# The continually evolving landscape of novel therapies in oncogene-driven advanced non-small-cell lung cancer

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Abstract: Non-small-cell lung cancer (NSCLC) is a highly heterogeneous disease that is frequently associated with a host of known oncogenic alterations. Advances in molecular diagnostics and drug development have facilitated the targeting of novel alterations such that the majority of NSCLC patients have driver mutations that are now clinically actionable. The goal of this review is to gain insights into clinical research and development principles by summary, analysis, and discussion of data on agents targeting known alterations in oncogenedriven, advanced NSCLC beyond those in the epidermal growth factor receptor (EGFR) and the anaplastic lymphoma kinase (ALK). A search of published and presented literature was conducted to identify prospective trials and integrated analyses reporting outcomes for agents targeting driver gene alterations (except those in EGFR and ALK) in molecularly selected. advanced NSCLC. Clinical efficacy data were extracted from eligible reports and summarized in text and tables. Findings show that research into alteration-directed therapies in oncogenedriven, advanced NSCLC is an extremely active research field. Ongoing research focuses on the expansion of new agents targeting both previously identified targets (particularly hepatocyte growth factor receptor (MET), human epidermal growth factor receptor 2 (HER2), and Kirsten rat sarcoma viral oncogene homolog (KRAS)) as well as novel, potentially actionable targets (such as neuregulin-1 (NRG1) and phosphatidylinositol 3-kinase (PI3K)). The refinement of biomarker selection criteria and the development of more selective and potent agents are allowing for increasingly specific and effective therapies and the expansion of clinically actionable alterations. Clinical advances in this field have resulted in a large number of regulatory approvals over the last 3 years. Future developments should focus on the continued application of alteration therapy matching principles and the exploration of novel ways to target oncogene-driven NSCLC.

*Keywords:* antibody-drug conjugates, monoclonal antibodies, non-small-cell lung cancer, oncogenic alterations, protein kinase inhibitors, targeted therapy

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#### Introduction

Lung cancer is one of the most common malignancies and the leading cause of cancer-related death.<sup>1–3</sup> Non-small-cell lung cancer (NSCLC) accounts for 85% of all lung malignancies and approximately 50% of NSCLC patients are diagnosed at the metastatic stage.<sup>4–6</sup> NSCLC is a heterogeneous disease that is frequently associated with multiple known oncogenic driver genes.<sup>7–10</sup> The earliest characterized of these are mutations involving the *epidermal growth factor receptor* (*EGFR*) and fusions involving *anaplastic lymphoma kinase* (*ALK*). Treatment with EGFR and ALK inhibitors is well established, with initial

Review

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approvals in biomarker-unselected and -selected populations in 2003 and 2011, respectively.<sup>7,11–14</sup>

Advances in cancer biology, molecular diagnostics, and drug development have improved our ability to identify and therapeutically target oncogenic alterations.<sup>9,10,15,16</sup> It is now estimated that the majority of NSCLC patients have alterations that are clinically actionable with a therapeutic agent that acts on the altered target (alterationdrug-matched).<sup>9,17–26</sup> Here we will update our initial review of novel (non-EGFR/ALK) targeted therapies<sup>8</sup> by identifying, summarizing, analyzing, and discussing recent data on agents targeting lesser-known alterations (Table 1) in oncogene-driven, advanced NSCLC to gain insights into clinical research and development principles.

Table 1	Select	actionable	molecular	alterations in	n oncogene	-driven	NSCLC.

Oncogene and molecular alteration	Biological function in regular and altered states	Common alterations	Incidence, %	Detection method
<i>ROS1</i> rearrangement <sup>7,9,27–29</sup>	<ul> <li>ROS1 is a tyrosine kinase receptor with significant structural homology to ALK</li> <li>Rearrangements/translocations give rise to fusions of functional ROS1 tyrosine kinase domain with other genes</li> <li>Resulting constitutive activation drives transformation and activates SHP-1/SHP-2, JAK/STAT, PI3K/AKT/mTOR, and MAPK/ERK signaling leading to enhanced tumor cell survival and proliferation</li> </ul>	Up to 24 fusion partners identified	1–3	FISH, RT-PCR, RNA NGS
<i>BRAF-</i> V600 mutation <sup>7,9,30</sup>	<ul> <li>BRAF is an intracellular serine/threonine kinase activated by RAS and subsequently activates MEK and ERK (MAPK pathway)</li> <li>Mutation leads to constitutive activation, cell growth, and proliferation</li> <li>Dual inhibition of BRAF and MEK may prevent reactivation of MAPK signaling</li> </ul>	V600E	1–2	DNA NGS
<i>NTRK</i> rearrangement <sup>7.9,31–34</sup>	<ul> <li>Neurotrophin kinase genes (<i>NTRK1</i>, <i>NTRK2</i>, and <i>NTRK3</i>) code for tropomyosin receptor tyrosine kinases (TRKA, TRKB, and TRKC)</li> <li>Ligand binding activates PI3K/AKT/mTOR, RAS/RAF/MAPK, and PLC-γ pathways, leading to the proliferation, growth, and survival of neurons in the peripheral and central nervous system</li> <li>Gene rearrangements result in the formation of fusion proteins that drive tumor growth and survival through constitutively active forms containing the TRK kinase domain</li> </ul>	NTRK1 NTRK2 NTRK3	0.1–1(3)	FISH, RT-PCR, DNA/RNA NGS
<i>MET</i> alteration <sup>7,9,35</sup>	<ul> <li>MET regulates cell growth, differentiation, motility, and epithelial-mesenchymal transition in tumor cells through activation of RAS/RAF/MAPK, PI3K/AKT/mTOR, WNT/β-catenin, and STAT pathways</li> <li>MET gene amplification may result in constitutive activation of MET receptor</li> <li>MET amplification is also a driver of acquired resistance to EGFR TKIs</li> <li>MET exon 14 skipping mutations lead to decreased MET degradation, leading to high expression and increased activation</li> </ul>	MET amplification (MET/CEP7 ratio >2 or GCN >5) MET exon 14 skipping mutation	0.34 2-3	FISH DNA NGS
<i>RET</i> rearrangement <sup>7,9,36,37</sup>	<ul> <li>RET is a tyrosine kinase receptor with giant cell-derived neurotrophic factor as its ligand</li> <li>Activation leads to RAS/RAF/MAPK, PI3K/AKT/mTOR, and PLC-signaling → cell proliferation, migration, and differentiation</li> <li>Chromosomal rearrangements involve fusion partners such as KIF5B, CCDC6, NCOA4, and TRIM33</li> <li>Chimeric proteins constitutively dimerize, activating the kinase domain and leading to uncontrolled activation of MAPK and PI3K pathways</li> </ul>	13 RET/PTC fusion proteins identified (RET/ PTC1-PTC9)	1–2	FISH, DNA/RNA NGS RT-PCR
				(Continued)

#### Table 1. (Continued)

Oncogene and molecular alteration	Biological function in regular and altered states	Common alterations	Incidence, %	Detection method
HER2 alteration <sup>7,9,38-40</sup>	• Altered ErbB, or HER, signaling has been implicated in many forms of cancer. HER2 is an emerging target for NSCLC	HER2 amplification	2–22	FISH
	<ul> <li>HER2 is an ErbB receptor tyrosine kinase. The binding of ligands to ErbB members induces homo- and beterodimerization and activation of downstream PI3K/</li> </ul>	HER2 overexpression	8-23	IHC
	<ul> <li>AKT signaling → cellular proliferation, migration, and differentiation</li> <li>Changes leading to altered HER signaling include HER2 amplification and mutations</li> </ul>	HER2 exon 20 duplication or YVMA 776–779 insertion (80%–90%)	1–7	DNA NGS
		HER2 rare point mutations: G660D, R678Q, E693K, and Q709L		
KRAS mutation <sup>7,9,41–44</sup>	<ul> <li>KRAS activated by GDP → GTP binding</li> <li>KRAS-GTP → MAPK/ERK and KRAS mutations prevent hydrolysis (KRAS-GTP → inactive KRAS-GDP) persistent activation of MAPK/ERK and PI3K</li> <li>KRAS is a downstream effector of EGFR which can promote tumor cell proliferation</li> </ul>	Point mutation at codons 12 (most common, >80%), 13, 14, and 60/61	Up to 30 KRASG12C: 3-15	DNA NGS

Source: Adapted from Melosky et al.8

AKT, protein kinase B; ALK, anaplastic lymphoma kinase; BRAF, v-raf murine sarcoma viral oncogene homolog B1; CCDC6, coiled-coil domain-containing protein 6; CEP, centromere of chromosome 7; DNA, deoxyribonucleic acid; EGFR, epidermal growth factor receptor; ErbB, avian erythroblastic leukemia viral oncogene homolog; ERK, extracellular-signal-regulated kinase; FISH, fluorescence in situ hybridization; GCN, gene copy number; GDP, guanosine diphosphate; GTP, guanosine triphosphate; HER2/3, human epidermal growth factor receptor 2/3; JAK, Janus kinase; KIF5B, kinesin family member 5B; KRAS, Kirsten rat sarcoma viral oncogene homolog; MAPK, mitogen-activated protein kinase; MEK, MAPK/ERK kinase; MET, hepatocyte growth factor receptor; mTOR, mammalian target of rapamycin; NCOA4, nuclear receptor coactivator 4; NGS, next-generation sequencing; NSCLC, non-small-cell lung cancer; NTRK1/2/3, neurotrophic tyrosine receptor kinase 1/2/3; PI3K, phosphatidylinositol 3-kinase; PLC, phospholipase C; PTC, papillary thyroid carcinomas; RAF, rapidly accelerated fibrosarcoma; RAS, rat sarcoma GTPase; RET, rearranged during transfection; RNA, ribonucleic acid; ROS1, c-ros oncogene 1; RT-PCR, reverse transcription polymerase chain reaction; SHP-1/2, Src homology 2 domain-containing protein tyrosine phosphatase 1/2; STAT, signal transducer and activator of transcription; TKI, tyrosine kinase inhibitor; TRIM33, tripartite motif containing 33; TRKA/B/C, tropomyosin receptor kinase A/B/C; WNT, wingless-related integration site.

### Methods

We have elected to support this narrative review with systematic search methods to ensure unbiased and comprehensive identification, assessment, and summary of relevant clinical studies in this field. A search of published and presented literature was conducted to identify prospective phase I-III trials and integrated analysis reporting efficacy outcomes for agents targeting novel driver gene alterations (i.e., excluding EGFR and ALK) in molecularly selected, advanced NSCLC populations. PubMed (all time to October 25, 2023), the proceedings from the American Society of Clinical Oncology (ASCO), the Medical Oncology European Society for (ESMO), and the World Conference on Lung Cancer 2022 and 2023 annual meetings were searched using the key search terms "NSCLC" AND "advanced"/"metastatic" AND "novel targets" AND "phase I-III" OR respective aliases (Figure 1). A supplemental bibliographic search of review articles and pooled/meta-analyses was also conducted. In addition, directed searches were performed after the database search cutoff date to ensure that the most up-to-date reports of eligible studies were considered. English language records were vetted at the abstract level and checked at the full text as needed by an initial reviewer (A.P.) and confirmed by a second independent reviewer (I.M.). All eligible studies were cited in the findings; however, only trials reporting outcomes since our initial review<sup>8</sup> (i.e., in the last 3 years, approximately) for at least 20 patients with alteration-drug-matched NSCLC were included in the tables. Additional search vetting details are summarized and in Supplemental Methods.

## Findings

The literature search identified a total of 2938 records, resulting in a total of 180 primary reports



Papers reporting outcomes in last 3 years and with ≥20 NSCLC alteration-matched patients and those otherwise considered key landmark reports in the respective molecularly-defined subsets were summarized in table, n=73

### Figure 1. PRISMA diagram.

<sup>a</sup>Primary or associated reports of eligible studies that were not identified through database search. <sup>b</sup>All types of ALK and EGFR alterations were included.

<sup>c</sup>A single trial may have multiple reports for different biomarker-selected patient cohorts or subsets; likewise, a single report may provide data from single or multiple studies on different biomarker-selected patient cohorts or subsets. ALK, anaplastic lymphoma kinase; ASCO, American Society of Clinical Oncology; BRAF, v-raf murine sarcoma viral oncogene homolog B1; EGFR, epidermal growth factor receptor; ESMO, European Society for Medical Oncology; FGFR, fibroblast growth factor receptor; HER2, human epidermal growth factor receptor 2; KRAS, Kirsten rat sarcoma viral oncogene homolog; MET, hepatocyte growth factor receptor; n, number; NRG1, neuregulin-1; NSCLC, non-small-cell lung cancer; NTRK, neurotrophic tyrosine receptor kinase; PI3K, phosphoinositide 3-kinase; PRISMA; Preferred Reporting Items for Systematic Reviews and Meta-Analyses; PTK7, tyrosine-protein kinase-like 7; RET, rearranged during transfection; ROS1, c-ros oncogene 1; WCLC, World Conference on Lung Cancer.

Table 2. Efficacy outcomes of clinical trials assessing novel targeted therapy in molecularly selected, target-matched advanced NSCLC.

Trial name, NCT# Phase	Molecular alteration	Line of therapy Pretreatment details	Regimen(s)	Patients, <i>n</i>	Overall response rate,ª % (95% CI)	Median duration of response,ª months (95% CI)	Median progression-free survival,ª months HR (95% CI)	Median overall survival, months HR (95% CI)
ROS1-rearranged								
ROS1-TKI-naïve								
EUCROSS, NCT02183870 Phase II <sup>45-47</sup>	<i>ROS1</i> rearrangement	First/Second line+ ROS1 TKI-naïve	Crizotinib 250 mg BID	30	73.3 (54.1–87.7)	19.0 (8.3-NYR)	19.4 <sup>b</sup> (10.1–32.2)	54.8 (20.3–NYR)
METROS, NCT02499614 Phase II Study + Expansion Cohorts <sup>4840</sup>	ROS1 rearrangement	Second line+ ROS1 TKI-naïve	Crizotinib 250 mg BID	64	65.4 <sup>b.c</sup> (44–82)	21.4 <sup>b.c</sup> [12.7–30.1]	13.8 <sup>b</sup> (7.4–20.2)	40.5 (27.9–53.1)
00 12-01, NCT01945021 Phase II <sup>s0,51</sup>	<i>ROS1</i> rearrangement, <i>ALK</i> rearrangement negative	First line +	Crizotinib 250 mg BID	127	71.7 (63.0–79.3)	19.7 [14.1–NYR]	15.9 [12.9–24.0]	44.2 (32.0-NYR)
STARTRK-2, STARTRK-1, and ALKA-372-001 Integrated Analysis <sup>s2</sup>	ROS1 rearrangement	First/second line+ TKI-naïve	Entrectinib 600 mg daily	168	67.9 (60.2–74.8)	20.5 (14.8–34.8)	15.7 (12.0–21.1)	47.8 (44.1–NE)
TQ-B3101-1-0001/TQ- B3101-II-01, NCT03019276/ NCT03972189 Phase I/II <sup>53</sup>	ROS1 rearrangement	First line +	Unecritinib 300 mg BID	111	80.2 (71.5–87.1)	20.3 (11.0–26.1)	16.5 (10.2–27.0)	Х
Barossa, JapicCTI-194851 Phase II Cohort 1 <sup>54</sup>	<i>ROS1</i> rearrangement	First line TKI-naïve	Brigatinib 180 mg daily <sup>d</sup>	28	67.9 (90% CI, 50.6–82.1)	NR	12.0 (5.8–NE)	NYR
ВТР-42723, NCT03608007 Phase II <sup>55</sup>	<i>ROS1</i> rearrangement	First/second line TKI-naïve	Ensartinib 225 mg daily	37	27.0 <sup>b</sup> [13.8–44.1]	4.8 <sup>b</sup> [1.8–10.8]	4.6 <sup>b</sup> [4.0–6.4]	NYR [14.9–NE]
TRIDENT-1, NCT03093116 Phase I/li <sup>56</sup>	<i>ROS1</i> rearrangement	First line + TKI naïve	Repotrectinib 40 mg daily to 160 mg BID, including the R2PD of 160 mg QD × 14 days followed by 160 mg BID	71	79 (68–88)	34.1 [25.6–NE]	35.7 (27.4-NE)	NE (44.4–NE)
TRUST, NCT04395677 Phase II <sup>57</sup>	<i>ROS1</i> rearrangement	First line + TKI-naïve	Taletrectinib 600 mg daily	67	92.5 [83.4–97.5]	NYR (range: 1.3–27.6)	NYR (range: 0.0–29.0)	NR
TRUST-II, NCT04919811 Phase II <sup>58</sup>	<i>ROS1</i> rearrangement	First line+ ROS1-TKI-naïve	Taletrectinib 600 mg daily	25	92.0 [74.0–99.0]	NR	NR	NR
TKI-pretreated								
TRIDENT-1, NCT03093116 Phase (/li <sup>56</sup>	<i>ROS1</i> rearrangement	Second line 1 Prior TKI, no prior CT	Repotrectinib 40 mg daily to 160 mg BID, including the RP2D of 160 mg QD × 14 days followed by 160 mg BID	56	38 (25–52)	14.8 (7.6-NE)	9.0 (6.8–19.6)	25.1 (17.8–NE)
TRUST, NCT04395677 Phase II <sup>s7</sup>	<i>ROS1</i> rearrangement	Second line+ Crizotinib- pretreated	Taletrectinib 600 mg daily	38	52.6 (35.8–69.0)	NYR (range: 1.4–22.2)	9.8 (range: 0.0–23.5)	NR
								(Continued)

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Table 2. (Continued)								
Trial name, NCT# Phase	Molecular alteration	Line of therapy Pretreatment details	Regimen(s)	Patients, <i>n</i>	Overall response rate,ª % (95% CI)	Median duration of response,ª months (95% CI)	Median progression-free survival,ª months HR (95% CI)	Median overall survival, months HR (95% CI)
TRUST-II, NCT04919811 Phase II <sup>38</sup>	<i>R0S1</i> rearrangement	Second line ≥1 prior ROS1-TKI	Taletrectinib 600 mg daily	21	57.1 (34.0-78.2)	NR	NR	NR
ARR0S-1, NCT05118789 Phase I <sup>59</sup>	R0S1 rearrangement	Second line ≥1 prior ROS1-TKI	NVL-520 25–125 mg daily	21	48	Х	NR Median time on treatment: 3.6	NR
BRAF mutant								
BRF113928, NCT01336634 Phase II <sup>60-62</sup>	BRAF V600E - mutation	First line	Dabrafenib 150 mg BID plus trametinib 2 mg QD	36	63.9 <sup>b</sup> (46.2–79.2)	10.2 <sup>b</sup> [8.3–15.2]	10.8 <sup>b</sup> [7.0–14.5]	17.3 [12.3–40.2]
		Second line+	Dabrafenib 150 mg BID plus trametinib 2 mg QD	57	68.4 <sup>b</sup> [54.8–80.1]	9.8 <sup>b</sup> (6.9–18.3)	10.2 <sup>b</sup> (6.9–16.7)	18.2 [14.3–28.6]
CDRB436ECN01, NCT04452877 Phase II <sup>63</sup>	BRAF V600E - mutation	First line +	Dabrafenib 150 mg BID plus trametinib 2 mg QD	20	75 (50.9–91.3)	NYR	NYR	NYR
PHAROS, NCT03915951 Phase Il <sup>44</sup>	BRAF V600E-mutation	First line Second line +	Encorafenib 450 mg QD plus Binimetinib 45 mg BID	59 39	75 (62–85) 46 (30–63)	NYR (23.1–NE) 16.7 (7.4–NE)	NYR (15.7–NE) 9.3 (6.2–NE)	NYR NYR
HL-085-102, NCT03781219 Phase I <sup>65</sup>	BRAF V600-mutation	Second line+	Tunlametinib 0.5 to 15 mg BID plus vemurafenib 960 mg BID q3w in dose escalation phase Tunlametinib 9/12 mg BID plus vemurafenib 720/960 mg BID in dose expansion phase	с б	60.6° (42.1-77.1)	11.3º (3.9-NE)	11.7º (5.6–NE)	R
NTRK-rearranged								
LOXO-TRK-14001, NAVIGATE and SCOUT Integrated analysis <sup>66</sup>	<i>NTRK</i> rearrangement	Lung subgroup First-line+	Larotrectinib 100 mg BID	20	73 <sup>b</sup> (45–92)	33.9 <sup>b</sup> [5.6–33.9]	35.4 <sup>b</sup> [5.3–35.4]	40.7 [17.2-NE]
STARTRK-2, STARTRK-1 and ALKA-372-001 Integrated analysis <sup>67</sup>	NTRK rearrangement	Lung subgroup First line +	Entrectinib 600 mg QD	51	62.7 (48.1–75.9)	27.3 (19.9–30.9)	28.0 [15.7–30.4]	41.5 (30.9–NE)
TRIDENT-1, NCT03093116 Phase II <sup>48</sup>	<i>NTRK</i> rearrangement	TKI naïve (52%)	Repotrectinib 160 mg QD×2 weeks → 160 mg BID	21	62 [38-82]	12 mos DoR: 92% (76–100)	12 mos PFS: 64% (43-86)	ХN
		TKI pretreated (29%)	Repotrectinib 160 mg QD×2 weeks → 160 mg BID	14	42 [18–71]	12 mos DoR: 44% (1–88)	12 mos PFS: 23% (0-49)	ХN
								(Continued)

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Trial name, NCT# Phase	Molecular alteration	Line of therapy Pretreatment details	Regimen(s)	Patients, <i>n</i>	Overall response rate,ª % (95% CI)	Median duration of response,ª months (95% CI)	Median progression-free survival,ª months HR (95% CI)	Median overall survival, months HR (95% CI)
<i>MET</i> -altered								
<i>MET</i> -amplified, overexpressed, and	d/or mutated							
PROFILE 1001, NCT00585195 Phase I <sup>69</sup>	<i>MET</i> amplification, MET/CEP7 ratio ≥1.8	First-line+	Crizotinib 250 mg BID	38	28.9 <sup>b</sup> (15.4–45.9) MET/CEP7 ratio ≥4.0: 38.1 (18.1–61.6)	5.2º [range: 3.3–25.8] MET/CEP7 ratio ≥4.0: 5.2 [range: 3.3–25.8]	5.1 <sup>b</sup> (1.9–7.0) MET/CEP7 ratio ≥4.0: 6.7 (3.4–9.2)	11.0 (7.1–15.9) MET/CEP7 ratio ≥4.0: 11.4 (7.2–19.3)
GEOMETRY mono-1, NCT02414139	<i>MET</i> amplification, GCN ≥10	Cohort 1a Second line+	Capmatinib 400 mg BID	69	29 (19–41)	8.3 (4.2–15.4)	4.1 (2.9–4.8)	NR
Thase I.'.	<i>MET</i> amplification, GCN 6 to 9	Cohort 1b Second line+	Capmatinib 400 mg BID	42	12 (4–26)	24.9 [2.7–24.9]	2.7 (1.4–3.1)	NR
	<i>MET</i> amplification, GCN 4 or 5	Cohort 2 Second line+	Capmatinib 400 mg BID	54	9 (3–20)	9.7 (4.2–NE)	2.7 (1.4–4.1)	NR
	<i>MET</i> amplification, GCN <4	Cohort 3 Second line+	Capmatinib 400 mg BID	30	7 (1–22)	4.2 [4.2-4.2]	3.6 [2.2-4.2]	NR
	<i>MET</i> amplification, GCN ≥10	Cohort 5a First line	Capmatinib 400 mg BID	15	40 (16–68)	7.5 [2.6–14.3]	4.2 [1.4–6.9]	NR
VISION, NCT02864992 Cohort B Phase II71	<i>MET</i> amplification, GCN ≥2.5	First line +	Tepotinib 500 mg QD	24	42	NE (2.8–NE)	NR	NR
16-019, NCT02750215 Phase II <sup>72</sup>	<i>MET</i> skipping alterations (75%) or amplification (25%)	Crizotinib pretreated	Capmatinib 400 mg BID	20	10 <sup>e</sup>	NR	5.5° (1.3–11.0)	11.3 (5.5–NYR)
265-101, NCT00697632 Phase  7 <sup>3</sup>	MET/AXL mutation or amplification	First line +	Glesatinib spray-dried dispersion (750 mg BID) and free-base suspension (1050 mg BID) formulations	27	25.9e	۲	4.1°	9.7
BD-CM-I02, NCT0292920 Phase lb <sup>74</sup>	c-MET overexpression and/or METex14 skipping mutation	First line +	BPI-9016M 300-600 mg QD or 400 mg BID	38	2.6° (0.1–13.8)	R	1.9° [1.9–3.7]	10.3 (7.3–NE)
R5093-ONC-1863, NCT04077099 Phase   <sup>75</sup>	$METex14 \text{ skipping, } MET amplification (GCN \geq 6 or MET/CPC7 \geq 4, or MET/CPC7 \geq 4, or MET gene fold change \geq 2), or change \geq 2, or over expression (IIHC3+ or H score \geq 200)$	First line +	REGN5093 2000 mg q3w	36	16.7°	۳	X	R
								(Continued)

Table 2. (Continued)								
Trial name, NCT# Phase	Molecular alteration	Line of therapy Pretreatment details	Regimen(s)	Patients, <i>n</i>	Overall response rate,ª % (95% CI)	Median duration of response,ª months (95% CI)	Median progression-free survival,ª months HR (95% CI)	Median overall survival, months HR (95% CI)
LUMINOSITY, NCT03539536 Phase II <sup>76</sup>	c-MET overexpression	Second line +	Telisotuzumab Vedotin 1.9 mg/kg q2w	122	22.1 NSQ EGFR WT: 36.5 [23.6–51.0] NSQ EGFR mutant: 11.6 (3.9–25.1] SQ: 11.1 [2.4–29.2]	NR NSQ EGFR WT: 6.9 (4.1–NE) NSQ EGFR mutant: NE (3.0–NE) SQ: 4.4 (3.0–NE)	R	ж Х
LUNG-MAP, NCT02154490 Phase II (platform) Sub-study S1400K77	c-MET overexpression	SQ lung cancer First line+	Telisotuzumab Vedotin 2.7 mg/kg QD q3w	23	9e (0–20)	R	2.4° [1.4–3.0]	5.6 (3.9–9.5)
<i>MET</i> exon 14-mutant								
GEOMETRY mono-1, NCT02414139	<i>MET</i> ex14 skipping mutation	Cohort 5b, First line	Capmatinib 400 mg BID	28	67.9 (47.6–84.1)	12.6 (5.6–NE)	12.4 (8.2–23.4)	20.8 (12.4–NE)
Phase II/0//8		Cohort 4, second/ third line		69	40.6 (28.9–53.1)	9.7 (5.6–13.0)	5.4 (4.2-7.0)	13.6 (8.6–22.2)
		Expansion cohort 6, second line		31	51.6 (33.1–69.8)	8.4 (4.2–NE)	6.9 (4.2–13.3)	NE (13.5–NE)
		Expansion cohort 7, first line		32	65.6 (46.8–81.4)	NE (5.5–NE)	10.8 (6.9–NE)	NE (10.6–NE)
GeoMETry-III, NCT04427072 Phase III <sup>79</sup>	<i>MET</i> ex14 mutation	Second line+	Capmatinib 400 mg BID	<u>ז</u>	53.3 (26.6–78.7)	9.9 (2.9–NE)	6.1 HR 0.46 [0.16–1.3] <i>p</i> =0.066	N
			Docetaxel 75 mg/m² q3w	7	0 (0-41.0)	NR	4.1	NR
CINC280J12201, NCT04323436 Phase II <sup>79</sup>	<i>MET</i> ex14 skipping mutation	First line Treatment naïve	Capmatinib 400 mg BID plus Spartalizumab 400 mg q4w	31	38.7 <sup>b</sup> (21.8–57.8)	NYR	13.3 <sup>b</sup> (9.3–NE)	N
VISION, NCT02864992 Cohorts	<i>MET</i> ex14 skipping	Firstline	Tepotinib 500 mg daily	164	57.3 (49.4-65.0)	46.4 [13.8-NE]	12.6 [9.7–17.7]	21.3 [14.2–25.9]
A and C Phase II <sup>80,81</sup>	mutation	Second line+	Tepotinib 500 mg daily	149	45.0 (36.8–53.3)	12.6 [9.5–18.5]	11.0 [8.2–13.7]	19.3 [15.6–22.3]
GLORY, NCT04270591 Phase I/II <sup>82</sup>	<i>MET</i> ex14 skipping mutation	First line+	Gumarontinib 300 mg QD	79	66 [54–76]	8.3 (6.3–NE)	8.5 [7.6–9.7]	17.3 [12.1–NE]
KUNPENG, NCT04258033 Phase II <sup>83</sup>	<i>MET</i> ex14 skipping mutation	First line+	Vebreltinib 200 mg BID q4w	52	75 [61.1–86.0]	15.9 (9.2–17.8)	14.1 (6.4–17.9)	20.7 (16.2-NE)
2016-504-00CH1, NCT02897479 Phase III <sup>84,85</sup>	<i>MET</i> ex14 skipping mutation	First line+	Savolitinib 400 or 600 mg daily	70	47.1 (35.1–59.5)	6.9 (4.9–12.5)	6.9 (4.6–8.3)	12.5 (10.5–21.4)
								(Continued)

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Table 2. (Continued)								
Triat name, NCT# Phase	Molecular alteration	Line of therapy Pretreatment details	Regimen(s)	Patients, <i>n</i>	Overall response rate,ª % (95% Cl)	Median duration of response,ª months (95% CI)	Median progression-free survival,ª months HR (95% CI)	Median overall survival, months HR (95% CI)
CHRYSALIS, NCT02609776 Phase 186	METex14 mutation	First line +	Amivantamab 1050– 1400 mg q1w ×4 then q2w	43	33.3 <sup>b</sup> [18.6–51.0]	NYR <sup>b</sup> (2.1–12.2)	N	NR
<i>RET</i> -rearranged								
ALL-RET, UMIN00020628 Phase I/II (expansion) <sup>87</sup>	<i>RET</i> fusion <i>EGFR</i> mutation and <i>ALK</i> rearrangement negative	Second line+ Prior CT, RET inhibitor-naïve	Alectinib 450 mg BID	25	4	ж	3.4 (2.0–5.4)	19 (5.4–NE)
LIBRETTO-001, NCT03157128	<i>RET</i> fusion	First line	Selpercatinib 160 mg BID	69	84 [73–92]	20.2 (13.0-NE)	22.0 (13.8-NE)	NE
Phase II dose expansion <sup>86,89</sup>		Second line+ (prior platinum)	Selpercatinib 160 mg BID	247	61 (55–67)	28.6 (20.4–NE)	24.9 (19.3–NE)	NE
LIBRETT0-321, NCT04280081 Phase II <sup>90</sup>	RET fusion	First line +	Selpercatinib 160 mg BID	26	69.2 (48.2–85.7)	NYR	NYR	NYR
LIBRETT0-431, NCT04194944 Phase III <sup>91</sup>	<i>RET</i> fusion	First line	Selpercatinib 160 mg BID q3w	129	84 [76–90]	24.2 (17.9–NE)	24.8 (16.9–NE) HR 0.46 (0.31–0.70) <i>p</i> < 0.001	NYR HR 0.96 (0.50–1.83)
			Pemetrexed plus CT <sup>f</sup>	83	65 (54–75)	11.5 [9.7–23.3]	11.2 (8.8–16.8)	NYR
ARROW, NCT03037385 Phase I/II92	RET fusion	Cohort A, first line +	Pralsetinib 400 mg daily	28	72 (60–82)	NYR	NYR	NR
		Cohort B, second line (prior platinum)	Pralsetinib 400 mg daily	136	599 (50–67)	22.3 [15.1–NYR]	16.5 [10.5–24.1]	
B0S172738-01, NCT03780517 Phase I <sup>93</sup>	<i>RET</i> fusion	Second line + (no alternative therapy approved)	BOS172738 10–150 mg daily	30	33° 8	NYR	NR	N
KL400-I/II-01, NCT05265091	RET fusion	First line	KL590586 40-120 mg	25	76e	NYR	NR	NR
Tase 2		Second line + Prior anti-PD-1/ PD-L1 therapy	daity	32	63e	NYR	ĸ	ХN
SY-5007-I, NCT05278364 Phase I <sup>95</sup>	<i>RET</i> fusion	Second line + (previously treated)	SY-5007 20 mg daily or 20–200 mg BID	55	75.0 <sup>e</sup> (53.3–90.2)	NR	NR	N
<i>HER2</i> -altered								
2016-0783, NCT03066206 Phase II%	HER2 exon 20 mutation	First line +	Poziotinib 16 mg daily q4w	30	27 <sup>b</sup> [12–46]	5 <sup>b</sup> (4.0–NE)	5.5 <sup>b</sup> (4.0–7.0)	15 (9.0–NE)
								(Continued)

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Table 2. (Continued)								
Trial name, NCT# Phase	Molecular alteration	Line of therapy Pretreatment details	Regimen(s)	Patients, <i>n</i>	Overall response rate,ª % (95% CI)	Median duration of response,ª months (95% CI)	Median progression-free survival,ª months HR (95% CI)	Median overall survival, months HR (95% CI)
ZENITH20, NCT03318939 Phase II <sup>97-99</sup>	<i>HER2</i> exon 20 insertions	Cohort 2 Second line +	Poziotinib 16 mg daily	06	27.8 (18.9–38.2)	5.1 (4.2–5.5)	5.5 (3.9–5.8)	NR
		Cohort 4 First line	Poziotinib 16 mg daily	80	39 (28–50)	5.7 (4.6–11.9)	5.6 [5.4–7.3]	NR
ChiCTR1800020262 Phase II <sup>100</sup>	HER2 exon 20 mutation (79.5%) HER2 non-exon 20 mutation (20.5%)	First line +	Pyrotinib 400 mg daily	78	19.2° (11.2–30.0)	9.9° (6.2–13.6)	5.6° (2.8–8.4)	10.5 (8.7–12.3)
TRUMP, NCT03574402 Phase II (platform) HER2 cohort <sup>101</sup>	HER2 mutation	First line	Pyrotinib 400 mg daily	28	35.7 <sup>b</sup> (18.0–53.5)	6.4 <sup>b</sup> [0.9–12.0]	7.3 <sup>b</sup> (1.3–13.4)	14.3 [6.0–22.7]
PATHER2, ChiCTR1900021684 Phase II <sup>102</sup>	<i>HER2</i> mutation or amplification	Second line+ Prior anti-HER2/ TKI and/or CT	Pyrotinib 400 mg plus Apatinib 250 mg daily	33	51.5 <sup>b</sup> (33.5–69.2)	6.0 <sup>b</sup> [4.4–8.6]	6.9 <sup>b</sup> (5.8–8.5)	14.8 [10.4–23.8]
21607, NCT05099172 Phase I <sup>103</sup>	HER2 exon 20 insertions	Second line +	BAY2927088 q3w following a Bayesian adaptive dose-selection model	20	60e.h	Ж	ж Z	ж
Beamion Lung 1, NCT04886804 Phase I <sup>104,105</sup>	HER2 TKD mutations	Second line +	Zongertinib 30–300 mg QD	27	46 <sup>e</sup>	NR	NR	NR
2021-FXY-191, NCT05016544 Phase Ib <sup>166</sup>	HER2 mutation	R	Inetetamab 8 mg/kg loading → 6 mg/kg plus Pyrotinib 320 mg daily	41	36.6 <sup>e</sup>	R	NR	NR
TAPUR, NCT02693535 Phase II (platform) HER2 cohort <sup>107</sup>	HER2 mutation or amplification	First line+ Lung cancer of any histology (96.4% NSCLC)	Pertuzumab 840 mg loading dose then 420 mg q3w plus Trastuzumab 8 mg/kg loading dose then 6 mg/kg q3w	28	11 <sup>b</sup> (2-28)	NR	3.7 <sup>b</sup> (range: 2.1–5.3) <sup>i</sup>	л
MyPathway, NCT02091141 Phase II (platform) HER2 cohort <sup>108</sup>	<i>HER2</i> amplified (43.2%) <i>HER2</i> mutated (56.8%)	Second line +	Pertuzumab 840 mg loading dose → 420 mg q3w plus Trastuzumab 8 mg/kg loading dose → 6 mg/kg q3w	16 21	13 <sup>b</sup> (2–38) 19 <sup>b</sup> (5–42)	7 <sup>b</sup> (6–8) 9 <sup>b</sup> (6–10)	2 <sup>b</sup> (1–6) 4 <sup>b</sup> (3–5)	NN NR
IFCT 1703-R2D2, NCT03845270 Phase II <sup>109</sup>	HER2 mutation	Second line+ Progressed on platinum-based CT	Pertuzumab 840 mg loading dose → 420 mg q3w plus Trastuzumab 8 mg/kg loading dose → 6 mg/kg q3w	45	29º (17.8-40.0)	11º (2.9–14.9)	6.8° (4.0−8.5)	N
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Trial name, NCT# Phase	Molecular alteration	Line of therapy Pretreatment details	Regimen(s)	Patients, <i>n</i>	Overall response rate,ª % (95% CI)	Median duration of response,ª months (95% CI)	Median progression-free survival,ª months HR (95% CI)	Median overall survival, months HR (95% CI)
JapicCTI-194620 Phase II <sup>110</sup>	<i>HER2</i> exon 20 insertion mutation	Second line + Prior CT	T-DM1 3.6 mg/kg q3w	21	38.1⁰ (90%Cl, 23.0–55.9)	3.5° (2.7–6.5)	2.8° [1.4−4.4]	8.1 (3.5–13.2)
TRAEMOS, NCT03784599 Phase I/I <sup>111</sup>	HER2 overexpression (IHC2+)	Second line+ Prior EGFR TKI	T-DM1 3.6 mg/kg q3w plus Osimertinib 80 mg QD	27	12 weeks ORR <sup>e</sup> : 4 (0–20)	NR	2.8° [1.4–4.6]	13.9 [10–16.9]
DESTINY-Lung01, NCT03505710 Phase II <sup>112-114</sup>	<i>HER2</i> alterations	Cohorts 1&2 Second line+	T-DXd 6.4 mg/kg q3w	91	55 (44–65)	9.3 (5.7–14.7)	8.2 (6.0–11.9)	17.8 (13.8–22.1)
	HER2 overexpression (IHC2+/3+)	Cohort 1 Second Line+ Prior CT (92%) and PD-L1 (73%)	T-DXd 6.4 mg/kg q3w	49	26.5 (15.0-41.1)	5.8 (4.3–NE)	5.7 (2.8–7.2)	12.4 [7.8–17.2]
		Cohort 1a Second Line + Prior CT (98%) and PD-1/PD-L1 (80%)	T-DXd 5.4 mg/kg q3w	41	34.1 (20.1–50.6)	6.2 (4.2-9.8)	6.7 [4.2–8.4]	11.2 (8.4–NE)
	HER2 mutation	Cohort 2 Second Line+ Prior PD-1/PD-L1 (54.8%)	T-DXd 6.4 mg/kg q3w	42	61.9 (45.6–76.4)	NYR (5.3–NE)	14.0 (6.4–14.0)	NYR [11.8–NE]
DESTINY-Lung02, NCT04644237 Randomized phase Il <sup>115</sup>	HER2 mutation	Second line + (prior platinum)	T-DXd 5.4 mg/kg q3w T-DXd 6.4 mg/kg q3w	102 50	49.0 (39.0–59.1) 56.0 (41.3–70.0)	16.8 (6.4–NE) NE (8.3–NE)	9.9 (7.4–NE) 15.4 (8.3–NE)	19.5 [13.6–NE] NE [12.1–NE]
KRAS G12C(X)-Mutant								
CodeBreaK 100, NCT03600883 Phase II <sup>116</sup>	KRAS G12C mutation	Second line+ Prior PD-1/PD-L1 therapy [91.3%]	Sotorasib 960 mg daily	174	41 (33.3–48.4)	12.3 (7.1–15.0)	6.3 (5.3–8.2)	12.5 [10.0–17.8]
CodeBreaK 200, NCT04303780 Phase III <sup>117</sup>	KRAS G12C mutation	Second line +	Sotorasib 960 mg daily	171	28.1 (21.5–35.4) <i>p</i> < 0.001	8.6 [7.1–18.0]	5.6 (4.3–7.8) HR: 0.66 (0.51– 0.86), <i>p</i> =0.0017	10.6 (8.9–14.0) HR 1.01 (0.77–1.33), <i>p</i> = NS
			Docetaxel 75 mg/m² q3w	174	13.2 [8.6–19.2]	6.8 (4.3–8.3)	4.5 (3.0-5.7)	11.3 [9.0–14.9]
KRYSTAL-1, NCT03785249 Phase I/II <sup>118</sup>	KRAS G12C mutation	Second line+ Prior CT and PD-1/ PD-L1 therapy	Adagrasib 600 mg BID	116	42.9 [33.5–52.6]	8.5 (6.2–13.8)	6.5 (4.7–8.4)	12.6i (9.2–19.2)
G042144, NCT04449874 Phase Ia <sup>119</sup>	KRAS G12C mutation	Second line+	Divarasib 50–400 mg QD q3w	58	53.4 <sup>b</sup> [39.9–66.7]	14.0 <sup>b</sup> (8.3–NE)	13.1 <sup>b</sup> [8.8–NE]	NR
D1553-102, NCT05383898 Phase I/II <sup>120</sup>	KRAS G12C mutation	Second line+	Garsorasib 600 mg BID	62	38.7 <sup>b</sup> [26.6–51.9]	6.9 <sup>b</sup> [5.4–NE]	7.6 <sup>b</sup> [5.7–NE]	NR
								(Continued)

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Table 2. (Continued)								
Trial name, NCT# Phase	Molecular alteration	Line of therapy Pretreatment details	Regimen(s)	Patients, <i>n</i>	Overall response rate,ª % (95% CI)	Median duration of response,ª months (95% CI)	Median progression-free survival,ª months HR (95% CI)	Median overall survival, months HR (95% CI)
KontRASt-01, NCT04699188 Phase Ib/II <sup>121</sup>	KRAS G12C mutation	Second line+	JDQ443 monotherapy in dose escalation and food effect cohorts	24	41.7e	NR	NR	NR
CodeBreaK 100/101, NCT03600883/NCT04185883 Phase Ib-II <sup>122</sup>	KRAS G12C mutation	Second line +	Sotorasib 960 mg/ day + Atezolizumab 1200 mg q3w or Pembrolizumab 200 mg q3w with or without lead- in Sotorasib 960 mg/day	58	29 [18-43]	17.9 (5.6–NE)	Я	15.7 [9.8–17.8]
CodeBreak 101, NCT04185883 Phase Ib/II <sup>123</sup>	KRAS G12C mutation	Second-line +	Sotorasib 960mg/ day + RMC-4630 100/140/200 mg twice q1w	5	27 <sup>b</sup> (6–61)	۳	ж Z	ж Z
NCT05288205 Phase I/IIa <sup>124</sup>	KRAS G12C mutation	Second line+ G12Ci naïve	Glecirasib plus JAB-3312	28	50e	NR	NR	NR
		KRAS G12Ci-pretreated		7	14.3 <sup>e</sup>	NR	NR	NR
RAMP 202, NCT04620330	KRAS G12V mutation	Second line+	Avutometinib 4 mg BID	16	0	7.9	NR	NR
Phase II 25			Avutometinib 3.2 mg plus Defactinib 200 mg BID	19	11	8.5	R	NR
SW0G S1507, NCT02642042 Phase II <sup>126</sup>	KRAS mutation	Second line+ Prior IO and/or CT	Trametinib 2 mg daily plus docetaxel 75 mg/m²	53	34 <sup>e</sup> (22–48)	5.0° (2.3–5.6)	4.1° (3.1–5.3)	10.9 (8.0–16.3)
KRYSTAL-7, NCT04613596 Phase II <sup>127</sup>	KRAS 612C mutation PD-L1 ≥50%	First line	Adagrasib 400 mg BID plus Pembrolizumab 200 mg q3w	148	63	NYR (12.6–NE)	NYR (8.2-NE)	NR
SCARLET, JRCT2051210086 Phase II <sup>128</sup>	KRAS G12C mutation	First line, NSQ	Sotorasib 960mg QD plus Carboplatin AUC5 and Pemetrexed 500mg/m <sup>2</sup> q3w ×4	27	88.9 (80% Cl: 78.5-94.8)	ж	NYR	6-mos OS: 87.0
RMC-6236-001, NCT05379985 Phase I <sup>129</sup>	KRAS G12X(non-C) mutation	Second line +	RMC-6236 80–400 mg daily	40	38e	Х	NR Median time on treatment: 3.1	NR
								(Continued)

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Table 2. (Continued)								
Trial name, NCT# Phase	Molecular alteration	Line of therapy Pretreatment details	Regimen(s)	Patients, <i>n</i>	Overall response rate,ª % (95% CI)	Median duration of response,ª months (95% CI)	Median progression-free survival,ª months HR (95% CI)	Median overall survival, months HR (95% CI)
<i>FGFR</i> -altered								
FIND, 2018-000399-13 Phase II <sup>130</sup>	<i>FGFR</i> alteration <sup>k</sup>	NR	Erdafitinib 3 mg-9 mg daily	22	9e.h,l	NR	NR	NR
NRG1-rearranged								
eNRGy, NCT02912949 Phase II <sup>131</sup>	NRG1 fusion	First line+ (72% prior platinum)	Zenocutuzumab 750 mg q2w	07	37.2 <sup>b</sup> (26.5–48.9)	14.9 <sup>b</sup> [7.4–20.4]	NR	NR
PTK7-positive								
M19-611, NCT04189614 Phase Ib <sup>132</sup>	PTK7-expressing	Second line+ (all patients enrolled)	Cofetuzumab pelidotin 2.8 mg/kg q3w	56	19.6 <sup>e</sup> [10.2–32.4]	7.2º [2.8-9.7]	5.3 <sup>e</sup> (3.6–5.9)	NR
		NSQ EGFR WT, PTK7 ≥90%/≥2+ evaluable subset		20	30.0° (11.9–54.3)	5.8° (2.8–NE)	5.5° (2.6–8.5)	NR
Study inclusion criteria: Presented or p last 3years and with >20 NSCLC patier studies included in that table were not! By independent review unless otherwit By investigator (local radiological) asse dwith 2 Acautod in considered on mo	ublished clinical trials of nov nts as well as select pivotal th included here unless their re se specified. essment. ctivity in 26 ROS1+ patients.	le l targeted therapy ager rials are included. Trials sults were updated sinc, enrolled in the respectiv	tts assessed in molecularly se exclusively in the locally advar a the cutoff date for the previo a study cohort. <sup>48</sup>	lected, alteral nced setting w us review.	ion-drug-matched ad ere not included. This	vanced/metastatic NSCLC table serves as an update	. Trials reporting efficacy s to Table 2 of our initial r	outcomes in the eview on this topic <sup>a</sup> —

<sup>4</sup>With a 7-day lead-in period at 90 mg.

eType of radiological assessment (by investigator or independent review) not specified.

fCT of investigator's choice with or without pembrolizumab 200 mg q3w.

9 Includes two patients still on treatment with partial responses pending confirmation. hIncludes unconfirmed responses.

<sup>1</sup>Transformed from weeks to months using a conversion factor of 4.35 weeks/month.

With an updated data cut-off date of January 15, 2022 (median follow-up of 15.6 months).

<sup>4</sup>Patients enrolled in three cohorts according to the type of alteration: High confidence activating FGFR translocations (1), high confidence activating FGFR alterations [3]. Both responses were observed in the cohort of patients with high confidence activating FGFR translocations. ORR in that cohort was 23%.

chemotherapy; DoR, duration of response; EGFR, epidermal growth factor receptor; FGFR, fibroblast growth factor receptor; GCN, gene copy number; HER2, human epidermal growth factor receptor 2; HR, hazard ratio; HRG, heregulin; IHC, immunohistochemistry; KRAS, Kirsten rat sarcoma viral oncogene homolog; MET, hepatocyte growth factor receptor; mos, months; n, number; NCT, national clinical trial; NE, not estimable; NR, not reported; NR01, neuregulin-1; NS, non-significant; NSCLC, non-small-cell lung cancer; NSQ, non-squamous cell; NTRK, neurotrophic tyrosine receptor kinase; NYR, not yet reached; ORR, objective response rate; OS, overall survival; PD-1, programmed cell death protein 1; PD-L1, programmed death ligand 1; PFS, progression-free survival; PTK7, tyrosine-protein kinase-like 7; QD, once daily; qXw, every X weeks; R2PD, recommended phase II dose; RET, rearranged during transfection; ROS1, c-ros oncogene 1; SQ, squamous cell; T-DM1, trastuzumab emtansine; T-DXd, trastuzumab deruxtecan; TKD, tyrosine kinase domain; TKI, tyrosine kinase inhibitor; WT, wild-type; #th ALK, anaplastic lymphoma kinase; BID, twice daily; BRAF, v-Raf murine sarcoma viral oncogene homolog B1; CEP, centromere of chromosome 7, CI, confidence interval; c-Met, hepatocyte growth factor receptor; CIT, line+, #th line of treatment in the advanced setting or higher.

from 174 clinical trials or integrated analyses reporting efficacy outcomes on novel oncogenedirected therapies in alteration-matched advanced NSCLC (PRISMA, Figure 1). Study analyses were grouped by molecular target and will be discussed chronologically based on the availability of a Food and Drug Administration (FDA) approved agent: c-ros oncogene 1 (ROS1)rearranged (n=23), v-Raf murine sarcoma viral oncogene homolog B1 (BRAF) V600-mutated (n=9), neurotrophic tyrosine receptor kinase (NTRK)-rearranged (n=4), hepatocyte growth factor receptor (MET)-altered (n=35), rearranged during transfection (RET)-rearranged (n=15), human epidermal growth factor receptor (HER)2altered (n=38), Kirsten rat sarcoma viral oncogene homolog (KRAS)-mutated (n=32), fibroblast growth factor receptor (FGFR)-altered (n=10), *HER3-/neuregulin-1* (*NRG1*)-altered (n=10), phosphoinositide 3-kinase (PI3K)-altered (n=2), and tvrosine-protein kinase-like 7 (PTK7)-mutated (n=1). Analyses with  $\geq 20$  NSCLC biomarkerselected patients reporting outcomes in the last 3 years (since September 2020) are summarized in Table 2 (n=73).

## ROS1-rearranged

The ROS1 tyrosine kinase domain shares 84% and 86% sequence similarity with ALK and tropomyosin receptor kinase (TRK), respectively.<sup>133,134</sup> Consequently, two main types of inhibitors have been assessed in patients with tyrosine kinase inhibitor (TKI)-naïve and -pretreated NSCLC harboring ROS1 rearrangements: those that co-inhibit ALK/ROS153,135-146 and those that co-inhibit TRK/ROS1.144-147 In TKI-naïve patients, the ALK/ROS1/MET coinhibitor crizotinib was the first agent to receive regulatory approval for NSCLC with ROS1 rearrangements in 2016 based on results from the phase I PROFILE-1001 study.148 Updated results confirmed initial findings of frequent (objective response rate (ORR) 72%) and durable (median duration of response (mDoR) 24.7 months) responses and showed strong median progression-free survival (mPFS 19.3 months) and median overall survival (mOS 51.4 months) outcomes.141 Multiple other phase I-II studies of crizotinib in ROS1-rearranged NSCLC have confirmed its clinical efficacy<sup>45,46,48,50,140</sup> and updated results from three of these studies demonstrated robust survival outcomes with mPFS of 13.8-19.4 months and mOS of 40.5-54.8 months at a median follow-up of 54.4-81.4 months 45,47,49,50

(Table 2). With few exceptions where ORRs were modest (ensartinib 27%, iruplinalkib 36.8%),<sup>55,138</sup> other ALK/ROS1 inhibitors (ceritinib, lorlatinib, brigatinib, and unecritinib) have shown high clinical activity as initial ROS1-directed therapy (ORR 62%-80.2%),<sup>53,54,136,142,143</sup> however have yet to receive regulatory approval for *ROS1*-rearranged NSCLC. In particular, unecritinib (a novel derivative of crizotinib) was recently associated with an 80.2% ORR, 20.3-month mDoR, and mPFS of 16.5 months.<sup>53</sup>

Entrectinib is a brain-penetrant agent and was the first TRK/ROS1 inhibitor to receive accelerated approval for TKI-naïve ROS1-rearranged NSCLC based on results from an NSCLCspecific integrated analysis of phase I-II studies in multiple tumors.149 At a median follow-up of 29.1 months, entrectinib continued to show frequent and durable responses (ORR 67.9%; mDoR 20.5 months), with a mPFS and mOS of 15.7 and 47.8 months, respectively.<sup>52</sup> Taletrectinib and repotrectinib are potent, next-generation TRK/ROS1 inhibitors designed to improve central nervous system activity and overcome treatment resistance with favorable safety profiles that showed early signs of activity in ROS1-rearranged NSCLC.<sup>146,147,150</sup> Treatment with repotrectinib resulted in frequent and durable responses and robust PFS in the ROS1-TKI-naïve cohort of the phase II trial TRIDENT-1 (ORR 79%; mDoR 34.1 months; mPFS 35.7 months),<sup>56,144</sup> leading to a priority review designation<sup>151</sup> and subsequent approval by the FDA.<sup>152</sup> After displaying promising activity in phase I studies,<sup>147,153</sup> taletrectinib showed the highest response rates across studies of ROS1 inhibitors in the phase II trials TRUST and TRUST-II (92.5% and 92.0%),57,58,145 leading to a breakthrough therapy designation by the FDA.154

Since the seminal approval of crizotinib, several studies have assessed the clinical activity of ROS1 inhibitors, in ROS1-TKI-pretreated patients. The ALK/ROS1 inhibitors, lorlatinib and brigatinib, were among the first to demonstrate activity in this setting with ORRs between 26.3% and 35%.<sup>135,143,155</sup> In a small study of patients with brain-only progression while on crizotinib, lorlatinib (an agent designed specifically to penetrate the blood–brain barrier)<sup>156</sup> led to an ORR of 67% at 12 weeks and 87% while on the study.<sup>137</sup> Recently, the next-generation TRK/ROS1 inhibitors, repotrectinib and taletrectinib, have also shown promise. Repotrectinib received

FDA approval in this setting based on an ORR of 38% and a mDoR of 14.8 months in the cohort of ROS1-TKI-pretreated patients from TRIDENT-1<sup>144,56,152</sup> and taletrectinib demonstrated impressive ORRs of 52.6% and 57.1% in the cohorts of ROS1-TKI-pretreated patients from TRUST and TRUST-II.<sup>57,58,145,146</sup> NVL-520, a ROS1-selective inhibitor designed to avoid neurotoxicity associated with TRK inhibition, showed promising clinical activity (ORR 48%) in a heavily pretreated population, including at least one prior ROS1-inhibitor, displaying both brain penetration and activity against resistance mutations.<sup>59</sup>

In summary, both ALK/ROS1 and TRK/ROS1 inhibitors are highly active and have been approved for the treatment of NSCLC with *ROS1* rearrangements; more potent and selective next-generation inhibitors continue to improve clinical efficacy and safety leading to additional regulatory approvals.

## BRAF-V600-mutant

In contrast with ROS1-altered and other oncogene-driven NSCLCs (see below), high clinical activity in BRAF-V600-mutated NSCLC was only achieved thus far with a combination of both direct and downstream inhibition with BRAF<sup>60,63-</sup> 65,108,157-161 and mitogen-activated protein kinase kinase (MEK)1/2 inhibitors.60,63-65,161,162 Similar to the targeting of BRAF mutations in melanoma, the use of these inhibitors as monotherapy (namely selumetinib or vemurafenib) produced minimal to modest clinical activity in NSCLC<sup>108,158,159,162</sup> leading to combination therapy trials. The first combination to be approved was the BRAF inhibitor dabrafenib plus the MEK1/2 inhibitor trametinib for BRAF-V600Emutated NSCLC based on outcomes from the phase II BRF113928 trial.61,62,163 At a median follow-up of 16.3-16.6 months, initial findings in both treatment-naïve and pretreated cohorts were confirmed with frequent and durable responses (ORR 63.9% and 68.4%; mDoR 10.2 and 9.8 months, respectively) and robust mPFS (10.8 and 10.2 months) and OS outcomes (17.3 and 18.2 months; Table 2).<sup>60</sup> The clinical activity of dabrafenib plus trametinib in this setting is also supported by an ORR of 75% from a recent phase II trial.63

Two additional inhibitor combinations were developed to increase the potency, selectivity, and

safety of at least one of the combination partners relative to prior BRAF and/or MEK inhibitors.<sup>30,164,165</sup> The PHAROS phase II study demonstrated good activity for the second-generation combination of encorafenib plus binimetinib in treatment-naïve and pretreated cohorts (ORRs of 75% and 46%, respectively), durable responses (mDoR not yet reached (NYR) and 16.7 months), and robust mPFS (NYR and 9.3 months).64 These findings supported approval of encorafenib plus binimetinib for the treatment of metastatic BRAF-V600E NSCLC on October 2023.166 Recently, the HL-085-102 trial reported favorable outcomes for vemurafenib plus the highly potent and selective MEK inhibitor tunlametinib in pretreated NSCLC patients with BRAF-V600 mutations (ORR 60.6%, mDoR 11.3 months, mPFS 11.7 months).65 Other BRAF inhibitor combinations have been tested in this setting with no breakthrough results to date.157,160,161

The development of BRAF and MEK inhibitor combinations continues to evolve with next-generation agents. A promising approach currently in early clinical testing is the use of BRAF dimer inhibitors (belvarafenib, DCC-3084, BGB-3245, PF-07799933)<sup>161,167-169</sup> which prevent the paradoxical activation of MAPK signaling leading to resistance observed with BRAF monomer inhibitors and the need for a MEK inhibitor. These new agents are also active against Class II and III BRAF mutations.<sup>170,171</sup>

## NTRK-rearranged

Inhibitors of TRK-A/B/C have been assessed in NTRK-rearranged solid tumors including the first-generation agents larotrectinib<sup>66,172</sup> and entrectinib67,173 and the next-generation TRK inhibitors taletrectinib<sup>146</sup> and repotrectinib.<sup>68,174</sup> Both larotrectinib and entrectinib were approved in 2018 and 2019, respectively, for tumor-agnostic indications in NTRK fusion-positive tumors based on integrated analyses of multicenter, single-arm trials.149,175 Up-to-date, tumor-agnostic and tumor-specific analyses have generally confirmed the benefit of these agents in lung cancer. Integrated analysis of phase I/II LOXO-TRK-14001, NAVIGATE, and SCOUT trials reported an ORR of 69% and mDoR, mPFS, and mOS of 32.9, 29.4, and NYR months for larotrectinib among 269 patients with solid tumors and an ORR of 73%, mDoR, mPFS, and mOS of 33.9, 35.4, and 40.7 months, respectively, among a subgroup of 20 lung cancer patients<sup>66</sup> (Table 2).

Similar analyses of the phase I/II STARTRK-2, STARTRK-1, and ALKA-372-001 studies evaluating entrectinib reported an ORR of 62.4% and mDoR, mPFS, and mOS of 29.4, 15.7, and 38.2 months among 194 patients with solid tumors<sup>173</sup> and an ORR of 62.7% and mDoR, mPFS, and mOS of 27.3, 28.0, and 41.5 months among 51 patients with NSCLC.<sup>67</sup>

The next-generation TRK inhibitor repotrectinib has also demonstrated clinical activity in patients with *NTRK*-rearranged solid tumors,<sup>174</sup> leading to a breakthrough therapy designation by the FDA in October 2021.<sup>176</sup> In a recent update of the TRIDENT-1 basket trial, repotrectinib continued to show promising clinical activity in solid tumors with ORRs of 58% and 50% in TKI-naïve and -pretreated cohorts and of 62% and 42% in the respective subsets of NSCLC patients.<sup>68</sup>

TRK inhibitors have shown strong activity and robust clinical outcomes across different *NTRK*fusion positive tumors including NSCLC, representing one of the most compelling examples of alteration-drug matching.

## **MET**-altered

A host of agents have been assessed in MET-altered NSCLC including nonselective MET inhibitors (crizotinib<sup>48,69,140,177-182</sup> and S49076<sup>183</sup>), selective MET inhibitors (capmatinib,<sup>70,72,78,79,184,185</sup> tepotinib,<sup>71,80,81</sup> savolitinib,<sup>84,85,186,187</sup> glumetinib,<sup>188,189</sup> bozitinib,190 ABN401,191 SAR125844,192 vebreltinib,83 and gumarontinib82), dual MET/X inhibitors (glesatinib,<sup>73</sup> BPI-9016M,<sup>74</sup> and OMO-1<sup>193</sup>), anti-MET antibodies (onartuzumab194 and emibetuzumab<sup>195</sup>), antibody mixtures (Sym015-01<sup>196</sup>), bispecific METxEGFR (amivantamab,86 CKD-702197) and METxMET (REGN509375) antibodies, and anti-MET antibody-drug conjugates (ADCs; telisotuzumab vedotin<sup>76,77,198</sup>). Multiple biomarkers and thresholds have also been used to select patients with variable clinical activity across studies with different agents and biomarker selection criteria.

MET-amplified or -overexpressed. In patients selected exclusively based on *MET* amplification, the multi-targeted-TKI crizotinib and the selective MET inhibitor capmatinib are the most well-studied agents and have generally shown only limited to modest clinical activity with an apparent relationship between higher *MET* amplification and improved outcomes in some

studies.<sup>48,69,70,140,177,179,184</sup> Other selective MET inhibitors have also shown preliminary efficacy signals in patients with *MET*-amplified tumors.<sup>71,184,192</sup>

Multiple MET inhibitors have been assessed in patients with MET overexpression or a variety of MET alterations. The first-in-class ADC telisotuzumab vedotin failed to meet the pre-specified response criteria for continuing enrolment in the subprotocol S1400K of Lung-MAP with an ORR of 9%77 and displayed only modest activity in the LUMINOSITY phase II trial (ORR 22.1%).<sup>76</sup> Interestingly, biomarker analyses from LUMINOSITY revealed higher ORR in nonsquamous NSCLC without EGFR mutations and high MET overexpression (≥50% by immunohistochemistry; ORR 52.2%).76 Studies assessing smallmolecule inhibitors or antibody-based agents with dual or bispecific targeting showed limited to modest activity (ORRs 2.6%-25.9%).73-75,196

METex14-mutant. Studies of MET inhibitors in patients with NSCLC harboring predominantly METex14 mutations generally resulted in more favorable clinical outcomes than those seen in MET-amplified/-overexpressed NSCLC.140,70,81,177,180,186,187 Crizotinib demonstrated variable activity in METex14 NSCLC (ORR 12%-65%),<sup>57,177,179-181</sup> and received an FDA breakthrough therapy designation in 2018<sup>199</sup> based on favorable results from the PROFILE-1001 study.<sup>182</sup> The first regulatory approval in this setting was granted to the selective MET inhibitor capmatinib based on results from the multi-cohort GEOMETRY mono-1 phase II trial.<sup>200</sup> Updated results from this study showed frequent and durable responses and robust PFS and OS outcomes in both treatment-naïve (ORR 65.6%-67.9%, mDoR 12.6-NYR months, mPFS 10.8-12.4 months, mOS 20.8-NYR months in initial and expansion cohorts) and previously treated patients (ORR 40.6%-51.6%, mDoR 8.4-9.7 months, mPFS 5.4-6.9 months, mOS 13.6-NYR months in initial and expansion cohorts).70,78 More recently, the GeoMETry-III phase III trial comparing capmatinib to standard-of-care docetaxel in previously treated METex14 NSCLC showed numerical differences in ORR (53.3% vs 0%) and PFS (6.1 vs 4.1 months; hazard ratio (HR) 0.46, 95% confidence interval (CI) 0.16-1.3, p = 0.066) that although consistent with GEOMETRY mono-1 results did not reach statistical significance after early trial

termination.79 Tepotinib was the second selective MET inhibitor to receive accelerated approval for METex14 NSCLC in February 2021 based on initial results from the large phase II VISION trial.<sup>201</sup> Updated results confirmed initial findings with frequent and durable responses and robust PFS and OS outcomes in both treatment-naïve and pretreated patients (ORR 57.3% and 45.0%, mDoR 46.4 and 12.6 months, mPFS 12.6 and 11.0 months, mOS 21.3 and 19.3 months, respectively).80 Additional selective MET inhibitors have also shown preliminary efficacy signals<sup>187,189-191</sup> that were confirmed in larger cohorts of phase II studies of savolitinib, gumarontinib, and vebreltinib (ORRs 47.1%, 66%, and 75%, respectively).82-86 Notably, vebreltinib showed high activity, durable responses, and robust PFS outcomes in both treatment-naïve and pretreated cohorts of the KUNPENG study (ORR 77.1% and 70.6%; mDoR 16.5 and 15.3 months; mPFS 14.5 and 7.1 months).83 The dual MET/OCT-2 inhibitor OMO-1 and the bispecific METxEGFR antibody CKD-702 have shown early signs of activity.<sup>193,197</sup> The combination of capmatinib with the immune checkpoint inhibitor (ICI) spartalizumab was assessed in treatment-naïve patients resulting in a modest ORR (38.7%) and high rates of treatment-related adverse events prompting early trial termination.<sup>185</sup>

In crizotinib-pretreated patients with predominantly skipping alterations (75%), capmatinib showed minimal activity (ORR 10%)<sup>72</sup> while in MET-inhibitor-pretreated patients, the bispecific METxEGFR antibody amivantamab demonstrated promising clinical activity (ORR 33%) in the *MET*ex14 cohort of the CHRYSALIS phase I trial.<sup>86</sup>

In summary, targeting *MET* dysregulation with MET inhibitors has been successful in *MET*ex14 NSCLC. More potent and selective next-generation TKIs have shown high clinical activity and are the only type of agents approved thus far in this setting. In *MET*-amplified/-overexpressed tumors, encouraging results have been observed particularly in *MET*-amplified subsets. An interesting relationship between levels of MET enrichment and clinical activity was apparent in multiple studies.

## **RET**-rearranged

Earlier generation multi-kinase inhibitors (cabozantinib, alectinib, vandetanib, lenvatinib, and ponatinib)87,202-208 and more selective RET TKIs (selpercatinib, pralsetinib, BOS172738, KL590586, SY-5007)88-95,209 have been assessed in patients with NSCLC harboring RET rearrangements. Small phase I-II trials (≤25 patients) assessing multitargeted TKIs for which RET is a secondary target generally reported minimal activity (ORRs 4%-28%)87,202,203,205,207 except the LURET phase II trial of vandetanib which reported a promising ORR of 53%.<sup>204,208</sup> More recently, studies of selective RET TKIs have demonstrated improved outcomes. Selpercatinib was the first agent approved by the FDA in this setting<sup>210</sup> based on initial results of large, multi-cohort non-randomized the LIBRETTO-001 phase II trial.89 Trial results were recently confirmed showing frequent and durable responses and robust PFS outcomes in both treatment-naïve (ORR 84%, mDoR 20.2 months, mPFS 22.0 months) and pretreated patients (ORR 61%, mDoR 28.6 months, mPFS 24.9 months; Table 2).88 The smaller phase II trial LIBRETTO-321 further confirmed the favorable clinical activity of selpercatinib in patients with RET-rearranged NSCLC with an ORR of 69.2% (87.5% in treatment-naïve and 61.1% in pre-treated subsets).90 Recently, the phase III trial LIBRETTO-431 comparing selpercatinib to chemotherapy as initial treatment of RET-rearranged NSCLC met its primary endpoint with a large improvement in mPFS (24.8 vs 11.2 months; HR 0.46, p<0.001) and more frequent and longer responses (ORR 84% vs 65%; mDoR 24.2 vs 11.5 months) for selpercatinib.91 In September 2022, selpercatinib received full FDA approval for RET-rearranged NSCLC based on the updated results from the NSCLC cohort of the LIBRETTO-001 trial.<sup>211</sup> The FDA has also granted full approval to pralsetinib for the treatment of RET fusion-positive NSCLC in August 2023<sup>212</sup> based on the recently updated results of the phase II ARROW trial which confirmed initial findings<sup>209</sup> with an ORR of 72% and mDoR NYR among chemotherapynaïve patients and ORR of 59% and mDoR of 22.3 months among platinum-pretreated patients.92 Median PFS was NYR and 16.3 months in chemotherapy-naïve and -pretreated patients, respectively. Other highly selective RET inhibitors potent and (BOS172738, KL590586, and SY-5007) have shown promising clinical activity in phase I trials (ORR 33%-76%).93-95 Similar to other alteration-matched settings, selective RET TKIs have improved outcomes relative to multitargeted

TKIs in the treatment of *RET*-arranged NSCLC; selpercatinib and pralsetinib are the only agents approved in this setting.

## HER2-altered

Four main types of inhibitors, dual- or pan-HER TKIs (BAY2927088, neratinib, dacomitinib, afatinib, pyrotinib, poziotinib, and tarloxotinibeffector),<sup>96–103,213–221</sup> selective HER2 TKIs (zongertinib),<sup>104,105,222</sup> anti-HER2 monoclonal antibodies (mAbs; trastuzumab, pertuzumab, and inetetamab),<sup>106–109,223–227</sup> and anti-HER2 ADCs (ado-trastuzumab emtansine (T-DM1) and trastuzumab deruxtecan (T-DXd))<sup>110–115,228– <sup>232</sup> have been assessed in patients with NSCLC with *HER2* alterations.</sup>

Second-generation small-molecule TKIs that were primarily developed as EGFR inhibitors in NSCLC (dacomitinib, afatinib, and neratinib) were tested in HER2-altered NSCLC showing activity as single agents (ORRs limited 0%-12%).<sup>213,215,216,218,219</sup> More recently, newer next-generation multi-HER TKIs (poziotinib, pyrotinib, tarloxotinib, BAY2927088, BDTX-189) and HER2-selective TKIs (zongertinib) have shown better yet generally modest activity in primarily HER2ex20-mutated NSCLC (ORR 19.2%-60%; Table 2).96-105,214,220-222 Of these, the highest ORR was observed with the multi-HER TKI BAY2927088 (60%)<sup>103</sup> leading to an FDA breakthrough designation for HER2mutated NSCLC.<sup>223</sup> No small-molecule HER2 TKI has been approved to date for the treatment of HER2-altered NSCLC.

Antibody-based agents have the potential to increase selectivity and specificity relative to multitargeted TKIs. However, the use of single or dual anti-HER2 mAb regimens with or without chemotherapy has resulted in minimal to modest activity in HER2-altered NSCLC (0%-45%; Table 2).<sup>106–109,224–228</sup> Recently, two ADCs, T-DM1 and T-DXd, have been prospectively assessed in this setting. T-DM1, which delivers a microtubule-inhibitory payload to HER2presenting cells, has shown minimal activity in HER2-amplified/patients with pretreated overexpressed NSCLC (ORR 6.7%-20%)229-231 and moderate activity in chemotherapy-pretreated patients with HER2ex20 insertions (ORR 38.1%).<sup>110</sup> T-DM1 also showed limited activity when combined with osimertinib in osimertinibpretreated patients with HER2 overexpression.111

T-DXd, which delivers a topoisomerase 1 inhibitor payload, has shown greater activity overall in HER2-altered (including overexpressed and mutated) NSCLC with ORRs of 55.6% and 55% in heavily pretreated patients from a phase I study dose-expansion cohort and the phase II DESTINY-Lung01 trial, respectively.<sup>113,114,232</sup> Both studies reported high ORRs in patients with HER2 mutations compared with HER2 overexpression (72.7% and 61.9% vs 26.5%-34.1%, respectively).<sup>112,113,232</sup> Longer mDoR, mPFS, and mOS in HER2-mutated relative to HER2overexpressed patients were also apparent in DESTINY-Lung01 (NYR vs 5.8-6.2 months, 14.0 vs 5.7-6.7 months, and NYR vs 11.2-12.4 months, respectively). T-DXd received a breakthrough therapy designation for use in platinum-pretreated HER2-mutant NSCLC patients from the FDA in May 2020 based on results of DESTINY-Lung01.233 More recently, results from the randomized phase II trial DESTINY-Lung2 comparing two doses of T-DXd (5.4 vs 6.4 mg/kg every 3 weeks (q3w)), confirmed the favorable outcomes (ORR 49.0% and 56.0%; mDoR 16.8 months and NYR; mPFS 9.9 and 15.4 months; mOS 19.5 months and NYR for the 5.4 and 6.4 mg/kg q3w doses, respectively)<sup>115</sup> leading to the FDA granting only the lower-dose regimen accelerated approval for use in HER2mutant NSCLC in August 2022 due to concerns of higher rates of interstitial lung disease/pneumonitis with 6.4 mg/kg q3w.234 This regimen is also being evaluated for a HER2-amplified, tumor-agnostic indication with promising efficacy.235 Other HER2-directed ADCs (A166 and ARX788) and bispecific antibodies (KN026) have shown promising results in early-phase studies in HER2-altered tumors; however, their efficacy in NSCLC has yet to be established.<sup>236-238</sup>

Several clinical studies now show a greater benefit for HER2-directed therapy in those with HER2 mutations compared to other types of HER2 alterations, with the best outcomes observed for the ADC T-DXd which was approved for HER2mutated NSCLC.

### **KRAS**-mutant

Multiple approaches have sought to target *KRAS* mutations in NSCLC, including direct inhibition with RAS/RAF blockers<sup>125,239,240</sup> and indirect approaches such as inhibition of downstream effectors,  $^{125,126,240-251}$  cyclin-dependent kinases 4/6,  $^{252-254}$  and other targets.  $^{125,242,247,249,250,255}$  The

first successful effort to directly target KRAS in NSCLC emerged from the development of agents that selectively and irreversibly bind and stabilize the KRAS-G12C inactive form (single-OFF KRAS-G12C inhibitors).118,256-259 Sotorasib and adagrasib received accelerated approval from the FDA in May 2021 and December 2022<sup>260,261</sup> for previously treated, KRAS-G12C-mutant NSCLC based on results from the multicenter, single-arm trials CodeBreaK100 and KRYSTAL-1, respectively.118,258 Initial results from CodeBreaK100 were confirmed in a 2-year update showing frequent and durable responses and robust time-toevent outcomes (ORR of 41% and mDoR, mPFS, and mOS of 12.3, 6.3, and 12.5 months, respectively).<sup>116</sup> After a median follow-up of 17.7 months, the confirmatory, phase III trial CodeBreaK200 met its primary endpoint of PFS (median 5.6 vs 4.5 months, HR 0.66, p = 0.0017) and showed significant improvement in ORR (28.1% vs 13.2%, p < 0.001) with sotorasib relative to docin etaxel platinum-pretreated patients.117 However, benefits in mDoR (8.6 months (95% CI 7.1-18.0) vs 6.8 months (95% CI 4.3-8.3)) and OS (10.6 vs 11.3 months, p=0.53) were not apparent which may be in part due to removal of OS as a co-primary endpoint, consequent reduction in sample size and introduction of crossover from docetaxel to sotorasib in a trial amendment.<sup>262</sup> Despite CodeBreaK200 meeting its primary endpoint, the FDA ruled that the primary endpoint data could not be reliably interpreted and postponed conversion to full approval.263 Initial results from the KRYSTAL-1 trial leading to accelerated approval of adagrasib were comparable to sotorasib's registrational data with an ORR of 42.9% and mDoR, mPFS, and mOS of 8.5, 6.5, and 12.6 months, respectively.<sup>118</sup> Adagrasib's confirmatory trial KRYSTAL-12 is ongoing. More recently, the new potent and selective G12C inhibitors divarasib, JDQ443, and garsorasib have shown promising activity as single agents with ORRs of 53.4%, 41.7%, and 38.7%, mDoR of 14.0, not reported (NR) and 6.9 months, and mPFS of 13.1, NR and 7.6 months, respectively.<sup>119-121</sup> Additional single-OFF G12C inhibitors are either in very early stages of clinical development or have been halted due to safety and/or efficacy concerns.<sup>264-268</sup>

New RAS inhibitors are now being developed toward different individual mutations (*KRAS*-G12X) or with a wider selectivity range (from multi-KRAS to multi-RAS), and targeting active (ON) forms.<sup>259</sup> Recently, the first-in-class,

RAS-selective, tri-complex multi-ON RAS inhibitor, RMC-6236, showed promising preliminary clinical activity in *KRAS*-G12X(D/V/A/ S/R) NSCLC (ORR 38%; Table 2).<sup>129</sup>

Data on combination regimens in patients with KRAS-G12C mutations have recently emerged. Combination of sotorasib with ICIs (atezolizumab or pembrolizumab) showed only moderate activity (ORR 29%) in cohorts of the CodeBreak100/101 trials where frequent grade 3/4 hepatotoxicity limited ability to maintain dosing.<sup>122</sup> Higher ORRs were observed with the selective KRAS-G12C inhibitors MK-1084 and adagrasib in combination with pembrolizumab (47% and 63%, respectively) in programmed death-ligand 1 (PD-L1)-positive (tumor proportion score (TPS)  $\geq 1\%$ ) and PD-L1-high respectively.127,269  $(\text{TPS} \ge 50\%)$ patients, Combinations of sotorasib or glecirasib with SHP2 inhibitors (RMC4630 or JAB-3312, respectively) in pretreated patients showed moderate ORRs overall (43% and 27%, respectively) with promising activity in G12C inhibitor-naïve subsets (ORR of 50% in both studies).123,124 Combinations of MEK inhibitors (binimetinib, trametinib, or avutometinib) with other systemic agents (chemotherapy, defactinib, or multi-TKIs (erlotinib, anlotinib, ponatinib)) have shown variable activity in pretreated patients with KRAS mutations (ORRs 0% -60%).<sup>125,126,242,243,246-249</sup> In chemotherapy-naïve non-squamous NSCLC patients, first-line sotorasib plus carboplatin-pemetrexed showed an impressive ORR of 88.9% and PFS and OS rate at 6 months of 81.2% and 87.0% in the SCARLET phase II trial.128

In summary, the development of agents that indirectly target KRAS (such as MEK/ERK inhibitors) has not been successful in *KRAS*-mutant NSCLC. KRAS-G12C single-OFF inhibitors have shown strong activity in previously treated, *KRAS*-G12C-mutant NSCLC and are the only type of targeted agents approved in this setting. New single- and multi-ON inhibitors are promising agents as they can more directly inhibit active RAS forms and have the potential to simultaneously inhibit different aberrant forms; however, these are still in very early stages of development.

### Other targets

Several targeted therapies are being developed in alteration-drug-matched settings without a

first-in-class regulatory approval to date, including *FGFR*-, *HER3*-, *NRG1*-, *PTK7*-, and *PI3K*altered NSCLC.

FGFR inhibition of FGFR-altered NSCLC was initially attempted with non-selective inhibitors mostly in FGFR-amplified/overexpressed tumors resulting in considerable toxicity with minimal activity.<sup>270-273</sup> The use of FGFR-selective, multior pan-FGFR inhibitors eased safety concerns; however, clinical activity remained minimal (ORRs 4%-11%).<sup>274-277</sup> The recently presented results of the FIND and RAGNAR trials of erdafitinib followed this trend with minimal to modest activity in NSCLC patients with FGFR alterations (ORRs of 9% and 26%, respectively).130,278 Moreover, rogaratinib treatment of squamous NSCLC with FGFR alterations produced no responses in SAKK19/18 which was closed prematurely due to futility.279

In addition to inhibition of HER2-altered NSCLC, multiple approaches have sought to address aberrant HER signaling, including anti-HER3 mAbs and small-molecule pan-HER inhibitors in patients with HER3 or NRG1 overexpression/amplification or NRG1 rearrangements. Testing of small-molecule pan-HER inhibitors in HER1-3-altered NSCLC had limited success.<sup>280-282</sup> Although circulating NRG1 levels were initially identified as potentially predictive of efficacy of the anti-HER3 mAb patritumab plus erlotinib in the randomized phase II HERALD trial,<sup>283</sup> the phase III HER3-Lung study failed to confirm this finding.<sup>284</sup> Similarly, the addition of the anti-HER3 mAbs lumretuzumab or seribantumab to either chemotherapy or EGFR inhibitors did not show meaningful benefit (ORRs of 6.3% and 19.7% in pretreated patients and 42.9% in a small subset of chemotherapy-naïve patients) despite early signals of higher activity in HER3- or NRG1-enriched NSCLC.285-288 The anti-HER3 mAb GSK2849330 showed minimal activity in HER3-expressing cancers (n=29)with a single yet durable response in an NSCLC patient with a cluster of differentiation 74-NRG1 rearrangement.<sup>289</sup> When NRG1 rearrangements were used as biomarker selection criteria, seribantumab and the HER2/HER3 bispecific antibody zenocutuzumab showed moderate vet promising activity with durable responses in previously treated NSCLC patients enrolled in the CRESTONE (ORR 36%)<sup>290</sup> and eNRGy trials (ORR 37.2%; mDoR 14.9 months).<sup>131</sup>

These agents have received fast-track or priority review designations from the FDA in *NRG1*rearranged tumor-agnostic or NSCLC-specific indications.<sup>291,292</sup>

Development of therapies targeted to PI3K and PTK7 in the respective biomarker alterationmatched NSCLC populations is in the very early stages of development without a clear breakthrough to date.<sup>132,293,294</sup>

## Discussion

Development of therapies directed toward driver genes in molecularly selected, advanced NSCLC is an extremely active research field with a large number of studies evaluating new agents in previously identified targets (particularly in MET-, HER2-, and KRAS-altered disease) and new potentially actionable molecular targets (NRG1 and PTK7). MET, HER2, KRAS, ROS1, RET, and BRAF alterations are both clinically actionable and relatively common in NSCLC patients (>1%). It is therefore not surprising that these are among the most studied populations. Although NTRK alterations are uncommon ( $\leq 1\%$ ), their clinical actionability has been convincingly demonstrated independent of tumor type, with high clinical activity across multiple tumors and several tumor-agnostic approvals.

The number of unique clinically actionable settings defined by oncogenic alterations (other than those of EGFR and ALK) continues to grow and clinical research efforts in this field have led to a large number of FDA approvals in the last 3 years (n=9).<sup>295</sup> Many of these are in patient populations with a high clinical need as oncogenic alterations tend toward more aggressive cancers with few treatment options. The clinical impact of alteration-matched therapies is also reflected in trial eligibility for new non-oncogenic-targeted agents (such as ICIs) which now often exclude patients with clinically actionable alterations (EGFR, ALK, ROS1, and others). Moreover, approval of tumor-agnostic indications for the same alteration-drug pairs previously approved in NSCLC<sup>296,297</sup> serves as further validation of the applicability of this strategy. However, despite efforts to standardize reporting and interpretation of alteration-drug-matched clinical trial data,<sup>298-302</sup> regulatory approvals and reimbursement vary across regions limiting access in certain jurisdictions.303-308



**Figure 2.** Clinical activity of selected types of agents used as initial targeted therapy across different oncogene-driven NSCLC settings.

Box and whiskers plot of full (horizontal line segments) and interquartile ranges (boxes), median (vertical lines inside the boxes) and mean (dots) ORR values from clinical studies grouped by setting and type of systemic agent. ORRs for first-line CT alone (platinum doublets),<sup>313</sup> with TT,<sup>314</sup> or ICIs<sup>315</sup> were obtained from meta-analyses and are provided as reference points. Studies of initial TT in alteration-drug-matched settings often include patients previously treated with standards of care for advanced, biomarker-unselected NSCLC. Studies in patients previously treated with alteration-matched TT were not include (e.g., studies of ROS1 inhibitors in patients previously treated with a ROS1 TKI).

<sup>a</sup> "Altered" was used to convey any alteration type, including amplification, overexpression, and mutation. Most of the alterations in "MET-altered" are in *MET*-amplified or -overexpressed but may also include a small fraction of patients with *MET* mutations.

<sup>b</sup>"Enriched" was used to convey increased levels of gene products (RNA or protein amplification or overexpression). ADC, antibody–drug conjugate; ALK, anaplastic lymphoma kinase; BRAF, v-Raf murine sarcoma viral oncogene homolog B1; CT, chemotherapy; HER2, human epidermal growth factor receptor 2; ICI, immune checkpoint inhibitor; KRAS, Kirsten rat sarcoma viral oncogene homolog; MA, meta-analysis; MEK, mitogen-activated protein kinase kinase; MET, hepatocyte growth factor receptor gene; NMA, network meta-analysis; NSCLC, non-small-cell lung cancer; NTRK, neurotrophic tyrosine receptor kinase; ORR, overall response rate; PK, pharmacokinetics; PLT, platinum (doublets); RET, rearranged during transfection; ROS1, c-ros oncogene 1; RNA, ribonucleic acid; TKI, tyrosine kinase inhibitor; TRK, tropomyosin receptor kinase; TT, targeted therapy; 1L, first-line.

Our review highlights the considerable development of targeted therapy in NSCLC, resulting in an overall increase in the antitumor activity of alteration-drug-matched strategies across multiple oncogene-driven settings (Figure 2). Fueled by developments in molecular diagnostic tools, patient selection has evolved from biomarkerunselected populations to those defined by an altered biomarker and, more recently, by specific alterations with known oncogenic potential. Target actionability has also improved through the development of increasingly selective and potent agents, with better pharmacokinetic profiles, that are capable of inhibiting specific alterations at lower doses and with fewer off-target effects. Although the initial use of multi-targeted TKIs allowed multiple alterations to become simultaneously actionable (e.g., crizotinib in *ALK-*, *ROS1-*, and *MET-*altered disease), these agents have generally been replaced with more potent, selective, and/or direct small-molecule inhibitors or antibody-based agents. For example, even though crizotinib had initially shown considerable activity in ROS1-rearranged NSCLC, ORRs in this setting continue to improve with next-generation inhibitors that display higher selectivity toward ROS1 and its mutant forms (Figure 2).57-59,309 Nonetheless, strategies involving simultaneous inhibition of multiple targets such as co- and pan-inhibitory approaches may still be useful in areas where a more stringent biological control is required due to compensatory mechanisms (such as functional redundancy and pathway feedback loops) or weak primary target inhibition. With the establishment of alteration-drug-matched approaches as firstline therapy in the advanced setting, there is an increasing need for strategies to overcome both innate and acquired resistance.310 These commonly involve co-inhibition with combination therapy or bispecific agents to address off-target mechanisms (e.g., KRAS-G12C plus SHP2 inhibitors against adaptative resistance to KRAS inhibition<sup>123,124,310</sup> or amivantamab to overcome reciprocal resistance and signaling crosstalk between EGFR and MET)310-312 and/or use of next-generation inhibitors which typically address on-target resistance mechanisms (e.g., taletrectinib against the ROS1 secondary solvent-front mutation G2032R).<sup>309</sup> Current research also increasingly favors direct alteration targeting over indirect strategies such as modulation of proximal "pathway" components or levels of effector molecules or by stabilizing inactive/OFF states. Newer antibody-based agents are improving the clinical actionability of alteration-matched approaches by directed delivery of cytotoxic moieties (ADCs) or by specifically and simultaneously targeting multiple alterations with potential synergistic effects (bispecific antibodies). Bispecific antibodies have also the potential of combining alteration-drug-matching with other therapeutic approaches that have been successful in the treatment of NSCLC, such as immune modulation of the tumor microenvironment with ICIs.

Development of effective therapeutic strategies has been challenging in some biomarker-selected settings, such as PI3K- and FGFR-altered NSCLC for which no agent was approved despite decades-long research efforts. In particular, alterations to PI3K and its efferent (PI3K-AKTmammalian target of rapamycin (mTOR)) pathway are relatively common in NSCLC and multiple direct and indirect inhibitory approaches have been attempted with pan-class I PI3K, PI3K subtype, AKT, mTOR, and PI3K/mTOR inhibitors in both alteration-drug-matched and populations.<sup>316–318</sup> -unmatched PI3K-AKTmTOR is an example of a pathway with complex

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regulatory mechanisms and intricate crosstalk, where target inhibition is challenged by multiple intra- and inter-pathway compensatory mechanisms (including functional redundancy of PI3K toxicities.316-320 isoforms) and on-target Moreover, PI3K pathway alterations are genetically diverse, occur in a clinically heterogenous group of patients, and are often associated with alterations in other oncogenes and high mutational load, where they may be "passengers" rather than "drivers" of the oncogenic process.<sup>320-322</sup> In addition to addressing issues with inhibitor selectivity and toxicity, and similar to MET inhibitors in MET-altered disease, a critical step in the development of PI3K inhibitors in NSCLC may be the identification and targeting of oncogenic drivers among the range of PI3K pathway alterations.320

It is important to note that many targeted agents are currently being developed in unselected/ non-matched populations, using indirect ("pathway") inhibition strategies and targeting non-oncogene tumor-associated alterations. For example, treatment of NFE2L2/KEAP1altered NSCLC is being attempted indirectly with glutaminase<sup>323</sup> and mTOR inhibitors.<sup>324,325</sup> ADCs targeting the human trophoblast cell surface glycoprotein antigen 2 (TROP2; datopotamab deruxtecan, sacituzumab govitecan, and SKB264) have recently shown promise in NSCLC in combination with ICIs<sup>326,327</sup> or as single agents.<sup>328-330</sup> However, their development has been directed toward TROP2-unselected populations as biomarker analyses have failed to establish TROP2 expression as a predictor of clinical activity.<sup>328,331</sup> Development of ADCs against other tumor-associated markers especially in populations with high levels of target expression is a promising approach that is currently being explored.332-334

## Summary

Research in alteration-drug matching continues to evolve at a rapid pace in NSCLC. The number of settings defined by oncogenic alterations has increased and alteration targeting has become increasingly specific and effective with the refinement of biomarker selection criteria and the use of newer, more selective, and potent agents. Future developments should focus on the continued application of these principles to new settings and the exploration of novel ways to target oncogene-driven NSCLC.

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## Author contributions

**Barbara Melosky:** Conceptualization; Data curation; Funding acquisition; Methodology; Supervision; Visualization; Writing – original draft; Writing – review & editing.

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#### Supplemental material

Supplemental material for this article is available online.

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