

| Discovery cohort | Dataset | N | Age (mean±SD) | Male/Female | FTND (mean±SD) | TTFC (mean±SD) |
|--------------------|-----------------------|--------|-------------------|---------------------|------------------|------------------|
| 1 | SAGE | 2,042 | 37.89±8.96 | 906/1,140 | 3.11±3.28 | 1.25±1.30 |
| 2 | SC | 2,479 | 40.73±10.18 | 1,076/1,403 | 5.48±2.37 | 1.57±0.86 |
| 3 | MGS | 2,496 | 52.25±16.10 | 939/917 | 3.28±2.92 | 1.33±1.19 |
| 4 | COPDGene1 | 320 | 57.83±7.96 | 159/134 | 4.79±2.53 | 1.90±1.02 |
| 5 | ISIB | 299 | 41.46±9.38 | 193/106 | 6.69±2.10 | 2.75±0.47 |
| 6 | CIDR370v1 | 574 | 44.80±8.24 | 114/52 | 2.92±1.95 | 0.30±0.70 |
| | CIDR370v3 | 598 | 46.03±10.13 | 151/99 | 3.45±2.19 | 0.54±0.94 |
| 7 | CIDRc3 | 1,710 | 36.14±8.90 | 994/716 | - | 2.20±1.08 |
| | CIDRc4 | 477 | 40.25±14.89 | 189/288 | - | 0.09±0.44 |
| 8 | EAGLE * | 3,051 | 66.34±6.88 | 2,538/477 | 3.84±2.64 | * |
| 9 | ALSPAC | 161 | 46.16±4.74 | 0/161 | 3.20±2.17 | 2.48±1.01 |
| 10 | AUTW | 190 | 26.81±3.42 | 83/107 | 3.46±2.62 | 1.29±1.12 |
| 11 | CEDAR | 294 | 23.65±5.13 | 201/93 | 1.41±2.36 | 0.65±1.11 |
| 12 | FTC1 | 1,563 | 44.86±15.17 | 906/657 | 3.36±2.33 | 1.37±1.01 |
| | FTC2 | 811 | 47.88±16.34 | 408/403 | 2.87±2.42 | 1.19±1.05 |
| 13 | NTR | 2,436 | 48.61±14.44 | 992/1,444 | 2.73±2.40 | 1.11±1.06 |
| 14 | GCD | 2,117 | 37.64±10.31 | 1,246/871 | 2.39±0.91 | 2.39±0.91 |
| | All samples | | 45.97±9.77 | 11,095/9,068 | 3.53±2.33 | 1.40±0.95 |
| | FTND Discovery Sample | 19,431 | | | | |
| | TTFC Discovery Sample | 18,567 | | | | |
| Replication cohort | Dataset | N | Age (mean±SD) | Male/Female | FTND (mean±SD) | TTFC (mean±SD) |
| 1 | VTSABD | 270 | 26.37±2.55 | 107/163 | 2.20±2.15 | 1.01±1.22 |
| 2 | COPDGene2 | 2,254 | 57.47±7.83 | 1,201/1,053 | 4.83±2.40 | 1.99±1.00 |
| 3 | S4S | 711 | 19.38±1.33 | 368/343 | 2.14±2.12 | 0.93±0.96 |
| 4 | PNAT2 | 934 | 46.2±11.2 | 544/390 | 5.34±1.99 | 2.07±0.81 |
| 5 | EAGLE * | 3,051 | 66.34±6.88 | 2,538/477 | * | 1.50±0.88 |
| 6 | FINRISK | 2,841 | 49.84±13.3 | 1,580/1,261 | 2.77±2.48 | 1.21±1.02 |

| | | | | | |
|-----------------------|--------|-------------------|--------------------|------------------|------------------|
| All samples | | 44.27±7.18 | 6,338/3,687 | 2.46±2.23 | 1.45±0.98 |
| FTND Replication | 7,010 | | | | |
| TTFC Discovery Sample | 10,061 | | | | |

FTND, Fagerström test for nicotine dependence; TTFC, time to smoke first cigarette in the morning;

* EAGLE samples were used in discovery analyses of FTND, and were used in replication analyses of TTFC;
SD, standard deviation.

| Genotype Array | # Genotyped SNPs | Imputation | Imputation QC |
|--|------------------|---------------|--------------------------------------|
| ILMN_Human-1 | 1,072,389 | IMPUTE2 | INFO ≥0.4 |
| HumanOmni2.5 | 2,379,515 | IMPUTE2 | INFO ≥0.4 |
| Affy 6.0 | 808,931 | IMPUTE2 | INFO ≥0.4 |
| HumanOmni1-Quad_v1-0_B | 1,051,295 | IMPUTE2 | INFO ≥0.4 |
| Affy 6.0 | 808,931 | IMPUTE2 | INFO ≥0.4 |
| HumanCNV370v1_C | 370,435 | IMPUTE2 | INFO ≥0.4 |
| HumanCNV370-Quadv3_C | 373,428 | IMPUTE2 | INFO ≥0.4 |
| Human660W-Quad_v1_C | 655,248 | IMPUTE2 | INFO ≥0.4 |
| Human610-Quadv1_B | 620,932 | IMPUTE2 | INFO ≥0.4 |
| 610QUAD | 515,922 | IMPUTE2 | INFO ≥0.4 |
| Illumina Human Hap 550-Quad | 557,124 | MACH 1.0.16 | INFO ≥0.4 |
| Illumina 610 Quad | 273,180 | IMPUTE2 | INFO ≥0.4 |
| Illumina Human 660W Quad | 519,138 | IMPUTE2 | INFO ≥0.4 |
| Illumina Human670-QuadCustom BeadChip | 528,415 | IMPUTE2 | INFO ≥0.4 |
| Illumina HumanCoreExome-12v1-0 BeadChip | 340,330 | IMPUTE2 | INFO ≥0.4 |
| Affymetrix 6.0, Perlegen-Affymetrix 5.0, Illumina 660, Illumina 1M, Illumina 370K | 1,099,846 | MACH/Minimach | R ² Mach ≥0.4 & INFO ≥0.6 |
| HumanOmni1-Quad_v1-0_B | 1,014,563 | IMPUTE2 | INFO ≥0.5 |

| Genotype Array | # Genotyped SNPs | Imputation | Imputation QC |
|---|---|------------|---------------|
| Illumina Human 660W Quad | 497,153 | IMPUTE2 | INFO ≥0.4 |
| HumanOmniExpress | 639,431 | IMPUTE2 | NONE |
| Affymetrix Biobank array | 628,679 | IMPUTE2 | INFO ≥0.4 |
| Illumina HumanOmniExpressExome-8v1.2 | 958,497 | IMPUTE2 | INFO ≥0.4 |
| 610QUAD | 515,922 | IMPUTE2 | INFO ≥0.4 |
| | Depending on the batch: 331 007, 551 | | |
| Illumina 610-quad BeadChip/ Illumina Human Core Exome BeadChip <i>in several batches</i> | 322 , 538 448, 323 784, 317 570, 536 | | |
| | 039, 612 239 | IMPUTE2 | INFO>0.8 |

| Sample Description | Reference |
|--|-----------|
| Smoking, cocaine and alcohol addiction | 1,2,3 |
| Smoking cessation | 4, 5 |
| Molecular genetic study of schizophrenia | 6 |
| Genetic study of COPD | 7 |
| Alcohol addiction | 8 |
| Heroin addiction | 9 |
| Heroin addiction | 9 |
| Heroin addiction | 9 |
| Heroin addiction | 9 |
| Genetic study of lung cancer | 10 |
| Birth Cohort | 11,12 |
| Brisbane Longitudinal Twin Sample, 19UP Project | 21 |
| longitudinal study of substance abuse risk | 26 |
| FinnTwin12 and 'Nicotine Addiction Genetics' subcohorts from the Finnish Twin Cohort | 13-15 |
| FinnTwin12, FinnTwin16 and 'Nicotine Addiction Genetics' subcohorts from the Finnish Twin Cohort | 13-15 |
| Netherlands Twin Register longitudinal surveys | 16-19 |
| Cocaine, opioid, and alcohol addiction | 20 |

| Sample Description | Reference |
|--|-----------|
| Virginia Twin Study of Adolescent Behavioral Development | 23, 24 |
| Genetic study of COPD | 7 |
| Study of genetic and environmental influences on substance use and emotional health at a large US university | 25 |
| Clinical sample | 22 |
| Genetic study of lung cancer | 10 |
| The National FINRISK study | 27 |

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