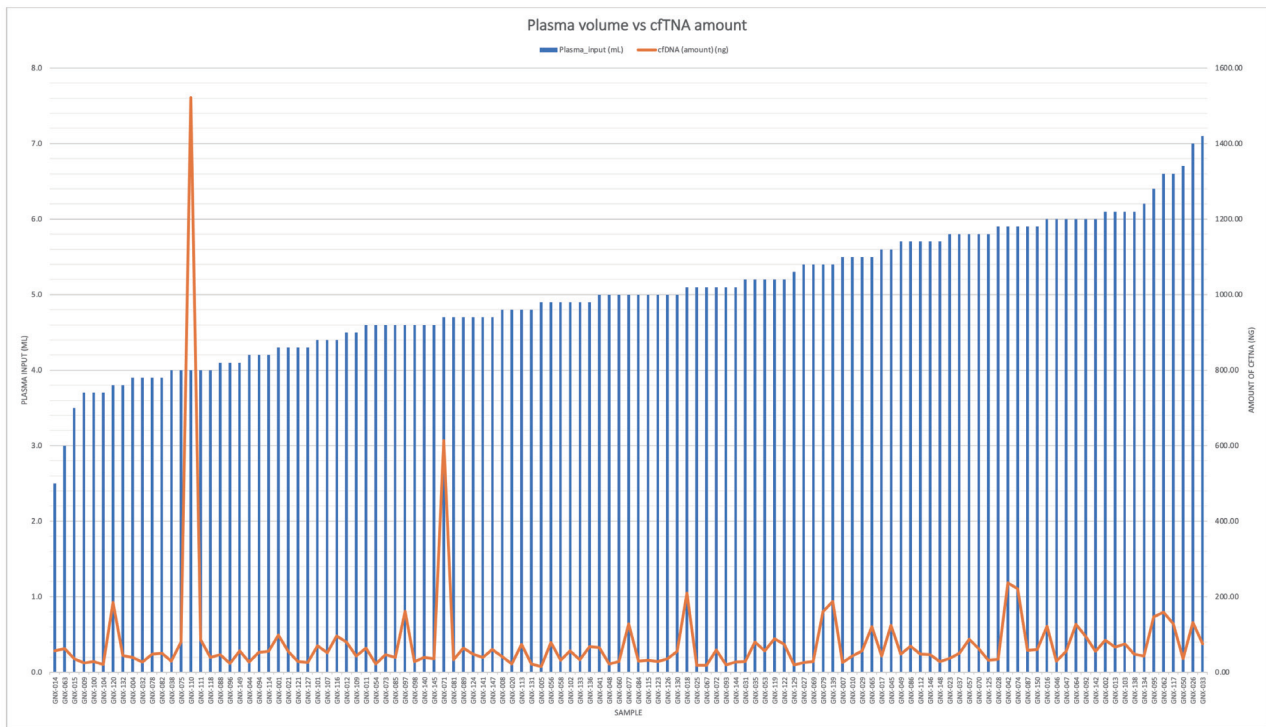


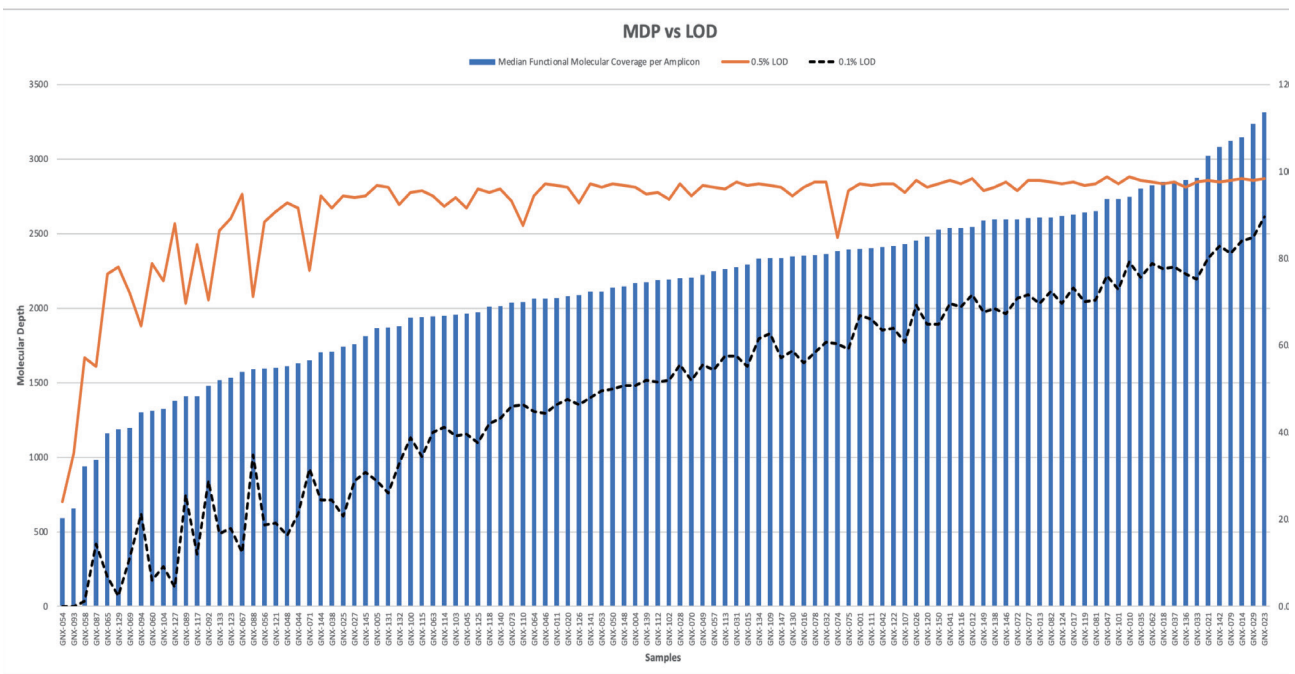
Rapid genomic profiling of circulating tumor DNA in non-small cell lung cancer using Oncomine Precision Assay with Genexus™ Integrated Sequencer

| DNA hotspots  |               |              |               |               | CNVs          |               | Inter-genetic fusions |              | Intra-genetic fusions |
|---------------|---------------|--------------|---------------|---------------|---------------|---------------|-----------------------|--------------|-----------------------|
| <i>AKT1</i>   | <i>CHEK2</i>  | <i>FGFR3</i> | <i>KIT</i>    | <i>NTRK3</i>  | <i>ALK</i>    | <i>FGFR1</i>  | <i>ALK</i>            | <i>NTRK1</i> | <i>AR</i>             |
| <i>AKT2</i>   | <i>CTNNB1</i> | <i>FGFR4</i> | <i>KRAS</i>   | <i>PDGFRA</i> | <i>AR</i>     | <i>FGFR2</i>  | <i>BRAF</i>           | <i>NTRK2</i> | <i>EGFR</i>           |
| <i>AKT3</i>   | <i>EGFR</i>   | <i>FLT3</i>  | <i>MAP2K1</i> | <i>PIK3CA</i> | <i>CD274</i>  | <i>FGFR3</i>  | <i>ESR1</i>           | <i>NTRK3</i> | <i>MET</i>            |
| <i>ALK</i>    | <i>ERBB2</i>  | <i>GNA11</i> | <i>MAP2K2</i> | <i>PTEN</i>   | <i>CDKN2A</i> | <i>KRAS</i>   | <i>FGFR1</i>          | <i>NUTM1</i> |                       |
| <i>AR</i>     | <i>ERBB3</i>  | <i>GNAQ</i>  | <i>MET</i>    | <i>RAF1</i>   | <i>EGFR</i>   | <i>MET</i>    | <i>FGFR2</i>          | <i>RET</i>   |                       |
| <i>ARAF</i>   | <i>ERBB4</i>  | <i>GNAS</i>  | <i>MTOR</i>   | <i>RET</i>    | <i>ERBB2</i>  | <i>PIK3CA</i> | <i>FGFR3</i>          | <i>ROS1</i>  |                       |
| <i>BRAF</i>   | <i>ESR1</i>   | <i>HRAS</i>  | <i>NRAS</i>   | <i>ROS1</i>   | <i>ERBB3</i>  | <i>PTEN</i>   | <i>MET</i>            | <i>RSPO2</i> |                       |
| <i>CDK4</i>   | <i>FGFR1</i>  | <i>IDH1</i>  | <i>NTRK1</i>  | <i>SMO</i>    |               |               | <i>NRG1</i>           | <i>RSPO3</i> |                       |
| <i>CDKN2A</i> | <i>FGFR2</i>  | <i>IDH2</i>  | <i>NTRK2</i>  | <i>TP53</i>   |               |               |                       |              |                       |

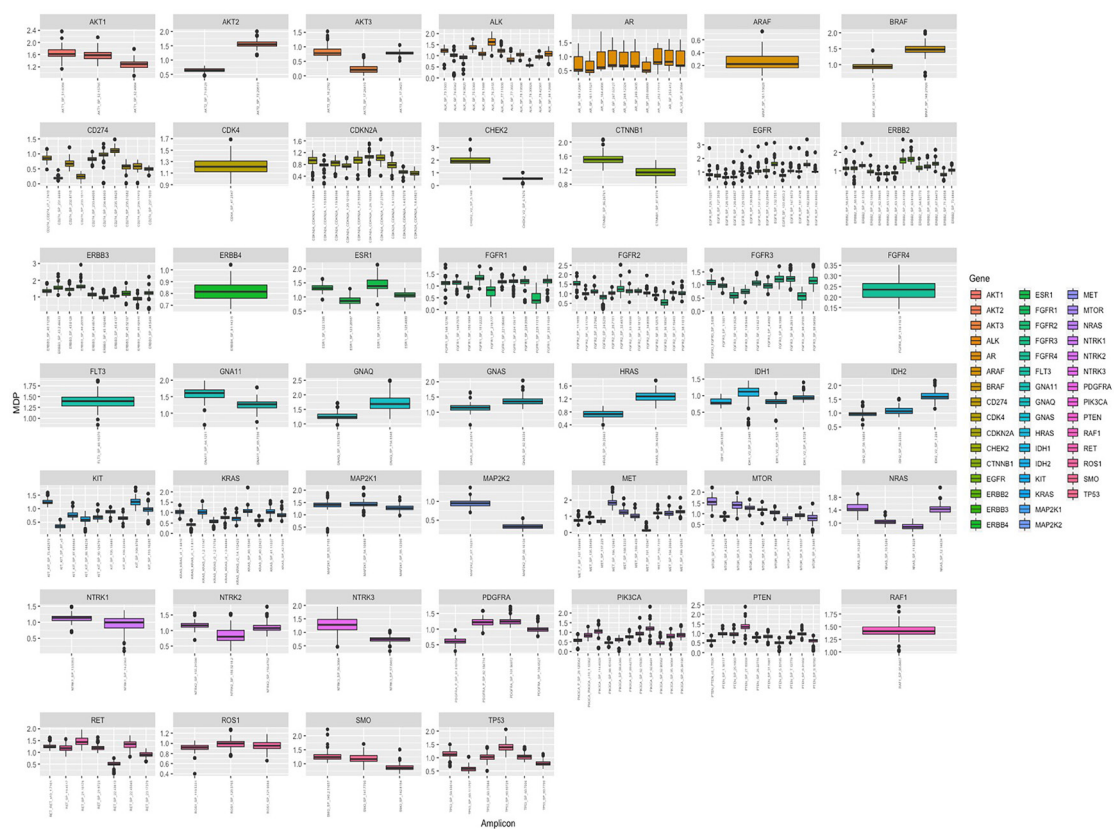
Figure S1 Oncomine Precision Assay gene list.



**Figure S2** Distribution of plasma volume and corresponding extracted cfTNA.



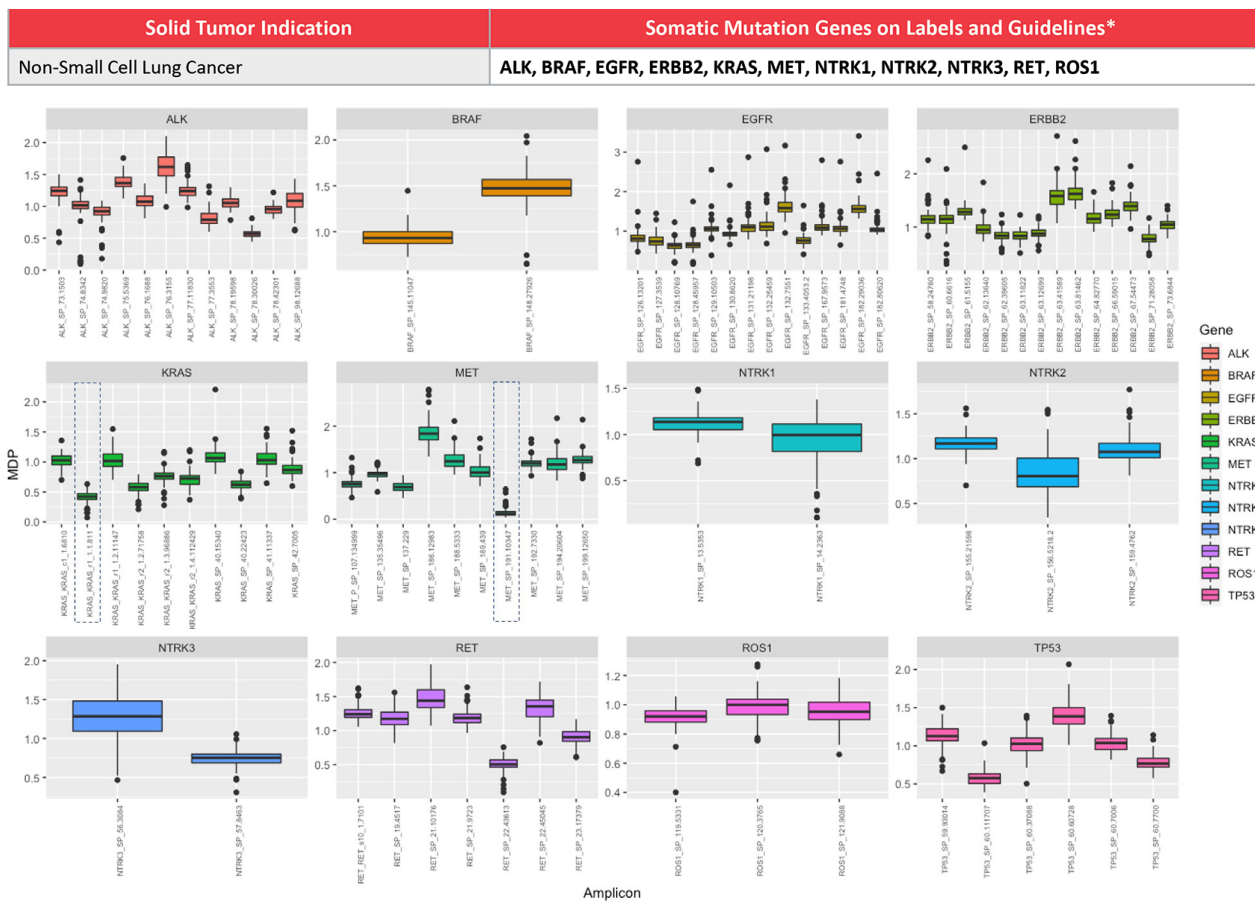
**Figure S3** Molecular depth and the percentage of amplicons at LOD of 0.5% and 0.1%.



|  |
|--|
| GENE_ID=MET;CNV_ID=MET;CNV_HS=1;HS_ONLY=1                                |
| GENE_ID=CD274;CNV_ID=CD274;CNV_HS=1;HS_ONLY=1                            |
| GENE_ID=AKT3;CNV_ID=AKT3;CNV_HS=0;HS_ONLY=1                              |
| GENE_ID=ARAF;CNV_ID=ARAF;CNV_HS=0;HS_ONLY=1                              |
| GENE_ID=FGFR4;CNV_ID=FGFR4;CNV_HS=0;HS_ONLY=1;min_fam_per_strand_cov=0   |
| GENE_ID=CD274;CNV_ID=CD274;CNV_HS=1;HS_ONLY=1                            |
| GENE_ID=MAP2K2;CNV_ID=MAP2K2;CNV_HS=0;HS_ONLY=1                          |
| GENE_ID=KIT;CNV_ID=KIT;CNV_HS=0;HS_ONLY=1                                |
| GENE_ID=FGFR1;CNV_ID=FGFR1;CNV_HS=1;HS_ONLY=1                            |
| GENE_ID=KRAS;CNV_ID=KRAS;CNV_HS=1;HS_ONLY=1                              |
| GENE_ID=PIK3CA;CNV_ID=PIK3CA;CNV_HS=1;HS_ONLY=1;min_fam_per_strand_cov=0 |
| GENE_ID=PIK3CA;CNV_ID=PIK3CA;CNV_HS=1;HS_ONLY=1                          |
| GENE_ID=CDKN2A;CNV_ID=CDKN2A;CNV_HS=1;HS_ONLY=1                          |
| GENE_ID=CD274;CNV_ID=CD274;CNV_HS=1;HS_ONLY=1                            |

- 14/250 amplicons, RMC<0.5 (under performed)
- *MET* (1), *CD274* (3), *FGFR1* (1), *FGFR4* (1), *AKT3* (1), *ARAF* (1), *MAP2K2* (1), *KIT* (1), *KRAS* (1), *PIK3CA* (2), *CDKN2A* (1)

Figure S4 Relative molecular coverage per amplicon in individual genes included in OPA.



**RMC=1.0**  
 (Coverage of the specific amplicon=median molecular coverage of sample)

**RMC<0.5**  
 (Coverage of the specific amplicon<50% of median molecular coverage of sample)

Figure S5 Relative molecular coverage per amplicon in NSCLC genes included in OPA.