proteomics analysis using mass spectrometry has been performed to evaluate the effect of storage conditions on the preservation of proteins. Protein yield and coverage were compared in four storage conditions to determine the optimum storage conditions for tissue samples to perform proteomics analysis. Unique proteins obtained from each condition were further analyzed to examine the effect of storage conditions on subcellular location. Differential analysis was performed on all individual conditions to compare the unique statistically differentially expressed proteins.

Results: TC tissues showed the highest protein yield compared to NC because the fat portion was higher in NC. The FFPE condition, followed by RNAlater, was determined to have the maximum protein coverage. Unique proteins could be detected from FFPE samples, providing a hint of the modifications induced during the paraffinization. However, the differential analysis showed more unique proteins in the Allprotect storage conditions, followed by RNAlater. The proteins CNDP2 and PLIN4 showed dysregulation in the TC sample despite the different storage conditions and may be used as therapeutic markers for breast cancer. Biological pathway analysis showed spliceosome and PPAR signaling pathways were enriched in TC compared to NC tissue.

Conclusions: This study evaluated the effects of different tissue preservation methods on proteomics analysis.

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114P Circulating microRNAs and response to oncological and surgical therapy in patients with locally advanced gastric cancer

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Background: Therapeutic management of locally advanced gastric cancer (LAGC) combines surgery with neo-adjuvant (NACT) and adjuvant chemotherapy (ACT). miRNAs have emerged as promising candidates for treatment efficacy prediction, hence, the present study aims at defining therapy response-specific profiles of circulating miRNAin LAGC.

Methods: A prospective cohort of 26 LAGC patients scheduled for NACT, surgery and ACT treatment was considered. Peripheral blood samples were collected prior to (preNACT) and after NACT (postNACT) as well as after tumor surgical excision and by completion of ACT (postACT). Patients were grouped according to Becker's tumor regression grade criteria into responders (R;TRG1-2) and non-responders (NR;TRG3). Serum RNA was isolated with magnetic bead technology and relative expression levels of miR21a, mir19a, mir20a, miR30a & miR15a were determined by qRT-PCR.

Results: PreNACT profiles revealed expression differences between R and NR patient groups, with Responders characterized by elevated miR21a and, particularly, miR30a and miR15a expression levels as compared to NR. In response to NACT, miR15a & miR30a downregulation was the most distinguished difference defining Responders. R profile also showed a distinct upregulation of mir21a and elevation of the initially low levels of mir20a & mir19a. In contrast, NR showed NACT-dependent upregulation of all targets except miR19a. Interestingly, it was surgical depletion of primary tumor that first led to a marked activation of studied miRNAs in both R and NR patients, an upregulation found further augmented after ACT treatment. Nevertheless, postACT miR15a and miR30a levels in R remained substantially lower than in NR, evidence adding to their potential as chemosensitivity indicators.

Conclusions: This study aimed at monitoring the consequential to oncological and surgical therapy response-dependent expression patterns of a panel of circulating miR and, despite the small case series, revealed the potential of, particularly, miR15a and miR30a as chemosensitivity predictors in LAGC. The evidence merits further investigation in larger patient cohorts to validate their clinical utility as biomarkes for stratifying GC patients for precision therapy.

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115P BrainStorm-NSE: Serum neuron-specific enolase as a biomarker for central nervous system metastases: A prospective cohort study

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Background: Improving clinical outcomes of patients with central nervous system (CNS) metastases remains an unmet medical need. Serum neuron-specific enolase (NSE) has been investigated as a non-invasive biomarker of brain damage, and we believe it may contribute to the early detection of CNS metastases.

Methods: We aim to assess the predictive value of NSE for the development of CNS metastases in patients recruited for BrainStorm study, an international, multicentre prospective cohort study. BrainStorm will recruit around 600 patients with newly diagnosed non-CNS metastatic solid tumors with high risk of developing CNS metastases (Part A) to obtain 280 patients at diagnosis of CNS metastases (Part B). NSE assessment was added in a protocol amendment approved on 28 Oct 2021. All patients underwent blood collection for NSE assessment and magnetic resonance imaging for screening (Part A) or confirming (Part B) CNS metastases, at baseline and at regular intervals. Here we report an exploratory comparison of the baseline NSE from the first patients tested in Part A vs B. We applied Mann-Whitney test for comparing NSE levels (ng/ml) and Fisher's exact test for proportion of patients with positive NSE (above upper limit of normal), using a two-sided statistical significance of 5%.

Results: We included 34 patients from Dec21 to Jun23, 26 in part A and 8 in part B - Table 115P. Median NSE was numerically higher in Part B (16.6, IQR 13.1-27.7 vs 12.4, 11.0-16.0) (p=0.26). NSE was positive for 62.5% of patients in Part B vs 34.6% in Part A (p=0.23). Median NSE levels were numerically lower in patients with breast cancer (Part B: 14.2 vs Part A: 12.7) and larger in patients with lung cancer (Part B: 19.0 vs Part A: 7.6).

Table: 115P Baseline characteristics at inclusion

	Part A (N=26)	Part B (N=8)
Age — median (IQR)	55.5 (47.5-63.5)	63.5 (58.3-67.8)
Female sex — n (%)	25 (96.1)	6 (75.0)
ECOG performance status — n (%), 1 missing		
0	13 (50.0)	2 (28.6)
1	12 (46.1)	4 (57.1)
2	1 (3.8)	1 (14.3)
Cancer type — n (%)		
TNBC	11 (42.3)	2 (25.0)
HER2+/ER- BC	8 (30.8)	-
HER2+/ER+ BC	3 (11.5)	3 (37.5)
NSCLC	2 (7.7)	3 (37.5)
SCLC	1 (3.8)	-
Melanoma	1 (3.8)	-
Disease type — n (%), 1 missing		
de novo	13 (52.0)	4 (50.0)
recurrent	12 (48.0)	4 (50.0)
Number of metastatic sites — median (IQR)	2 (1-3)	2.5 (1-3.3)
Months from non-CNS metastases to NSE — median (IQR)	6.5 (1.8-25.8)	5.8 (1.3-65.1)
Weeks from CNS metastases to NSE — median (IQR)	-	2.4 (1.5-3.6)

Conclusions: Our preliminary results suggest a numerical trend for higher serum NSE levels in patients with established brain metastases supporting the need to formally investigate serum NSE as a circulating biomarker of CNS metastases once study accrual is completed and follow-up mature.