Supplementary Table S1. Gene range and numbers of analyzed SNPs within *PDCD1*, *CD274*, and *PDCD1LG2*

|  |  |  |  |
| --- | --- | --- | --- |
| Gene name | Gene range | Total SNP numbers | SNPs passing genotype quality controla |
| *PDCD1* | chr2: 242,792,033–242,801,060 | 344 | 36 (5) |
| *CD274* | chr9: 5,450,503–5,470,566 | 606 | 58 (9) |
| *PDCD1LG2* | chr9: 5,510,512–5,571,282 | 1928 | 137 (21) |

Abbreviations: SNP, single nucleotide polymorphism.

a Minor allele frequency > 0.01 (numbers of tagged SNPs with a PLINK pruning threshold of R2 < 0.2).

Supplementary Table S2. Correlation between identified *PDCD1LG2* SNPs and pulmonary TB history is associated with lung adenocarcinoma risk

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| SNP | Allelea | With TB | Multivariate ORb | 95%CIb | *p*-value for correlationb |
| rs2381282# | T/C | Yes | 0.553 | (0.148, 2.058) | 0.266 |
| No | 1.172 | (1.010, 1.361) |
| rs4742103# | C/T | Yes | 1.555 | (0.503, 4.811) | 0.244 |
| No | 0.788 | (0.663, 0.937) |
| rs4237162 | C/T | Yes | 0.589 | (0.214, 1.626) | 0.135 |
| No | 1.292 | (1.079, 1.548) |
| rs4742104# | C/T | Yes | 0.716 | (0.267, 1.924) | 0.766 |
| No | 0.834 | (0.716, 0.971) |
| rs12237624# | C/T | Yes | 0.247 | (0.044, 1.398) | 0.040 |
| No | 1.579 | (1.094, 2.279) |
| rs78096119# | A/G | Yes | 0.216 | (0.038, 1.240) | 0.031 |
| No | 1.533 | (1.084, 2.167) |
| rs6476988# | A/G | Yes | 1.133 | (0.390, 3.291) | 0.939 |
| No | 1.182 | (1.002, 1.395) |
| rs7857315# | T/C | Yes | 1.132 | (0.390, 3.291) | 0.924 |
| No | 1.194 | (1.012, 1.409) |
| rs10975178# | A/G | Yes | 0.929 | (0.328, 2.631) | 0.631 |
| No | 1.202 | (1.023, 1.413) |
| rs7854413 | C/T | Yes | 0.461 | (0.145, 1.469) | 0.408 |
| No | 0.760 | (0.597, 0.968) |
| rs56001683# | G/T | Yes | 0.588 | (0.182, 1.900) | 0.621 |
| No | 0.795 | (0.631, 1.002) |
| rs7858319# | C/A | Yes | 0.588 | (0.182, 1.900) | 0.622 |
| No | 0.795 | (0.629, 1.003) |

Abbreviations: CI, confidence interval; MAF, minor allele frequencies; OR, odds ratio; SNP, single nucleotide polymorphism; TB, tuberculosis.

a Coding allele/Reference allele

b Covariates of age, education levels, body mass index, first-degree family with a history of lung cancer, history of pulmonary tuberculosis infection, cooking time in years, cooking with fume extractor, and environmental tobacco smoking exposure were used as adjusted variables.

# Imputed SNP

Supplementary Table S3. Results of eQTL analyses for 12 identified *PDCD1LG2* SNPs in lung tumor and adjacent normal tissues

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  |  | Chr:Position  (GRCH37/hg19) |  | *PDCD1LG2* | | |
| SNP | Minor allele | Tissue | beta |  | *p*-value |
| rs2381282# | T | 9:5514839 | Normal | -0.148 |  | < 0.001 |
| Tumor | -0.059 |  | 0.232 |
| rs4742103# | C | 9:5526077 | Normal | 0.050 |  | 0.260 |
| Tumor | -0.048 |  | 0.373 |
| rs4237162 | C | 9:5526124 | Normal | -0.053 |  | 0.259 |
| Tumor | -0.033 |  | 0.568 |
| rs4742104# | C | 9:5532871 | Normal | -0.051 |  | 0.189 |
| Tumor | 0.032 |  | 0.500 |
| rs12237624# | C | 9:5549080 | Normal | -0.247 |  | 0.019 |
| Tumor | 0.111 |  | 0.391 |
| rs78096119# | A | 9:5555489 | Normal | -0.247 |  | 0.019 |
| Tumor | 0.111 |  | 0.391 |
| rs6476988# | A | 9:5555554 | Normal | 0.057 |  | 0.194 |
| Tumor | 0.008 |  | 0.882 |
| rs7857315# | T | 9:5555897 | Normal | 0.057 |  | 0.194 |
| Tumor | 0.008 |  | 0.882 |
| rs10975178# | A | 9:5556434 | Normal | 0.053 |  | 0.233 |
| Tumor | -0.034 |  | 0.530 |
| rs7854413 | C | 9:5557708 | Normal | 0.118 |  | 0.169 |
| Tumor | 0.041 |  | 0.691 |
| rs56001683# | G | 9:5559495 | Normal | 0.134 |  | 0.106 |
| Tumor | 0.070 |  | 0.487 |
| rs7858319# | C | 9:5564748 | Normal | 0.134 |  | 0.106 |
| Tumor | 0.070 |  | 0.487 |

Abbreviations: eQTL, expression quantitative trait loci; SNP, single nucleotide polymorphism.

#Imputed SNP