

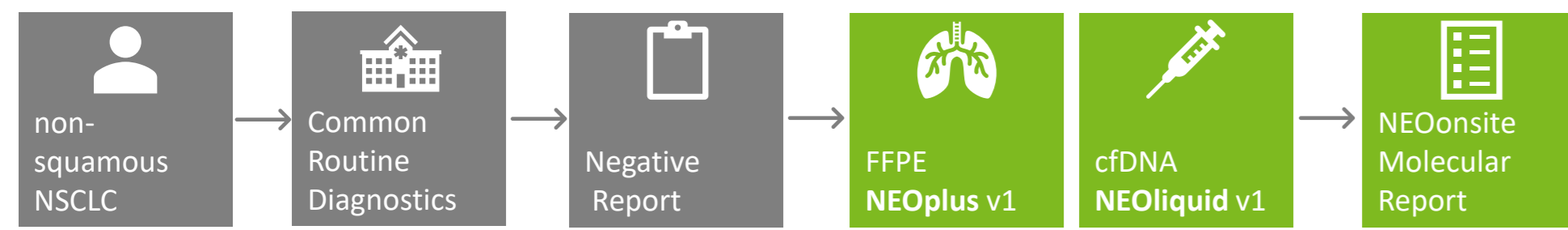
Hybrid Capture-Based Assays in Primary Diagnostics of NSCLC Patients

Results from the NEOlung Study

Balazs Jori¹, Oliver Gautschi², Martin Kimmich³, Sophie Beaucaire Danel⁴, Niels Reinmuth⁵, Pilar Garrido⁶, Federico Cappuzzo⁷, Martin Forster⁸, Krishna Patel⁸, Christian Grohé⁹, Annette Müller¹⁰, Claas Wesseler¹¹, Roopika Menon¹, Judith Müller¹, Erika Mariotti¹, Julia Brinkmann¹², Lukas Heukamp¹³, Frank Griesinger¹⁴

¹NEO New Oncology, Cologne, Germany, ²University of Berne and Cantonal Hospital of Lucerne, Switzerland, ³Department of Pneumology, Clinic Schillerhoehe, Gerlingen, Germany, ⁴Institut du Thorax Curie-Montsouris, Institut Curie, Paris, France, ⁵Asklepios Lung Clinic, Munich-Gauting, Germany, ⁶Medical Oncology Department, Hospital Ramón y Cajal, Madrid, Spain, ⁷Department of Oncology & Hematology, AUSL Romagna, Ravenna, Italy, ⁸Cancer Clinical Trials Unit, University College Hospitals, London, United Kingdom, ⁹Evangelische Lungenklinik Berlin, Berlin, Germany, ¹⁰Department of Hematology and Oncology, University Hospital of Mannheim, Mannheim, Germany, ¹¹Thoraxonkologie, Asklepios Klinikum, Hamburg, Germany, ¹²Oncology, Pfizer Pharma GmbH, Berlin, Germany, ¹³Lung Cancer Network, NOWEL, Oldenburg, Germany, ¹⁴Hematology and Oncology, Pius Hospital, University of Oldenburg, Oldenburg, Germany

Routine molecular screening of non-small cell lung cancer (NSCLC) patients for actionable mutations is often challenging due to limited tumor material and assay sensitivity. **NEOlung**, a multi-centric exploratory study evaluated the usefulness of hybrid capture-based next generation sequencing (HC-NGS) assays NEOliquid v1 and NEOplus v1 in the primary diagnostic setting. Our aim was to evaluate the added value of both assays in a presumed negative, untreated NSCLC patient population.



NSCLC Samples	Methods	Alterations detected
<ul style="list-style-type: none"> 183 blood and 30 FFPE samples Prior, common routine diagnostics resulted: <ul style="list-style-type: none"> - negative for <i>EGFR</i> - negative or untested for <i>KRAS, ALK, MET, ERBB2, RET, ROS1, BRAF, NTRK1</i> 	<ul style="list-style-type: none"> DNA-based HC-NGS NEOliquid v1 for cfDNA NEOplus v1 for FFPE NEO proprietary bioinformatic pipeline 	<ul style="list-style-type: none"> Point mutations Small InDels Copy Number Variations Gene Fusions

Genes in NEOliquid v1													
<i>ALK</i>	<i>ARAF</i>	<i>ATM</i>	<i>ATR</i>	<i>BRAF</i>	<i>BRCA1</i>	<i>BRCA2</i>	<i>CDK4</i>	<i>CDKN2A</i>	<i>CDKN2B</i>	<i>CTNNB1</i>	<i>DDR2</i>		
<i>EGFR</i>	<i>ERBB2</i>	<i>FGFR1</i>	<i>FGFR2</i>	<i>FGFR3</i>	<i>HRAS</i>	<i>IDH1</i>	<i>IDH2</i>	<i>KEAP1</i>	<i>KIT</i>	<i>KRAS</i>	<i>MAP2K1</i>		
<i>MDM2</i>	<i>MET</i>	<i>MTOR</i>	<i>NFE2L2</i>	<i>NRAS</i>	<i>PDGFRA</i>	<i>PIK3CA</i>	<i>PTEN</i>	<i>RB1</i>	<i>RET</i>	<i>ROS1</i>	<i>STK11</i>		
	<i>TP53</i>	<i>TSC1</i>	<i>TSC2</i>										

In addition to SNVs and small InDels, the test covers genes applicable for CNV (bold) and for fusion detection (italic).

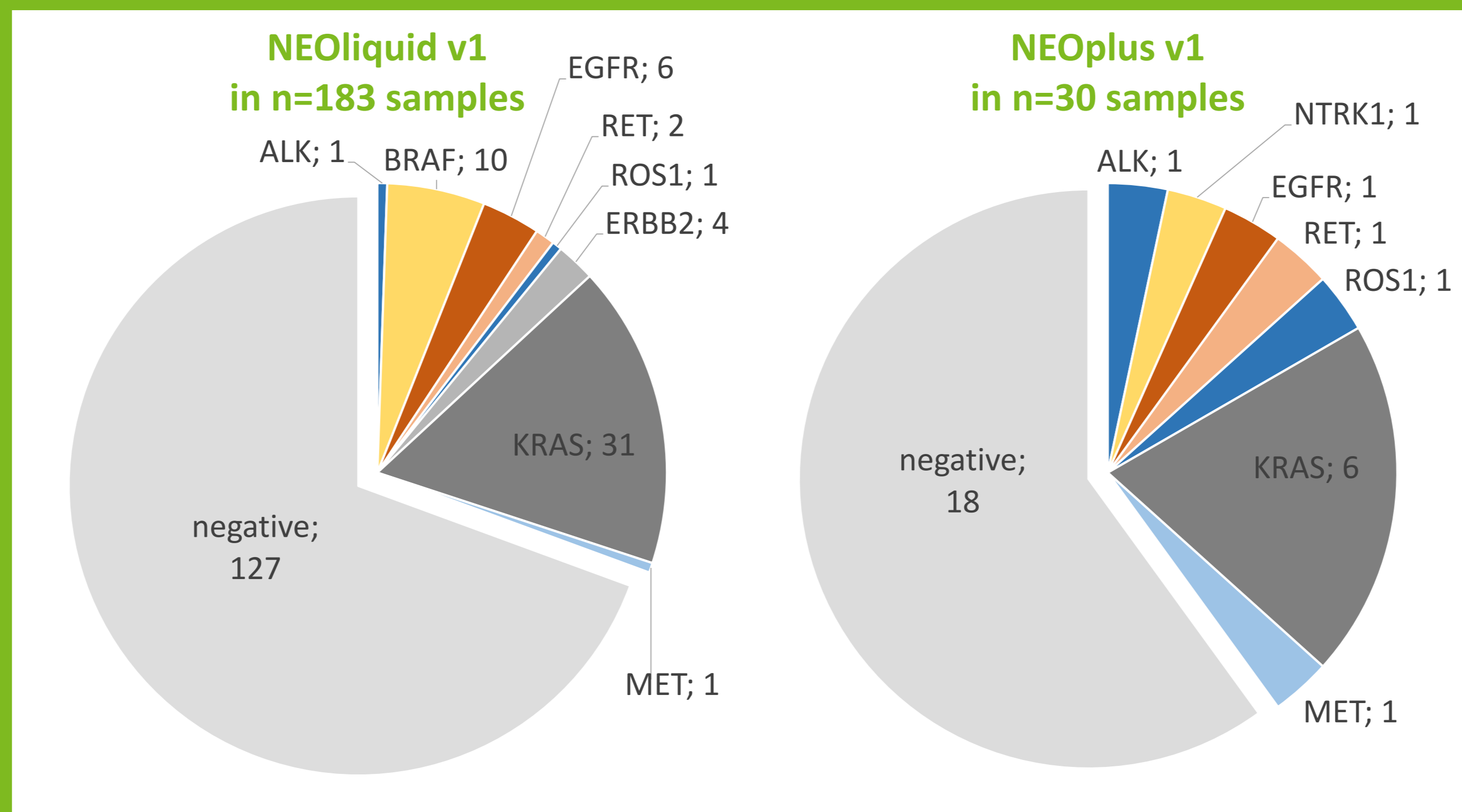
Genes in NEOplus v1													
<i>ABL1</i>	<i>AKT1</i>	<i>ALK</i>	<i>APC</i>	<i>AR</i>	<i>ARAF</i>	<i>ARID1A</i>	<i>ARID1B</i>	<i>ATM</i>	<i>ATR</i>	<i>B2M</i>	<i>BCL6</i>		
<i>BRAF</i>	<i>BRCA1</i>	<i>BRCA2</i>	<i>BRD4</i>	<i>BRIP1</i>	<i>CCND1</i>	<i>CCNE1</i>	<i>CD274</i>	<i>CD74</i>	<i>CDH1</i>	<i>CDK4</i>	<i>CDK6</i>		
<i>CDKN2A</i>	<i>CDKN2B</i>	<i>CHEK1</i>	<i>CHEK2</i>	<i>CTNNB1</i>	<i>DDR2</i>	<i>EGFR</i>	<i>EML4</i>	<i>ERBB2</i>	<i>ERBB3</i>	<i>ESR1</i>	<i>FBXW7</i>		
<i>FGFR1</i>	<i>FGFR2</i>	<i>FGFR3</i>	<i>FGFR4</i>	<i>GNA11</i>	<i>GNA13</i>	<i>GNAI2</i>	<i>GNAQ</i>	<i>GNAS</i>	<i>GNAT2</i>	<i>HRAS</i>	<i>IDH1</i>		
<i>IDH2</i>	<i>JAK2</i>	<i>KDR</i>	<i>KEAP1</i>	<i>KIF5B</i>	<i>KIT</i>	<i>KRAS</i>	<i>MAP2K1</i>	<i>MAP2K2</i>	<i>MDM2</i>	<i>MET</i>	<i>MTOR</i>		
<i>MYC</i>	<i>MYCL1</i>	<i>MYCN</i>	<i>NF1</i>	<i>NFE2L2</i>	<i>NRAS</i>	<i>NRG1</i>	<i>NTRK1</i>	<i>PALB2</i>	<i>PDGFRA</i>	<i>PDGFRB</i>	<i>PIK3CA</i>		
<i>PIK3R1</i>	<i>POLD1</i>	<i>POLE</i>	<i>PRKDC</i>	<i>PTCH1</i>	<i>PTEN</i>	<i>RAD50</i>	<i>RAD51</i>	<i>RAF1</i>	<i>RB1</i>	<i>RET</i>	<i>RICTOR</i>		
	<i>ROS1</i>	<i>RPTOR</i>	<i>SMO</i>	<i>STK11</i>	<i>TERT</i>	<i>TP53</i>	<i>TP53BP1</i>	<i>TSC1</i>	<i>TSC2</i>	<i>VHL</i>			

In addition to SNVs, small InDels and CNV, the test covers genes applicable for fusion detection (italic).

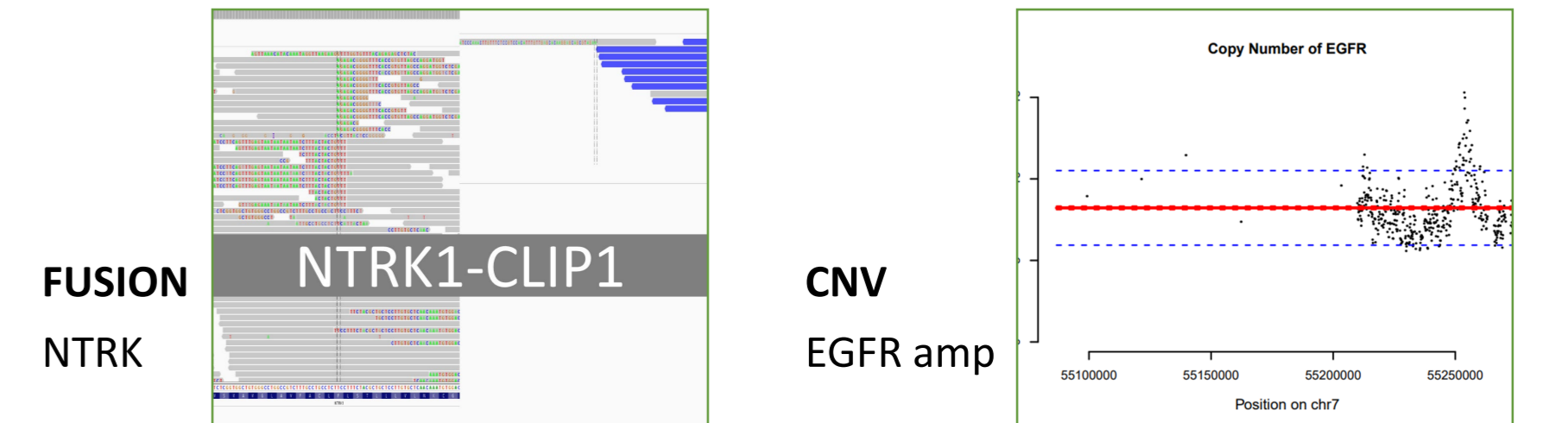
Within a previously negatively reported NSCLC cohort, using hybrid capture assays we identified

additional
12 (6.6%) patients with NEOliquid and
5 (16.5%) patients with NEOplus

with druggable alterations.



Distribution of driver alterations detected with NEOliquid v1 and NEOplus v1 in NSCLC samples that were previously reported as negative in routine molecular analysis.



- ### Results
- We analysed 213 samples that were previously documented to be, based on previous routine screening (i.e. IHC, PCR), negative for *EGFR* and negative or untested for *ALK, BRAF, EGFR, ERBB2, KRAS, MET, RET, ROS1, NTRK1*.
 - NEOliquid v1 (cfDNA) identified driver events in *ALK* (1), *BRAF* (10), *EGFR* (6), *RET* (2), *ROS1* (1), *ERBB2* (4), *KRAS* (31), *MET* (1) in 56 out of the **183 blood** samples.
 - NEOplus v1 (FFPE) identified driver events in *NTRK1* (1), *ALK* (1), *EGFR* (1), *KRAS* (6), *MET* (1), *RET* (1), *ROS1* (1), in 12 out of the **30 tumor** samples.
 - Out of these, druggable alterations were identified in 12 patients analysed with NEOliquid (6.6%), and in further 5 patients with NEOplus (16.5%).

- ### Conclusions
- HC-NGS can detect less prevalent, novel or complex and even druggable alterations that would not be detectable with commonly used routine diagnostic methods.
 - Due to the broad landscape of driver events in NSCLC, basic routine screening methods often fail to detect actionable and druggable alterations, such as *BRAF, RET, MET* or *NTRK*.
 - The detection of actionable *EGFR* mutations in a pre-screened, potential *EGFR*-negative cohort might be explained by the lower sensitivity or lack of testing in routine assays, especially with respect to non-classical *EGFR* mutations such as p.(I744_E746delinsMK) or p.(G719C), p.(S768I).

Conflict of interest
B. Jori, R. Menon, E. Mariotti, J. Müller are employed by NEO New Oncology GmbH. J. Brinkmann is employed by Pfizer Pharma GmbH. P. Garrido declares conflict of interest as of Roche, Speaker, Advisory Role, AstraZeneca, Speaker, Advisory Role, Bristol (BMS), Speaker, Advisory Role, Guardant Health, Advisory Role, MSD, Speaker, Advisory Role, Pfizer, Speaker, Advisory Role, Janssen, Advisory Role, Boehringer Ingelheim, Speaker, Advisory Role, Novartis, Speaker, Advisory Role, Gilead, Speaker, Rovi, Speaker, Abbvie, Advisory Role Lilly, Advisory Role, Takeda, Advisory Role, Speaker, Sysmex, Speaker Blueprint Medicines, Advisory Role, Bayer, Advisory Role. M. Forster has research grants from AstraZeneca, Boehringer Ingelheim, Bristol-Myers Squibb, Daiichi Sankyo, MSD & Merck and honoraria for advisory and consultancy work from Achilles, AstraZeneca, Bayer, Bristol-Myers Squibb, Celgene, Guardant Health, Merck, MSD, Nanobiotix, Novartis, Oxford VacMedix, Pfizer, PharmaMar, Roche & Takeda.

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Contact
NEO New Oncology GmbH, Gottfried-Hagen-Str. 20, 51105 Köln, Germany www.newoncology.de, email jori@newoncology.de