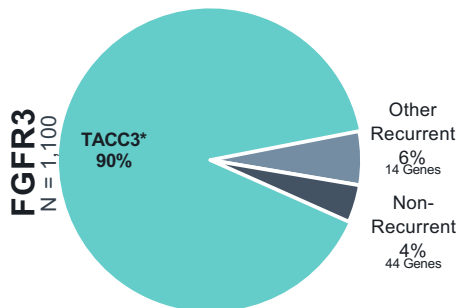
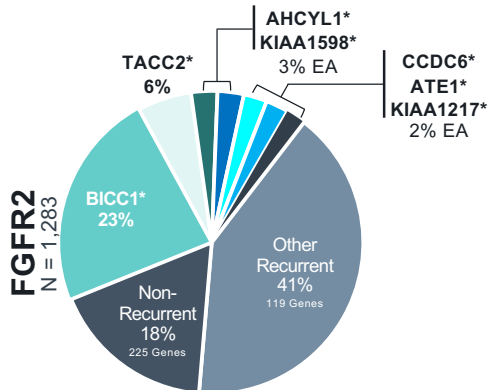
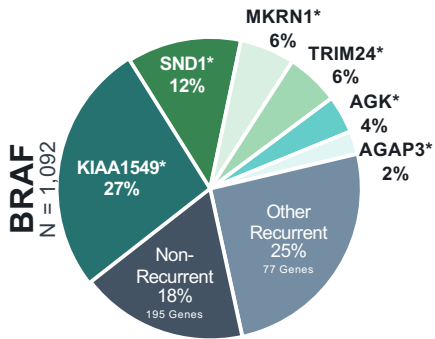
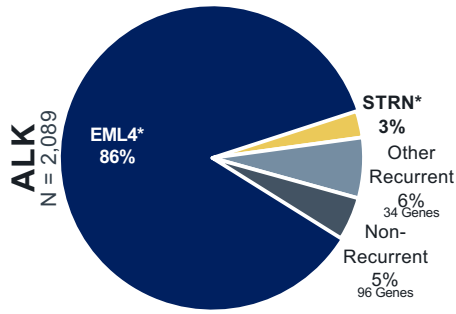


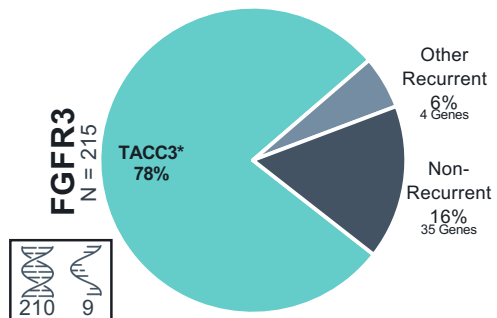
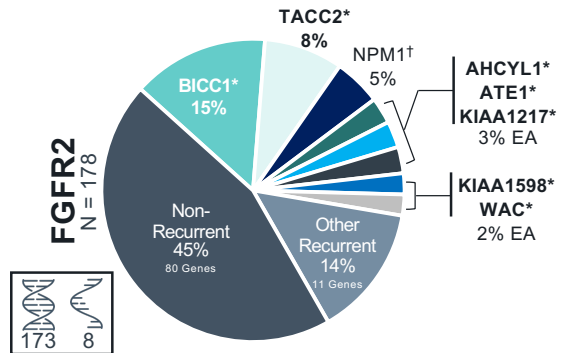
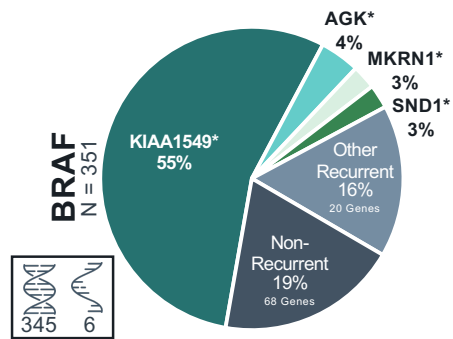
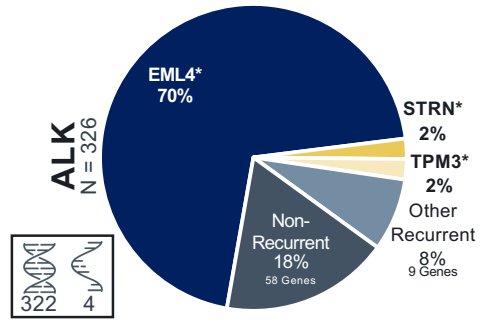
FMI DNA CGP

N = 459,751

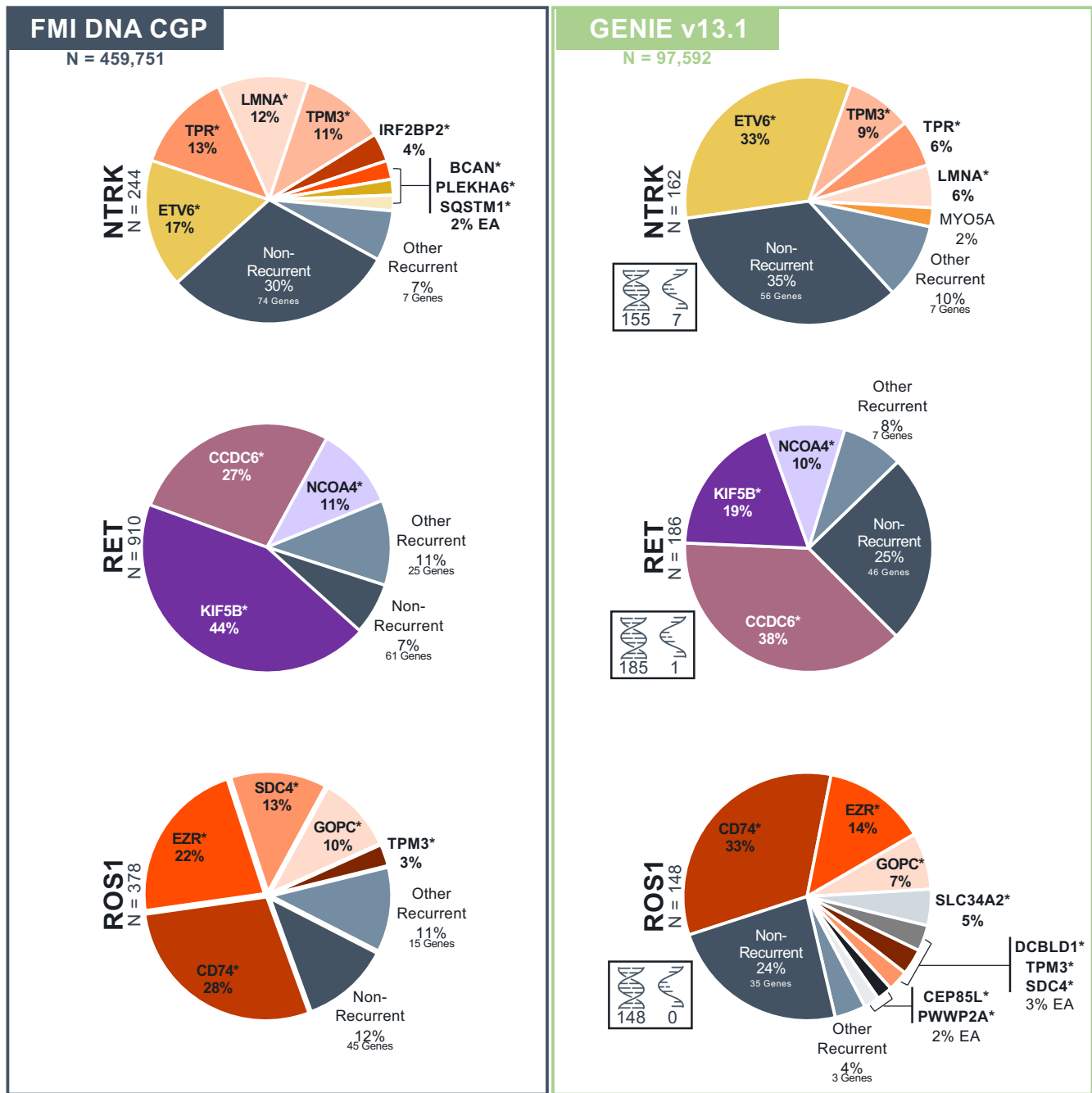


GENIE v13.1

N = 97,592

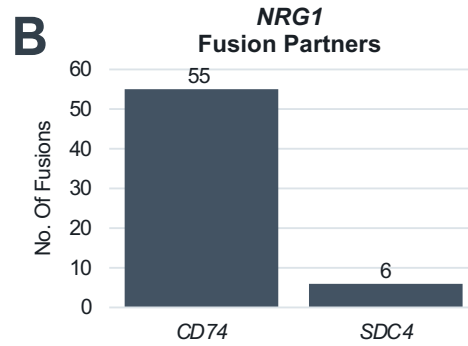
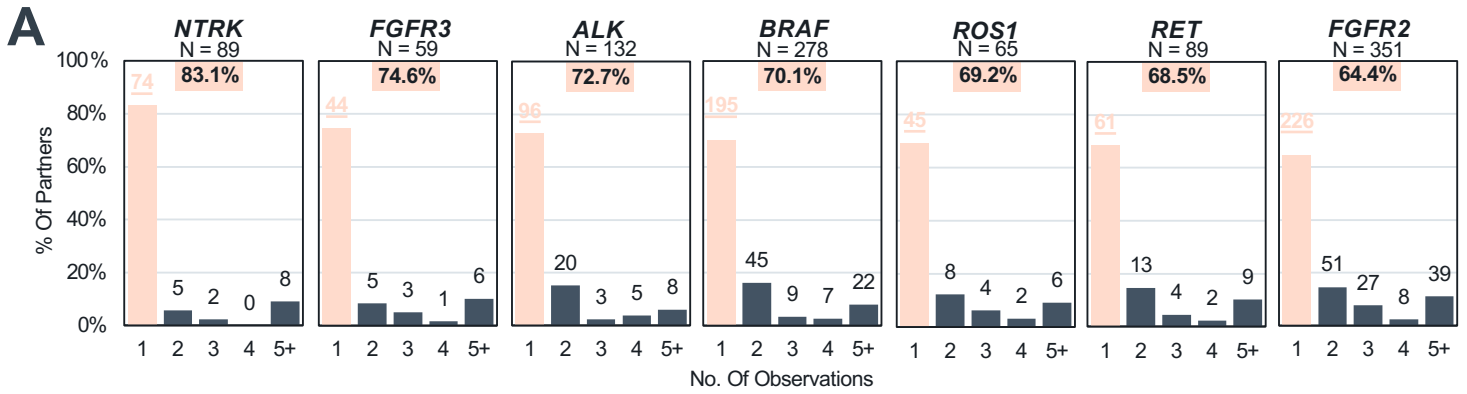


GENE NAME* = OBSERVED AS FUSION PARTNER IN BOTH COHORTS

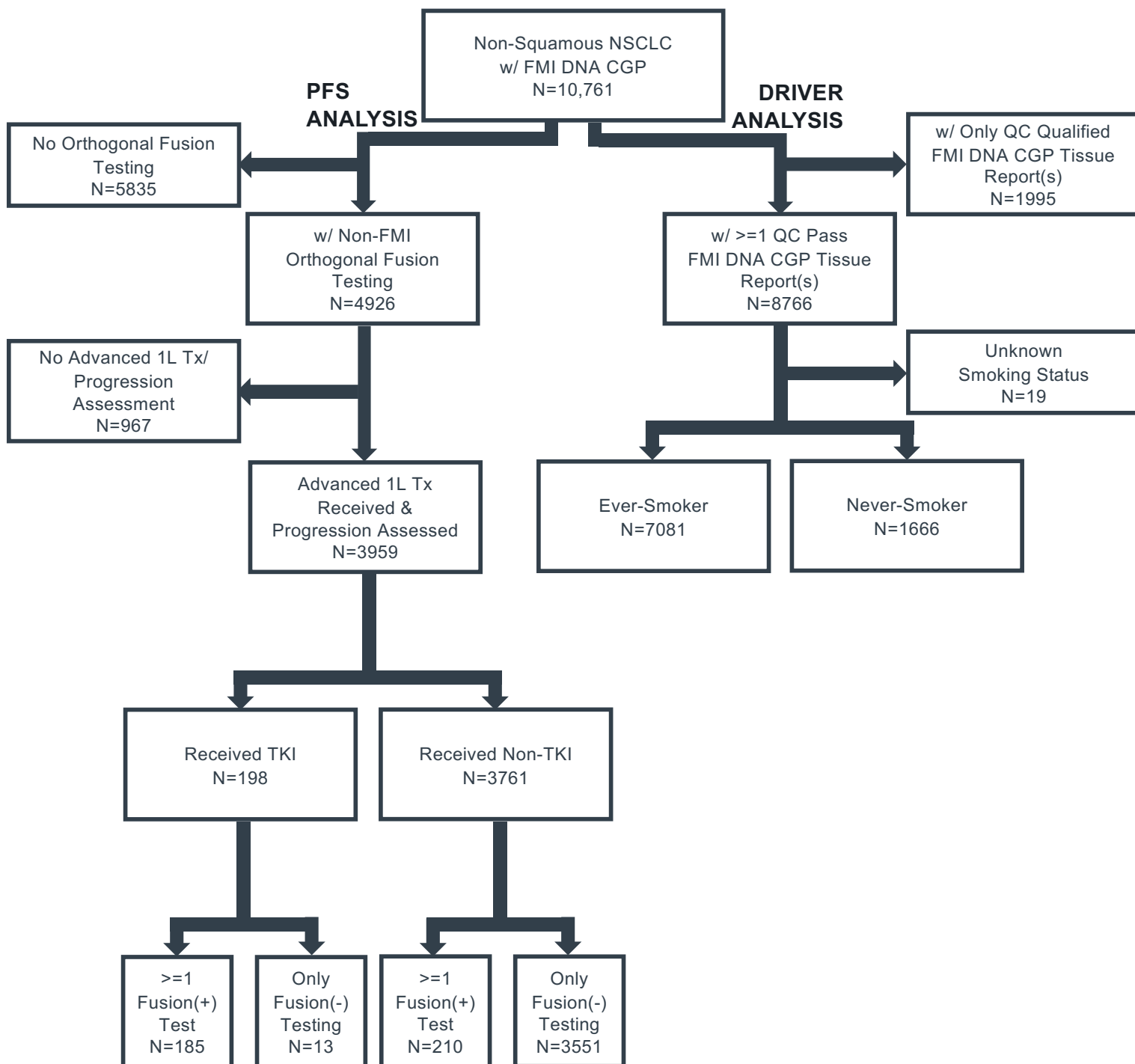


GENE NAME* = OBSERVED AS FUSION PARTNER IN BOTH COHORTS

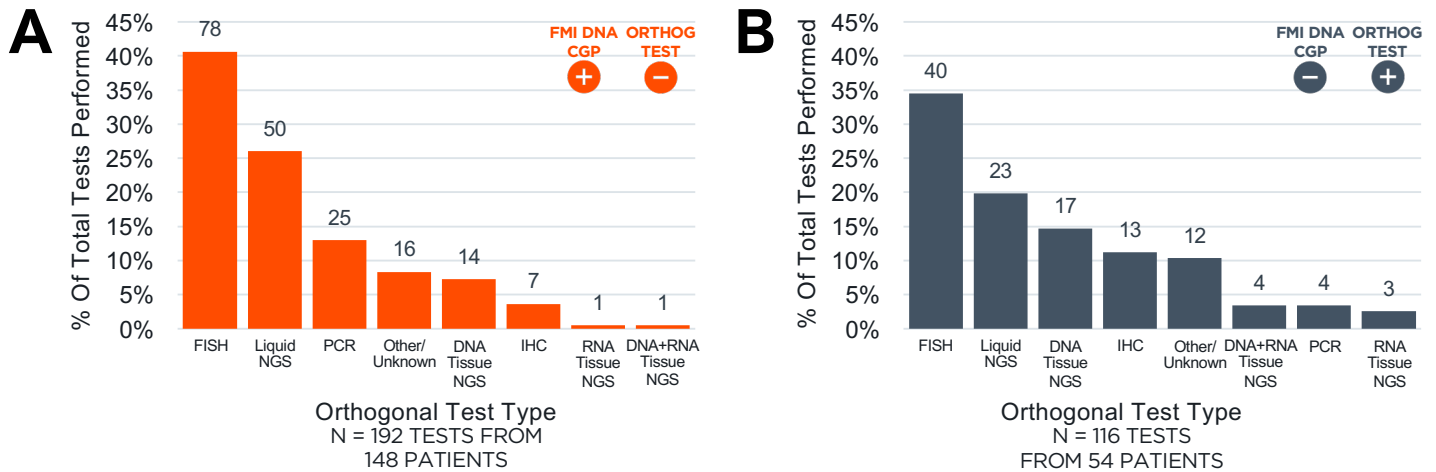
Supplemental Figure 1. FMI DNA CGP Fusion Partner Diversity Prevalence of partner genes involved in *ALK*, *BRAF*, *FGFR2*, *FGFR3*, *NTRK1/2/3*, *RET*, and *ROS1* fusions. Partner genes representing $\geq 2\%$ of observed fusions are plotted individually while recurrent partners representing $< 2\%$ of observed fusions and non-recurrent partners are grouped. Asterisk (*) indicates partner gene was detected using both FMI DNA CGP and non-FMI assays in the AACR GENIE v13.1 data set. Ns below assay names denote the number of unique patients with structural variant profiling in the relevant cohort. Ns adjacent to gene names denote the number of fusion events detected in the relevant cohort. The number of fusion events with DNA and RNA evidence in GENIE is also indicated. (Note that fusions may be supported by both types of evidence.) †While *FGFR2-NPM1* rearrangements were detected on F1CDx/F1, they were considered variants of uncertain significance (VUS). FMI DNA CGP, Foundation Medicine Tissue DNA Comprehensive Genomic Profiling.



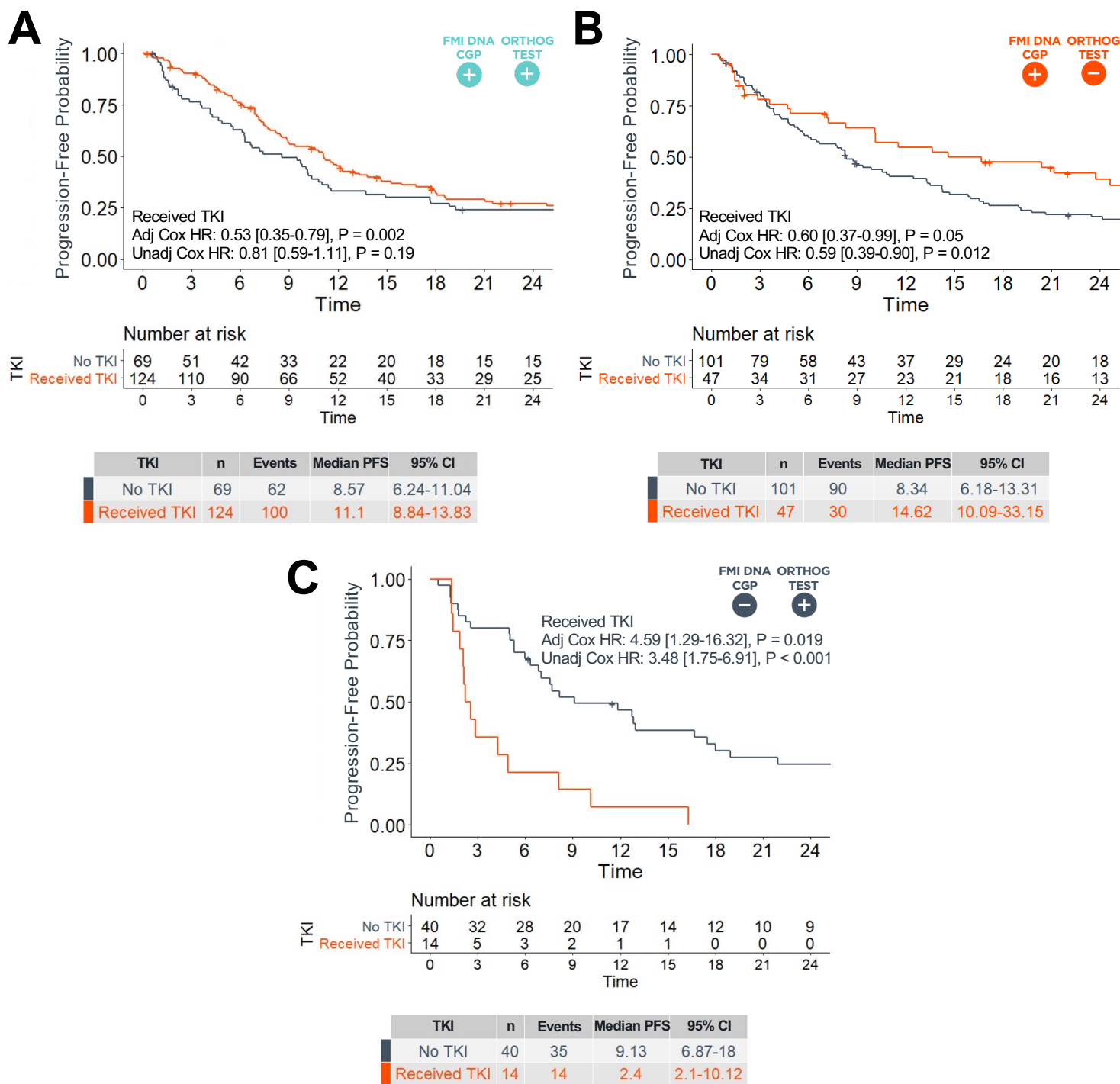
Supplemental Figure 2. FMI DNA CGP Fusion Detection Additional Data (Related To Figure 2). A) Percentage of fusion partners observed a single –versus– multiple times with each clinically actionable fusion gene. The total number of fusion partners observed with each gene is indicated above the plots. The number of fusions partners observed with each gene in each observation category (1-5+) is also indicated. B) No. of detected *NRG1* fusions involving baited gene partners in tissue biopsies profiled using F1CDx (N = 316,152). FMI DNA CGP, Foundation Medicine Tissue DNA Comprehensive Genomic Profiling.



Supplemental Figure 3. CONSORT Diagram For Non-Squamous NSCLC Clinicogenomic Analyses The clinicogenomic cohort consisted of patients with histology/genomics consistent with non-squamous NSCLC who underwent FMI DNA CGP (N = 10,761). (Left) For the PFS analysis (Figure 3), patients 1) with both tissue-based FMI DNA CGP and fusion testing using an orthogonal method through which 2) an *ALK*, *NTRK*, *RET*, or *ROS1* fusion was identified in ≥ 1 test and who 3) received a matched TKI in the advanced 1L and 4) were assessed for progression were included. (Right) For the oncogenic driver analysis (Figure 4), patients with qualified reports were excluded due to the possibility of reduced sensitivity for alteration detection. The cohort was divided into ever-smokers and never-smokers based on self-reported smoking history and patients with unknown smoking history were excluded. FMI DNA CGP, Foundation Medicine Tissue DNA Comprehensive Genomic Profiling.



Supplemental Figure 4. Orthogonal Testing Methods For Non-Squamous NSCLC Patients With Discordant FMI DNA CGP And Orthogonal Fusion Testing Results Distribution of orthogonal testing modalities undergone by A) N = 148 patients who were assessed for progression and were found to be fusion-positive on FMI DNA CGP and fusion-negative on orthogonal testing (FMI DNA CGP+/Orthog-) and B) N = 54 patients who were assessed for progression and were found to be fusion-negative on FMI DNA CGP and fusion-positive on orthogonal testing (FMI DNA CGP-/Orthog+). Each testing modality is only counted once per patient. However, a single patient could be counted towards multiple modalities if a patient underwent multiple types of testing such that the sum of all bars may exceed 100%. FMI DNA CGP, Foundation Medicine Tissue DNA Comprehensive Genomic Profiling.



Supplemental Figure 5. Non-Squamous NSCLC rwPFS Associations According To Fusion Testing Results And 1L Therapy Class Received Patients with non-squamous NSCLC who were assessed for progression and underwent both FMI DNA CGP and additional fusion testing were stratified by 1L therapy class (i.e., matched TKI versus other). Unadjusted Kaplan-Meier plots are shown for patients who (A) had *ALK*, *NTRK*, *RET*, or *ROS1* fusions detected on both FMI DNA CGP and orthogonal testing (FMI DNA CGP+/Orthog+), (B) had *ALK*, *NTRK*, *RET*, or *ROS1* fusions detected on FMI DNA CGP but not orthogonal testing (FMI DNA CGP+/Orthog-) or (C) had *ALK*, *NTRK*, *RET*, or *ROS1* fusions detected on orthogonal testing but not FMI DNA CGP (FMI DNA CGP-/Orthog+). Analyses are indexed to the start of 1L therapy. In addition to univariable Cox model HRs, adjusted HRs are presented for a multivariable Cox model that includes established prognostic variables (see **Supplementary Figure 6**). FMI DNA CGP, Foundation Medicine Tissue DNA Comprehensive Genomic Profiling; HR, Hazard Ratio; TKI, Tyrosine Kinase Inhibitor; rwPFS, Real-World Progression Free Survival.

A

FMI DNA ORTHOG
CGP TEST
+ +

N = 178

Variable		N Events	Hazard ratio	p
TKI	No TKI	62 55	Reference	
	Received TKI	116 93	0.53 (0.35, 0.79)	0.002
Socioeconomic status	1 - Lowest SES	16 13	Reference	
	2	25 16	0.71 (0.32, 1.59)	0.404
	3	45 43	1.41 (0.71, 2.82)	0.329
	4	41 32	1.25 (0.61, 2.56)	0.542
	5 - Highest SES	51 44	1.92 (0.94, 3.92)	0.072
Practice type	Academic	43 37	Reference	
	Academic/Community	8 7	0.85 (0.33, 2.20)	0.738
	Community	127 104	1.00 (0.65, 1.54)	0.993
Gender	Female	95 83	Reference	
	Male	83 65	1.19 (0.79, 1.80)	0.407
Race	Asian	14 11	Reference	
	Black or African American	12 10	0.80 (0.30, 2.10)	0.650
	Other Race	27 24	0.60 (0.27, 1.34)	0.211
	Unknown/not documented	5 2	0.34 (0.07, 1.73)	0.193
	White	120 101	0.65 (0.32, 1.32)	0.233
Stage at diagnosis	Stage I-III	34 28	Reference	
	Stage IV	144 120	0.83 (0.50, 1.38)	0.472
Smoking status	History of smoking	65 54	Reference	
	No history of smoking	113 94	0.90 (0.60, 1.34)	0.605
Age at start of systemic line of therapy	0	178	Reference	
	1	67 53	1.74 (1.08, 2.81)	0.023
	2	57 45	1.71 (0.71, 4.09)	0.229
	3	4 4	2.40 (0.74, 7.84)	0.146
	Unknown	40 39	1.64 (0.97, 2.75)	0.063
Opioids immediately prior to therapy	44	1.28 (0.80, 2.04)	0.300	
Presence of pretherapy bone metastases	92	1.58 (1.01, 2.47)	0.043	
Presence of pretherapy CNS metastases	54	1.34 (0.89, 2.01)	0.162	
Presence of pretherapy liver metastases	48	1.86 (1.14, 3.02)	0.012	
Presence of pretherapy adrenal metastases	18	1.34 (0.70, 2.57)	0.374	
Presence of other pretherapy metastases	124	1.17 (0.76, 1.80)	0.482	

B

FMI DNA ORTHOG
CGP TEST
+ -

N = 130

Variable		N Events	Hazard ratio	p
TKI	No TKI	87 78	Reference	
	Received TKI	43 28	0.60 (0.37, 0.99)	0.05
Socioeconomic status	1 - Lowest SES	12 10	Reference	
	2	17 13	0.42 (0.16, 1.07)	0.07
	3	42 36	0.64 (0.27, 1.48)	0.30
	4	24 19	0.69 (0.28, 1.70)	0.42
	5 - Highest SES	35 28	0.60 (0.26, 1.41)	0.24
Practice type	Academic	28 19	Reference	
	Academic/Community	2 2	2.04 (0.39, 10.70)	0.40
	Community	100 85	1.18 (0.63, 2.21)	0.61
Gender	Female	78 63	Reference	
	Male	52 43	0.98 (0.60, 1.61)	0.95
Race	Asian	2 1	Reference	
	Black or African American	8 5	2.71 (0.29, 24.88)	0.38
	Other Race	22 19	4.66 (0.57, 38.04)	0.15
	Unknown/not documented	11 11	3.08 (0.37, 25.43)	0.30
	White	87 70	2.95 (0.38, 22.88)	0.30
Stage at diagnosis	Stage I-III	27 22	Reference	
	Stage IV	103 84	0.98 (0.54, 1.81)	0.96
Smoking status	History of smoking	50 47	Reference	
	No history of smoking	80 59	0.59 (0.37, 0.93)	0.02
Age at start of systemic line of therapy	0	130	Reference	
	1	48 42	1.00 (0.97, 1.02)	0.66
	2	8 8	0.86 (0.51, 1.45)	0.57
	3	11 11	1.11 (0.40, 3.08)	0.84
	Unknown	23 17	1.19 (0.60, 2.36)	0.62
Opioids immediately prior to therapy	31	1.32 (0.72, 2.41)	0.36	
Presence of pretherapy bone metastases	47	1.34 (0.79, 2.26)	0.27	
Presence of pretherapy CNS metastases	35	0.98 (0.53, 1.81)	0.95	
Presence of pretherapy liver metastases	16	1.39 (0.69, 2.79)	0.35	
Presence of pretherapy adrenal metastases	7	3.41 (1.17, 10.00)	0.03	
Presence of other pretherapy metastases	85	1.38 (0.81, 2.37)	0.24	

C

FMI DNA ORTHOG
CGP TEST
- +

N = 47

Variable		N Events	Hazard ratio	p
TKI	No TKI	35 32	Reference	
	Received TKI	12 12	4.59 (1.29, 16.32)	0.019
Socioeconomic status	1 - Lowest SES	10 10	Reference	
	2	6 5	2.98 (0.58, 15.37)	0.192
	3	5 5	1.28 (0.18, 9.29)	0.804
	4	14 13	0.33 (0.10, 1.08)	0.066
	5 - Highest SES	12 11	0.10 (0.02, 0.45)	0.003
Practice type	Academic	8 8	Reference	
	Academic/Community	1 1	1.49 (0.10, 23.06)	0.775
	Community	38 35	5.33 (1.09, 26.18)	0.039
Gender	Female	24 22	Reference	
	Male	23 22	0.81 (0.29, 2.28)	0.692
Race	Asian	1 1	Reference	
	Black or African American	2 2	0.00 (0.00, 0.07)	0.003
	Other/unknown	6 5	0.02 (0.00, 0.75)	0.034
Stage at diagnosis	Stage I-III	38 36	Reference	
	Stage IV	15 14	0.57 (0.21, 1.56)	0.270
Smoking status	History of smoking	34 32	Reference	
	No history of smoking	13 12	0.63 (0.15, 2.64)	0.531
Age at start of systemic line of therapy	0	47	Reference	
	1	18 16	8.62 (2.98, 24.96)	<0.001
	2	26 25	76.67 (6.05, 972.389)	0.001
Opioids immediately prior to therapy	10	0.31 (0.09, 1.13)	0.077	
Presence of pretherapy bone metastases	13	4.77 (1.63, 13.92)	0.004	
Presence of pretherapy CNS metastases	13	7.21 (1.96, 26.48)	0.003	
Presence of pretherapy liver metastases	8	7.21 (1.62, 32.18)	0.010	
Presence of pretherapy adrenal metastases	7	1.97 (0.47, 8.27)	0.355	
Presence of other pretherapy metastases	22	0.32 (0.11, 0.94)	0.038	

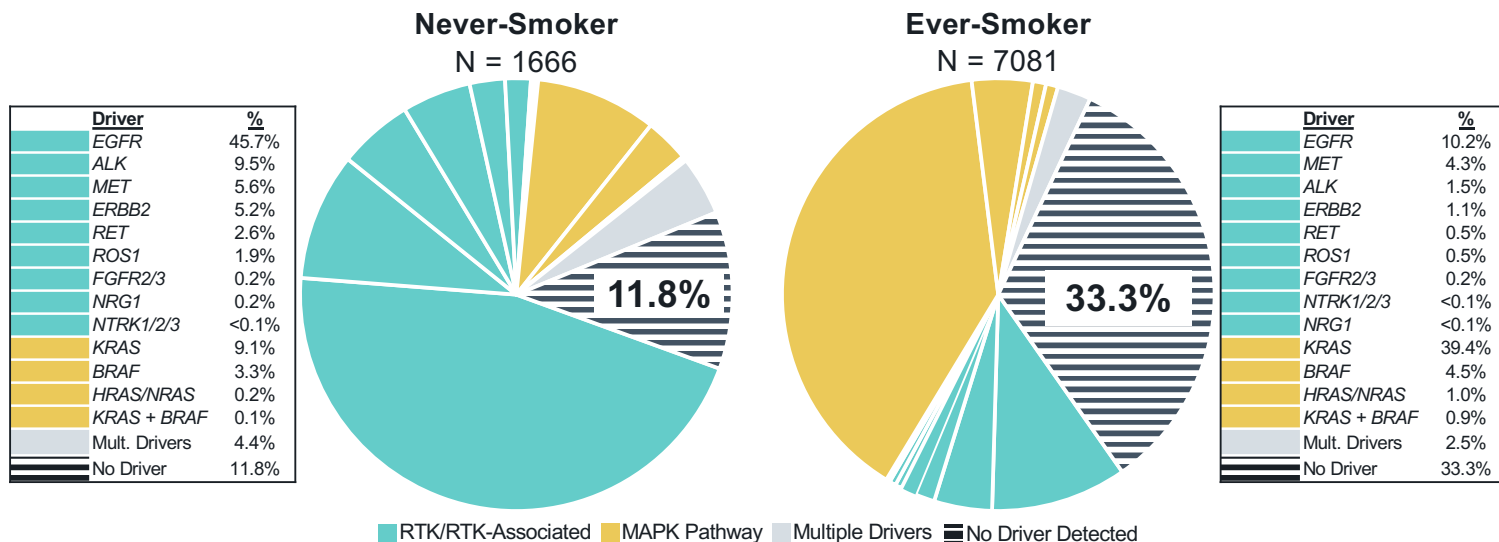
D

1L TKI

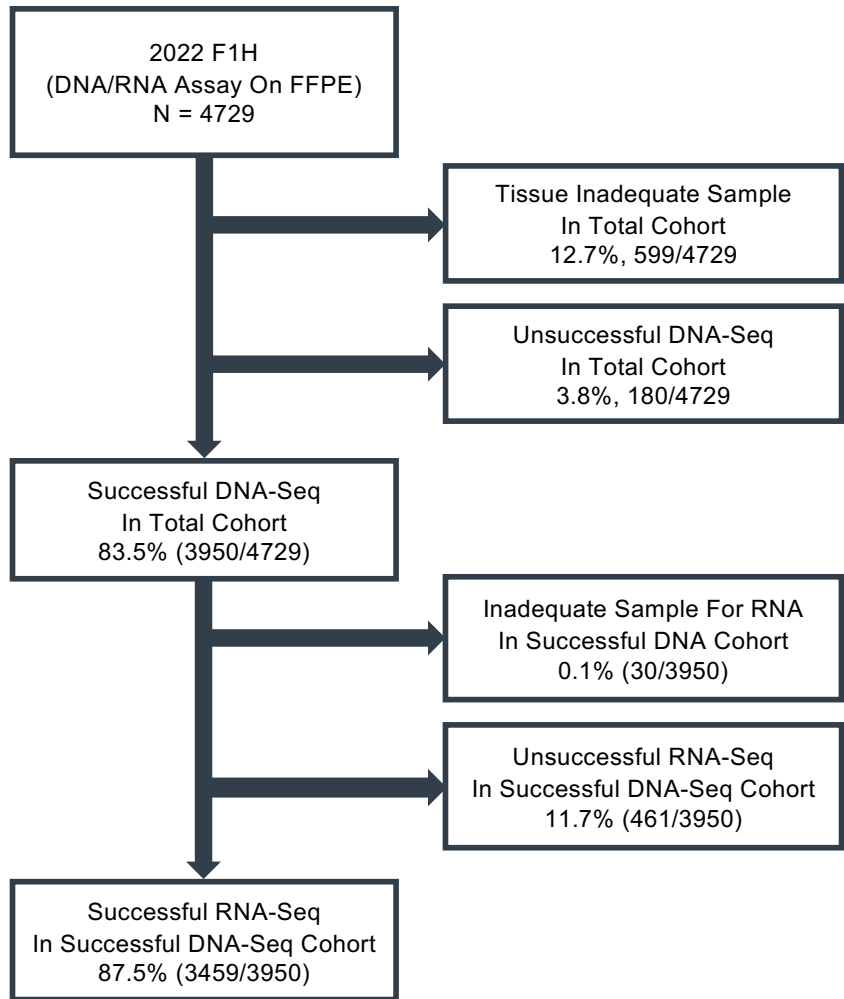
N = 173

Variable		N Events	Hazard ratio	p
Fusion results	FMI DNA CGP-/Orthog+	14 14	Reference	
	FMI DNA CGP+/Orthog-	43 28	0.15 (0.07, 0.33)	<0.001
	FMI DNA CGP+/Orthog+	116 93	0.17 (0.08, 0.36)	<0.001
Socioeconomic status	1 - Lowest SES	19 15	Reference	
	2	21 13	0.68 (0.29, 1.60)	0.38
	3	42 36	1.39 (0.69, 2.78)	0.35
	4	38 29	1.01 (0.51, 2.02)	0.97
	5 - Highest SES	53 42	1.37 (0.70, 2.68)	0.36
Practice type	Academic	40 30	Reference	
	Academic/Community	9 8	1.11 (0.44, 2.81)	0.82
	Community	124 97	1.03 (0.63, 1.67)	0.90
Gender	Female	96 79	Reference	
	Male	77 56	0.86 (0.55, 1.32)	0.48
Race	Asian	10 6	Reference	
	Black or African American	9 5	0.93 (0.26, 3.28)	0.91
	Other Race	28 24	0.92 (0.34, 2.47)	0.88
Stage at diagnosis	Stage I-III	7 6	Reference	
	Stage IV	119 94	1.19 (0.33, 4.26)	0.79
Smoking status	History of smoking	119 94	Reference	
	No history of smoking	24 20	0.95 (0.40, 2.41)	0.96
Age at start of systemic line of therapy	0	149 115	Reference	
	1	62 52	1.05 (0.59, 1.87)	0.86
	2	111 83	0.77 (0.50, 1.18)	0.23
ECOG Performance Score	0	173	Reference	
	1	63 48	1.00 (0.98, 1.02)	0.92
	2	55 40	1.13 (0.72, 1.78)	0.60
	3	11 8	1.21 (0.52, 2.82)	0.66
Opioids immediately prior to therapy	41	1.58 (0.40, 6.21)	0.51	
Presence of pretherapy bone metastases	41	1.12 (0.66, 1.93)	0.68	
Presence of pretherapy CNS metastases	41	1.08 (0.67, 1.75)	0.74	
Presence of pretherapy liver metastases	44	1.17 (0.74, 1.84)	0.51	
Presence of pretherapy adrenal metastases	20	1.24 (0.80, 1.93)	0.34	
Presence of other pretherapy metastases	119	1.62 (0.99, 2.64)	0.05	

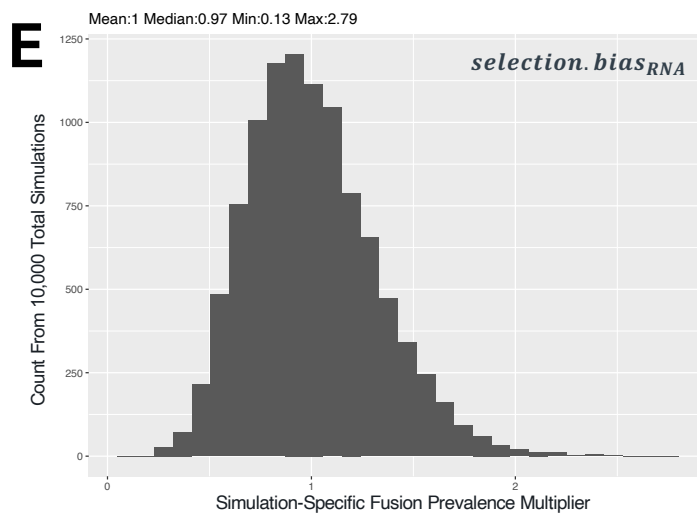
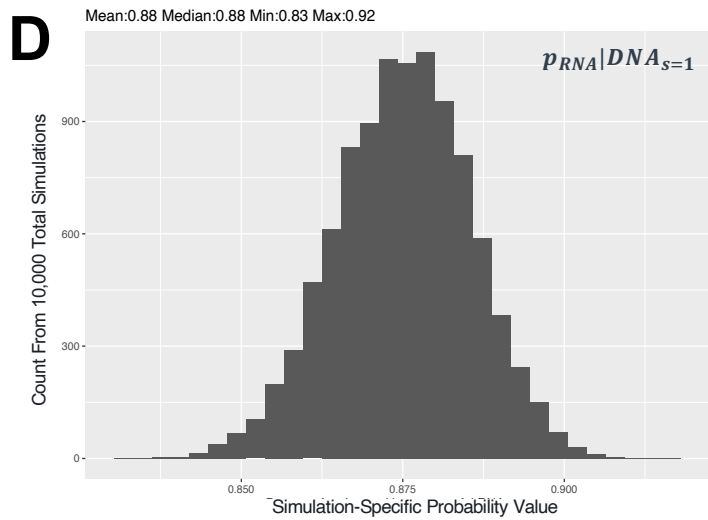
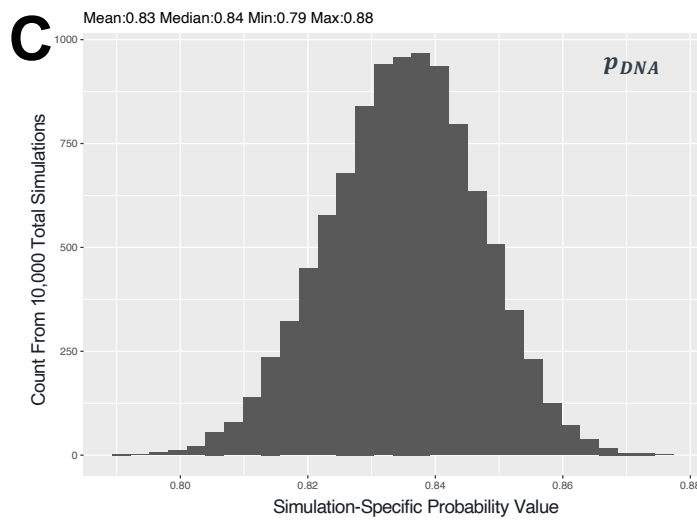
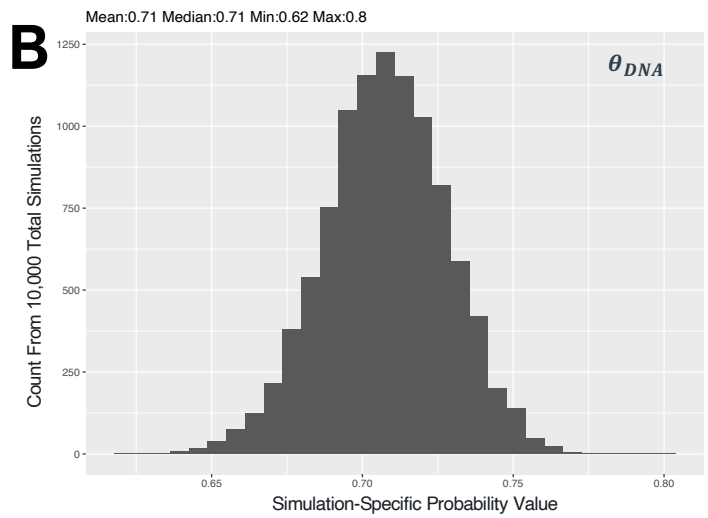
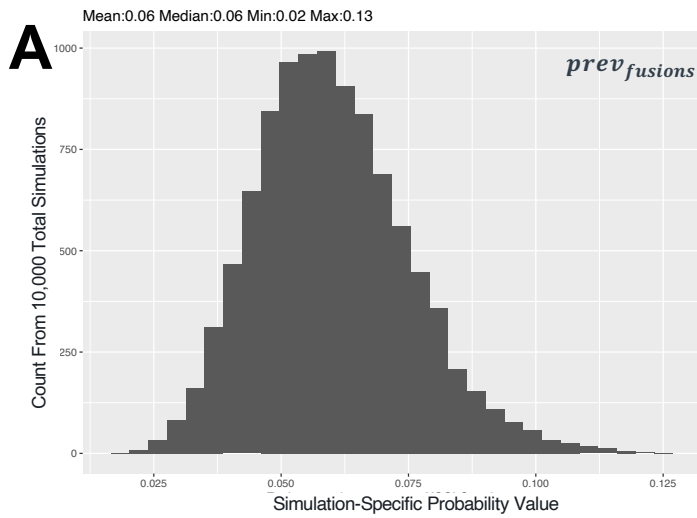
Supplemental Figure 6. Multivariable Cox Models For Non-Squamous NSCLC rwPFS On 1L Therapy rwPFS for (A) patients who had *ALK*, *NTRK*, *RET*, or *ROS1* fusions detected on both FMI DNA CGP and orthogonal testing (FMI DNA CGP+/Orthog+; N = 178) stratified by receipt of a matched TKI in 1L; (B) patients who had *ALK*, *NTRK*, *RET*, or *ROS1* fusions detected on FMI DNA CGP but not orthogonal testing (FMI DNA CGP+/Orthog-; N = 130) stratified by receipt of a matched TKI in 1L; (C) patients who had *ALK*, *NTRK*, *RET*, or *ROS1* fusions detected on orthogonal testing but not FMI DNA CGP (FMI DNA CGP-/Orthog+; N = 47) stratified by receipt of a matched TKI in 1L; and (D) all patients who received a matched TKI for *ALK*, *NTRK*, *RET*, or *ROS1* fusions in 1L stratified by fusion testing results (N = 173). Patients who were negative for *ALK*, *NTRK*, *RET*, or *ROS1* fusions by both FMI DNA CGP and orthogonal testing (FMI DNA CGP-/Orthog-) were excluded from this analysis. Adjustment variables included clinical characteristics which could impact prognosis. Missing Socioeconomic Status and ECOG Performance Score were not imputed, therefore patients missing either of these values were also excluded. For binary variables (pretherapy opioids and pretherapy metastases), the N column shows the number of patients positive for that characteristic. In all analyses, either missing values were imputed or cases with missing values were excluded, as noted above. FMI DNA CGP, Foundation Medicine Tissue DNA Comprehensive Genomic Profiling; HR, Hazard Ratio; TKI, Tyrosine Kinase Inhibitor; rwPFS, Real-World Progression Free Survival.



Supplemental Figure 7. An Oncogenic Driver Is Not Detected In A Minority (12-33%) Of Non-Squamous NSCLC Using DNA CGP Tumors were classified as having an oncogenic driver if activating alterations were detected in select RTK/MAPK pathway genes (see **Supplementary Table 3**). The distribution of detected oncogenic drivers in ever-smoker and never-smoker subpopulations is shown. MAPK, Mitogen-Activated Protein Kinase; RTK, Receptor Tyrosine Kinase.



Supplemental Figure 8. FoundationOne®Heme (F1H) DNA/RNA Analyte Sequencing Success Rates (2022)



Supplemental Figure 9. Parameter Distributions For Probabilistic Sensitivity Analysis Distributions of individual parameter draws with summary statistics used to generate the probabilistic sensitivity analysis (see **Figure 5B**). Distributional parameters are defined in **Supplementary Table 3**. **A:** *prev_fusions* **B:** θ_{DNA} **C:** p_{DNA} **D:** $p_{RNA|DNA_{s=1}}$ **E:** *selection.bias_{RNA}*.

Supplemental Table 1. Summary Of Intronic Coverage On FoundationOne®CDx For Rearrangement Detection

EXONIC + SELECT INTRONIC COVERAGE N = 21

ALK Introns 18,19	BCL2 3' UTR	BRAF Introns 7-10	BRCA1 Introns 2,7,8,12,16,19,20	BRCA2 Intron 2
EGFR Introns 7, 15, 24-27	FGFR1 Introns 1, 5, 17	FGFR2 Introns 1, 17	FGFR3 Introns 17	KIT Intron 16
KMT2A (MLL) Introns 6-11	MSH2 Intron 5	MYC Intron 1	NOTCH2 Intron 26	NTRK1 Introns 8-11
NTRK2 Intron 12	PDGFRA Introns 7, 9, 11	RAF1 Introns 4-8	RARA Intron 2	RET Introns 7-11
ROS1 Introns 31-35				

SELECT INTRONIC COVERAGE ONLY N = 13

Gene	Introns Covered	Solid Tumor Common Fusion Partner Gene(s)
BCR	8, 13, 14	<i>NTRK2</i> (CNS Tumors)
CD74	6-8	<i>NRG1</i> (NSCLC); <i>NTRK1</i> (Pan-Solid); <i>ROS1</i> (NSCLC, Pan-Solid)
ETV4	8	<i>TMPRSS2</i> (Prostate)
ETV5	6, 7	<i>TMPRSS2</i> (Prostate)
ETV6	5, 6	<i>NTRK3</i> (Pan-Solid)
EWSR1	7-13	Multiple Partners (Sarcoma, Prostate)
EZR	9-11	<i>ROS1</i> (NSCLC, Pan-Solid)
MYB	14	<i>NFIB</i> (Adenoid Cystic Carcinomas)
NUTM1	1	<i>BRD4</i> (NUT Midline Carcinoma)
RSPO2	1	Multiple Partners, e.g., <i>EIF3E</i> (CRC)
SDC4	2	<i>NRG1</i> (Pan-Solid); <i>ROS1</i> (NSCLC)
SLC34A2	4	<i>ROS1</i> (NSCLC)
TMPRSS2	1-3	<i>ERG</i> , <i>ETV1</i> , <i>ETV4</i> , <i>ETV5</i> (Prostate)

Supplemental Table 2. Non-Squamous NSCLC Patient Cohort Clinical Characteristics

	Total Cohort
	<i>N</i> =10761
Age At Diagnosis, Years, Median (IQR)	67.0 [60.0;74.0]
Sex, <i>n</i> (%)	
Female	5971 (55.5%)
Male	4790 (44.5%)
Self-Reported Race, <i>n</i> (%)	
Asian	361 (3.35%)
Black or African American	722 (6.71%)
Hispanic or Latino	8 (0.07%)
Other Race	1502 (14.0%)
White	7166 (66.6%)
Unknown/Not Documented	1002 (9.31%)
AJCC Stage At Diagnosis, <i>n</i> (%)	
I	1330 (12.4%)
II	843 (7.83%)
III	2084 (19.4%)
IV	6164 (57.3%)
Other/Unknown/Not Documented	340 (3.16%)
Smoking History, <i>n</i> (%)	
History Of Smoking	8643 (80.3%)
No History Of Smoking	2095 (19.5%)
Unknown/Not Documented	23 (0.21%)
Practice Type, <i>n</i> (%)	
Academic	1270 (11.8%)
Academic/Community	608 (5.65%)
Community	8883 (82.5%)
Socioeconomic Status, <i>n</i> (%)	
1 - Lowest SES	1459 (13.6%)
2	1865 (17.3%)
3	2187 (20.3%)
4	2248 (20.9%)
5 - Highest SES	2073 (19.3%)
Unknown	929 (8.63%)
ECOG PS At Diagnosis, <i>n</i> (%)	
0	2179 (20.2%)
1	2253 (20.9%)
2	578 (5.37%)
3+	153 (1.42%)
Unknown	5598 (52.0%)

Supplemental Table 3. Parameter Inputs For Deterministic And Probabilistic Sensitivity Analyses

Parameter Description		Base Case Estimate	Min	Max	Distribution	Justification
$prev_{fusions}$	Estimated NCCN driver fusion prevalence in the NSCLC patient population	6.0%	1.6%	10.4%	Beta(15,235)	Based on combined fusion prevalence estimates for <i>ALK</i> , <i>RET</i> , <i>ROS1</i> , and <i>NTRK1/2/3</i> from the literature (see Methods)
θ_{DNA}	Probability of detecting an oncogenic driver alteration on DNA CGP	70.8%	66.7%	88.2%	Beta(354,146)	6,194/8,747 patients observed with driver alterations on FMI DNA CGP (4,724/7,081 Ever-Smoker & 1,470/1,666 Never-Smoker; see Figure 4)
p_{DNA}	Probability of DNA CGP assay technical success	83.5%	80%	90%	Beta(835,165)	Calculated based on experience w/ FoundationOne Heme (see Supplementary Figure 6)
$p_{RNA DNA_{s=1}}$	Probability of RNA CGP assay technical success given prior DNA CGP assay technical success	87.5%	85%	92%	Beta(875,125)	Calculated based on experience w/ FoundationOne Heme (see Supplementary Figure 6); 92% UB based on Benayed et al. ¹⁴
$selection.bias_{RNA}$	Multiplier for enrichment of fusion-positive patients in the cohort without a driver identified on DNA CGP	1	1	1.2	Gamma(10,10)	BC and LB selection bias assumed as 0 (x1 multiplier for fusion prevalence). UB based on % fusion-positive patients from MSK-IMPACT versus reflex to MSK-Fusion testing (~x1.2) [Benayed et al. ¹⁴]

BC, Base Case; FMI DNA CGP, Foundation Medicine Tissue DNA Comprehensive Genomic Profiling; LB, Lower Bound; UB, Upper Bound

Supplemental Table 4. NSCLC RTK/MAPK Oncogenic Driver Alterations

Gene	Classification	Activating Alteration Types
<i>ALK</i>	RTK	RE
<i>EGFR</i>	RTK	MUT
<i>ERBB2</i>	RTK	MUT
<i>FGFR2</i>	RTK	RE
<i>FGFR3</i>	RTK	RE
<i>MET</i>	RTK	MUT, AMP
<i>NRG1</i>	RTK-Associated	RE
<i>NTRK1</i>	RTK	RE
<i>NTRK2</i>	RTK	RE
<i>NTRK3</i>	RTK	RE
<i>RET</i>	RTK	RE
<i>ROS1</i>	RTK	RE
<i>BRAF</i>	MAPK	MUT
<i>HRAS</i>	MAPK	MUT
<i>KRAS</i>	MAPK	MUT
<i>NRAS</i>	MAPK	MUT

AMP, Amplification; MUT, Mutation (Substitutions & Short Insertions/Deletions); RE, Rearrangement; MAPK, Mitogen-Activated Protein Kinase; RTK, Receptor Tyrosine Kinase

Supplemental Table 5. Fusion Partner Genes Detected Using FMI DNA CGP & Non-FMI Assays In AACR Project GENIE v13.1.xlsx

Supplemental Table 6. Estimates From One-Way Sensitivity Analysis Corresponding to Figure 5A

Parameter	Expected % Of Patients With RNA-Only Fusion Result		
	Base Case	Min	Max
$prev_{fusions}$	1.28	0.34	2.22
θ_{DNA}		1.46	0.52
p_{DNA}		1.23	1.38
$p_{RNA DNA_{S=1}}$		1.24	1.35
$selection.bias_{RNA}$		1.28	1.54