

Utilizing serum-derived lipidomics with protein biomarkers and machine learning for early detection of ovarian cancer in the symptomatic population

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Key Takeaways

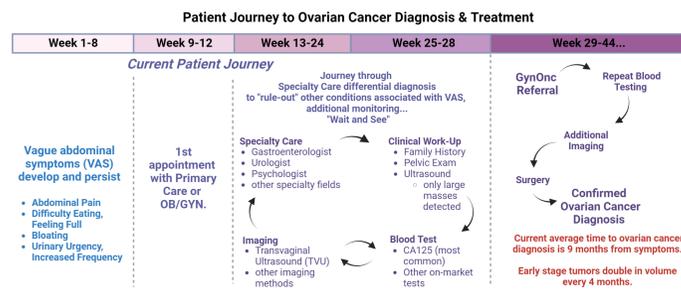
- Ovarian cancer is lethal due to lack of robust biomarkers and vague symptoms that present at early stages.
- A robust, non-invasive, early detection diagnostic test for the symptomatic population will improve the poor prognosis of OC.
- We are developing a serum-based blood test to detect OC earlier in women with vague abdominal symptoms (VAS).
- Our novel machine learning (ML)-based multi-omic model achieves high AUCs in early-stage OC across independent, heterogeneous patient populations.
- ML + multi-omics shows improved performance over current methods, allowing for earlier cancer detection, shortening time to diagnosis, and improving patient outcomes.

Current standard of care offers limited options for early-stage OC detection

- <50% diagnosed within 1 mo. of first doctor visit¹
- Avg. time to OC diagnosis is 9 months in the U.S.²
- >70% diagnosed with late-stage OC, 5-year survival 10-30%³
- Lack of effective diagnostic tools available for early-stage OC
- If OC is diagnosed at earlier stages, survival can jump to >90%⁴

Addressing diagnostic challenges in women with vague abdominal symptoms

- >80% individuals with early-stage OC present with VAS
- Many OC patients undergo gastrointestinal, general abdominal and/or urological evaluations first because symptoms overlap⁴
- While some advances are reported for asymptomatic individuals, the **biological complexity of the symptomatic population requires novel approaches**

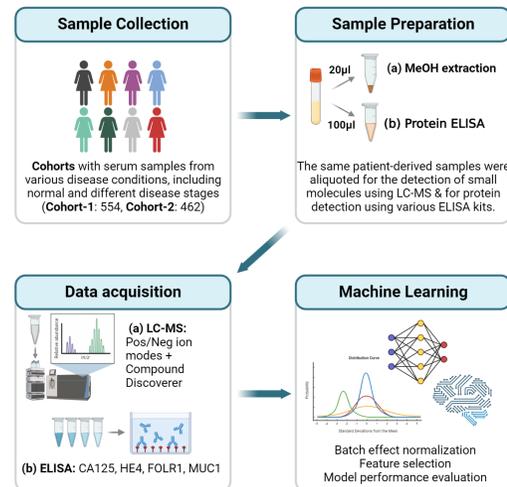


- To address this, our study includes serum from healthy individuals (normal), early- and late-stage OC, and non-cancerous conditions that share symptoms common in OC:
 - Gyn: Endometriosis, fibroids, cysts, adnexal masses (benign)
 - Gastrointestinal (GI) disorders

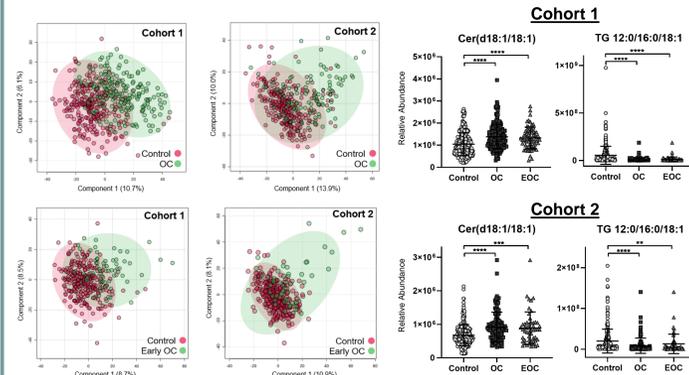
LC-MS for lipid detection + ELISA-based protein panel + Machine Learning

We conducted a multi-omics analysis of two independent, clinically annotated cohorts. Cohort 1 was obtained from the University of Colorado Gynecologic Tissue and Fluid Bank + commercial vendors. Cohort 2 specimens were collected from a **prospectively enrolled symptomatic population** through Manchester University NHS Foundation Trust + commercial vendors. Samples were blinded and cohorts were processed independently.

Diagnosis	Group	Cohort 1	Cohort 2	Combined
Cancer	All OC	218	109	327
	Early-stage OC	82	52	134
	Late-stage OC	136	57	193
	Borderline	25	20	45
Non-Cancer	All Controls	301	294	595
	Normal	82	208	290
	Benign	169	85	254
	GI Disorders	50	0	50
	Pre-cancer	0	1	1
Grand Totals		544	423	967

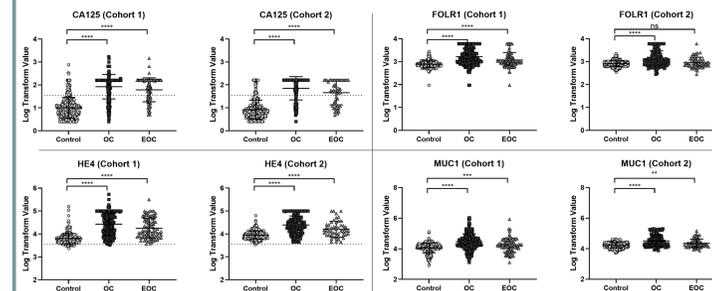


Ovarian cancer serum shows a distinct lipidomic profile compared to controls



- PLSDA comparing controls v. all OC (top left) and controls v. early-stage OC (bottom left) show **clear lipid profile differences**.
- There are a range of significantly altered lipid classes in OC when compared to the diverse symptomatic population.
- Divergence is more clearly observed for specific lipid species (right), highlighting **individual lipids as potential biomarkers** for early-stage OC in the complex VAS population.

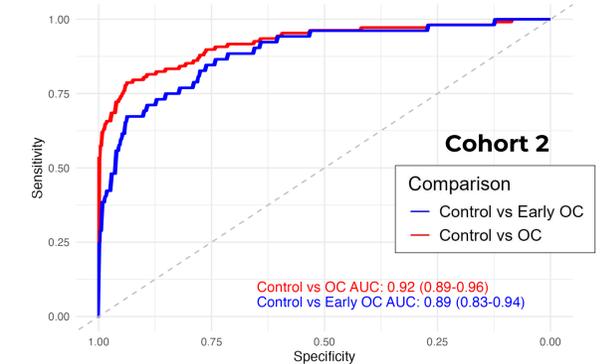
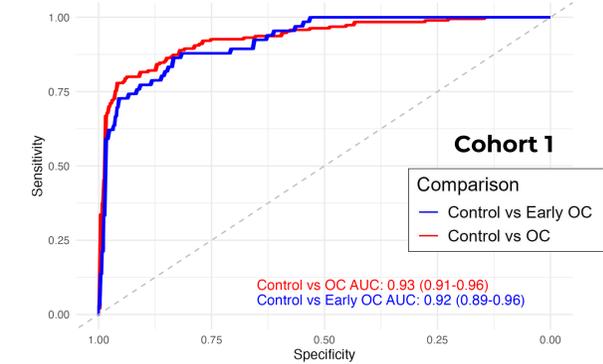
Protein biomarkers differ in OC but lack early-stage diagnostic power



- Levels of CA125 and HE4 (used in clinical practice) with FOLR1 and MUC1 (promising diagnostic/therapeutic targets) were elevated in OC and early-stage OC.
- However, wide ranges and modest differences highlight the limitations of using these proteins as stand-alone biomarkers.

Multi-omic modeling distinguishes OC & early-stage OC in the VAS population

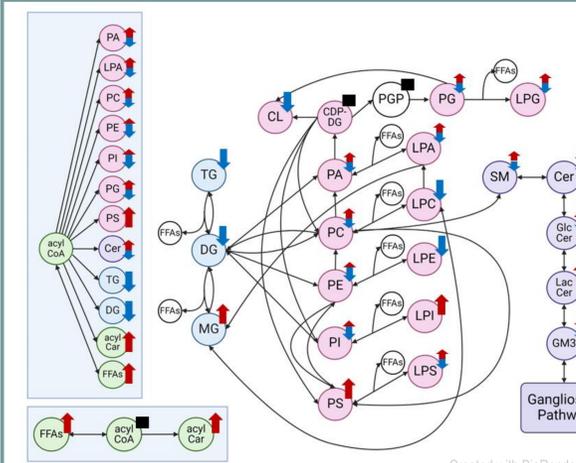
- Wide distributions and subtle alterations in lipid and protein biomarkers illustrate the need for **combinatorial approaches**.
- Machine learning-based modeling was performed to assess multi-omics as a tool to distinguish OC from VAS controls.



- For Cohort 1, the top-performing model showed **AUCs of 93% for controls vs. OC, and 92% for controls vs. early-stage OC** (top).
- The model demonstrates high performance when tested on Cohort 2 as an independent hold-out set, achieving AUCs of 92% for controls vs. OC and 89% for controls vs. early-stage OC. (bottom) This performance is underscored by the heterogeneous nature of the cohorts and prospective collection in the complex intended use population.
- These data illustrate the power of a multi-omic approach leveraging lipid and protein profiling to distinguish OC.**

Multi-omic modeling distinguishes OC & early-stage OC in the VAS population

- Lipid metabolism is a highly dynamic and deeply interconnected network of species.
- When comparing normal and OC serum, class level alterations in the lipid profile can be observed:
 - Increases in LacCer, LPI, PS, MG, acyl-Cer, FFAs
 - Decreases in LPC, LPE, TG, DG
 - A mix of increased and decreased species in gangliosides, Cer, SM, LPS, PI, PE, PC, PA
- This illustrates the potential of specific lipid classes and individual species for their utility as diagnostic biomarkers in a clinical diagnostic assay.



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