The 200 word abstract should be a brief and concise summary of the background/motivation for the study, method and result(s), as well as conclusion/statement of significance.

"Integrating mutational profiles and single-cell transcriptional data using LASSO regularized regression to elucidate key molecular functions involved in the pathogenesis of myelodysplastic/myeloproliferative neoplasm (MDS/MPN) with neutrophilia"

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MDS/MPN with neutrophilia, previously known as aCML, is a rare and aggressive hematologic malignancy. The options for treating aCML are limited, and the prognosis is very poor. The mutational landscape of this disease is highly heterogeneous, and the presence of specific mutations can affect the prognosis and require a different therapeutic approach. To better understand the genetic mechanisms underlying aCML, we performed a combined analysis of single-cell RNA sequencing and whole-exome sequencing mutation profiling in 4 healthy donors and 12 aCML patients. The integration of these high-dimensional data is challenging, so we developed a novel computational framework based on regularized regression with the LASSO penalty. Our approach first compares healthy donors *vs* patients to estimate gene expression in different conditions, and then quantifies the impact of specific mutations on gene expression returned as fold change compared to the inferred expression in normal samples.
This analysis revealed dysregulated genes in aCML patients, such as the upregulation of calcium-binding protein S100A10, associated to mutations in ASXL1 and RUNX1, and the downregulation of the phospholipid-binding protein ANXA1, related to SETBP1 mutations. This study may improve our understanding of the molecular machinery of aCML and provide new insights into therapeutic targets for this disease.