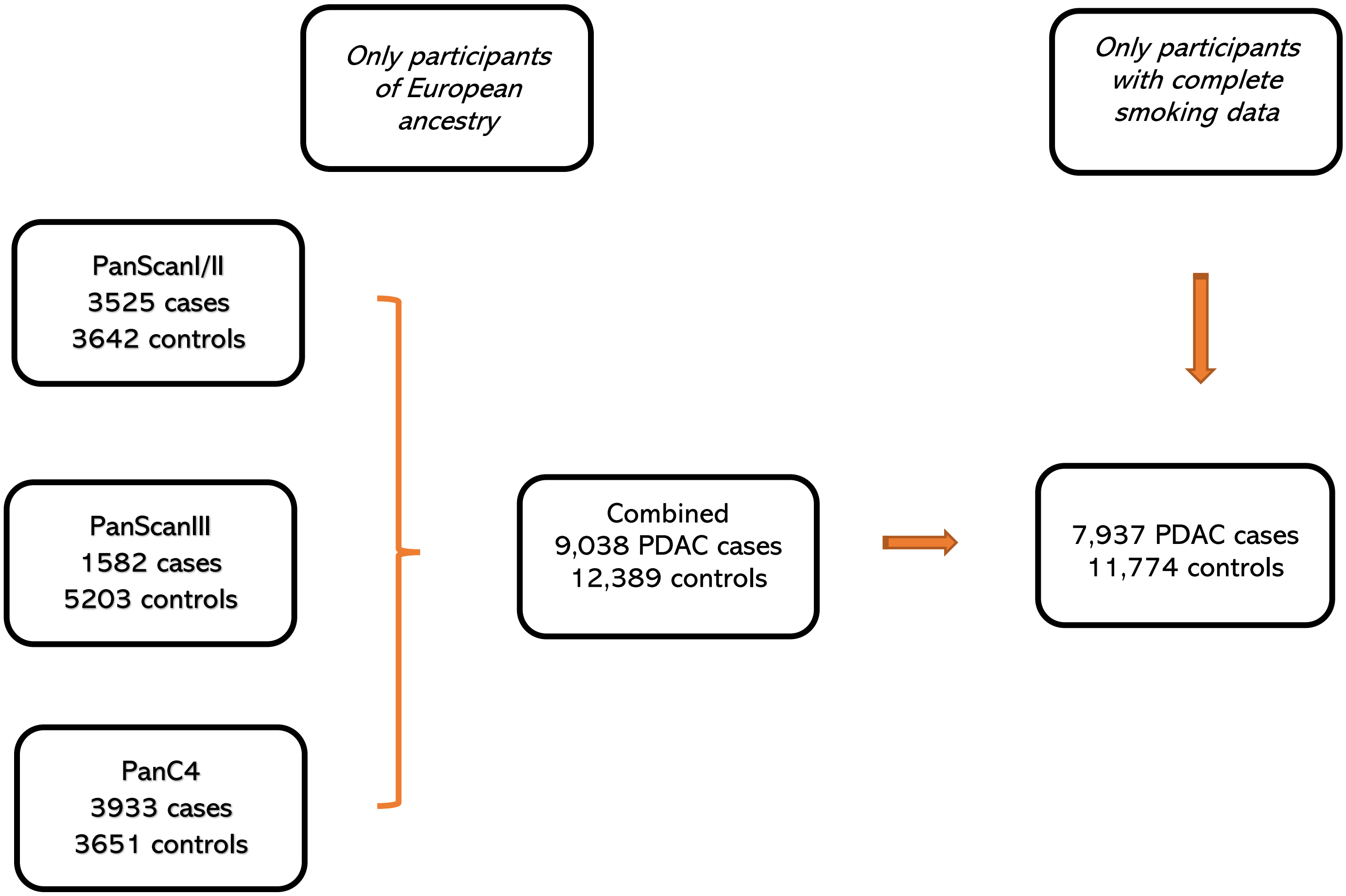
Supplemental Figure 1. Flowchart for participant selection for analytic data set.



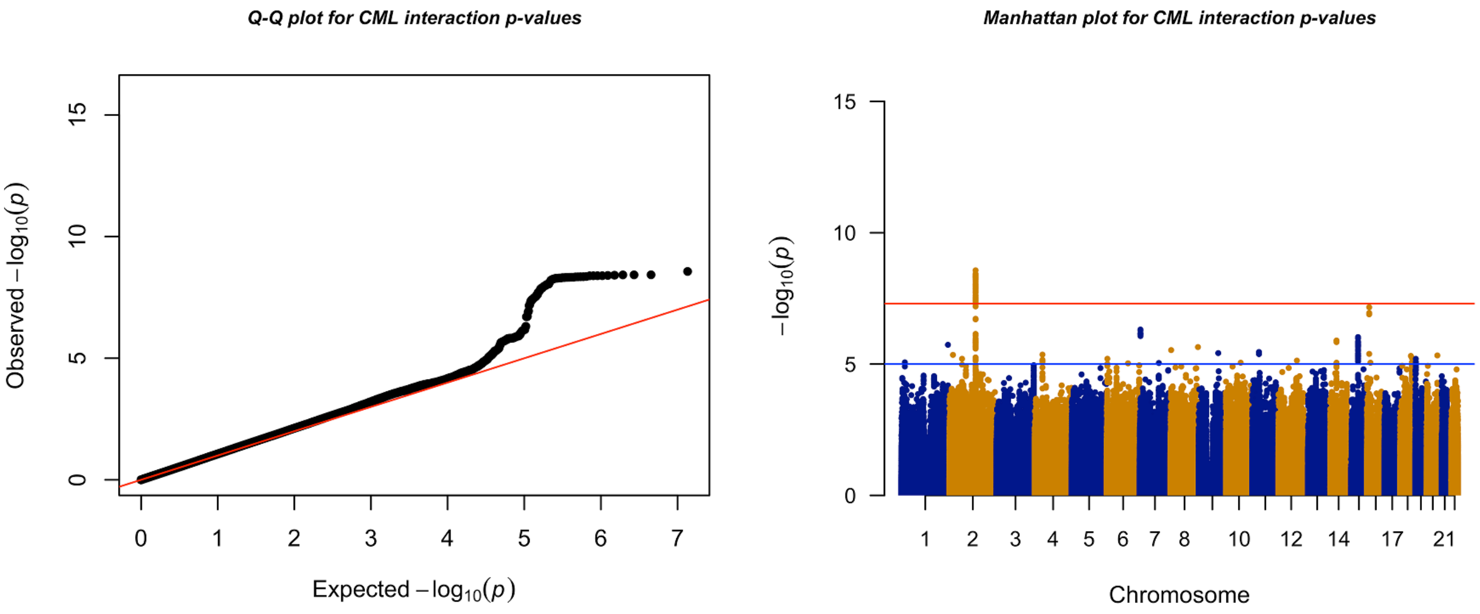
Abbreviations: PDAC: pancreatic ductal adenocarcinoma

Klein A, Wolpin BM, Risch HA, Stolzenberg-Solomon RZ, Mocci E, Zhang M, *et al.* Genome-wide meta-analysis identifies five new susceptibility loci for pancreatic cancer. Nat Comm **2018**.

**Supplemental table 1. Case and control count by study phase**

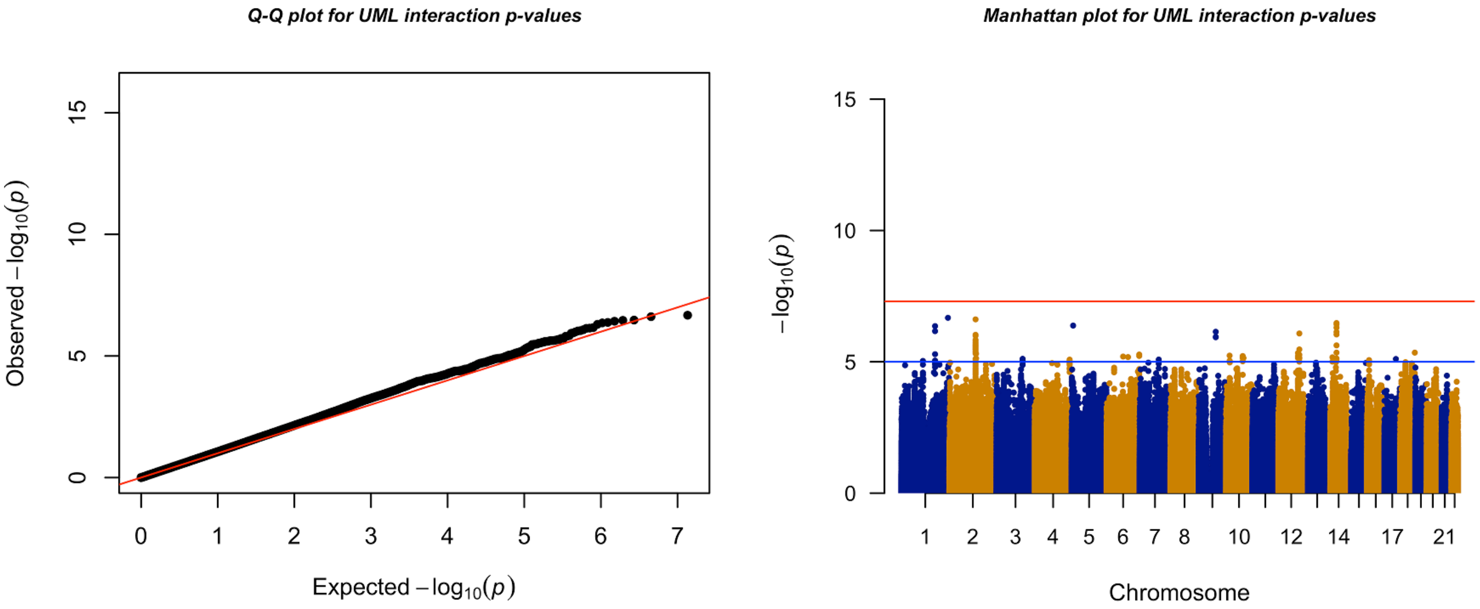
| | | PanScan1/2 | | PanScan3 | | PanC4 | | Total | |
|---|---|---|---|---|---|---|---|---|---|
| | Study | Case | Control | Case | Control | Case | Control | Case | Control |
| Cohorts | | | | | | | | | |
| | AgHealth | | | 23 | 0 | | | 23 | 0 |
| | ATBC | 194 | 206 | 44 | 217 | | | 238 | 423 |
| | CLUE II | 67 | 70 | | | | | 67 | 70 |
| | CPS II | 107 | 112 | 146 | 105 | | | 253 | 217 |
| | EPIC Denmark | 83 | 86 | | | | | 83 | 86 |
| | EPIC IARC | 216 | 228 | 150 | 256 | | | 366 | 484 |
| | EPIC Umea | 79 | 98 | 19 | 0 | | | 98 | 98 |
| | HPFS | 52 | 49 | 23 | 84 | | | 75 | 133 |
| | MCCS | | | 34 | 75 | | | 34 | 75 |
| | MEC | | | 27 | 198 | | | 27 | 198 |
| | NHS | 81 | 82 | 29 | 436 | | | 110 | 518 |
| | NYU-WHS | 6 | 11 | | | | | 6 | 11 |
| | PHS | 43 | 56 | 13 | 0 | | | 56 | 56 |
| | PLCO | 176 | 205 | 91 | 3042 | | | 267 | 3247 |
| | SELECT | | | 54 | 0 | | | 54 | 0 |
| | VITAL | | | 47 | 0 | | | 47 | 0 |
| | WHI | 206 | 207 | 166 | 222 | | | 372 | 429 |
| | WHS | 23 | 33 | | | | | 23 | 33 |
| Case-control or case series | | | | | | | | | |
| | DFCI | | | 356 | 0 | | | 356 | 0 |
| | JHU | 173 | 137 | | | 216 | 58 | 389 | 195 |
| | MAYO | 635 | 612 | | | 755 | 866 | 1390 | 1478 |
| | MDA | 256 | 266 | | | 550 | 471 | 806 | 737 |
| | MSKCC | 126 | 134 | | | 252 | 116 | 378 | 250 |
| | Spain | | | 95 | 397 | | | 95 | 397 |
| | Toronto | 257 | 259 | | | 351 | 350 | 608 | 609 |
| | UCSF | 198 | 199 | | | 208 | 204 | 406 | 403 |
| | Yale | 198 | 271 | | | 132 | 329 | 330 | 600 |
| | Queenland | | | | | 534 | 585 | 534 | 585 |
| | IARC | | | | | 446 | 442 | 446 | 442 |
| Total | | 3176 | 3321 | 1317 | 5032 | 3444 | 3421 | 7937 | 11774 |

**Supplemental figure 2. Q-Q and Manhattan plots for the CML and UML methods**



*Q-Q plot for CML interaction p-values*

*Manhattan plot for CML interaction p-values*



*Q-Q plot for UML interaction p-values*

*Manhattan plot for UML interaction p-values*

**Supplemental table 2. Top-1 SNP for locus 2q21.3 with association reaching genome wide significance**

| Chr<br>BP<br>SNP<br>A1/A2<br>Gene | Dataset | Info | MAF | Statistic Method | OR_SNP (95%CI) | OR_SNP*Former_Smoker (95%CI) | ORSNP*Current_Smoker (95%CI) | Interaction P-value |
|---|---|---|---|---|---|---|---|---|
| **2q21.3**<br>**135356285**<br>**rs1818613**<br>**G/T**<br>***TMEM163* (intronic)** | **Meta-Analysis** | | | **CML** | 0.87 (0.81,0.92) | 1.11 (1.04,1.18) | 1.33 1.24,1.42) | 2.70E-09 |
| | | | | **EB** | 0.87 (0.81,0.93) | 1.13 (1.04,1.23) | 1.35 (1.25,1.44) | 3.08E-09 |
| | | | | **UML** | 0.89 (0.83,0.96) | 1.11 (1.02,1.21) | 1.4 (1.27,1.52) | 1.02E-06 |
| | **PanScan** | 0.99 | 0.39 | **CML** | 0.88 (0.8,0.95) | 1.14 (1.04,1.23) | 1.39 (1.26,1.51) | 8.22E-07 |
| | | | | **EB** | 0.9 (0.81,0.99) | 1.11 (0.99,1.23) | 1.39 (1.27,1.51) | 1.01E-06 |
| | | | | **UML** | 0.92 (0.83,1.01) | 1.07 (0.95,1.2) | 1.41 (1.25,1.57) | 1.24E-04 |
| | **PanC4** | 0.984 | 0.39 | **CML** | 0.85 (0.76,0.94) | 1.08 (0.98,1.19) | 1.27 (1.13,1.4) | 2.49E-03 |
| | | | | **EB** | 0.85 (0.76,0.94) | 1.13 (0.98,1.28) | 1.28 (1.13,1.43) | 4.96E-03 |
| | | | | **UML** | 0.86 (0.75,0.96) | 1.17 (1.02,1.32) | 1.32 (1.12,1.53) | 1.30E-02 |

Abbreviations: Chr, chromosome; BP, base pair position according to the human genome Build 37; A1, effect allele (minor allele); A2, alternative allele (major allele)
Info, imputation quality score; MAF, minor allele frequency; CML, Constrained maximum-likelihood; EB, Empirical Bayes; UML Unconstrained maximum-likelihood; OR (95%CI), odds ratios and confidence intervals.

**Supplemental Table 3. Top-1 SNP for locus 2q21.3 association by study phase and study design**

| Chr<br>BP<br>SNP<br>A1/A2<br>Gene | Dataset | MAF | Statistic Method | OR_SNP (95%CI) | OR_SNP*Former_Smoker (95%CI) | ORSNP*Current_Smoker (95%CI) | Interaction P-value |
|---|---|---|---|---|---|---|---|
| 2q21.3<br>135356285<br>rs1818613<br>G/T<br>*TMEM163* (intronic) | **PanScan I** | 0.36/0.64 | **CML** | 0.87 (0.76, 1.00) | 1.23 (1.05, 1.45) | 1.52 (1.25, 1.85) | 1.06E-04 |
| | | | **EB** | 0.89 (0.76, 1.03) | 1.21 (1.00, 1.47) | 1.52 (1.25, 1.84) | 1.12E-04 |
| | | | **UML** | 0.92 (0.79, 1.08) | 1.15 (0.92, 1.44) | 1.55 (1.19, 2.01) | 4.37E-03 |
| | | | | | | | |
| | **PanScan II** | 0.40/0.60 | **CML** | 0.86 (0.75, 0.98) | 1.15 (0.99, 1.34) | 1.38 (1.11, 1.72) | 1.19E-02 |
| | | | **EB** | 0.87 (0.75, 1.00) | 1.15 (0.98, 1.34) | 1.38 (1.11, 1.72) | 1.28E-02 |
| | | | **UML** | 0.89 (0.77, 1.04) | 1.12 (0.91, 1.39) | 1.43 (1.03, 1.98) | 9.32E-02 |
| | | | | | | | |
| | **PanScan III** | 0.40/0.60 | **CML** | 0.91 (0.80, 1.03) | 1.02 (0.86, 1.20) | 1.15 (0.91, 1.45) | 4.78E-01 |
| | | | **EB** | 0.91 (0.80, 1.03) | 1.02 (0.86, 1.20) | 1.15 (0.91, 1.46) | 4.76E-01 |
| | | | **UML** | 0.93 (0.79, 1.09) | 0.99 (0.80, 1.23) | 1.18 (0.88, 1.59) | 4.57E-01 |
| | | | | | | | |
| | **PanC4** | 0.39/0.61 | **CML** | 0.85 (0.76,0.94) | 1.08 (0.98,1.19) | 1.27 (1.13,1.4) | 2.49E-03 |
| | | | **EB** | 0.85 (0.76,0.94) | 1.13 (0.98,1.28) | 1.28 (1.13,1.43) | 4.96E-03 |
| | | | **UML** | 0.86 (0.75,0.96) | 1.17 (1.02,1.32) | 1.32 (1.12,1.53) | 1.30E-02 |
| | | | | | | | |
| | **Cohorts** | | **CML** | 0.97 (0.87, 1.08) | 1.08 (0.94, 1.24) | 1.24 (1.05, 1.47) | 3.82E-02 |
| | | | **EB** | 1.00 (0.88, 1.14) | 0.96 (0.79, 1.16) | 1.23 (1.03, 1.47) | 2.76E-02 |
| | | | **UML** | 1.03 (0.90, 1.18) | 0.92 (0.77, 1.10) | 1.18 (0.95, 1.46) | 7.25E-02 |
| | | | | | | | |
| | **Case-control** | | **CML** | 0.84 (0.79, 0.91) | 1.13 (1.04, 1.23) | 1.35 (1.21, 1.51) | 2.18E-07 |
| | | | **EB** | 0.85 (0.79, 0.91) | 1.17 (1.07, 1.29) | 1.37 (1.21, 1.54) | 3.95E-07 |
| | | | **UML** | 0.86 (0.80, 0.94) | 1.18 (1.05, 1.33) | 1.43 (1.21, 1.68) | 4.56E-05 |

Abbreviations: Chr, chromosome; BP, base pair position according to the human genome Build 37; A1, effect allele (minor allele); A2, alternative allele (major allele) Info, imputation quality score; MAF, minor allele frequency; CML, Constrained maximum-likelihood; EB, Empirical Bayes; UML Unconstrained maximum-likelihood; OR (95%CI), odds ratios and confidence intervals. Case/control counts: PanScan1 1696/1780, PanScan2 1480/1541, PanScan3 1317/5032, PanC4 3949/3673, cohorts 2199/6070, case-control studies 6243/5948.

**Supplementary table 4: Top index SNPs after LD clumping on the meta-analyzed SNPs in regions with suggestive evidence of interaction (empirical Bayes interaction p-value ≤ 5E-06).**

| CHR | SNP Position | Effect Allele/Ref Allele | MAF Panc4-PanScan | INFO Panc4-PanScan | OR | | | EB Interaction p-value |
|---|---|---|---|---|---|---|---|---|
| | | | | | SNP (95% CI) | SNP*Former Smoker (95% CI) | SNP*Current Smoker (95% CI) | |
| 14q22.1 | rs8003600<br>52209869 | T/A | 0.24-.024 | .94-.93 | 0.87 (0.81, 0.93) | 1.31 (1.18, 1.44) | 1.04 (0.92, 1.17) | 2.10E-07 |
| 1q12 | rs3765814<br>241773027<br>*OPN3*<br>(intronic) | T/C | 0.17-0.16 | 1-0.75 | 0.90 (0.83. 0.97) | 0.83 (0.74, 0.94) | .82 (0.70, 0.96) | 1.90E-06 |
| 16q12.1 | rs78013006<br>11462404<br>*LOC105371082*<br>(Intronic) | G/A | 0.10-0.10 | .90-.86 | 0.97 (0.87, 1.08) | 0.80 (0.70, 0.92) | 1.23 (1.05, 1.43) | 3.53E-06 |

Note: 1000 genome phase 3 was chosen as the reference panel. SNPs in a clump were selected based on a threshold of $r^2$ equal to 0.05 and a physical distance of 250kb from the index SNPs. Computation was done using plink 1.9.

**Supplemental Table 5: Tests of interaction between Established PDAC Risk loci and smoking**

| Chr<br>SNP<br>Position$^{a}$<br>Gene | Effect Allele/ Ref Allele | MAF PanC4-PanScan | INFO$^{b}$ PanC4-PanScan | Method GxE | OR SNP (95% CI) | OR SNP*Former Smoker (95% CI) | OR SNP*Current Smoker (95% CI) | Interaction P -value |
|---|---|---|---|---|---|---|---|---|
| **1q32.1<br>rs2816938<br>199,985,368<br>NR5A2** | A/T | .26-.24 | .99-.99 | CML | 1.19 (1.12-1.27) | .99 (.91-1.08) | 1.05 (.94-1.17) | .58 |
| | | | | UML | 1.18 (1.08-1.29) | .98 (.88-1.09) | 1.16 (1.01-1.33) | .06 |
| | | | | EB | 1.19 (1.12-1.27) | .99 (.90-1.08) | 1.09 (.95-1.26) | .33 |
| **1q32.1<br>rs3790844<br>200,007,432<br>NR5A2** | G/A | .22- .22 | 1-1 | CML | .83 (.78-.88) | .94 (.87-1.03) | 1.02 (.92-1.14) | .23 |
| | | | | UML | .83 (.76-.91) | .96 (.86-1.08) | .99 (.85-1.14) | .81 |
| | | | | EB | .83 (.78-.89) | .94 (.86-1.03) | 1.01 (.90-1.13) | .37 |
| **2p13.3<br>rs1486134<br>67,639,769<br>ETAA1 2236bp 3'** | G/T | .289-.286 | 1-1 | CML | .91 (.86-.97) | .99 (93-1.06) | .99 (91-1.08) | .97 |
| | | | | UML | .89 (.84-.95) | 1.01 (90-1.12) | 1.04 (91-1.20) | .80 |
| | | | | EB | .91 (.85-.96) | .99 (91-1.09) | 1.00 (90-1.12) | .97 |
| **3q29<br>rs9854771<br>189,508,471<br>TP63** | A/G | .344-.354 | 1-.998 | CML | .89 (.84-.95) | 1.00(.93-1.08) | .99 (.90-1.09) | .96 |
| | | | | UML | .90 (.84-.95) | .99 (.89-1.09) | 1.03 (.91-1.17) | .82 |
| | | | | EB | .89 (.84-.95) | 1.00 (.92-1.09) | 1.00 (.91-1.11) | .99 |
| **5p15.33<br>rs2736098<br>1,294,086<br>TERT** | T/C | .252- .265 | .921-.84 | CML | .83 (.78-.88) | 1.04 (.95-1.13) | .96 (.87-1.07) | .37 |
| | | | | UML | .77 (.70-.84) | 1.13 (1.02-1.26) | 1.10 (.94-1.27) | .089 |
| | | | | EB | .79 (.73-.87) | 1.09 (.98-1.21) | 1.04 (.89-1.21) | .37 |
| **5p15.33<br>rs401681<br>1,322,087<br>CLPTM1L** | T/C | .466-.463 | 1-1 | CML | 1.19 (1.12-1.27) | .98 (.91-1.05) | .97 (.89-1.06) | .78 |
| | | | | UML | 1.20 (1.13-1.28) | .97 (.88-1.06) | .99 (.88-1.12) | .78 |
| | | | | EB | 1.19 (1.12-1.27) | .98 (.91-1.05) | 1.00 (.89-1.12) | .79 |
| | A/C | .252-.259 | | CML | .87 (.82-.93) | 1.01 (.93-1.09) | 1.03 (.93-1.14) | .82 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **7p13**<br>**rs17688601**<br>**40,866,663**<br>**SUGCT** | | | 1-1 | UML | .87 (.82-.93) | 1.00 (.89-1.11) | 1.10 (.96-1.27) | .31 |
| | | | | EB | .87 (.82-.93) | 1.00 (.90-1.10) | 1.06 (.94-1.20) | .55 |
| **7p12**<br>**rs73328514**<br>**47,488,569**<br>**TNS3** | T/A | .109-.111 | .965-.929 | CML | .83 (.76-.90) | .98 (.88-1.09) | 1.01 (.86-1.17) | .93 |
| | | | | UML | .83 (.74-.92) | 1.02 (.87-1.18) | 1.04 (.85-1.28) | .91 |
| | | | | EB | .83 (.76-.90) | 1.00 (.88-1.13) | 1.01 (.87-1.18) | .98 |
| **7q32.3**<br>**rs6971499**<br>**130,680,521**<br>**LINC-PINT** | C/T | .146-.142 | 1- .954 | CML | .84 (.77-.91) | .98 (.89-1.08) | .97 (.86-1.11) | .89 |
| | | | | UML | .84 (.77-.92) | .99 (.86-1.13) | .97 (.81-1.17) | .96 |
| | | | | EB | .84 (.77-.91) | .98 (.89-1.09) | .97 (.81-1.17) | .92 |
| **8q21.11**<br>**rs2941471**<br>**76,470,404**<br>**HNF4G** | G/A | .419-.418 | .997-.997 | CML | 1.14 (1.07-1.21) | .96 (.90-1.02) | .88 (.81-.96) | .026 |
| | | | | UML | 1.15 (1.08-1.22) | .99 (.90-1.08) | .88 (.77-.99) | .11 |
| | | | | EB | 1.14 (1.07-1.21) | .96 (.90-1.02) | .88 (.81-.96) | .028 |
| **8q24.21**<br>**rs10094872**<br>**128,719,884**<br>**MYC** | T/A | .371-.375 | .964-.943 | CML | 1.14 (1.07-1.21) | .95 (.88-1.02) | 1.02 .93-1.12) | .2 |
| | | | | UML | 1.12 (1.06-1.20) | .96 (.87-1.06) | 1.09 (.96-1.24) | .16 |
| | | | | EB | 1.14 (1.07-1.21) | .95 (.87-1.03) | 1.03 (.93-1.15) | .23 |
| **8q24.21**<br>**rs1561927**<br>**129,568,078**<br>**MIR1208** | C/T | .25-.26 | 1-1 | CML | 1.12 (1.06-1.19) | .99 (.91-1.08) | .98 (.88-1.09) | .92 |
| | | | | UML | 1.12 (1.05-1.19) | 1.00 (.90-1.11) | 1.04 (.91-1.20) | .83 |
| | | | | EB | 1.13 (1.06-1.20) | .99 (.90-1.08) | 1.01 (.89-1.14) | .94 |
| **9q34**<br>**rs505922**<br>**136,149,229**<br>**ABO** | C/T | .373-.366 | 1-1 | CML | 1.26 (1.18-1.34) | .98 (.91-1.05) | 1.05 (.96-1.16) | .31 |
| | | | | UML | 1.23 (1.16-1.31) | 1.02 (.93-1.13) | 1.11 (.98-1.27) | .24 |
| | | | | EB | 1.25 (1.18-1.34) | .99 (.91-1.08) | 1.07 (.95-1.20) | .40 |
| **13q12.2**<br>**rs9581943**<br>**28,493,997**<br>**PDX1-AS1-PDX1** | A/G | .41-.414 | 1- .987 | CML | 1.16 (1.09-1.23) | 1.01 (.94-1.08) | .98 (.90-1.07) | .85 |
| | | | | UML | 1.15 (1.08-1.22) | 1.05 (.96-1.16) | .94 (.83-1.06) | .19 |
| | | | | EB | 1.16 (1.09-1.23) | 1.02 (.94-1.11) | .98 (.88-1.08) | .68 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **13q22.1**<br>**rs9543325**<br>**73,916,628**<br>**KLF5 and KLF12** | C/T | .409-.391 | 1-1 | CML | 1.29 (1.21-1.37) | .98 (.92-1.05) | .94 (.86-1.03) | .43 |
| | | | | UML | 1.27 (1.20-1.36) | 1.04 (.94-1.15) | .91 (.80-1.03) | .13 |
| | | | | EB | 1.28 (1.20-1.36) | 1.00 (.92-1.09) | .93 (.84-1.03) | .33 |
| **16q23.1**<br>**rs7190458**<br>**75,263,661**<br>**BCAR1** | A/G | .056-.051 | 1-.739 | CML | 1.51 (1.32-1.74) | .87 (.74-1.03) | .83 (.67-1.02) | .13 |
| | | | | UML | 1.50 (1.29-1.75) | .86 (.69-1.08) | .88 (.65-1.18) | .40 |
| | | | | EB | 1.51 (1.31-1.73) | .87 (.73-1.04) | .86 (.65-1.14) | .28 |
| **17q12**<br>**rs4795218**<br>**36,078,510**<br>**HNF1B** | A/G | .218-.222 | .954-.958 | CML | .88 (.82-.93) | .97 (.89-1.06) | .99 (.88-1.10) | .79 |
| | | | | UML | .90 (.83-.99) | .93 (.83-1.05) | .93 (.80-1.08) | .43 |
| | | | | EB | .88 (.83-.94) | .96 (.88-1.06) | .98 (.85-1.12) | .73 |
| **17q25.1**<br>**rs11655237**<br>**70,400,166**<br>**LINC00673** | T/C | .13-.120 | .955-1 | CML | 1.34 (1.23-1.47) | .88 (.79-.98) | .83 (.73-.96) | .013 |
| | | | | UML | 1.32 (1.19-1.47) | .95 (.82-1.09) | .84 (.70-1.02) | .21 |
| | | | | EB | 1.34 (1.23-1.46) | .90 (.79-1.02) | .84 (.73-.97) | .038 |
| **18q21.32**<br>**rs1517037**<br>**56,878,274**<br>**GRP** | T/C | .177- .182 | 1-1 | CML | .87 (.82-.93) | 1.03 (.94-1.13) | .96 (.86-1.08) | .48 |
| | | | | UML | .85 (.78-.93) | 1.06 (.93-1.20) | 1.01 (.87-1.19) | .66 |
| | | | | EB | .86 (.79-.94) | 1.07 (.96-1.19) | .97 (.85-1.11) | .31 |
| **22q12.1**<br>**rs16986825**<br>**29,300,306**<br>**ZNRF3** | T/C | .165-.158 | 1- .996 | CML | 1.14 (1.04-1.24) | 1.00 (.91-1.10) | 1.20 (1.07-1.36) | .0053 |
| | | | | UML | 1.18 (1.08-1.28) | .96 (.85-1.10) | 1.06 (.90-1.25) | .05 |
| | | | | EB | 1.15 (1.05-1.26) | .99 (.88-1.10) | 1.12 (.95-1.32) | .28 |

Abbreviations: Chr:chromosome; MAF:Minor Allele Frequency; GxE: Gene by Environment ; OR 95% CI: Odds Ratio and its 95% confidence interval

a) SNP position according to NCBI Human Genome Build 37
b) Quality of imputation metric

**Supplemental table 6. Expression quantitative trait loci (eQTL) for rs1818613 in normal tissues from GTEx8, false discovery rate (FDR) threshold of ≤0.05**

| SNP Id | Ref/Effect allele | Gene Symbol | P-Value | NES# | Tissue |
|---|---|---|---|---|---|
| rs1818613 | G/T | TMEM163 | 1.20E-27 | 0.55 | Heart - Atrial Appendage |
| rs1818613 | G/T | TMEM163 | 1.10E-21 | 0.4 | Whole Blood |
| rs1818613 | G/T | TMEM163 | 3.10E-17 | -0.45 | Testis |
| rs1818613 | G/T | TMEM163 | 7.00E-15 | 0.41 | Esophagus - Muscularis |
| rs1818613 | G/T | TMEM163 | 1.80E-11 | 0.28 | Pituitary |
| rs1818613 | G/T | TMEM163 | 3.00E-11 | 0.37 | Artery - Aorta |
| rs1818613 | G/T | CCNT2 | 1.90E-09 | -0.13 | Nerve - Tibial |
| rs1818613 | G/T | TMEM163 | 6.90E-08 | 0.25 | Artery - Tibial |
| rs1818613 | G/T | CCNT2 | 9.40E-08 | -0.14 | Lung |
| rs1818613 | G/T | TMEM163 | 4.60E-07 | 0.23 | Esophagus - Mucosa |
| rs1818613 | G/T | TMEM163 | 6.50E-07 | 0.28 | Esophagus - Gastroesophageal Junction |
| rs1818613 | G/T | CCNT2 | 1.30E-06 | -0.12 | Esophagus - Muscularis |
| rs1818613 | G/T | TMEM163 | 1.40E-06 | 0.22 | Nerve - Tibial |
| rs1818613 | G/T | TMEM163 | 3.80E-06 | 0.21 | Brain - Frontal Cortex (BA9) |
| rs1818613 | G/T | CCNT2 | 1.80E-05 | -0.087 | Thyroid |
| rs1818613 | G/T | TMEM163 | 1.90E-05 | 0.1 | Lung |
| rs1818613 | G/T | CCNT2-AS1 | 2.30E-05 | 0.41 | Brain - Cerebellar Hemisphere |
| rs1818613 | G/T | CCNT2 | 2.70E-05 | -0.097 | Skin - Not Sun Exposed (Suprapubic) |
| rs1818613 | G/T | CCNT2 | 4.10E-05 | -0.13 | Heart - Left Ventricle |
| rs1818613 | G/T | ZRANB3 | 4.10E-05 | -0.3 | Brain - Hippocampus |
| rs1818613 | G/T | CCNT2 | 4.90E-05 | -0.12 | Heart - Atrial Appendage |
| rs1818613 | G/T | CCNT2-AS1 | 4.90E-05 | 0.35 | Brain - Cerebellum |
| rs1818613 | G/T | CCNT2 | 6.10E-05 | -0.15 | Brain - Cortex |
| rs1818613 | G/T | VDAC2P4 | 6.60E-05 | 0.38 | Brain - Cerebellar Hemisphere |
| rs1818613 | G/T | CCNT2 | 7.20E-05 | -0.14 | Pituitary |
| rs1818613 | G/T | TMEM163 | 9.50E-05 | 0.19 | Thyroid |
| rs1818613 | G/T | CCNT2 | 1.00E-04 | -0.12 | Testis |
| rs1818613 | G/T | CCNT2 | 2.00E-04 | -0.071 | Artery - Tibial |

# Normal effect size

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**Supplemental Table 7: Results of the SNP with the highest CLPP after thresholding CLPP to 0.001. Effect sizes/slope and the p-values are shown based on the eQTL analysis from the GTEx v7 data. Colocalization analysis is performed using eCAVIAR package.**

| **SNP ID** | **Tissue Name** | **Gene Name** | **Ref/Alt Allele** | **CLPP** | **Interaction.EB p-value** | **eQTL Slope** | **eQTL p-value** |
|---|---|---|---|---|---|---|---|
| rs842357 | Adipose Subcutaneous | MGAT5 | G/A | 0.002 | $1.75 \times 10^{-08}$ | -0.014 | 0.745 |
| rs842357 | Artery Tibial | MGAT5 | G/A | 0.002 | $1.75 \times 10^{-08}$ | -0.011 | 0.716 |
| rs842357 | Brain Anterior Cingulate cortex BA24 | TMEM163 | G/A | 0.031 | $1.75 \times 10^{-08}$ | -0.204 | 0.023 |
| rs842357 | Brain Caudate Basal ganglia | R3HDM1 | G/A | 0.002 | $1.75 \times 10^{-08}$ | -0.005 | 0.912 |
| rs842357 | Brain Nucleus Accumbens basal ganglia | CCNT2 | G/A | 0.002 | $1.75 \times 10^{-08}$ | 0.124 | 0.033 |
| rs842357 | Brain Putamen Basal ganglia | RAB3GAP1 | G/A | 0.001 | $1.75 \times 10^{-08}$ | 0.018 | 0.838 |
| rs842357 | Cells EBV-transformed lymphocytes | ZRANB3 | G/A | 0.001 | $1.75 \times 10^{-08}$ | -0.02 | 0.835 |
| rs842357 | Cells Transformed fibroblasts | CCNT2 | G/A | 0.033 | $1.75 \times 10^{-08}$ | 0.085 | 0.01 |
| *rs842357* | *Heart Atrial Appendage* | *TMEM163* | *G/A* | *0.982* | $1.75 \times 10^{-08}$ | *-0.501* | $1.43 \times 10^{-15}$ |
| rs842357 | Liver | MGAT5 | G/A | 0.001 | $1.75 \times 10^{-08}$ | 0.037 | 0.599 |
| rs842357 | Nerve Tibial | TMEM163 | G/A | 0.002 | $1.75 \times 10^{-08}$ | -0.184 | 0.002 |
| rs842357 | Prostate | CCNT2 | G/A | 0.077 | $1.75 \times 10^{-08}$ | 0.185 | 0.011 |
| rs842357 | Skin Sun Exposed Lower leg | MGAT5 | G/A | 0.002 | $1.75 \times 10^{-08}$ | -0.013 | 0.675 |
| rs842357 | Small Intestine Terminal Ileum | CCNT2 | G/A | 0.012 | $1.75 \times 10^{-08}$ | 0.191 | 0.006 |
| rs842357 | Stomach | TMEM163 | G/A | 0.032 | $1.75 \times 10^{-08}$ | -0.104 | 0.008 |
| rs842357 | Testis | MGAT5 | G/A | 0.004 | $1.75 \times 10^{-08}$ | 0.059 | 0.31 |
| rs842357 | Vagina | ZRANB3 | G/A | 0.003 | $1.75 \times 10^{-08}$ | -0.098 | 0.409 |

# Co-localization posterior probability

* Interaction p-value from the empirical Bayes approach