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BASTION – FROM BASIC TO
TRANSLATIONAL RESEARCH
IN ONCOLOGY

Report on the stay of Dr Michał Świerniak at the University of Ferrara, Italy, within the 7PR21/BASTION/WP1 (Twinning)

From May 30th till June 27th, 2015 I visited the research group of Professor Stefano Volinia at the University of Ferrara, Italy.

It was my second visit in Ferrara (the first was in the end of 2014) and I was continuing the project of detection, annotation and statistical analyses of circular RNAs from the Next Generation Sequencing (NGS) data of patients diagnosed with the acute myeloid leukemia (AML). After testing available tools for exploring circRNA I decided to create my own algorithm which allow to detect potential circRNAs in sensitive and specific way.

Algorithm is based on the STAR (Spliced Transcripts Alignment to a Reference) aligner output and includes following steps:

1. Detection of potential circRNAs.

2. Annotation based on known human genes.

3. Creation of custom reference of known circRNAs from the database and potential new circRNAs identified in step 1.

4. Remapping reads unmapped to the genome to the custom reference.

5. Counting reads including the junctions.

6. Filtering the circRNAs based on number of reads across all analyzed samples.

I have analyzed 250 AML samples resulting in identification of over 1000 circRNAs expressed in AML samples. These circRNAs need to be analyzed statistically and validated on the independent group of samples.