**Supplementary materials:**

**Multiple genome pattern analysis and signature gene identification for the Caucasian lung adenocarcinoma patients with different tobacco exposure patterns**

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**Materials and Methods**

**The measurement of the classification performance**

To evaluate the performance of the classification model, the prediction accuracy, specificity and sensitivity were calculated as the following equations:

In general:

* True positive (TP): correctly classified as positive samples
* False positive (FP): incorrectly classified as positive samples
* True negative (TN): correctly classified as negative samples
* False negative (FN): incorrectly classified as negative samples

In our study, nonsmokers were used as the positive samples and current-smokers were used as the negative samples. Sensitivity, SN, is the proportion of nonsmokers that are correctly classified as the nonsmokers. Specificity, SP, is the proportion of current-smokers which are correctly classified as the current-smokers. Accuracy, ACC, is the proportion of samples which are correctly classified.

There are four types of smoking history in TCGA dataset: current-smoker, reformed less than 15 years, reformed longer than 15 years and lifelong nonsmoker. On the contrary, there are only three types of smoking history in EDRN: current-smoker, former-smoker and lifelong nonsmoker. For SPORE data, only ever or never smoking status is available. Due to the different types in these datasets and the arbitrary cutoff and definition of smoking history, in order to identify the most significant signature genes, only typical samples *i.e.* current-smokers and lifelong nonsmokers in TCGA were used as training samples in our study. EDRN (current-smokers and lifelong nonsmokers) and SPORE (ever/never smokers) data were used as independent validation samples.

**Table S1. The list of experimental proved important genes**

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| No. | Gene | Location | No. | Gene | Location | No. | Gene | Location | No. | Gene | Location |
| 1 | GSTM1[[1](#_ENREF_1)] | 1p13.3 | 7 | EGFR[[2](#_ENREF_2)] | 7p12 | 13 | MGMT[[3](#_ENREF_3)] | 10q26 | 19 | MEK1[[4](#_ENREF_4)] | 15q22.1-q22.33 |
| 2 | LCK[[5](#_ENREF_5)] | 1p34.3 | 8 | MET[[6](#_ENREF_6)] | 7q31 | 14 | KRAS[[7](#_ENREF_7)] | 12p12.1 | 20 | CHRNA5[[8](#_ENREF_8)] | 15q24 |
| 3 | ALK[[2](#_ENREF_2)] | 2p23 | 9 | AKR1B10[[9](#_ENREF_9)] | 7q33 | 15 | ERBB3[[10](#_ENREF_10)] | 12q13 | 21 | MMD[[11](#_ENREF_11)] | 17q |
| 4 | STAT1[[12](#_ENREF_12)] | 2q32.2 | 10 | BRAF[[13](#_ENREF_13)] | 7q34 | 16 | MDM2[[14](#_ENREF_14)] | 12q14.3-q15 | 22 | XRCC1[[15](#_ENREF_15)] | 19q13.2 |
| 5 | FHIT[[16](#_ENREF_16)] | 3p14.2 | 11 | NAT2[[17](#_ENREF_17)] | 8p22 | 17 | DUSP6[[18](#_ENREF_18)] | 12q22-q23 | 23 | ERCC2[[15](#_ENREF_15)] | 19q13.3 |
| 6 | ROS-1[[19](#_ENREF_19)] | 6q22 | 12 | RET[[19](#_ENREF_19)] | 10q11.2 | 18 | OLFM4[[20](#_ENREF_20)] | 13q21.1 | 24 | RASSF2[[21](#_ENREF_21)] | 20p13 |

**Table S2. The list of 43 GE signature genes\***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| No. | Gene | Location | Median Value | |
| Never Smokers | Current Smokers |
| 1 | BCL2L15 | 1p13.2 | 8.713 | 7.265 |
| 2 | GSTM1 | 1p13.3 | 7.727 | 1.546 |
| 3 | ZYG11A | 1p32.3 | 4.147 | 5.557 |
| 4 | HPDL | 1p34.1 | 3.255 | 4.998 |
| 5 | C1orf61 | 1q22 | 1.352 | 2.993 |
| 6 | FAM72A | 1q32.1 | 3.178 | 4.962 |
| 7 | GNG4 | 1q42.3 | 4.048 | 5.319 |
| 8 | ALK | 2p23 | 2.317 | 2.059 |
| 9 | CGREF1 | 2p23.3 | 5.100 | 6.926 |
| 10 | FHIT | 3p14.2 | 5.084 | 5.054 |
| 11 | GPR15 | 3q11.2-q13.1 | 0.922 | 3.986 |
| 12 | HHLA2 | 3q13.13 | 7.629 | 4.218 |
| 13 | UCHL1 | 4p14 | 7.461 | 9.535 |
| 14 | FGB | 4q28 | 1.814 | 5.777 |
| 15 | FGG | 4q28 | 7.516 | 9.828 |
| 16 | HPGD | 4q34-q35 | 10.935 | 9.535 |
| 17 | UGT3A1 | 5p13.2 | 0 | 0 |
| 18 | PCSK1 | 5q15-q21 | 2.248 | 3.727 |
| 19 | EGFR | 7p12 | 10.409 | 10.048 |
| 20 | WBSCR17 | 7q11.23 | 6.424 | 4.661 |
| 21 | AKR1B10 | 7q33 | 4.866 | 4.279 |
| 22 | BARX1 | 9q12 | 2.003 | 4.068 |
| 23 | MCM10 | 10p13 | 5.636 | 7.641 |
| 24 | MSMB | 10q11.2 | 3.229 | 5.218 |
| 25 | RET | 10q11.2 | 4.650 | 4.442 |
| 26 | MGMT | 10q26 | 8.089 | 8.360 |
| 27 | CALCA | 11p15.2 | 0.700 | 1.562 |
| 28 | B4GALNT4 | 11p15.5 | 4.570 | 7.014 |
| 29 | RCOR2 | 11q13.1 | 4.707 | 6.272 |
| 30 | KRAS | 12p12.1 | 10.220 | 10.348 |
| 31 | ERBB3 | 12q13 | 12.093 | 12.168 |
| 32 | DDN | 12q13.12 | 1.814 | 3.531 |
| 33 | MDM2 | 12q14.3-q15 | 10.914 | 10.768 |
| 34 | POU4F1 | 13q31.1 | 0.499 | 3.241 |
| 35 | ERN2 | 16p12.2 | 7.562 | 5.426 |
| 36 | YBX2 | 17p13.1 | 2.125 | 5.960 |
| 37 | DLL3 | 19q13 | 0.903 | 3.946 |
| 38 | LGALS4 | 19q13.2 | 5.170 | 3.407 |
| 39 | PLUNC | 20q11.2 | 6.367 | 8.314 |
| 40 | CYP24A1 | 20q13 | 6.781 | 9.092 |
| 41 | MYBL2 | 20q13.1 | 8.539 | 10.085 |
| 42 | UBE2C | 20q13.12 | 7.885 | 9.494 |
| 43 | PRAME | 22q11.22 | 2.856 | 7.054 |

\* genes are sorted according to their contribution to the classification model.

**Table S3. The list of 48 methylation signature genes\***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| No. | Gene | Location | Median Value | |
| Never Smokers | Current Smokers |
| 1 | GSTM1 | 1p13.3 | 0.354 | 0.430 |
| 2 | LCK | 1p34.3 | 0.616 | 0.602 |
| 3 | C1orf64 | 1p36.13 | 0.771 | 0.690 |
| 4 | CA6 | 1p36.2 | 0.804 | 0.759 |
| 5 | ANKRD45 | 1q25.1 | 0.404 | 0.483 |
| 6 | GNLY | 2p11.2 | 0.775 | 0.746 |
| 7 | ALK | 2p23 | 0.121 | 0.131 |
| 8 | PAX8 | 2q12-q14 | 0.773 | 0.725 |
| 9 | STAT1 | 2q32.2 | 0.093 | 0.087 |
| 10 | HTR2B | 2q36.3-q37.1 | 0.656 | 0.724 |
| 11 | FHIT | 3p14.2 | 0.484 | 0.469 |
| 12 | UCHL1 | 4p14 | 0.383 | 0.314 |
| 13 | PCDHB11 | 5q31 | 0.416 | 0.359 |
| 14 | LEAP2 | 5q31.1 | 0.645 | 0.695 |
| 15 | TCP11 | 6p21.3-p21.2 | 0.702 | 0.662 |
| 16 | EGFR | 7p12 | 0.121 | 0.126 |
| 17 | WBSCR17 | 7q11.23 | 0.212 | 0.320 |
| 18 | MET | 7q31 | 0.182 | 0.179 |
| 19 | C7orf45 | 7q32.2 | 0.857 | 0.887 |
| 20 | AKR1B10 | 7q33 | 0.733 | 0.708 |
| 21 | NAT2 | 8p22 | 0.901 | 0.898 |
| 22 | ZNF572 | 8q24.13 | 0.177 | 0.145 |
| 23 | GLDC | 9p22 | 0.116 | 0.181 |
| 24 | SPAG6 | 10p12.2 | 0.358 | 0.434 |
| 25 | CALML3 | 10p15.1 | 0.775 | 0.730 |
| 26 | PPYR1 | 10q11.2 | 0.415 | 0.480 |
| 27 | RET | 10q11.2 | 0.187 | 0.195 |
| 28 | SRGN | 10q22.1 | 0.248 | 0.398 |
| 29 | MGMT | 10q26 | 0.493 | 0.481 |
| 30 | B4GALNT4 | 11p15.5 | 0.169 | 0.164 |
| 31 | GPR152 | 11q13.1 | 0.799 | 0.746 |
| 32 | KRAS | 12p12.1 | 0.094 | 0.087 |
| 33 | ERBB3 | 12q13 | 0.178 | 0.174 |
| 34 | GTSF1 | 12q13.2 | 0.757 | 0.677 |
| 35 | MDM2 | 12q14.3-q15 | 0.043 | 0.042 |
| 36 | DUSP6 | 12q22-q23 | 0.052 | 0.053 |
| 37 | OLFM4 | 13q21.1 | 0.529 | 0.451 |
| 38 | RNASE6 | 14q11.2 | 0.325 | 0.414 |
| 39 | CHRNA5 | 15q24 | 0.209 | 0.209 |
| 40 | MMP25 | 16p13.3 | 0.081 | 0.139 |
| 41 | CYBA | 16q24 | 0.190 | 0.237 |
| 42 | FGF11 | 17p13.1 | 0.507 | 0.465 |
| 43 | MMD | 17q | 0.227 | 0.223 |
| 44 | ZFP28 | 19q13.43 | 0.165 | 0.091 |
| 45 | CPXM1 | 20p13-p12.3 | 0.233 | 0.319 |
| 46 | PXMP4 | 20q11.22 | 0.195 | 0.266 |
| 47 | CD40 | 20q12-q13.2 | 0.192 | 0.268 |
| 48 | SULT4A1 | 22q13.2-q13.31 | 0.311 | 0.290 |

\* genes are sorted according to their contribution to the classification model.

**Table S4. The list of 75 CNV signature genes\***

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Gene | Location | Current smoker | Never smoker | Gene | Location | Current smoker | Never smoker |
| RET | 10q11.2 | 2.0441 | 1.9317 | LCA5L | 21q22.2 | 1.9687 | 2.1224 |
| ALK | 2p23 | 2.101 | 2.0218 | HMGN1 | 21q22.3|21q22.2 | 1.9695 | 2.1224 |
| LCK | 1p34.3 | 2.0082 | 2.1125 | WRB | 21q22.3 | 1.9677 | 2.1224 |
| RASSF2 | 20p13 | 2.0519 | 1.9471 | EFCAB6 | 22q13.1-q13.33 | 1.8891 | 1.9791 |
| STAT1 | 2q32.2 | 2.0906 | 2.037 | GDI2 | 10p15 | 2.0514 | 1.9339 |
| KRAS | 12p12.1 | 2.171 | 2.0627 | ARFGAP3 | 22q13.2-q13.3 | 1.8912 | 1.9794 |
| MGMT | 10q26 | 1.9714 | 1.8937 | PACSIN2 | 22q13.2 | 1.8893 | 1.9794 |
| MET | 7q31 | 2.2231 | 2.1386 | GNB1 | 1p36.33 | 2.0063 | 2.1228 |
| GSTM1 | 1p13.3 | 2.0859 | 2.1693 | DYRK1A | 21q22.13 | 1.9692 | 2.0907 |
| MDM2 | 12q14.3-q15 | 2.2075 | 2.5284 | DSCR3 | 21q22.2 | 1.9693 | 2.0907 |
| TSPAN17 | 5q35.3 | 1.9796 | 2.1148 | CPNE3 | 8q21.3 | 2.3434 | 2.1682 |
| UIMC1 | 5q35.2 | 1.9786 | 2.1148 | CHRAC1 | 8q24.3 | 2.4062 | 2.2497 |
| DDX41 | 5q35.3 | 1.9759 | 2.1023 | GTPBP4 | 10p15-p14 | 2.0379 | 1.9294 |
| PRELID1 | 5q35.3 | 1.9784 | 2.1013 | TRAPPC9 | 8q24.3 | 2.3727 | 2.2497 |
| ATG12 | 5q21-q22 | 1.8957 | 2.0293 | ATAD2 | 8q24.13 | 2.4438 | 2.2841 |
| COX7C | 5q14 | 1.895 | 2.0697 | STAU1 | 20q13.1 | 2.1446 | 2.062 |
| PGGT1B | 5q22.3 | 1.8994 | 2.0295 | OSTM1 | 6q21 | 1.8006 | 1.9566 |
| FEM1C | 5q22 | 1.9011 | 2.0293 | SEC63 | 6q21 | 1.8022 | 1.9566 |
| TAF7 | 5q31 | 1.9261 | 2.0329 | CD164 | 6q21 | 1.8044 | 1.9585 |
| DNAJA3 | 16p13.3 | 2.0561 | 2.192 | FIG4 | 6q21 | 1.8035 | 1.9585 |
| NMRAL1 | 16p13.3 | 2.0561 | 2.192 | SMPD2 | 6q21 | 1.8072 | 1.9585 |
| TMEM167A | 5q14.2 | 1.9027 | 2.0587 | ZBTB24 | 6q21 | 1.8067 | 1.9585 |
| MGRN1 | 16p13.3 | 2.0585 | 2.2007 | IMPACT | 18q11.2-q12.1 | 2.0188 | 1.9105 |
| RAB18 | 10p12.1 | 2.0792 | 1.9404 | ZFP64 | 20q13.2 | 2.1829 | 2.1053 |
| ABI1 | 10p11.2 | 2.0724 | 1.9398 | MRPS30 | 5q11 | 2.4329 | 2.3092 |
| YME1L1 | 10p14 | 2.0757 | 1.9398 | NUP155 | 5p13.1 | 2.5062 | 2.3741 |
| WAC | 10p12.1 | 2.0805 | 1.9404 | PANK4 | 1p36.32 | 2.0142 | 2.1231 |
| UBR5 | 8q22 | 2.3961 | 2.1848 | PEX10 | 1p36.32 | 2.0127 | 2.1231 |
| N4BP1 | 16q12.1 | 2.0035 | 2.1744 | TMEM68 | 8q12.1 | 2.2637 | 2.2064 |
| ICMT | 1p36.21 | 1.998 | 2.1299 | PVT1 | 8q24 | 2.5434 | 2.3937 |
| CAMTA1 | 1p36.31 | 1.9995 | 2.1227 | SPATA7 | 14q31.3 | 1.9974 | 2.1381 |
| INTS8 | 8q22.1 | 2.3634 | 2.167 | TTC8 | 14q31.3 | 2.0015 | 2.1972 |
| BRD7 | 16q12 | 1.9897 | 2.154 | TPD52 | 8q21 | 2.4283 | 2.323 |
| C8orf37 | 8q22.1 | 2.3605 | 2.1766 | ZBTB10 | 8q21.13 | 2.432 | 2.323 |
| PLEKHF2 | 8q22.1 | 2.3634 | 2.1766 | TRAPPC6B | 14q21.1 | 2.2548 | 2.2152 |
| SH3BGR | 21q22.3 | 1.9681 | 2.1224 | TBC1D15 | 12q21.1 | 2.0764 | 2.1976 |
| ZFAT | 8q24.22 | 2.4229 | 2.2267 | RAB21 | 12q21.1 | 2.077 | 2.1976 |
| MLLT10 | 10p12 | 2.0481 | 1.9358 |  |  |  |  |

\* genes are sorted according to their contribution to the classification model.

**Table S5. KEGG pathways analysis for GE signatures**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| No. | KEGG ID | Pathways | *p*-value | Genes |
| 1 | hsa05219 | Bladder cancer | 0.0057 | EGFR, KRAS, MDM2 |
| 2 | hsa05223 | Non-small cell lung cancer | 0.0093 | EGFR, FHIT, KRAS |
| 3 | hsa05214 | Glioma 3 | 0.0125 | EGFR, KRAS, MDM2 |
| 4 | hsa04144 | Endocytosis | 0.0126 | EGFR, RET, ERBB3, MDM2 |
| 5 | hsa05218 | Melanoma | 0.0157 | EGFR, KRAS, MDM2 |
| 6 | hsa04012 | ErbB signaling pathway | 0.0230 | EGFR, KRAS, ERBB3 |
| 7 | hsa05215 | Prostate cancer | 0.0240 | EGFR, KRAS, MDM2 |

**Table S6. KEGG pathways analysis for ME signatures**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| No. | KEGG ID | Pathways | *p*-value | Genes |
| 1 | hsa05218 | Melanoma | 2.529E-4 | EGFR, KRAS, MET, FGF11, MDM2 |
| 2 | hsa05200 | Pathways in cancer | 4.339E-4 | EGFR, RET, KRAS, MET, PAX8, FGF11, MDM2, STAT1 |
| 3 | hsa05214 | Glioma | 0.0027 | EGFR, KRAS, CALML3, MDM2 |
| 4 | hsa05216 | Thyroid cancer | 0.0073 | RET, KRAS, PAX8 |
| 5 | hsa04144 | Endocytosis | 0.0086 | EGFR, RET, ERBB3, MET, MDM2 |
| 6 | hsa05219 | Bladder cancer | 0.0151 | EGFR, KRAS, MDM2 |
| 7 | hsa05223 | Non-small cell lung cancer | 0.0243 | EGFR, FHIT, KRAS |
| 8 | hsa05212 | Pancreatic cancer | 0.0413 | EGFR, KRAS, STAT1 |
| 9 | hsa04020 | Calcium signaling pathway | 0.0434 | EGFR, CALML3, ERBB3, HTR2B |

**Table S7. KEGG pathways analysis for CNV signatures**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **No.** | **KEGG ID** | **Pathways** | ***p*-value** | **Genes** |
| 1 | hsa05200 | Pathways in cancer | 0.0017 | MDM2, MET, RET, STAT1, KRAS |
| 2 | hsa04144 | Endocytosis | 0.0018 | ARFGAP3, MDM2, MET, RET |
| 3 | hsa05218 | Melanoma | 0.0020 | MDM2, MET, KRAS |
| 4 | hsa04120 | Ubiquitin mediated proteolysis | 0.0068 | MDM2, MGRN1, UBR5 |
| 5 | hsa05216 | Thyroid cancer | 0.0088 | RET, KRAS |

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