# Changes in gene expression during immortalization of haematopoietic cells

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Signalling pathways are crucial for correct cell functioning and communication. The pathways respond to various extracellular signalling molecules including growth factors and their disruption can lead to pathological conditions, such as tumor diseases and other malignancies. We studied an Epo/EpoR-dependent haematopoietic cell line from zebrafish (*Danio rerio*) that lost dependence on stem cell factor (SCF) in two consecutive steps of immortalization. In a time-series based experiment, gene expression was analysed on a whole genome scale using RNA-Seq. The resulting data was analysed to obtain genes that changed in transcription level most significantly. Large number of differentially expressed genes indicated that there were several processes, which accounted for observed changes. Thus, we divided the differentially expressed genes in clusters according to time dependence of their expression profiles. We characterized the resulting gene clusters functionally with respect to the Gene Ontology terms and KEGG signalling and metabolic pathways.