**Supplementary table 1: List of Genes for targeted sequencing in the ctDNA assay**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Point Mutations/InDels (Bold = all exons; \*=all exons covered in v2.11; \*\*\*=added coverage in v2.11)** | | | | | | | | | |
| *AKT1* | *ALK* | ***APC*** | ***AR*** | *ARAF* | *ARID1A* | ***ATM\**** | ***BRAF*** | ***BRCA1*** | ***BRCA2*** |
| *CCND1* | *CCND2* | *CCNE1* | *CDH1* | ***CDK4\**** | ***CDK6\**** | ***CDK12\*\**** | *CDKN2A* | *CTNNB1* | *DDR2* |
| ***EGFR*** | ***ERBB2*** | *ESR1* | *EZH2* | *FBXW7* | *FGFR1* | *FGFR2* | *FGFR3* | *GATA3* | *GNA11* |
| *GNAQ* | *GNAS* | *HNF1A* | ***HRAS*** | *IDH1* | *IDH2* | *JAK2* | *JAK3* | ***KIT*** | ***KRAS*** |
| *MAP2K1* | *MAP2K2* | ***MAPK1*** | ***MAPK3*** | ***MET*** | *MLH1* | *MPL* | *MTOR* | ***MYC*** | *NF1* |
| *NFE2L2* | *NOTCH1* | *NPM1* | ***NRAS*** | *NTRK1* | *NTRK3* | *PDGFRA* | ***PIK3CA*** | *PTEN* | *PTPN11* |
| *RAF1* | ***RB1*** | *RET* | *RHEB* | *RHOA* | *RIT1* | *ROS1* | *SMAD4* | *SMO* | ***STK11*** |
| *TERT* | ***TP53*** | *TSC1* | *VHL* |  |  |  |  |  |  |
| **Amplifications** | | | | | | | | | |
| AR | BRAF | CCND1 | CCND2 | CCNE1 | CDK4 | CDK6 | EGFR | ERBB2 | ESR1\*\* |
| FGFR1 | FGFR2 | KIT | KRAS | MET | MYC | PDGFRA | PIK3CA | RAF1 |  |
| **Fusions** | | | | | | | | | |
| *ALK* | *FGFR2* | *FGFR3* | *NTRK1* | *RET* | *ROS1* |  |  |  |  |

**Supplementary Table 2: Percentage of CANTOS lung cancer patients assayed for ctDNA with mutations in various oncogenic driver genes detected at baseline and time closest to lung cancer diagnosis**

|  |  |  |
| --- | --- | --- |
| **Oncogenic Driver Gene** | **Baseline**  **All Arms**  **N=33** | **Closest to cancer diagnosis**  **All Arms**  **N=49** |
| *ATM* | 3.0% | 2.0% |
| *BRAF* | 3.0% | 0 |
| *CDKN2A* | 3.0% | 6.1% |
| *CTNNB1* | 0 | 4.1% |
| *EGFR* | 6.1% | 8.2% |
| *FGFR2* | 6.1% | 0 |
| *HNF1A* | 9.1% | 0 |
| *JAK2* | 0 | 4.1% |
| *KRAS* | 6.1% | 6.1% |
| *MTOR* | 0 | 2.0% |
| *NF1* | 0 | 2.0% |
| *NFE2L2* | 3.0% | 2.0% |
| *NTRK1* | 3.0% | 0 |
| *PDGFRA* | 0 | 2.0% |
| *PIK3CA* | 0 | 2.0% |
| *PTEN* | 0 | 4.1% |
| *TP53* | 54.5% | 53.1% |
| *VHL* | 3.0% | 2.0% |

**Supplementary Table 3: Percentage of CANTOS lung cancer patients assayed for ctDNA with mutations in various oncogenic driver genes detected at baseline and time closest to lung cancer diagnosis stratified by treatment**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Gene** | **Baseline** | | | | **Closest to lung cancer diagnosis** | | | | |
| **Canakinumab 300 mg**  **N=3** | **Canakinumab 150 mg**  **N=7** | **Canakinumab 50 mg**  **N=7** | **Placebo**  **N=16** | **Canakinumab 300 mg**  **N=3** | **Canakinumab 150 mg**  **N=10** | **Canakinumab 50 mg**  **N=13** | **Placebo**  **N=23** |
|
|
| *ATM* | 0 | 0 | 0 | 6.3% | 0 | 0 | 0 | 4.3% |
| *BRAF* | 0 | 0 | 0 | 6.3% | 0 | 0 | 0 | 0 |
| *CDKN2A* | 0 | 14.3% | 0 | 0 | 0 | 10.0% | 0 | 8.7% |
| *CTNNB1* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 8.7% |
| *EGFR* | 0 | 0 | 14.3% | 6.3% | 0 | 10.0% | 7.7% | 8.7% |
| *FGFR2* | 0 | 0 | 14.3% | 6.3% | 0 | 0 | 0 | 0 |
| *HNF1A* | 0 | 0 | 0 | 18.8% | 0 | 0 | 0 | 0 |
| *JAK2* | 0 | 0 | 0 | 0 | 0 | 0 | 7.7% | 4.3% |
| *KRAS* | 0 | 14.3% | 0 | 6.3% | 0 | 10.0% | 0 | 8.7% |
| *MTOR* | 0 | 0 | 0 | 0 | 33.3% | 0 | 0 | 0 |
| *NF1* | 0 | 0 | 0 | 0 | 0 | 0 | 7.7% | 0 |
| *NFE2L2* | 0 | 14.3% | 0 | 0 | 0 | 0 | 0 | 4.3% |
| *NTRK1* | 0 | 0 | 14.3% | 0 | 0 | 0 | 0 | 0 |
| *PDGFRA* | 0 | 0 | 0 | 0 | 0 | 0 | 7.7% | 0 |
| *PIK3CA* | 0 | 0 | 0 | 0 | 0 | 10.0% | 0 | 0 |
| *PTEN* | 0 | 0 | 0 | 0 | 0 | 0 | 7.7% | 4.3% |
| *TP53* | 100.0% | 42.9% | 57.1% | 50.0% | 66.7% | 50.0% | 61.5% | 47.8% |
| *VHL* | 0 | 14.3% | 0 | 0 | 0 | 10.0% | 0 | 0 |