**Supplementary Tables**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Supplementary Table 1:** Primer and probe sequences for methylation analysis of *SOX17* by qMSP. | | | | | |
| **Gene** | **Forward (5' - 3')** | **Reverse (5' - 3')** | **Probe (5' - 3')** | **Amplicon size (bp)** | |
| *SOX17* | TTTGGGCGCGGGGTCG | CCCACGTCCCAATCCAACC | DFO - CCC {C}T{T} ACC C{C}T CCC - BHQ2 | 57 | |
| Locked nuclear acids are indicated by {base}. qMSP = quantitative methylation-specific PCR. | | | |  |  |

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Supplementary Table 2**: Parameter estimates of DNA methylation levels of *CDO1,* *SOX17* and *TAC1* measured in NSCLC patients (n=23) and controls (n=60) according to the fitted linear mixed model. | | | | | | | | | | | |
|  | *CDO1* | | | *SOX17* | | | | *TAC1* | | | |
| **Fixed effects** | **Estimates** | **95%-CI** | ***p*** |  | **Estimates** | **95%-CI** | ***p*** |  | **Estimates** | **95%-CI** | ***p*** |
| (Intercept) | 0·76 | (0·48, 1·04) |  |  | 1·41 | (1·24, 1·59) |  |  | 0·44 | (0·35, 0·53) |  |
| casecontrol [control] | -0·05 | (-0·34, 0·23) | 0·711 |  | -0·26 | (-0·50, -0·03) | **0·030** |  | -0·14 | (-0·28, 0·01) | 0·059 |
| sex [male]\* | 0·30 | (0·03, 0·57) | **0·031** |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |
| **Random Effects** |  |  |  |  |  |  |  |  |  |  |  |
| σ2 | 0·19 |  |  |  | 0·24 |  |  |  | 0·17 |  |  |
| τ00 subject | 0·27 |  |  |  | 0·14 |  |  |  | 0·02 |  |  |
| ICC | 0·59 |  |  |  | 0·38 |  |  |  | 0·10 |  |  |
| N subject | 83 |  |  |  | 83 |  |  |  | 83 |  |  |
| Observations\*\* | 193 |  |  |  | 193 |  |  |  | 193 |  |  |
| DNA methylation level estimates are presented as square root transformed ct ratios. σ2 = within-subject variability; τ00 = between-subject variability; ICC = Intraclass Correlation Coefficient; NSCLC = non-small cell lung cancer. | | | | | | | | | | | |
| \*Only *CDO1* methylation levels were corrected for sex, following backward stepwise selection.  \*\*Five urine samples of patients were excluded from the analysis based on an *ACTB* Ct value of  ≥ 32. | | | | | | | | | | | |