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## POSTER PRESENTATION

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# Copy number alteration signature defines undifferentiated pleomorphic sarcomas and leiomyosarcomas with poor prognosis

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## Background
Undifferentiated high-grade pleomorphic sarcomas (UPS) display an aggressive clinical behavior with frequent development of distant metastasis and local recurrence. Since these tumors, particularly leiomyosarcomas (LMS), present a similar morphological pattern with other entities, the classification criterion by exclusion is frequently used.

## Methodology
In this study, array-based comparative genomic hybridization (array CGH) was applied in 20 UPS and 17 LMS (untreated cases). Array CGH (Agilent Technologies, 44K) data were analyzed by Nexus Software (v 6.0, BioDiscovery). Multivariate analysis was performed in order to identify the most important prognostic factors.

## Results
LMS presented lower frequency of genomic alterations in comparison with UPS. None of the variables were identified as independent prognostic factors, but gains at 1q21.3 were significantly associated with poor survival and showed almost significance as an independent prognostic factor (relative risk 13.8, $P$ = 0.019). In addition, copy number profile of UPS and LMS was indistinguishable by unsupervised hierarchical clustering analysis, one out of three clusters presented cases associated with poor prognosis ($P$ = 0.022). Relative copy number analysis for *ARNT*, *SLC27A3*, *PBXIP1* and *CCND1* genes was performed by quantitative real time PCR in 11 LMS and 16 UPS confirming the array CGH findings. Gains on 1q21-q22 involving *ARNT*, *PXIP1* and *SCL27A3* were observed exclusively in a subset of UPS.

## Conclusions
These findings describing a poor prognosis genomic signature in a subgroup of UPS and LMS can contribute to better stratify these patients for treatment.

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