Financial Interests, Personal, Other, Travel funding: Roche; Financial Interests, Institutional, Research Funding: AstraZeneca. C. Ho: Financial Interests, Institutional, Research Grant: AstraZeneca, Roche; Financial Interests, Personal, Advisory Board: AbbVie, Amgen, AstraZeneca, Bayer, BMS, Janssen, Jazz Pharmaceuticals, Novartis, Pfizer, Roche, Sanofi, GSK. All other authors have declared no conflicts of interest.

https://doi.org/10.1016/j.annonc.2025.08.3399

2789P Real-world molecular epidemiology study of select biomarkers in extensive-stage small-cell lung cancer (ES-SCLC)

C.M. Rudin[1], C.M. Gay[2], N. Choudhury[3], A.C. Chiang[4], H. Hu[5], J. Ma[5], C. Chen[5], R. Cristescu[5], E.J. Dettman[5], K. Zu[5], J.E. Gray[6]

[1]Department of Medicine, Memorial Sloan Kettering Cancer Center, New York, United States of America; [2]Department of Thoracic/Head & Neck Medical Oncology, The University of Texas MD Anderson Cancer Center, Houston, United States of America; [3]Department of Medicine, Memorial Sloan Kettering Cancer Center and Weill Cornell Medical College, New York, United States of America; [4]Department of Medicine, Yale University School of Medicine, New Haven, United States of America; [5]Oncology Research, Merck & Co., Inc., Rahway, United States of America; [6]Department of Thoracic Oncology, Moffitt Cancer Center, Tampa, United States of America

Background: Small prospective analyses have shown patients (pts) with select biomarkers or distinct ES-SCLC transcriptional subtypes may have distinct clinical outcomes. To investigate the potential prognostic value of these factors, we evaluated the association between SCLC subtypes and select biomarkers with clinical outcomes in pts with ES-SCLC.

Methods: Based on real-world (rw), deidentified patient-level data from the Tempus database (Tempus AI, Inc., Chicago, IL), this retrospective cohort study identified adult pts diagnosed with ES-SCLC from 2018 to 2022 who started first-line systemic therapy containing any immune checkpoint inhibitor, and had available tumor RNA (Tempus xR) and DNA (Tempus xT) sequencing data. Baseline characteristics at start of first-line therapy (ie, index date for survival analyses) and T-cell inflamed gene expression profile ($Tcell_{inf}GEP$) were descriptively analyzed by subtype based on transcription factor expression: neuroendocrine (NE) subtypes SCLC-A (high ASCL1) and SCLC-N (high NEUROD1), and non-NE subtypes SCLC-P (high POU2F3) and triple negative (TN). Associations between subtypes and $Tcell_{inf}GEP$ with rwPFS and rwOS were assessed using risk set-adjusted Cox regression models. Database cutoff: 6/30/24.

Results: Among 298 pts, 157 (52.7%) were female, median age was 66.3 (range, 22.4−85.8) y, and median follow-up was 11.8 (range, 0.1−62.1) mo. High $Tcell_{inf}GEP$ was associated with longer rwPFS (HR = 0.54; 95% CI, 0.35−0.82) and rwOS (HR = 0.58; 95% CI, 0.42−0.80). TN and SCLC-P subtypes had higher $Tcell_{inf}GEP$; SCLC-P (vs SCLC-A) was associated with higher risk of progression (Table).

Table: 2789P

	SCLC-A	TN	SCLC-N	SCLC-P
$Tcell_{inf}GEP$[a]	106 (35.6)	40 (13.4)	107 (35.9)	45 (15.1)
Low (1st/2nd tertiles), n (%)	80 (75.5)	14 (35.0)	84 (78.5)	21 (46.7)
High (3rd tertile), n (%)	26 (24.5)	26 (65.0)	23 (21.5)	24 (53.3)
rwPFS[a]	46 (43.4)	18 (45.0)	49 (45.8)	18 (40.0)
HR (95% CI)[b]	-	0.73 (0.39−1.35)[c]	0.88 (0.57−1.35)[c]	2.62 (1.44−4.76)[c]
rwOS[a]	101 (95.3)	34 (85.0)	96 (89.7)	40 (88.9)
HR (95% CI)[b]	-	0.80 (0.48−1.32)[c]	1.03 (0.74−1.44)[c]	1.34 (0.85−2.11)[c]

[a]Data are n (%) with available data. [b]Based on risk set-adjusted Cox regression models. [c]HRs adjusted for $Tcell_{inf}GEP$; SCLC-A as reference.

Conclusions: Non-NE subtypes, with higher $Tcell_{inf}GEP$, are more inflamed. With mutual adjustment, high $Tcell_{inf}GEP$ was associated with reduced risk of progression or death, but among SCLC subtypes, only SCLC-P was associated with shorter rwPFS. These rw data compliment similar RNA-based biomarker findings from clinical trials.

Editorial acknowledgement: Medical writing assistance was provided by Young-A Heo, PhD, of ICON plc (Blue Bell, PA, USA). This assistance was funded by Merck Sharp & Dohme LLC, a subsidiary of Merck & Co., Inc., Rahway, NJ, USA.

Legal entity responsible for the study: Merck Sharp & Dohme LLC, a subsidiary of Merck & Co., Inc., Rahway, NJ, USA.

Funding: Merck Sharp & Dohme LLC, a subsidiary of Merck & Co., Inc., Rahway, NJ, USA.

Disclosure: C.M. Rudin: Financial Interests, Personal, Advisory Board, Consulting re: oncology drug development: Amgen, AstraZeneca, Daiichi Sankyo, Hoffmann-La Roche, Novartis, Jazz Pharmaceuticals; Financial Interests, Personal, Advisory Board, SAB member: Auron, Earli; Financial Interests, Personal, Advisory Board, Licensing fees and royalties for DLL3-directed therapies: Memorial Sloan Kettering. C.M. Gay: Financial Interests, Personal, Invited Speaker: ACHL, AstraZeneca, Dava Oncology, IDEOlogy, Onclive, Peerview, Physician Education Resource (PER), Research to Practice, Targeted Healthcare; Financial Interests, Personal, Advisory Board: Abdera Therapeutics, Amgen, Aptitude Health, AstraZeneca, BeOne, Boehringer Ingelheim, Daiichi Sankyo, G1 Therapeutics, Jazz Pharmaceuticals, Monte Rosa Therapeutics; Financial Interests, Personal, Royalties: UpToDate; Financial Interests, Institutional, Research Grant: AstraZeneca; Financial Interests, Personal and Institutional, Steering Committee Member: AstraZeneca, BioNTech, Amgen, Roche − Genentech. N. Choudhury: Financial Interests, Personal, Invited Speaker: OncLive, IDEOlogy; Financial Interests, Personal, Advisory Board: Eli Lilly, AbbVie, Merck, Harpoon Therapeutics; Financial Interests, Personal, Royalties, Pocket Oncology 3rd Edition: Wolters Kluwer; Financial Interests, Institutional, Local PI: Amgen, Merck, Monte Rosa Therapeutics, AbbVie, Harpoon Therapeutics, Janux, Pyxis, DualityBio, Seagen. A.C. Chiang: Financial Interests, Personal, Other, Principal investigator on trials: AbbVie, AstraZeneca, BMS, Amgen, Zai Labs; Financial Interests, Personal, Advisory Board: AstraZeneca, Daiichi Sankyo, Fosun Pharma, GNE, Janssen, Zai Lab; Financial Interests, Personal, Other, Internal education: Jazz Pharmaceuticals; Financial Interests, Personal, Other, DSMB: AstraZeneca. H. Hu, J. Ma, C. Chen, R. Cristescu, E.J. Dettman, K. Zu: Financial Interests, Full or part-time Employment: Merck Sharp & Dohme LLC, a subsidiary of Merck & Co., Inc., Rahway, NJ, USA; Financial Interests, Stocks or ownership: Merck & Co., Inc., Rahway, NJ, USA. J.E. Gray: Financial Interests, Advisory Role: AstraZeneca, Coherus, Daiichi Sankyo, Inc (DSI), Eli Lilly, EMD Serono − Merck KGaA, Gilead Sciences, Inc, GO2 for Lung Cancer, IDEOlogy Health, Janssen Scientific Affairs, LLC, Jazz Pharmaceuticals, Merck Sharp & Dohme LLC, a subsidiary of Merck & Co., I; Financial Interests, Research Funding: AstraZeneca, Boehringer Ingelheim, Bristol Myers Squibb, Eli Lilly, EMD Serono − Merck KGaA, Genentech, Gilead Sciences, Inc, GO2 for Lung Cancer, Merck Sharp & Dohme LLC, a subsidiary of Merck & Co., Inc., Rahway, NJ, USA, Novartis, Panbela Therapeutics. All other authors have declared no conflicts of interest.

https://doi.org/10.1016/j.annonc.2025.08.3400

2790P Machine learning classification of small cell lung cancer using plasma multiomics in IMPower133

M. Reck[1], R. Gupte[2], T. Qing[2], V. Cheung[2], A. Tang[3], V. Gayevskiy[4], J. Sullivan[5], A. Cauwels[6], A. Tseng[7], K. Walter[8], E. Tabari[9], V. Chubukov[10], A. Lovejoy[11], J. Lin[12], D. Shames[13], M. Ballinger[14], S.V. Liu[15], M. Srivastava[16], B. Nabet[17]

[1]Thoracic Oncology Department, LungenClinic Grosshansdorf, Grosshansdorf, Germany; [2]Computational Biologist, Freenome Ltd, Nottingham, United Kingdom; [3]Computational Biologist, Freenome Holdings Inc., South San Francisco, United States of America; [4]Bioinformatics, Genentech, Inc., South San Francisco, United States of America; [5]Diagnostics, Genentech, Inc., South San Francisco, United States of America; [6]Translational Cancer Research, Freenome Holdings Inc., South San Francisco, United States of America; [7]Data Scientist, Freenome Holdings Inc., South San Francisco, United States of America; [8]Biomarker Strategist, Freenome Holdings Inc., South San Francisco, United States of America; [9]Data Science, Freenome Holdings Inc., South San Francisco, United States of America; [10]Computational Biology, Freenome Holdings Inc., South San Francisco, United States of America; [11]Molecular research, Freenome Holdings Inc., South San Francisco, United States of America; [12]Oncology Department, Freenome Holdings Inc., South San Francisco, United States of America; [13]Global Head of Clinical Biomarkers and CDx Development, BeiGene, Ltd., San Mateo, United States of America; [14]Global Development Lead, Lung and Head & Neck Cancer Immunotherapy, Genentech, Inc. - Member of the Roche Group, South San Francisco, United States of America; [15]Medical Oncology Department, Lombardi Cancer Center Georgetown University, Washington, United States of America; [16]Translational Medicine, Genentech, Inc., South San Francisco, United States of America; [17]Oncology Biomarker Development Department, Genentech - Building 42, South San Francisco, United States of America

Background: Tissue RNA-Seq analysis of extensive-stage small cell lung cancer (ES-SCLC) tumors in the IMpower133 trial (NCT02763579) identified four ES-SCLC subsets (SCLC-N, SCLC-A, SCLC-I-NE, SCLC-I-non-NE), with the SCLC-I-NE subset showing longer overall survival with atezolizumab plus chemotherapy compared to chemotherapy alone, in contrast to the SCLC-I-non-NE subset (Nabet et al, Cancer Cell). To assess the feasibility of determining ES-SCLC subsets based on liquid biopsy, we developed machine learning models using plasma multiomics data.

Methods: We analyzed cell-free DNA (cfDNA) and circulating proteins from 140 patients from IMpower133. We measured CpG methylation at over 250,000 loci by targeted sequencing and inferred gene expression and transcription factor activities from cfDNA fragment patterns. Logistic regression models were trained on individual analyte classes as well as their combinations to classify tumors into one of four subsets.

Results: Plasma multiomics assays effectively differentiate SCLC subsets, with the methylation-based model showing average area under curve (AUC) of 0.84 across the four subsets, while models based on inferred gene expression and proteomics showed AUCs of 0.80 and 0.75. All models were also effective in distinguishing NE from non-NE tumors as a two-class problem (AUCs 0.78-0.89). Features related to subset-associated markers identified in tumors were detected in plasma and contributed to classifier performance. This included lower promoter methylation of NEUROD1 and REST in SCLC-N and SCLC-I-non-NE tumors, respectively. Inferred expression of immune biomarkers such as IFNG (IFN-γ) and CSF3 (G-CSF), was significantly different ($p<0.01$) between I-NE tumors and I-non-NE tumors. Among proteins quantified in serum, there was an enrichment for protein abundance patterns that matched tumor RNA expression, e.g. TFF3 in ASCL1-driven tumors.

Conclusions: We demonstrate that plasma multiomics assays accurately differentiate ES-SCLC subsets, particularly in distinguishing NE from non-NE tumors. These data underscore the potential of plasma multiomics as a noninvasive tool for clinically relevant SCLC subtyping.

Clinical trial identification: NCT02763579.

Legal entity responsible for the study: F. Hoffmann-La Roche.

Funding: F Hoffmann-La Roche.

Disclosure: M. Reck: Financial Interests, Personal, Invited Speaker: Amgen, AstraZeneca, BMS, Boehringer Ingelheim, Lilly, MSD, Merck, Novartis, Regeneron, Roche, Sanofi, GSK, Pfizer, Pierre Fabre; Financial Interests, Personal, Advisory Board: Amgen, AstraZeneca, BMS, BioNTech, Boehringer Ingelheim, Daiichi Sankyo, Gilead, MSD, Mirati, Pfizer, Regeneron, Roche, Sanofi, GSK, Lilly, Pierre Fabre; Financial Interests, Personal, Other, Member of DMSB: Daiichi Sankyo; Financial Interests, Personal, Other, Member of Data Monitoring Committee: Servier, CureVac; Financial Interests, Personal, Coordinating PI: AstraZeneca; Financial Interests, Institutional, Steering Committee Member: Amgen, Boehringer Ingelheim, BeiGene, Daiichi Sankyo, GSK, BMS, Lilly, MSD, Regeneron, Roche; Financial Interests, Institutional, Local PI: Pfizer Seagen, Nuvalent. R. Gupte: Financial Interests, Personal, Full or part-time Employment: Freenome; Financial Interests, Personal, Stocks/Shares, Employee: Freenome. T. Qing: Financial Interests, Institutional, Full or part-time Employment, I am a current employee of Freenome Holdings: Freenome Holdings; Financial Interests, Institutional, Stocks/Shares: Freenome Holdings. V. Cheung, A. Tang, A. Cauwels, A. Tseng, K. Walter, E. Tabari, V. Chubukov, A. Lovejoy, J. Lin: Financial Interests, Personal, Full or part-time Employment: Freenome Holdings. V. Gayevskiy, J. Sullivan, M. Ballinger, M. Srivastava, B. Nabet: Financial Interests, Personal, Full or part-time Employment: Genentech, Inc. D. Shames: Financial Interests, Personal, Full or part-time Employment: BeiGene. S.V. Liu: Financial Interests, Personal, Advisory Board, Consultant: AstraZeneca, Daiichi Sankyo, Genentech / Roche, Jazz Pharmaceuticals, Merck, Novartis, Regeneron; Financial Interests, Personal, Advisory Board: Bristol Myers Squibb, RAPT Therapeutics, Gilead, Guardant Health, Merus, Takeda, Revolution Medicines, Amgen, AbbVie, Boehringer Ingelheim, Mirati, Pfizer, Lilly, Natera, Johnson & Johnson; Financial Interests, Personal, Invited Speaker: OSE Immunotherapeutics, Yuhan; Financial Interests, Personal, Other, Consultant: GSK; Financial Interests, Institutional, Local PI: Alkermes, Elevation Oncology, Gilead, Merck, Merus, Nuvalent, RAPT, AbbVie, AstraZeneca, Puma, Ellipses, Bristol Myers Squibb, Cogent Biosciences, Duality, Synthekine, SystImmune, Medilink; Financial Interests, Institutional, Steering Committee Member: Genentech; Financial Interests, Institutional, Coordinating PI: OSE Immunotherapeutics; Non-Financial Interests, Member: ASCO, IASLC.

https://doi.org/10.1016/j.annonc.2025.08.3401

2791P Advancing SCLC biomarker discovery: AI-driven MHC-I quantification and impact of MHC-I on the tumor microenvironment

C. Eisen[1], F. Pollastri[1], M. Vuko[1], J. Lesniak[1], A. Andoni[1], K. DaCosta[1], E. Mahieu[1], E. Badhri[1], M. Schick[1], G. Schmidt[1], G. Fabbri[2]

[1]*Oncology R&D, AstraZeneca Computational Pathology GmbH, Munich, Germany;* [2]*Translational Medicine, AstraZeneca, Gaithersburg, United States of America*

Background: Small cell lung cancer (SCLC) is a highly aggressive malignancy with alarmingly low survival rates. Immune checkpoint blockade (ICB) has improved treatment outcomes but shows heterogeneous responses. The quest for predictive biomarkers is urgent. MHC-I expression has emerged as a key factor associated with superior ICB outcomes, yet conventional IHC scoring is hampered by stain variability. To revolutionize MHC-I assessment, this study introduces a cutting-edge computational pathology method, promising novel insights into SCLC biomarker discovery.

Methods: A Convolutional Neural Network was trained to segment the invasive epithelium within manually identified tumor areas and was divided into a grid of 1 μm^2 tiles. MHC-I expression was quantified through Optical Density (OD), categorizing tiles via varied thresholds. Utilizing a diverse commercial sample set of 126 SCLC specimens we used a multiplexed immunofluorescence panel to study the impact of MHC-I expression on the tumor immune contexture.

Results: Our model, tested against 50 annotated Field of Views, exhibited remarkable concordance with expert pathologists (0.88 F1 Score). Furthermore, high MHC-I expression was associated with higher densities of CD8+ T-cells, indicating an active immune status and infiltration of distinct immune cells. Conversely, low MHC-I expression correlated with an immunosuppressive tumor microenvironment. Our findings suggest that high MHC-I expression affects the tumor microenvironment, promoting an active immune status and immune cell infiltration, while low MHC-I expression is linked to an immunosuppressive microenvironment.

Conclusions: Our cutting-edge computational pathology approach for MHC-I scoring shows high concordance with manual scoring and provides a promising alternative to traditional methods in clinical settings. This method can automatically measure target expression, significantly aiding in the stratification of SCLC patients. Spatial analysis of the immune contexture underscores MHC-I's potential as a biomarker for identifying patients with an inflamed tumor microenvironment who are likely to benefit most from cancer immunotherapies.

Legal entity responsible for the study: AstraZeneca.

Funding: AstraZeneca.

Disclosure: C. Eisen, F. Pollastri, M. Vuko, J. Lesniak, A. Andoni, K. DaCosta, E. Mahieu, E. Badhri, M. Schick, G. Schmidt, G. Fabbri: Other, Full or part-time Employment: AstraZeneca.

https://doi.org/10.1016/j.annonc.2025.08.3402

2792TiP A phase Ib/II study of gocatamig (MK-6070; HPN328) and ifinatamab deruxtecan for relapsed/refractory extensive-stage small cell lung cancer (ES-SCLC)

J. Bar[1], J.C. Benitez Montanez[2], A.F. Navarro Mendivil[3], M. Gutierrez[4], M.L. Johnson[5], C. Caglevic[6], N. Peled[7], T. Shentzer Kutiel[8], J. Sands[9], C.I. Rojas[10], P.F. Simoes da Rocha[11], E. Algin[12], H. Udagawa[13], R. Ariyasu[14], T.M. Kim[15], C. Rathi[16], V.V. Karantza[17], Q. Liu[17], A.W. Gramza[17], J-M. Sun[18]

[1]*Institute of Oncology, Jusidman Cancer Center, Sheba Medical Center, Ramat Gan, Israel;* [2]*Medical Oncology, Thoracic Tumors Unit, University Hospital Virgen de la Victoria, Biomedicine Research Institute of Malaga (IBIMA plataforma BIONAND), Malaga, Spain;* [3]*Thoracic Oncology Group, Medical Oncology Department, Translational Genomics and Targeted Therapies in Solid Tumors, IDIBAPS Department of Medicine, University of Barcelona Hospital Clinic de Barcelona, Barcelona, Spain;* [4]*Department of Medical Oncology, John Theurer Cancer Center - Hackensack University Medical Center, Hackensack, United States of America;* [5]*Lung Cancer Research, SCRI Oncology Partners, Nashville, United States of America;* [6]*Cancer Research Department, Fundación Arturo López Pérez-Unidad de Investigación de Drogas Oncológicas, Santiago, Chile;* [7]*Cancer Center, Shaare Zedek Medical Center, Jerusalem, Israel;* [8]*Oncology Department, Rambam Health Care Campus, Haifa, Israel;* [9]*Thoracic Medical Oncology, Dana Farber Cancer Institute, Boston, United States of America;* [10]*Medical Oncology, Bradford Hill Investigación Clínica, Santiago, Chile;* [11]*Medical Oncology, Vall d'Hebron University Hospital, Barcelona, Spain;* [12]*Department of Medical Oncology, Ankara Bilkent City Hospital, Ankara, Türkiye;* [13]*Department of Thoracic Oncology, National Cancer Center Hospital East, Kashiwa, Japan;* [14]*Thoracic Medical Oncology, Cancer Institute Hospital of Japanese Foundation for Cancer Research, Tokyo, Japan;* [15]*Internal Medicine Department, Seoul National University Hospital, Seoul, Republic of Korea;* [16]*Clinical, Daiichi Sankyo USA, Boston, United States of America;* [17]*MRL, Merck & Co., Inc., Rahway, United States of America;* [18]*Medical Oncology, Samsung Medical Center, Seoul, Republic of Korea*

Background: Delta-like ligand 3 (DLL3) and B7-H3 are proteins that are highly expressed on the cell surface of SCLC. Gocatamig is a DLL3-targeted T-cell engager. Ifinatamab deruxtecan (I-DXd) is a B7-H3—targeted antibody-drug conjugate (ADC) linked to a potent topoisomerase I inhibitor. Gocatamig monotherapy and I-DXd monotherapy have each shown manageable safety and encouraging antitumor activity as second- or later-line treatment for ES-SCLC. With distinct mechanisms of action and minimally overlapping safety profiles, the combination of gocatamig and I-DXd has the potential to substantially enhance efficacy without compromising tolerability.

Trial design: In the ongoing, open-label 6070-002 study (NCT06780137), adults ($\geq$18 years) with ES-SCLC and ECOG PS 0-1 who had prior platinum-based chemotherapy (with or without PD-(L)1 inhibitors) are eligible. Part 1 comprises of a safety run-in phase followed by a dose-expansion phase. Target doses and schedules of gocatamig combined with I-DXd or I-DXd monotherapy to be used in part 1 will be determined based on results of the ongoing 6070-001 study (NCT04471727). Part 2 consists of a gocatamig monotherapy arm enrolling participants in Japan only. Additional monotherapy and combination cohorts are planned. The primary objectives are to evaluate safety and tolerability (parts 1 and 2), including the incidence and causality of adverse events (AEs), dose-limiting toxicities (part 1 safety run-in phase; part 2), and treatment discontinuations due to AEs, and to evaluate the objective response rate by investigator assessment per RECIST v1.1 (part 1). Secondary objectives are to evaluate duration of response and progression-free survival by investigator assessment per RECIST v1.1 (part 1) and to characterize the pharmacokinetics and immunogenicity of gocatamig plus I-DXd combination therapy (part 1), I-DXd monotherapy (part 1), and gocatamig monotherapy (part 2). The 6070-002 study will enroll participants in Australia, Chile, China, Israel, Japan, South Korea, Spain, Türkiye, the United States of America, and other sites as the expansion gets underway.

Clinical trial identification: NCT06780137.

Editorial acknowledgement: Anna Lau of Merck & Co., Inc., Rahway, NJ, USA provided medical writing assistance.

Legal entity responsible for the study: Merck Sharp & Dohme LLC, a subsidiary of Merck & Co., Inc., Rahway, NJ, USA.

Funding: Merck Sharp & Dohme LLC, a subsidiary of Merck & Co., Inc., Rahway, NJ, USA.

Disclosure: J. Bar: Financial Interests, Personal, Advisory Board: MSD, Takeda, Roche, Pfizer, AbbVie, Bayer, AstraZeneca, Merck-Serono, J-C healthcare, Medison Pharma, Amgen, NectinTx; Financial Interests, Personal, Invited Speaker: BMS; Financial Interests, Personal, Other, Steering committee: AbbVie, Merck Healthcare KGaA, Roche, AstraZeneca; Financial Interests, Institutional, Local PI: MSD, Roche, Takeda, AbbVie; Financial Interests, Institutional, Other, local sub-investigator: Novartis; Financial Interests, Institutional, Research Grant: OncoHost, ImmuneAI, AstraZeneca; Non-Financial Interests, Other, Committee member: IASLC. J.C. Benitez Montanez: Financial Interests, Personal, Invited Speaker, Local symposium: AstraZeneca; Financial Interests, Personal, Advisory Board, Expert opinion in national meeting: Roche; Financial Interests, Personal, Invited Speaker, National Symposium: Roche; Financial Interests, Personal, Advisory Board, Advisoring national meeting: BMS; Financial Interests, Personal, Invited Speaker, Local meeting: Regeneron, Takeda; Financial Interests, Institutional, Research Grant, Translational Research Grant for MAPs-LUNG project: Gilead. A.F. Navarro Mendivil: Financial Interests, Personal, Advisory Board: MSD, AstraZeneca, Pfizer, Hengenix Biotech, MedSIR, Oryzon Genomics, Boehringer Ingelheim, Janssen, Daiichi Sankyo; Financial Interests, Personal, Invited Speaker: Roche, Takeda, BMS, AstraZeneca, Boehringer Ingelheim, Adium, Tecnoframa, Regeneron, Eczacibasi; Financial Interests, Personal, Other, travel support to scientific meetings: Roche, Pfizer, Takeda, Janssen; Financial Interests, Institutional, Principal Investigator: BMS, Roche, Celgene, PharmaMar, AstraZeneca, MSD, Amgen, IPSEN, Daiichi Sankyo, Debiopharm, AbbVie; Financial Interests, Personal, Steering Committee