of metastases, we collected 32 blood samples from breast cancer female patient. We performed a Kaplan-Meier analysis on metastatic free survival, without highlighting an increased risk due to the presence of the mutation (HR 1.01; 95% CI 0.41-2.45; P = 0.976). By using Cox Regression Analysis, after adjusting the model, to confound for Triple Negative status, MIB-1 levels, neoadjuvant and adjuvant therapy, the presence of GPX6 polymorphism confers an increased risk of metastasis onset (HR 2.1; 95% CI 0.76-5.8; P = 0.15). We have genotyped further 80 triple negative breast cancer blood samples and are in the process of collecting all clinical-pathological information to strengthen the statistical analysis.

Conclusions: Further analysis will be performed to confirm data obtained, to make in vitro study to investigate it possible role in metastatic process of breast cancer.

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49P The metastatic potential of grade I breast carcinoma of no special type: A deep insight into putative molecular mechanisms

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Background: Metastasis continues to be a crucial problem for the clinical management and treatment of breast cancer (BC). Among breast carcinoma of no special type (BC-NST), grade 1 tumors do have the best prognosis in terms of recurrence and overall survival. However, rarely they metastasize to the axilla, suggesting a more aggressive behaviour. Our study aimed to uncover the mechanism responsible for the dissemination of tumor cells of grade 1 BC-NST into axillary lymph nodes in order to better understand lymph node metastasis phenomenon in BC.

Methods: Whole-exome sequencing technique was used to analyze a total of 7 BC with lymph node metastases and 8 without, all Luminal A BCs. Analysis compared the molecular profiles of the selected cases by Enlis Genome Research software, Cravat application and QueryOr software.

Results: Analyzing the data, we can explain the presence of metastasis for 3 different samples because of the presence of mutation in AKT1 and PI3K. However, surprisingly, the group of patients with positive lymph node shared the same polymorphism (rs406113) in GPX6 gene. The rs406113 polymorphism is a missense variation, which in combination with other mutations, had previously been associated with the risk of breast cancer. To further investigate the role of the GP6X polymorphism on the onset