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DSMZCellDive: a web tool for browsing and analyzing transcriptomic data of hematological cell lines

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Hematological cell lines are important *in vitro* models for research. For many cancer cell lines, including hematological cell lines, most molecular data like RNA-sequencing (RNA-seq) data are available from different sources but not from the cell line repository itself. This fact ultimately confronts the selection of cell lines as models with the question from which resource the cell line with the appropriate molecular characteristics is actually available. To overcome this limitation we developed DSMZCellDive (https://celldive.dsmz.de/), a novel web portal that offers access to uniformly generated and evaluated RNA-seq data from authenticated leukemia and lymphoma cell lines and further human cancer cell lines. Several starting points ease entering the database via browsing, searching or visualizing gene expression data in bar plots or heat maps. *In silico* transcriptomic analysis might thus precede or supplement laboratory experiments. Our web tool also contains authentication tools and HLA types and is designed for further expansion on meta and high-throughput data to be generated in future. As an example we show here analysis of oncogenic nuclear factor I (NFI) encoding genes in cell lines derived from selected B-cell malignancies. Recently, we have established the lymphoid TALE-code which describes physiological activities of TALE-class homeobox genes in most developing and mature lymphoid cell entities. This code allows identification of aberrantly expressed homeobox genes of this class in corresponding malignancies. Thus, we revealed aberrant expression of PBX1 in Hodgkin lymphoma (HL) patients and cell lines. Target gene analysis of PBX1 in HL cell lines revealed NFIB – a member of the NFI-family of transcription factor encoding genes. Extended expression analysis using DSMZCellDive shows that all four NFI family members are aberrantly expressed in HL cell lines, and that PBX1 may drive NFIB expression in primary effusion lymphoma cell lines as well, indicating an oncogenic role of this group of transcription factors in these types of lymphoma.