CARIS LIFE SCIENCES

Caris Abstracts and Presentation Schedule

AACR 2026

POSTERS

1200/1: **Spatially resolved tumor-cell MHC class II shapes adaptive immunity and therapeutic response in triple-negative breast cancer.**

Presenter: Saranya Chumsri

Author(s): Y. Liu, S. Deshmukh, T. Susiriwantananont, P. Eiamprapaporn, B. Wu, H. Joensuu, R. Leon-Ferre, D. Zahrieh, J. Boughey, J. Ingle, F. Couch, S. Wu, S. Gandhi, M. Lustberg, G. Sledge, M. Goetz, K. Knutson, E. Thompson, J. Carter, S. Chumsri.

Session: PO.CL01.12 – Spatial Proteomics and Transcriptomics 1

Time: 2:00 PM – 5:00 PM PST

Date: Sunday, April 19, 2026

Location: Poster Section 47

Key Findings:

- Tumor-cell MHC class II (HLA-DRA) expression was associated with an adaptive immune microenvironment in triple-negative breast cancer.
- High tumor-cell HLA-DR expression was associated with response to immune checkpoint blockade.
- In pembrolizumab-treated cohorts, responders had higher proportions of HLA-DRA-expressing tumor cells and increased local adaptive immune signatures.

2434/4: **Prognostic and predictive effects of *TP53* co-mutations and *RET* fusion partners in *RET*-rearranged advanced NSCLC.**

Presenter: Daniela Miliziano

Author(s): D. Miliziano, J. Rotow, M. Lomibao, T. Adeyelu, A. Marinello, H. Bote-de Cabo, J. Feng, A. De Giglio, M. Brandão, F. Guisier, M. Duruisseaux, C. Falcon, M. Cani, F. Colamartini, B. Waissengrin, I. Monnet, A. Eisert, E. Bria, A. Nassar, A. Aijaz, P. Iranzo, C. Lindsay, E. Fabre, V. Cordeiro de Lima, J. Raimbourg, L. Mezquita, N. Minatta, S. Cousin, K. Szymczak, V. Fallet, C. Audigier-Valette, H. Doubre, P. Rochigneux, A. Avanzo, A. Calles, M. Tagliamento, D. Cortinovis, B. Halmos, N. Girard, A. Elliott, J. Bar, A. Cortellini, D. Ionescu, F. Shepherd, F. Barlesi, K. Reckamp, D. Planchard, B. Besse, A. Drilon, M. Aldea.

Session: PO.CL01.03 – Biomarkers Predictive of Therapeutic Benefit 3

Time: 9:00 AM – 12:00 PM PST

Date: Monday, April 20, 2026

Location: Poster Section 40

Key Findings:

- Clinico-genomic analyses of tumors from patients with *RET*-rearranged advanced NSCLC treated with selective RET inhibitors demonstrated correlations between outcomes and genomic features.
- *TP53* co-mutation was associated with shorter progression-free and overall survival, indicating adverse prognostic significance.
- *RET* fusion partner was associated with differences in clinical outcomes.

3910/16: **AR copy number amplification and AR/*KLK3* expression patterns reveal mechanisms of AR signaling inhibitor (ARSI) resistance and highlight the need for AR-directed therapeutic innovation in metastatic castration resistance prostate cancer (mCRPC).**

Presenter: Celine Robert-Tissot

Author(s): C. Robert-Tissot, P. Nguyen, E. Murphy, Y. Yang, E. Gjini, M. Bowden.

Session: PO.CL07.02 – Molecular Targeted Therapy

Time: 2:00 PM - 5:00 PM PST

Date: Monday, April 20, 2026

Location: Poster Section 47

Key Findings:

- AR alterations and AR/*KLK3* expression were evaluated in mCRPC and correlated with treatment outcomes.
- AR copy number amplification (CNA) was associated with increased AR signaling and shorter time on treatment with ARSIs.
- These findings support a role for transcriptionally active AR in CNA-driven resistance.

4097/2: **cBioPortal for cancer genomics.**

Presenter: Ino de Bruijn

Author(s): T. Mazor, G. Zhao, M. Wilson, A. Wang, F. Vleugels, P. van Nierop, H. van den Ham, S. Sumer, J. Singh, B. Satravada, O. Plantalech, A. Ochoa, Z. Nasir, R. Madupuri, P. Lukasse, A. Lisman, J. Lindsay, X. Li, B. Lai, R. Kundra, P. Kumari, S. Kumar, T. Kuijpers, J. Ko, Z. Karagöz, K. Kalletla, P. Jagannathan, J. Hwee, G. Huelsz Prince, C. Haynes, B. Gross, Z. Fu, R. Forostianov, C. Chennault, R. AlHamad, U. Dogrusoz, A. Heath, A. Resnick, T. Pugh, C. Sander, J. Gao, N. Schultz, E. Ceram.

Session: PO.MD01.02 – AACR Project GENIE: Genomic Characterization

Time: 9:00 AM – 12:00 PM PST

Date: Tuesday, April 21, 2026

Location: Poster Section 1

Key Findings:

- cBioPortal integrates large-scale clinico-genomic datasets, including data from AACR Project GENIE and the Biopharma Collaborative.
- The platform is a global resource for cancer genomics analysis, with recent updates enhancing scale, interpretation, and usability.
- New features, including a natural language-based interface, enhance accessibility for complex genomic analyses within an open-source framework.

5336/4: **Distinct *KRAS* mutation codons differentially associate with microsatellite instability in colorectal carcinoma.**

Presenter: Julian Bryan

Author(s): M. Evans, V. Chandan, K. Shaw, S. Kopetz, A. Maitra, J. Bryan.

Session: PO.CL09.01 – Precision Oncology and Real World Data

Time: 9:00 AM – 12:00 PM PST

Date: Tuesday, April 21, 2026

Location: Poster Section 46

Key Findings:

- Microsatellite instability-high (MSI-H) prevalence in CRC was lower in tumors with *KRAS* codon 12 mutations.
- *KRAS* mutations in codons 13, 61, and 146 were associated with higher prevalence of MSI-H.
- These findings suggest that MSI-H prevalence differs by KRAS protein change.

6647/16: ***MCM2* and the origin licensing complex: A putative node of ER+/HER2- breast cancer therapy resistance.**

Presenter: Alekya Raghavan

Author(s): A. Raghavan, R. Plagens, C. Ma, S. Graff, M. Lustberg, A. Elliott, G. Sledge, C. Osborne, M. Rimawi, A. Elkhanany, R. Schiff.

Session: PO.CL09.02 – Real World Data to Provide Real World Evidence

Time: 2:00 PM – 5:00 PM PST

Date: Tuesday, April 21, 2026

Location: Poster Section 47

Key Findings:

- Histologic and genomic features were analyzed in ER+/HER2- breast cancer tumors stratified by expression of *MCM2* and its origin licensing complex (LC).
- High *MCM2* expression was associated with features linked to endocrine therapy and CDK4/6 inhibitor resistance.
- High *MCM2*/LC expression was also associated with the Luminal B breast cancer subtype.

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