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SERS-based DNA methylation profiling allows the differential diagnosis of malignant lymphadenopathy



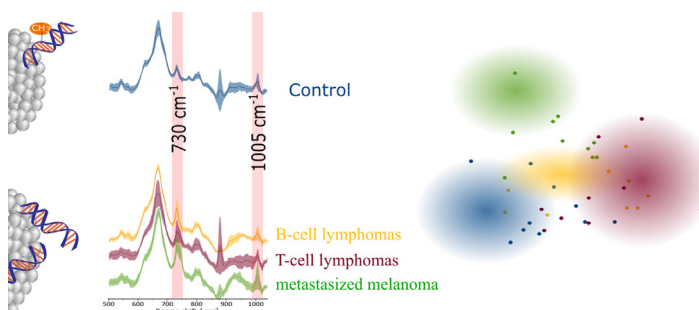
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HIGHLIGHTS

- SERS of lymph node DNA enables the discrimination of malignant and benign DNA.
- SERS of genomic DNA allows the univariate discrimination of B- and T-cell lymphoma.
- SERS allows the classification of lymphoma, melanoma and control genomic DNA samples.

GRAPHICAL ABSTRACT



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ABSTRACT

This study highlights the potential of surface-enhanced Raman scattering (SERS) to differentiate between B-cell lymphoma (BCL), T-cell lymphoma (TCL), lymph node metastasis of melanoma (Met) and control (Ctr) samples based on the specific SERS signal of DNA extracted from lymph node tissue biopsy. Differences in the methylation profiles as well as the specific interaction of malignant and non-malignant DNA with the metal nanostructure are captured in specific variations of the band at 1005 cm⁻¹, attributed to 5-methylcytosine and the band at 730 cm⁻¹, attributed to adenine. Thus, using the area ratio of these two SERS marker bands as input for univariate classification, an area under the curve (AUC) of 0.70 was achieved in differentiating between malignant and non-malignant DNA. In addition, DNA from the BCL and TCL groups exhibited differences in the area of the SERS band at 730 cm⁻¹,

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