Data integration of high-throughput microarray outputs to identify important microRNAs involved in ATLL pathogenesis, based on providing a model of the signaling network involved and then laboratory verification of the resulting model using a relative quantitative Real Time PCR on patient samples.

**References**

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**Abstract**

The study aimed to identify important microRNAs involved in ATLL pathogenesis by integrating high-throughput microarray outputs. A signaling network model was developed, and the resulting model was verified using relative quantitative Real Time PCR on patient samples.