Caris Abstracts and Presentation Schedule

ASCO 2026

CARIS® LIFE SCIENCES

Where Molecular Science Meets Artificial Intelligence.

Accelerating Precision Oncology Through Data-Driven Discovery

Caris Life Sciences® (Caris) is a leading next-generation AI TechBio company and precision medicine pioneer advancing cancer research and care through comprehensive molecular profiling, artificial intelligence, and large-scale clinico-genomic analysis. The studies in this book highlight how Caris leverages multiomic biomarker research and real-world data to advance understanding of tumor biology and support precision oncology approaches.

At the 2026 American Society of Clinical Oncology® (ASCO) Annual Meeting, Caris and collaborators from more than 60 institutions - including members of the Caris Precision Oncology Alliance® (Caris POA) - will present 32 studies, including one Rapid Oral presentation and four Posters with Merit Awards. Spanning 10 tumor types in addition to pan-cancer analyses, these studies reflect the growing impact of multiomic biomarker research and real-world evidence in precision oncology.

Caris' ASCO 2026 Research Highlights

The research presented by Caris and collaborators focuses on immuno-oncology, tumor microenvironment characterization, treatment response and resistance, molecular subtype discovery, and biomarker development. Highlights include:

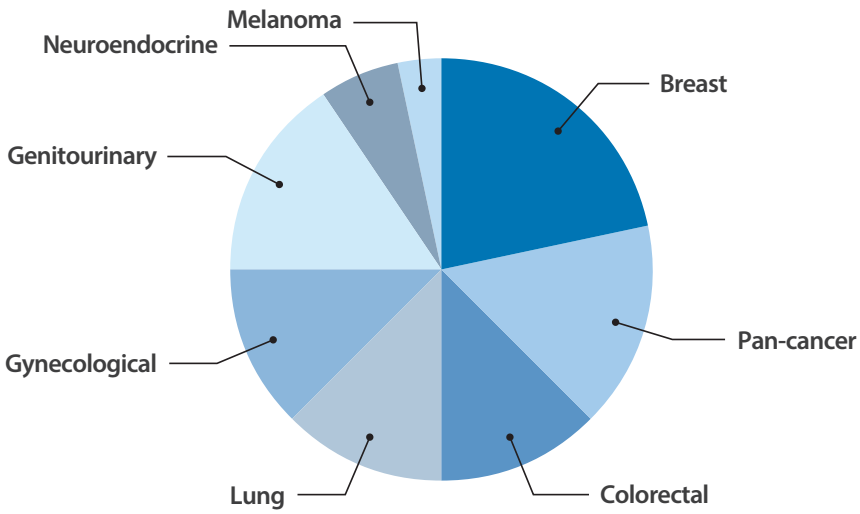
- Large-scale genomic profiling to investigate ancestry-associated mutational signatures in melanoma.
- Analysis of *ESR1* amplification and its association with outcomes and therapeutic response in breast cancer.
- Use of whole transcriptome sequencing to identify actionable genomic alterations beyond conventional DNA-based approaches.

Together, these studies demonstrate the value of comprehensive molecular profiling and large-scale clinico-genomic data in accelerating precision oncology research and personalized cancer care.

"Caris is proud to collaborate with leading academic and clinical institutions to advance large-scale, multiomic research and real-world evidence generation. The breadth of research being presented at ASCO reflects the importance of comprehensive molecular profiling and data-driven discovery to support continued progress in precision oncology."

— Caris EVP and Chief Medical Officer George W. Sledge, Jr., MD.

Accepted Caris Abstracts by Tumor Type Group



Caris Abstracts and Presentation Schedule

SATURDAY, MAY 30, 2026

9:00 AM – 12:00 PM CDT: HALL A

POSTER SESSION: GASTROINTESTINAL CANCER — COLORECTAL AND ANAL

Survival outcomes of human epidermal growth factor receptor 2 (HER2)-amplified and HER2-mutated left-sided colorectal cancer (CRC) patients treated with anti-epidermal growth factor receptor (EGFR) monoclonal antibodies (mAbs).

Y. Jan, K. Sweeney, A. Elliott, R. Hsieh, C. Kuang, P. Habibzadeh, S. Rahman, R. Shroff, H.-J. Lenz, S. Goel, A. Singhi, V. Gorantla, J. Rhee, J. Zhang, A. Saeed, D. Hsu.

Abstract: 3543 **Poster:** 297 **Presenter:** Yu Jen Alexander Jan, MD

Association of *FBXW7* mutation with prolonged survival in microsatellite instability-high colorectal cancer treated with immune checkpoint blockade.

M. Pruitt, S. Deshmukh, A. Saadeh, E. Hill, S. Wu, T. Adeyelu, K. Sweeney, J. Xiu, M. Malla, S. Goel, E. Antonarakis, M. Gordon.

Abstract: 3657 **Poster:** 424 **Presenter:** Margaret R. Pruitt, MD, PhD

Key Findings from this Session

- Analysis of 3,217 *KRAS/NRAS/BRAF* wild-type left-sided CRCs profiled by Caris showed that HER2-mutated tumors had worse outcomes following anti-EGFR therapy than HER2-normal tumors, whereas HER2-amplified tumors showed no significant difference in overall survival.
- In a cohort of 29,446 CRCs profiled by Caris, *FBXW7*-mutated MSI-H tumors were associated with improved overall survival following immune checkpoint blockade, supporting *FBXW7* mutation as a potential biomarker of response to immunotherapy in MSI-H CRC.
- **These studies demonstrate how comprehensive molecular profiling can identify clinically meaningful genomic subgroups in colorectal cancer, enabling biomarker discovery and refinement of targeted treatment strategies.**

SATURDAY, MAY 30, 2026

9:00 AM – 12:00 PM CDT: HALL A

POSTER SESSION: GASTROINTESTINAL CANCER— GASTROESOPHAGEAL, PANCREATIC, AND HEPATOBILIARY

Immune microenvironment signatures as prognostic biomarkers in gastroenteropancreatic neuroendocrine carcinoma (GEP-NEC).

R. Miao, N. Gandhi, J. Xiu, P. Del Desai, J. Rivero, G. Joseph, M. Oyenuga, U. Grewal, J. Handler, H. Yusuf, V. Avadhani, O. Alese.

Abstract: 4180 **Poster:** 163 **Presenter:** Ruoyu Miao, MD

Key Findings from this Session

- Molecular profiling of 4,863 neuroendocrine carcinomas by Caris revealed that GEP-NECs exhibit a distinct and relatively immunosuppressive tumor microenvironment compared to thoracic-NECs, with B-cell, NK-cell, and macrophage signatures associated with survival across disease subtypes.
- **These findings show how comprehensive molecular profiling and immune microenvironment analysis can identify prognostic immune signatures in rare cancers, supporting biomarker-driven therapeutic development in GEP-NEC.**

SATURDAY, MAY 30, 2026

1:30 PM – 4:30 PM CDT: HALL A

POSTER SESSION: DEVELOPMENTAL THERAPEUTICS—IMMUNOTHERAPY

MERIT AWARD

Mitochondrial DNA (mtDNA) expression as used to define metabolic and immune states in colorectal cancer (CRC).

M. Bartolini, S. Wu, J. Xiu, N. Kulkarni, S. Soni, S. Algaze, P. Mittal, L. Torres-Gonzalez, U. Shah, S. Trujillo, Y. Goretsky, J. Ho-Lo, Z. Wu, Y. Yang, J. Millstein, M. Khushman, R. Goldberg, A. Seeber, A. Puccini, H.-J. Lenz.

Abstract: 2647 **Poster:** 437 **Presenter:** Michela Bartolini, MD

Key Findings from this Session

- Analysis of 30,887 CRCs profiled by Caris identified mtDNA-encoded oxidative phosphorylation gene expression as a marker of distinct metabolic and immune tumor states, with mtDNA-low tumors associated with improved outcomes with immunotherapy.
- **This study demonstrates the value of comprehensive molecular profiling in identifying biologically distinct colorectal cancer subgroups and potential biomarkers of immunotherapy sensitivity, including in microsatellite stable (MSS) disease.**

SATURDAY, MAY 30, 2026

1:30 PM – 4:30 PM CDT: HALL A

POSTER SESSION: DEVELOPMENTAL THERAPEUTICS — MOLECULARLY TARGETED AGENTS AND TUMOR BIOLOGY

CARIS HIGHLIGHT

Influence of genetic ancestry on UV mutational signatures linked to immunotherapy response in melanoma, beyond TMB.

K. Magnaye, B. Gilg, L. Dickman, R. Plagens, D. Deacon, I. Brownell, L. Carvajal-Carmona, S. Holmen, S. Shalhout, A. Elliott, J. Klemp, J. Xiu, J. Yang, M. Radovich, M. Oberley, J. Hamrick, D. Spetzler, G. Sledge Jr., S. Raj, F. Abdulla.

Abstract: 3087 **Poster:** 224 **Presenter:** Kevin Magnaye, PhD

Key Findings

- Molecular profiling of 8,872 melanomas by Caris revealed significant ancestry-linked differences in UV-related COSMIC mutational signatures, with SBS7a and SBS7b enriched in patients of European ancestry.
- Among melanoma patients treated with first-line immune checkpoint inhibitors (ICI), SBS7a positivity was associated with improved overall survival and time to next treatment after ICI independent of TMB.
- SBS7a was largely absent in non-UV-driven cancers and did not predict immunotherapy outcomes in uveal melanoma or renal cell carcinoma, supporting its specificity as a UV-associated prognostic biomarker.
- **This study shows how large-scale genomic profiling and ancestry-informed analyses can identify biologically distinct tumor subgroups and support development of immunotherapy biomarkers.**

CARIS HIGHLIGHT

Clinical utility of whole transcriptome sequencing for fusion detection in advanced solid tumors: SCRUM-Japan MONSTAR-SCREEN-2.

T. Fujisawa, Y. Nakamura, N. Sakamoto, R. Yamashita, T. Kuwata, M. Nagamine, G. Ishii, C. Morizane, N. Nonomura, H. Iwata, S. Okano, H. Watari, K. Namikawa, T. Hashimoto, T. Shibuki, M. Imai, H. Bando, M. Radovich, G. Sledge Jr., T. Yoshino.

Abstract: 3127 **Poster:** 264 **Presenter:** Takao Fujisawa, MD, PhD

Key Findings

- Whole transcriptome sequencing (WTS) identified pathogenic fusion variants in 5.4% of advanced solid tumors in the SCRUM-Japan MONSTAR-SCREEN-2 study, including clinically actionable kinase fusions.
- More than half of pathogenic fusions identified by WTS would theoretically have been missed by conventional targeted DNA panel sequencing, including *FGFR2*, *FGFR3*, and *BRAF* rearrangements.
- WTS identified clinically relevant fusions that informed targeted therapy selection, including a *BRAF* fusion in melanoma undetected by conventional DNA panel testing.
- **These findings demonstrate how WTS can expand detection of actionable genomic alterations beyond conventional DNA-based approaches, supporting broader implementation of RNA profiling in precision oncology.**

Identification of high-grade neuroendocrine carcinoma (HGNEC) biology across tumor types through transcriptomic profiling and validation in lung cancer.

Y. Yang, N. Gandhi, A. Elliott, P. Vaidiswaran, T. Sen, S. Puri, B. Halmos, H. Borghaei, A. Thomas, S. Liu, P. Desai.

Abstract: 3121 **Poster:** 258 **Presenter:** Parth Anil Desai, MD, MBBS

Association of treatment-induced decrease of tumor chromosome Y and prognosis.

D. Theodorescu, S. Wu, E. Lou, A. Shields, J. Xiu, G. Sledge Jr., D. Spetzler.

Abstract: 3136 **Poster:** 273 **Presenter:** Dan Theodorescu, MD, PhD

Validation of SNHG11 as a prognostic and predictive biomarker for anti-EGFR benefit in colorectal cancer using real-world data.

M. Bartolini, Y. Baca, J. Xiu, S. Soni, P. Mittal, U. Shah, L. Torres-Gonzalez, S. Trujillo, Y. Goretsky, S. Algaze, W. Zhang, Y. Yang, J. Millstein, J. Ho-Lo, R. Goldberg, A. Shields, A. Seeber, A. Puccini, H.-J. Lenz.

Abstract: 3138 **Poster:** 275 **Presenter:** Michela Bartolini, MD

Genomic and transcriptomic correlates of HER3 expression in prostate cancer.

S. Balkhi, A. Mullasseril, M. Cookson, K. Stratton, A. McIntosh, S. Patel, A. De Souza, T. Mattox, S. Nazari, A. Elliott, K. Doytcheva, A. Annan, A. Naqash, J. Ciuro, K. Moore, D. Kilari, R. McKay, S. Patel, M. Jain, A. Ayanambakkam.

Abstract: 3142 **Poster:** 279 **Presenter:** Syed Saqib Balkhi, MD, MBBS

Key Findings from this Session

- Among 8,872 melanomas profiled by Caris, the UV-related SBS7a mutational signature was associated with improved immunotherapy outcomes independent of TMB and differed significantly by genetic ancestry.
- Whole transcriptome sequencing in the SCRUM-Japan MONSTAR-SCREEN-2 study identified clinically actionable fusion variants that would have been missed by conventional DNA panel sequencing, supporting the value of transcriptome-wide profiling in precision oncology.
- Transcriptomic analysis of 49,144 tumors profiled by Caris identified an HGNEC-like subset of NSCLC with poor survival, immune suppression, and enrichment of targetable neuroendocrine-associated biomarkers.
- In a longitudinal paired tumor analysis of 1,343 patients from the Caris real-world clinico-genomic cohort, post-treatment decreases in chromosome Y score were linked to worse survival across multiple cancer types, supporting further investigation of chromosome Y loss as a prognostic biomarker.
- Analysis of 15,456 colorectal cancers profiled by Caris confirmed that elevated expression of *SNHG11,* a long non-coding RNA, was associated with CMS2 biology, longer overall survival, and longer time on anti-EGFR therapy, supporting *SNHG11* as a potential prognostic and predictive biomarker in colorectal cancer.
- Across 19,238 prostate cancers profiled by Caris, HER3-high tumors were associated with luminal androgen receptor-dependent biology, an immune-cold phenotype, and improved survival in metastatic and castration-resistant disease.
- **Collectively, these studies highlight how comprehensive molecular profiling can uncover clinically relevant molecular subgroups, prognostic biomarkers, and therapeutic targets across diverse tumor types, supporting more precise biomarker-driven research and treatment strategies.**

SATURDAY, MAY 30, 2026

1:30 PM – 4:30 PM CDT: HALL A

POSTER SESSION: GENITOURINARY CANCER — KIDNEY AND BLADDER

Genomic and clinical correlates of belzutifan treatment in renal cell carcinoma (RCC): A retrospective analysis of 150 RCC patients.

H. Dudipala, Y.-W. Chen, S. Nazari, A. Elliott, N. Kulkarni, R. Nawfal, L. Ascione, M. Machaalani, D. McDermott, S. Signoretti, P. Barata, B. Rose, A. Bagrodia, N. Agarwal, S. Pal, T. Choueiri, R. McKay.

Abstract: 4541 **Poster:** 20 **Presenter:** Harshitha Reddy Dudipala, MD

Comprehensive characterization of HIF-2α and carbonic anhydrase IX expression and the genomic landscape in clear cell and *VHL*-altered renal cell carcinoma.

Y.-W. Chen, S. Nazari, A. Elliott, N. Kulkarni, R. Nawfal, L. Ascione, M. Machaalani, D. McDermott, S. Signoretti, P. Barata, B. Rose, A. Bagrodia, N. Agarwal, S. Pal, T. Choueiri, R. McKay.

Abstract: 4543 **Poster:** 22 **Presenter:** Yu-Wei Chen, MD, MS

CXCL9:SPP1 ratio: Macrophage polarization and outcomes with pembrolizumab or enfortumab vedotin plus pembrolizumab in metastatic urothelial cancer.

S. Atiq, T. Adeyelu, S. Izadmehr, J. Anker, E. Miller, T. Ganta, B. Liaw, S. Bohlman, A. Karol, B. Cho, A. Elliott, P. Barata, R. McKay, R. Mehrazin, A. Horowitz, J. Sfakianos, N. Bhardwaj, M. Galsky.

Abstract: 4573 **Poster:** 52 **Presenter:** Saad Omar Atiq, MD

Key Findings from this Session

- Evaluation of molecular profiling data from 150 belzutifan-treated RCCs showed that *HIF-2α* RNA expression alone did not predict treatment response, while responders demonstrated enrichment of PI3K/AKT/mTOR and DNA damage response pathway alterations.
- Genomic and transcriptomic profiling of 1,935 RCCs by Caris helped identify a canonical VHL/HIF-driven subtype characterized by high *HIF-2α* and *CA9* expression, favorable genomic features, and improved overall survival.
- In metastatic urothelial cancer, low CXCL9:SPP1 ratios derived from Caris molecular profiling were associated with reduced immune infiltration and worse outcomes following pembrolizumab or enfortumab vedotin plus pembrolizumab therapy.
- **These studies' findings show how integrated genomic, transcriptomic, and immune microenvironment profiling can identify biologically distinct genitourinary cancer subgroups and potential biomarkers of therapeutic response and resistance.**

SUNDAY, MAY 31, 2026

9:00 AM – 12:00 PM CDT: HALL A

POSTER SESSION: LUNG CANCER — NON–SMALL CELL LOCAL-REGIONAL/SMALL CELL/OTHER THORACIC CANCERS

Antigen presentation suppression as a hallmark of immune evasion and poor outcomes in small cell lung cancer.

T. Sen, E. Gobbini, V. Jethalia, S. Chakraborty, A. Vanderwalde, B. Halmos, H. Borghaei, D. Demircioglu, D. Hasson, A. Elliott.

Abstract: 8084 **Poster:** 558 **Presenter:** Triparna Sen, PhD

Key Findings from this Session

- Transcriptomic analysis of SCLC samples from large real-world and clinical trial cohorts identified a predominant classical antigen-presenting MHCs (CAMs)-low subset characterized by immune evasion, reduced expression of several druggable targets, and worse outcomes following chemoimmunotherapy.
- **This study demonstrates that integrated molecular and immune profiling can identify immunosuppressive tumor states and potentially inform development of biomarker-driven therapeutic strategies in SCLC.**

SUNDAY, MAY 31, 2026

9:00 AM – 12:00 PM CDT: HALL A

POSTER SESSION: LUNG CANCER — NON–SMALL CELL METASTATIC

Smoking signature as used to define a genomically distinct subset of class I *BRAF*-mutant NSCLC.

S. Wang, R. Odabashian, N. Gandhi, A. Elliott, B. Ricciuti, A. Di Federico, H. Borghaei, H. Mamdani, B. Halmos.

Abstract: 8538 **Poster:** 328 **Presenter:** Shuai Wang, MD

Use of LIF and LIFR expression to characterize survival and tumor microenvironment composition in lung adenocarcinoma.

M. Borecky, W.J. Jeon, A. Lau, A. Hagele, D. de Semir, Y. Baca, A. Elliott, G. Sledge Jr., S. Mirshahidi, H. Mirshahidi.

Abstract: 8553 **Poster:** 343 **Presenter:** Michael Borecky, MD, MA

Molecular and immune profiling of *BRAF*-mutated (*BRAF*^{MUT}) non-small cell lung cancer (NSCLC).

R. Odabashian, S. Wang, N. Gandhi, B. Ricciuti, A. Di Federico, H. Borghaei, B. Halmos, H. Mamdani.

Abstract: 8653 **Poster:** 443 **Presenter:** Roupen Odabashian, MD, FRCP

Key Findings from this Session

- Retrospective review of 33,217 NSCLCs profiled by Caris supported SBS4 as a genomic marker of smoking-related biology that defined distinct molecular and immune subsets of class I *BRAF*-mutant NSCLC, with overall survival benefit over wild-type disease preserved in SBS4-positive tumors.
- Analysis of Caris molecular profiling data from 10,041 lung adenocarcinomas showed that low *LIF* and high *LIFR* expression were associated with distinct immune microenvironment states and improved survival, with additional *LIF*-associated survival differences in osimertinib-treated *EGFR*-mutant tumors.
- Among 51,692 NSCLCs molecularly profiled by Caris, distinct *BRAF*-mutant classes demonstrated divergent molecular, immune, and survival profiles, with class 1 and VUS tumors associated with improved outcomes compared with *BRAF* wild-type disease.
- **In these studies, integrated genomic, transcriptomic, and immune profiling was shown to refine molecular classification and identify clinically relevant biomarkers of therapeutic response and prognosis in NSCLC.**

SUNDAY, MAY 31, 2026

9:00 AM – 12:00 PM CDT: HALL A

POSTER SESSION: GYNECOLOGIC CANCER

HPV-stratified tissue factor expression and multi-omic correlates of overall survival after tisotumab vedotin in cervical cancer.

S. Bruce, S. Wu, W. Gu, M. Dean, T. Nicolaides, N. Kulkarni, R. Jaehne, K. Moore, B. Erickson, R. Coleman, R. Eskander, R. Arend, J. Liu, T. Herzog, M. Oberley.

Abstract: 5537 **Poster:** 203 **Presenter:** Wen Gu, PhD

The role of combined T cell and NK cell activity in immune checkpoint inhibitor (ICI) therapy in endometrial cancer (EC).

D. Greenberg, P. Penalosa, W. Gu, S. Wu, M. Oberley, M. Toboni, B. Erickson, K. Tewari.

Abstract: 5609 **Poster:** 275 **Presenter:** Danielle Greenberg, MD

Antibody drug conjugate (ADC) biomarker targets in endometrial cancer (EC): Molecular characterization and implications for therapeutic decision-making.

B. Erickson, M. Toboni, S. Wu, M. Mullen, K. Moore, R. Eskander, T. Nicolaides, R. Arend, J. Liu, S. Bruce, B. Manning-Geist, R. Coleman, T Herzog.

Abstract: 5616 **Poster:** 282 **Presenter:** Britt Kristina Erickson, MD

Racial disparities in endometrial cancer (EC) survival persist after molecular classification (MC).

J. Roberts, S. Wu, M. Toboni, B. Erickson, N. Kulkarni, M. Oberley, N. Nair, W. Khadraoui, A. Sinno.

Abstract: 5620 **Poster:** 286 **Presenter:** Jill Roberts, MD

Key Findings from this Session

- In a cohort of cervical cancer patients treated with tisotumab vedotin (TV) who underwent Caris DNA/RNA sequencing, high TF expression was associated with longer overall survival following TV in HPV-negative but not HPV-positive disease.
- In Caris-profiled pMMR/MSS endometrial cancers treated with pembrolizumab or dostarlimab, T-cell, NK-cell, and combined T/NK immune signatures were independently associated with improved overall survival following immune checkpoint inhibition.
- Analysis of 13,731 endometrial cancers profiled by Caris showed that ADC target expression varied by molecular subtype, supporting subtype-specific biomarker evaluation for future ADC development.
- Among 10,162 Caris-profiled endometrial cancers, racial survival disparities persisted after molecular classification, with the largest disparity observed in No Specific Molecular Profile tumors.
- **Collectively, these studies highlight how genomic, transcriptomic, immune, and biomarker profiling can refine gynecologic cancer subgroups, inform therapeutic development, and reveal clinically relevant differences in treatment response and outcomes.**

SUNDAY, MAY 31, 2026

10:51 AM – 10:57 AM CDT: S403

SESSION: PREVENTION, RISK REDUCTION, AND GENETICS

RAPID ORAL

Clinical impact of *MSH3* loss-of-function alterations in patients treated with immune checkpoint blockade across cancer types.

E. Alouani, V. Randrian, A. Elliott, A. Nasir, D. Mieles, S. Abdelfattah, M. Foote, S. Maron, G. Vlachos, M. Abbass, O. Artz, M. Patel, W. Chatila, P. Johannet, D. Mandelker, M. Berger, A. Cercek, L. Diaz Jr., Z. Stadler, B. Rousseau.

Abstract: 10516 **Presenter:** Emily Linda Alouani, MD

Key Findings

- Analysis of 65,570 tumors identified *MSH3* loss-of-function (LOF) alterations in 1.2% of cases, with findings independently validated in a Caris pan-cancer cohort.
- Patients with *MSH3* LOF tumors had significantly improved overall survival following immune checkpoint blockade, including in MMRp/MSS tumors despite largely low TMB (<10 mutations/Mb).
- Somatic and germline *MSH3* LOF alterations define a distinct immunotherapy-sensitive subset and support *MSH3* LOF as a potential predictive biomarker beyond classic MSI-associated mechanisms.
- **These findings highlight how large-scale clinico-genomic profiling can identify novel immunotherapy-sensitive cancer subsets and support biomarker discovery beyond established MSI-associated mechanisms.**

MONDAY, JUNE 1, 2026

1:30 PM – 4:30 PM CDT: HALL A

POSTER SESSION: BREAST CANCER — LOCAL/REGIONAL/ADJUVANT

MERIT AWARD

Distinct late recurrence patterns and immune landscape of HER2-positive invasive lobular carcinoma (ILC): Analysis of NCCTG N9831 (Alliance) trial and real-world cohort.

Thiti Susiriwatananont, S. Deshmukh, P. Eiamprapaporn, Z. Li, S. Wu, K. Knutson, A. Nassar, Y. Liu, E. Perez, D. Trapani, M. Lustberg, G. Sledge Jr., E. Thompson, S. Chumsri.

Abstract: 564 **Poster:** 49 **Presenter:** Thiti Susiriwatananont, MD, MS

Association of patient-reported stress and depression symptoms with ER-specific tumor transcriptional signatures in breast cancer (BC).

S. Gandhi, S. Yasmeen, S. Rosario, H. Minderman, O. Maguire, S. Deshmukh, S. Wu, G. Sledge Jr., Z. Gong, A. Ruffin, M. Abdelbary, C. Paulos, N. Iyengar, E. Repasky, C. Ambrosone, S Yao, S. Badve, A. Madabhushi, K. Kalinsky, C-C. Hong.

Abstract: 565 **Poster:** 50 **Presenter:** Shipra Gandhi, MD, MS

Key Findings from this Session

- Analysis of the NCCTG N9831 trial, with validation in a real-world Caris cohort, showed that HER2-positive ILC demonstrated increased late recurrence risk despite initial trastuzumab benefit and exhibited a distinct immune landscape.
- Tumor transcriptomic analysis, with survival evaluation using Caris CODEai, demonstrated that patient-reported stress and depressive symptoms were associated with distinct ER-specific transcriptional signatures in breast cancer.
- **These studies demonstrate how transcriptomic and clinico-genomic analyses can identify distinct biological and immune features in breast cancer, potentially supporting more personalized approaches to risk stratification and therapeutic development.**

MONDAY, JUNE 1, 2026

1:30 PM – 4:30 PM CDT: HALL A

POSTER SESSION: BREAST CANCER — METASTATIC

MERIT AWARD

Organ- and histology-specific molecular and immune landscape of metastatic breast cancer.

G. Marta, S. Deshmukh, K. Fanucci, A. Lee, S. Oesterreich, S. Wu, J. Xiu, P. Advani, P. Coelho, M. Lustberg, S. Schnitt, N. Lin, S. Tolaney, E. Mayer, O. Metzger, G. Sledge Jr., R. Jeselsohn.

Abstract: 1024 **Poster:** 138 **Presenter:** Guilherme Nader Marta, MD

MERIT AWARD

TP53 status and licensing complex/IFNγ transcriptional profiles to stratify endocrine-related outcomes with CDK4/6i exposure in 10,833 real-world ER+/HER2- breast cancers and a treatment-naïve subset.

A. Raghavan, R. Plagens, C. Ma, J. Weber, A. Mabry, S. Graff, M. Lustberg, A. Elliott, G. Sledge Jr., C. Osborne, M. Rimawi, A. Elkhanany, R. Schiff.

Abstract: 1032 **Poster:** 146 **Presenter:** Alekya Raghavan, BS

CARIS HIGHLIGHT

Association of *ESR1* amplification with survival and benefit from CDK4/6 inhibition in breast cancer.

G. Sledge Jr., J. Xiu, M. Oberley, M. Radovich, D. Spetzler, A. Lee, S. Oesterreich.

Abstract: 1093 **Poster:** 207 **Presenter:** George W. Sledge, MD, FASCO

Key Findings

- Analysis of 27,979 breast cancers profiled by Caris identified *ESR1* amplification as a rare genomic alteration enriched in Luminal B disease.
- *ESR1*-amplified tumors exhibited genomic instability and enrichment of proliferative signaling pathways, including G2M checkpoint and MYC target gene sets.
- Clinically, *ESR1* amplification was associated with reduced overall survival and shorter palbociclib time on treatment, supporting its potential role as a negative predictive biomarker for CDK4/6 inhibition.
- **In this study, large real-world clinico-genomic analysis was used to identify rare molecular subsets associated with therapeutic resistance and clinically relevant treatment stratification in breast cancer.**

Time on treatment for systemic therapies for patients with hormone receptor-positive breast cancer and *BRCA1, BRCA2,* or *PALB2* pathogenic variants.

G. Parkinson, S. Nazari, M. Lustberg, A. Elliott, G. Sledge Jr., A. Soto, J. Caswell-Jin, A. Kurian, S. Graff.

Abstract: 1096 **Poster:** 210 **Presenter:** Gerneiva Parkinson, MD, MHS

Influence of *TONSL* on tumor suppressor function of *RAD51* and resistance to CDK4/6 inhibitors in ER+ breast cancer.

H. Nakshatri, S. Deshmukh, A. Khatpe, S. Wu, N. Kulkarni, S. Liu, J. Wan, S. Gandhi, M. Radovich, M. Lustberg, G. Sledge Jr., K. Miller, P Bhat-Nakshatri.

Abstract: 1097 **Poster:** 211 **Presenter:** Harikrishna Nakshatri, PhD

Real-world evaluation of CXCL9/10 with PD-L1 and TMB as predictors of pembrolizumab benefit in triple-negative breast cancer (TNBC).

S. Gandhi, S. Deshmukh, M. Canning, D. Trapani, S. Wu, J. Leone, K. Kalinsky, E. Roussos Torres, S. Badve, M. Jana, A. Madabhushi, S. Almahfouz, H. Al-Shakshir, M. Lustberg, K. Takabe, G. Curigliano, G. Sledge Jr., P. Kalinski.

Abstract: 1125 **Poster:** 239 **Presenter:** Shipra Gandhi, MD, MS

Key Findings from this Session

- Marked organ- and histology-specific molecular and immune heterogeneity was observed across 2,645 metastatic breast cancer biopsies, supporting site-aware interpretation of metastatic biopsies and biomarker assessment in advanced disease.
- Among 10,833 ER+/HER2- breast cancers profiled by Caris, licensing complex and IFNγ transcriptional profiles stratified endocrine therapy ± CDK4/6 inhibitor outcomes and may provide additional predictive value in *TP53* wild-type disease.
- Analysis of 27,979 Caris-profiled breast cancers identified *ESR1* amplification as a rare Luminal B-associated alteration linked to genomic instability, proliferative signaling, reduced overall survival, and shorter palbociclib time on treatment.
- Evaluation of 8,263 HR-positive breast cancers profiled by Caris showed that tumors with *BRCA1/2* or *PALB2* pathogenic variants had shorter time on endocrine therapy and CDK4/6 inhibitors, but longer time on PARP inhibitor therapy, compared with wild-type disease.
- In 10,980 ER-positive breast cancers profiled by Caris, high *TONSL* expression was associated with poorer outcomes following endocrine therapy and CDK4/6 inhibition, supporting further study of TONSL-directed strategies in resistant disease.
- High *CXCL9/10* expression was associated with an immune-active tumor microenvironment and improved overall survival following pembrolizumab, independent of PD-L1 and TMB, in a large cohort of TNBCs profiled by Caris.
- **Collectively, these studies demonstrate how integrated genomic, transcriptomic, and immune profiling can identify biologically distinct breast cancer subgroups, refine therapeutic stratification, and uncover potential biomarkers of treatment response and resistance across metastatic, hormone receptor–positive, and triple-negative disease.**

MONDAY, JUNE 1, 2026

1:30 PM – 4:30 PM CDT: HALL A

POSTER SESSION: CENTRAL NERVOUS SYSTEM TUMORS

Distinct genomic and microenvironmental profiles of brain metastases in renal cell carcinoma: Insights into hypoxia-driven adaptation and therapeutic vulnerabilities.

J. Avila, N. Sadeghipour, T. Nicolaides, A. Elliott, R. Kotecha, Y. Ged, M. Ahluwalia, E. Pack, S. Aulakh.

Abstract: 2033 **Poster:** 398 **Presenter:** Jorge Avila, MD

Key Findings from this Session

- Analysis of 3,913 renal cell carcinoma samples profiled by Caris identified distinct genomic and hypoxia-associated transcriptional features in brain metastases, while demonstrating conserved expression of multiple actionable therapeutic targets across primary tumors and brain metastases.
- **These findings demonstrate that comprehensive molecular profiling can characterize biologically distinct metastatic disease states and support development of biomarker-informed therapeutic strategies in renal cell carcinoma.**

MONDAY, JUNE 1, 2026

1:30 PM – 4:30 PM CDT: HALL A

POSTER SESSION: PREVENTION, RISK REDUCTION, AND GENETICS

Distinct immunogenomic features of cancers arising in solid organ transplant recipients.

S. Ahmed, C. Blosser, T. Adeyelu, K. Margolin, G. Ansstas, A. Elliott, F. Abdulla, E. Engels.

Abstract: 10587 **Poster:** 548 **Presenter:** Eric Engels, MD, MPH

Key Findings from this Session

- Molecular profiling of 1,024 tumors from solid organ transplant recipients identified reduced adaptive immune infiltration and lower IFN-γ signaling despite higher TMB and MSI prevalence in select cancer types.
- **Comprehensive molecular profiling can characterize distinct immunogenomic features in transplant-associated cancers that may inform development of immunotherapy strategies in solid organ transplant recipients.**

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