

## **Supplementary Information**

**Copy number gains of clinically relevant genes in advanced solid tumors.**

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**Table S1:** Characteristics of patients included in the prospective cohort

<b>Histology</b>	<b>Total of patients</b>	<b>N=243 (%)</b>
<b>Lung (NSCLC)</b>	<b>74 (30.4%)</b>	
Baseline		54
Progression		20
<b>Colorectal carcinoma</b>	<b>148 (61%)</b>	
Baseline		142
Progression		6
<b>Other tumors</b>	<b>21 (8.6%)</b>	
Baseline		18
Progression		3

Other tumors include Melanoma (6 cases, three after progression to therapy), Ovary (4), GIST (5), Thyroid (2), Esophagus (2), Renal (1), and Bile Duct (1).

**Table S2:** Description of gene and exons included in the GeneRead™ QIAact Custom Solid Tumor Panel

<b>GENE</b>	<b>Exons</b>
<i>ALK</i>	22, 23, 24, 25
<i>BRAF</i>	11, 15
<i>CDK4</i>	CNV only
<i>CDK6</i>	CNV only
<i>EGFR</i>	12, 18, 19, 20, 21
<i>ERBB2</i>	8, 17, 19, 20, 21
<i>ERBB4</i>	8, 17, 19, 20, 21
<i>FGFR1</i>	CNV only
<i>IDH1</i>	4
<i>IDH2</i>	4
<i>KIT</i>	8, 9, 11, 13, 14, 17
<i>KRAS</i>	2, 3, 4
<i>MET</i>	13, 15 (METΔ14)
<i>NRAS</i>	2, 3, 4
<i>PDGFRA</i>	12, 18
<i>PIK3CA</i>	10, 21
<i>RICTOR</i>	CNV only
<i>ROS1</i>	38
<i>STK11</i>	2, 3, 4, 5, 6, 7, 8, 9
<i>TP53</i>	4, 5, 6, 7, 8, 9

**Table S3:** Results of CNVs alterations observed in the twenty cell lines included in the validation cohort. FISH analysis of *EGFR*, *ERBB2* or *MET* were performed.

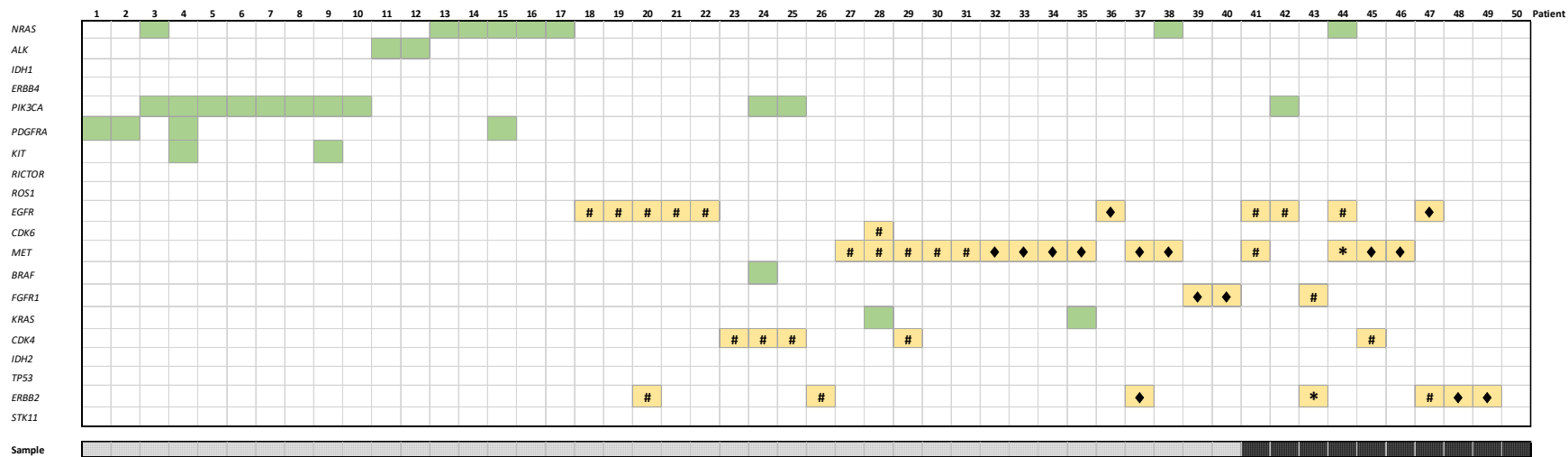
Cell lines	CNVs detected by GeneRead™ QIAact Custom Solid Tumor Panel (in house algorithm)		FISH confirmation
<b>PC9</b>	<i>EGFR</i>	<i>CKIT</i>	<i>EGFR</i> amplification
<b>PC9-ER</b>	<i>EGFR</i>	<i>CDK6</i>	<i>EGFR</i> amplification
<b>PC9-GR1</b>	<i>EGFR</i>	<i>CDK6</i>	<i>EGFR</i> amplification
<b>PC9-GR2</b>	<i>CDK6</i>	<i>RICTOR</i>	<i>EGFR</i> not amplified
<b>PC9-GR3</b>	<i>EGFR</i>	<i>CDK6</i>	<i>EGFR</i> amplification
<b>PC9-GR4</b>	<i>EGFR</i>	<i>CKIT</i>	<i>EGFR</i> amplification
<b>PC9-GR5</b>	<i>EGFR</i>	<i>CKIT</i>	<i>EGFR</i> amplification
<b>PC9-GR1-AZD1</b>	<i>CDK6</i>	<i>RICTOR</i>	<i>EGFR</i> not amplified
<b>PC9-GR1-AZD2</b>	<i>CDK6</i>	<i>RICTOR</i>	<i>EGFR</i> not amplified
<b>PC9-GR1-AZD3</b>	<i>CDK6</i>		<i>EGFR</i> not amplified
<b>PC9-GR1-AZD4</b>	<i>CDK6</i>		<i>EGFR</i> not amplified
<b>PC9-GR4-AZD1</b>	<i>CDK6</i>		<i>EGFR</i> not amplified
<b>PC9-GR4-AZD2</b>	<i>CDK6</i>		<i>EGFR</i> not amplified
<b>11-18</b>	<i>NRAS</i>	<i>CKIT</i>	<i>EGFR</i> not amplified
<b>11-18 GR1</b>	<i>NRAS</i>	<i>CKIT</i>	<i>EGFR</i> not amplified
<b>11-18 GR4</b>	<i>NRAS</i>	<i>CKIT</i>	<i>EGFR</i> not amplified
<b>EBC1</b>	<i>MET</i>		<i>MET</i> amplification
<b>Hs746T</b>	<i>MET</i>		<i>MET</i> amplification
<b>CRL-2351</b>	<i>ERBB2</i>		<i>ERBB2</i> amplification
<b>HCC827</b>	<i>EGFR</i>	<i>CDK4</i>	<i>EGFR</i> amplification

**Table S4:** Characteristics of commercial GeneRead™ QIAact Lung DNA Panel (Qiagen). The panel includes analysis of CNVs in 5 genes: *EGFR*, *ERBB2*, *MET*, *FGFR1* and *RICTOR*.

<b>Total number of variants</b>	<b>549</b>
<b>Number of unique variant positions</b>	<b>335</b>
<b>SNVs</b>	<b>320</b>
<b>MNVs</b>	<b>52</b>
<b>Insertions</b>	<b>106</b>
<b>Deletions</b>	<b>31</b>
<b>Replacements</b>	<b>40</b>
<b>CNV genes</b>	<b>5</b>

## SUPPLEMENTAL FIGURE LEGENDS

**Figure S1.** Heatmap of the FFPE NSCLC patients included in the retrospective cohort (n=50). All samples were analyzed by the GeneRead™ QIAact Custom Solid Tumor Panel using an “in-house” CNV algorithm and an alternative technique, either commercial NGS GeneRead™ QIAact Lung DNA Panel or FISH for *EGFR*, *ERBB2*, *MET* and *FGFR1* genes. In green, patients with CNVs in other genes not analyzed by FISH or commercial panel.



- ◆ CNV detected by NGS custom (in-house algorithm) and commercial NGS panel. Confirmed by FISH
- # CNV detected by NGS custom (in-house algorithm) and commercial NGS panel. FISH not done
- \* CNV detected by NGS custom (in-house algorithm) and commercial NGS panel. Discordance with FISH results
- Green CNV detected by NGS custom panel (in-house algorithm). FISH not done. CNV analysis not included in the commercial NGS panel

- Baseline
- Progression