**Supplemental Table 1:** Clinical characteristics and sequencing summary of lung cancer patient’s participants in this study

|  |  |  |
| --- | --- | --- |
| **Clinical characteristics** | **ADCA subtype (n=10)** | **SQCC subtype (n=9)** |
| **Age at diagnosis** |
|  Median (years) | 53 | 60 |
|  Range (years) | 35-69 | 41-76 |
| **Gender** |
|  Male | 8 | 8 |
|  Female | 2 | 1 |
| **Smoking status** |
|  Smoker | 7 | 8 |
|  Non-Smoker | 3 | 1 |
| **Summary statistics for exome sequencing**(On an average per tumor sample) |
| Raw data (GB) | 13.48 | 13.76 |
| Processed data (GB) | 11.98 | 12.24 |
| Aligned reads (%) | 98.87 | 97.40 |
| GC content (%) | 49.74 | 48.50 |

**Supplemental Table 2:** Variants summary identified by whole exome sequencing

|  |  |  |
| --- | --- | --- |
|  | **ADCA subtype** | **SQCC subtype** |
| * **Variants summary**
 |  |  |
| Single nucleotide variants (SNVs) | 1,157,921 | 1,076,209 |
|  Heterozygous SNVs | 266,952 | 229,733 |
|  Homozygous SNVs | 890,840 | 846,336 |
| Known variants | 616,999 | 537,980 |
| Variants rate | 1/2667 base | 1/2869 base |
|  Transition (Ts) | 1,189,997 | 1,060,798 |
|  Transversion (Tv) | 700,815 | 713,892 |
| * **Number variants by type**
 |  |  |
|  Single nucleotide polymorphisms (SNPs) | 1,066,489 | 991,400 |
|  Insertion (INS) | 38,751 | 35,799 |
|  Deletions (DEL) | 52,681 | 49,010 |
| * **Number of effects by impact**
 |  |  |
| High | 576 | 610 |
| Low | 16,425 | 21,022 |
|  Moderate | 10,748 | 14,628 |
|  Modifier | 7,180,332 | 6,696,386 |
| * **Number of effects by region**
 |  |  |
| Downstream | 272,529 | 238,006 |
| Exon | 45,083 | 50,719 |
| Gene | 64 | 2 |
| Intergenic | 673,653 | 627,209 |
| Intron | 2,862,687 | 2,692,471 |
| Splice\_site\_acceptor | 95 | 56 |
| Splice\_site\_donor | 120 | 118 |
| Splice\_site\_region | 3,071 | 4,120 |
| Transcript | 2,935,999 | 2,771,126 |
| Upstream | 390,031 | 325,737 |
| Utr\_3\_prime | 18,320 | 17,062 |
| Utr\_5\_prime | 6,429 | 6,020 |
|  **ADCA:** adenocarcinoma, **SQCC:** squamous cell carcinoma |

**Supplemental Fig. 1.** Chromatogram of validated genes via Sanger sequencing. a) *HRNR,* b) *TEKT4, c) KCNJ18, d) MPRIP, e) TBP, f) FBXo6, g) FOLR, h) GRPIN2* and *i) ESSRA*

