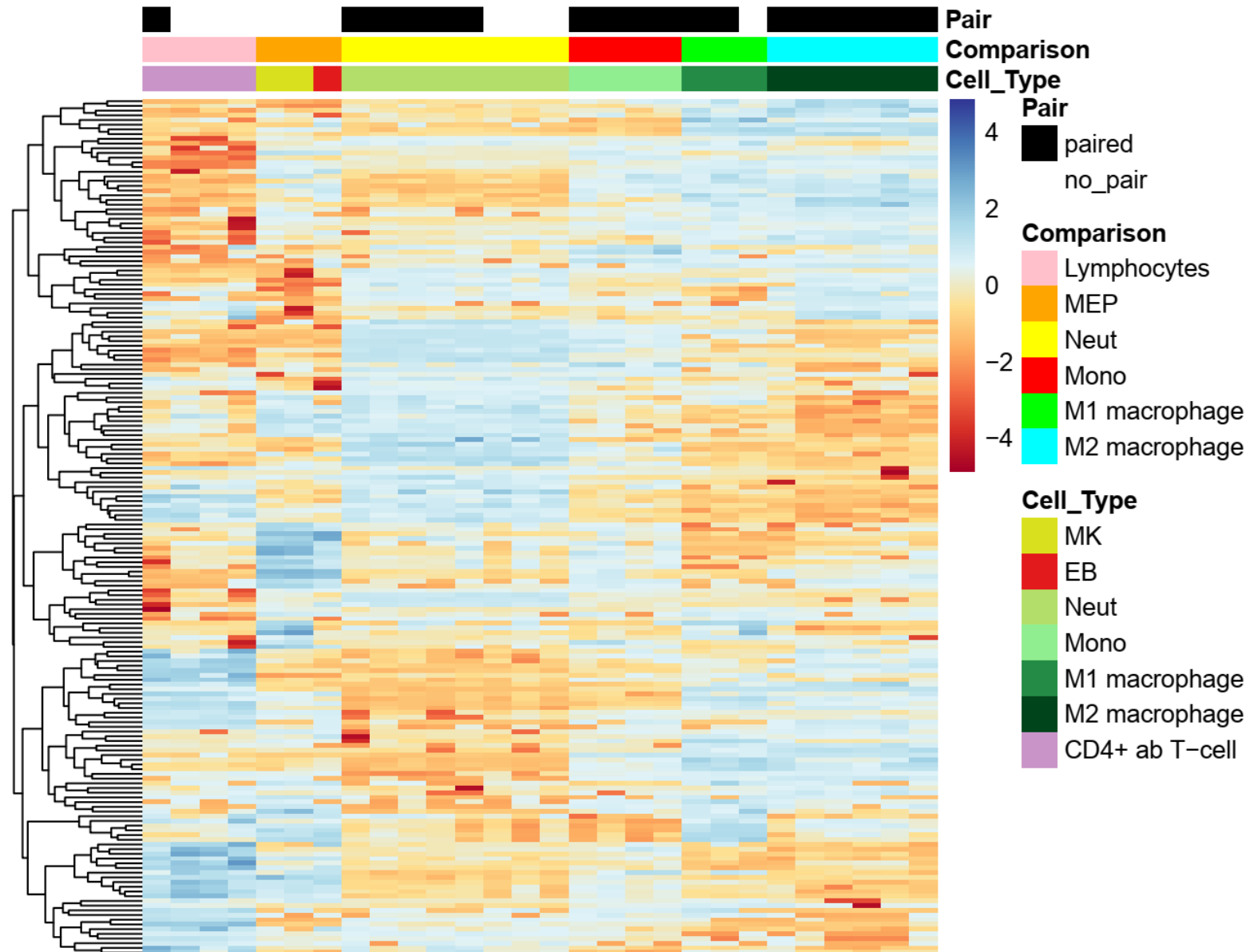
The screenshot shows a web browser window with the following elements:

- Browser Tab:** Blood RNAexpress
- Address Bar:** <https://blueprint.haem.cam.ac.uk/bloodatlas/>
- Search Bar:** Pesquisa
- Header:** A blue horizontal bar with the text **Blood RNAexpress** in white.
- Navigation:** Two circular icons representing a book, labeled **mRNA** and **miRNA**.
- Footer:** A link labeled **Help and info.** with an information icon.
- Background:** A red-to-white gradient background with a microscopic image of blood cells at the bottom.

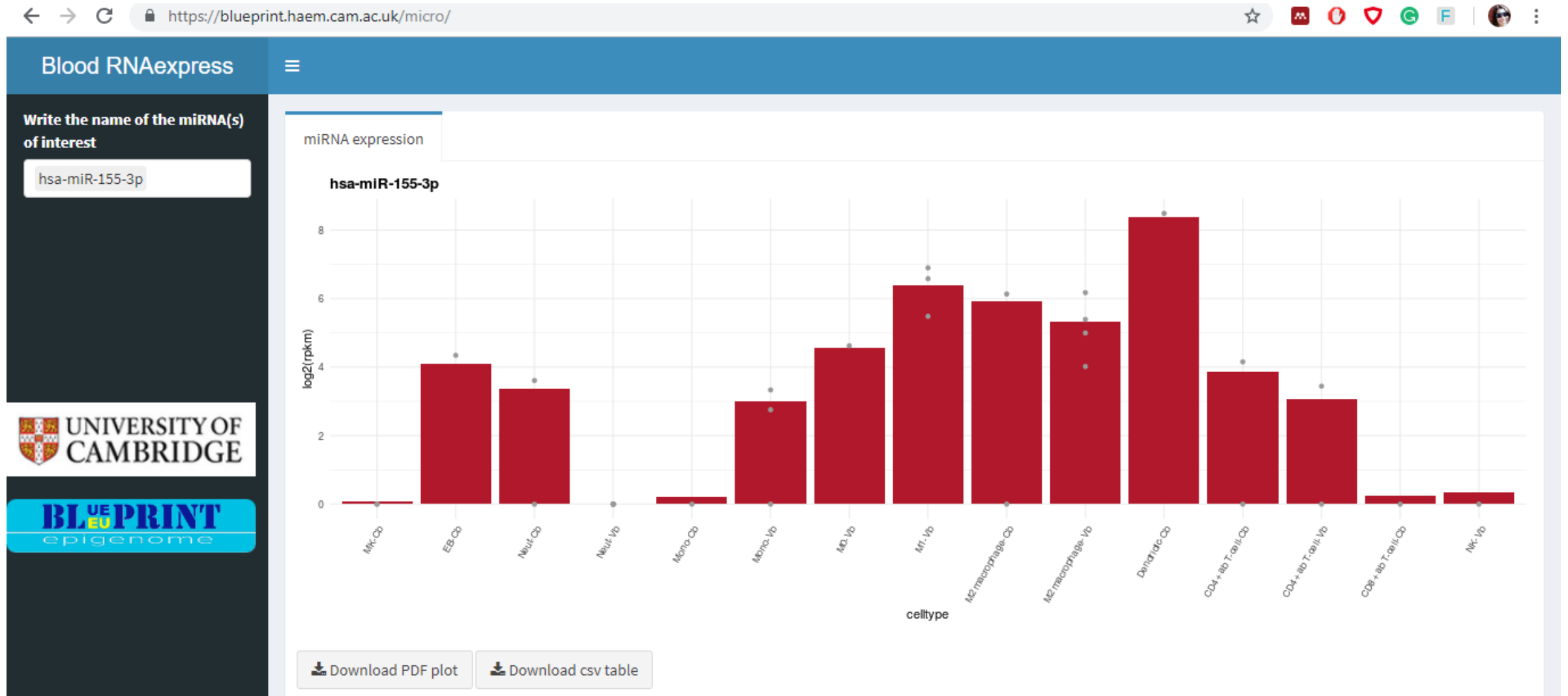
The BLUEPRINT atlas of mature hematopoietic cells transcriptomes (*miRNAs & mRNAs*)



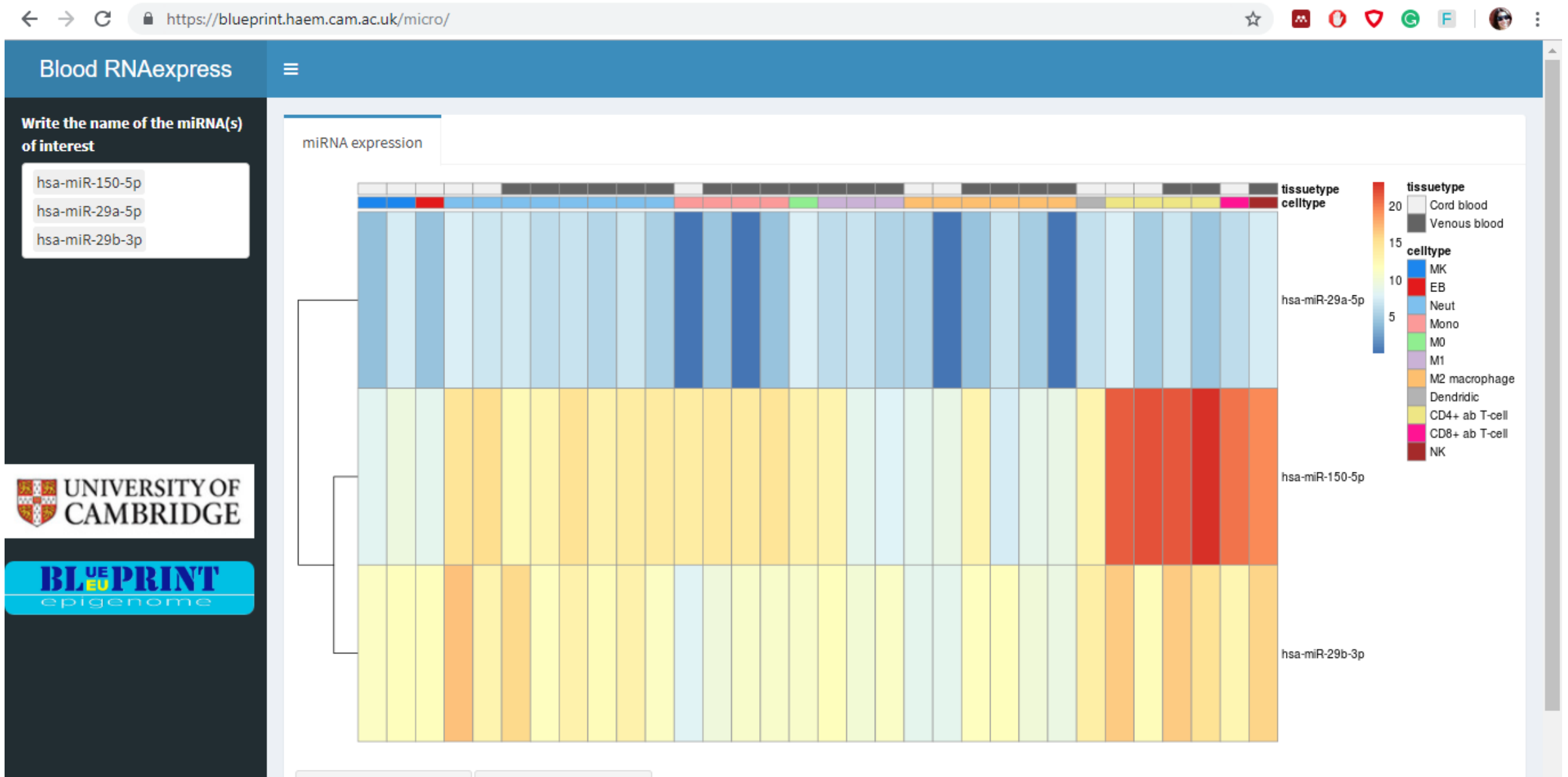
The BLUEPRINT atlas of mature hematopoietic cells transcriptomes. (*miRNAs*)



The BLUEPRINT atlas of mature hematopoietic cells transcriptomes. (*miRNAs*)



The BLUEPRINT atlas of mature hematopoietic cells transcriptomes. (*miRNAs*)



The BLUEPRINT atlas of mature hematopoietic cells transcriptomes.

- Gene expression atlas of mature blood cells (27 different cell types) (90 RNA and 32 small RNA-seq).
- Homogeneity in sample preparation and bioinformatic analysis.
- User can easily retrieve gene and transcript expression values.

спасибо 谢谢
GRACIAS 谢谢
THANK YOU

ありがとうございました MERCI

DANKE धन्यवाद

شُكراً OBRIGADO

