Genome-Wide Meta-Analysis of 241,258 Adults Accounting for Smoking Behavior Identifies Novel Loci for Obesity Traits

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73

74

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AEJ, TWW, MFF, MGr, VAF, KY, and LB contributed equally to this manuscript. LAC, KEN, IBB, TOK, RJFL, and CTL supervised this project together. LAC, KEN, IBB, TOK, TWW, RJFL and AEJ conceived and

designed the study. LAC, RJFL, AEJ and TOK coordinated the collection of genome-wide association and interaction study results from the participating studies. The association and interaction results were contributed by SWvdL, MASi, SH, GJdB, HMDR and GP (AtheroExpress); AVS, TBH, GE, LJL, and VG (AGES study); KEN, MGr, AEJ, KY, EBoe, and PGL (ARIC study); JBW, NGM, RPSM, PAFM, ACH and GWM (AUSTWIN study); DPS (B58C study); GC, LJP, JoH, AWM, ALJ, and JBe (BHS study); CSch, TA, EBot and RJFL (BioMe); TT, DHe, LF (BLSA); BM, TMB, KDT, SC and BMP (CHS); YW, NRL, LSA and KLM (CLHNS study); ZK, PMV, TC, SBe, GWa, and PV (COLAUS study); JMart, IR, and CH (Croatia-Korcula study); VV, IK, and OPo (Croatia-Vis study); LY, AB, DT, SLo, BB and PF (DESIR study); RRau, TAL, PK, MHa, KSa, and RM (DR's EXTRA study); KF, NP, TE, and AMe (EGCUT study); JL, RAS, CL, and NJW (Ely study); CL, JL, RAS and NJW (EPIC), JHZ, RL, RAS, and NJW (EPIC-Norfolk study); NA, MCZ and CMvD (ERF study); IBB, MFF, JC and LB (Family Heart Study); JL, RAS, CL, RJFL and NJW (Fenland study); FX, JW, JSN, VAF, NLHC, CTL, CSF, and LAC (FramHS); MBo, FSC, KLM, and RNB (FUSION study); JT, LK, CSa, and HAK (FUSION2 study); MGo, BKK and CAB (Gendian); DJP, JEH, LJH, SP, CH and BHS (Generation Scotland); LFB, SLRK, MAJ, and PAP (GENOA study); SAh, FR, IB, GHa and PWF (GLACIER study); JE, CO, JOJ, MLor, AE and LV (GOOD study); TSA, THa and TIAS (GOYA study); BOT, CAM, SLV, TF, JNH and RSC (GxE); MHol, MNH, CP, AL and HVe (Health06 study); YJS, TRi, TRa, MASa, DCR and CB (HERITAGE Family Study); JASm, JDF, SLRK, WZhao, and DRW (HRS study); AUJ, KK, OLH, LLB, AJW, and KH (HUNT2 study); MC, DBr, SLu, NGl, JASt and DC (HYPERGENES); RJS, BS, KG, UdF, AH, ET and DBa (IMPROVE); TT, DHe, and SBa (InCHIANTI study); JMJ, MEJ, NGr, and OPe (Inter99 study); TWW, IMH, MEZ, MMN, MO, ALD, HG, MW, RRaw, BT, AP and KSt (KORA S3 and S4 studies); JVvVO, JMV, SSch, MASw and BHRW (Lifelines); WZhang, MLo, UA, SAf, JCC, and JSK (LOLIPOP study); MEK, GED, TBG, GS, JiH, and WM (LURIC study); UL, CAH, LLeM, SBu, and LH (MEC study); AMan, LJRT and YdIC (MESA study); MLa, JK, AJS, HMS, PSC, and NN (METSIM study); MKa, DM and CO (MrOS); MHor, MRJ and MIM (NFBC66 study); LQ, THu, QQ and DJH (NHS study); DK, KKO, JL, and AW (NSHD study); JMV, GWi, GL, JJH, EJCdG and DIB (NTR study); PN, AFW,

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ABSTRACT

Few genome-wide association studies (GWAS) account for environmental exposures, like smoking, potentially impacting the overall trait variance when investigating the genetic contribution to obesity-related traits. Here, we use GWAS data from 51,080 current smokers and 190,178 nonsmokers (87% European descent) to identify loci influencing BMI and central adiposity, measured as waist circumference and waist-to-hip ratio both adjusted for BMI. We identify 23 novel genetic loci, and 9 loci with convincing evidence of gene-smoking interaction (GxSMK) on obesity-related traits. We show consistent direction of effect for all identified loci and significance for 18 novel and for 5 interaction loci in an independent study sample. These loci highlight novel biological functions, including response to oxidative stress, addictive behavior, and regulatory functions emphasizing the importance of accounting for environment in genetic analyses. Our results suggest that tobacco smoking may alter the genetic susceptibility to overall adiposity and body fat distribution.

INTRODUCTION

Recent genome-wide association studies (GWAS) have described loci implicated in obesity, body mass index (BMI), and central adiposity. Yet most studies have ignored environmental exposures with possibly large impacts on the trait variance[1, 2]. Variants that exert genetic effects on obesity through interactions with environmental exposures often remain undiscovered due to heterogeneous main effects and stringent significance thresholds. Thus, studies may miss genetic variants that have effects in subgroups of the population, such as smokers[3].

It is often noted that currently-smoking individuals display lower weight/BMI and higher waist circumference (WC) as compared to nonsmokers[4, 5, 6, 7, 8]. Smokers also have the smallest fluctuations in weight over approximately 20 years compared to those who have never smoked or have stopped smoking [9, 10]. Also, heavy smokers (>20 cigarettes per day [CPD]) and those that have smoked for more than 20 years are at greater risk for obesity than non-smokers or light to moderate smokers (<20 CPD)[11, 12]. Men and women gain weight rapidly after smoking cessation, suggesting that many people intentionally smoke for weight management[13]. It remains unclear why smoking cessation leads to weight gain or why long-term smokers maintain weight throughout adulthood, although studies suggest that tobacco use suppresses appetite[14, 15] or alternatively, smoking may result in an increased metabolic rate[14, 15]. Identifying genes that influence adiposity and interact with smoking may help us clarify pathways through which smoking influences weight and central adiposity[15].

A comprehensive study that evaluates smoking in conjunction with genetic contributions is warranted. Using GWAS data from the Genetic Investigation of Anthropometric Traits (GIANT) Consortium, we identified 23 novel genetic loci, and 9 loci with convincing evidence of gene-smoking interaction

(GxSMK) on obesity, assessed by BMI, and central obesity independent of overall body size, assessed by WC adjusted for BMI (WCadjBMI) and waist-to-hip ratio adjusted for BMI (WHRadjBMI). By accounting for smoking status, we focus both on genetic variants observed through their main effects and GxSMK effects to increase our understanding of their action on adiposity-related traits. These loci highlight novel biological functions, including response to oxidative stress, addictive behavior, and regulatory functions emphasizing the importance of accounting for environment in genetic analyses. Our results suggest that smoking may alter the genetic susceptibility to overall adiposity and body fat distribution.

RESULTS

GWAS discovery overview

We meta-analyzed study-specific association results from 57 Hapmap-imputed GWAS and 22 studies with Metabochip, including up to 241,258 (87% European descent) individuals (51,080 current smokers and 190,178 nonsmokers) while accounting for current smoking (SMK) (**Methods, Supplementary Fig. 1, Supplementary Tables 1-4**). For primary analyses, we conducted meta-analyses across ancestries and sexes. For secondary analyses, we conducted meta-analyses in European-descent studies alone and sex-specific meta-analyses (**Tables 1-4**, **Supplementary Data 1-6**). We considered four analytical approaches to evaluate the effects of smoking on genetic associations with adiposity traits (**Figure 1, Methods**). Approach 1 (SNPadjSMK) examined genetic associations after adjusting for SMK. Approach 2 (SNPjoint) considered the joint impact of main effects adjusted for SMK + interaction effects[16]. Approach 3 focused on interaction effects (SNPint); Approach 4 followed up loci from Approach 1 for interaction effects (SNPscreen). Results from Approaches 1-3 were considered genome-wide significant (GWS) with a P-value$<5\times10^{-8}$ while Approach 4 used Bonferroni adjustment after screening. Lead variants >500 kb from previous associations with BMI, WCadjBMI, and WHRadjBMI were considered novel. All association

results are reported with effect estimates oriented on the trait increasing allele in the current smoking stratum.

Across the three adiposity traits, we identified 23 novel associated genetic loci (6 for BMI, 11 for WCadjBMI, 6 for WHRadjBMI) and nine having significant GxSMK interaction effects (2 for BMI, 2 for WCadjBMI, 5 for WHRadjBMI) (**Figure 1, Tables 1-4**, **Supplementary Data 1-6**). We provide a comprehensive comparison with previously-identified loci[1, 2] by trait in supplementary material (**Supplementary Data 7, Supplementary Note 1**).

Accounting for Smoking Status

For primary meta-analyses of BMI (combined ancestries and sexes), 58 loci reached GWS in Approach 1 (SNPadjSMK) (**Supplementary Data 1, Supplementary Fig. 2-3**), including two novel loci near *SOX11*, and *SRRM1P2* (**Table 1**). Three more BMI loci were identified using Approach 2 (SNPjoint), including a novel locus near *CCDC93* (**Supplementary Fig. 4-5**). For WCadjBMI, 62 loci reached GWS for Approach 1 (SNPadjSMK) and two more for Approach 2 (SNPjoint), including eight novel loci near *KIF1B*, *HDLBP*, *DOCK3*, *ADAMTS3*, *CDK6*, *GSDMC*, *TMEM38B*, and *ARFGEF2* (**Table 1**, **Supplementary Data 2**, **Supplementary Fig. 2-5**). Lead variants near *PSMB10* from Approaches 1 and 2 (rs14178 and rs113090, respectively) are >500 kb from a previously-identified WCadjBMI-associated variant (rs16957304); however, after conditioning on the known variant, our signal is attenuated ($P=3.02\times10^{-2}$ and $P=5.22\times10^{-3}$), indicating that this finding is not novel. For WHRadjBMI, 32 loci were identified in Approach 1 (SNPadjSMK), including one novel locus near *HLA-C*, with no additional loci in Approach 2 (SNPjoint) (**Table 1**, **Supplementary Data 3, Supplementary Fig. 2-5**).

607 We used GCTA[17] to identify loci from our primary meta-analyses that harbor multiple independent SNPs
608 (**Methods, Supplementary Tables 5-7**). Conditional analyses revealed no secondary signals within 500
609 kb of our novel lead SNPs. Additionally, we performed conditional association analyses to determine if
610 our novel variants were independent of previous GWAS loci within 500 kb that are associated with
611 related traits of interest. All BMI-associated SNPs were independent of previously-identified GWS
612 associations with anthropometric and obesity-related traits. Seven novel loci for WCadjBMI were near
613 previous associations with related anthropometric traits. Of these, association signals for rs6743226
614 near *HDLBP*, rs10269774 near *CDK6*, and rs6012558 near *ARFGEF2* were attenuated (P>1E-5 and β
615 decreased by half) after conditioning on at least one nearby height and hip circumference adjusted for
616 BMI (HIPadjBMI) SNP, but association signals remained independent of other related SNP-trait
617 associations. For WHRadjBMI, our GWAS signal was attenuated by conditioning on two known height
618 variants (rs6457374 and rs2247056), but remained significant in other conditional analyses. Given high
619 correlations among waist, hip, and height, these results are not surprising.
620
621 Several additional loci were identified for Approaches 1 and 2 in secondary meta-analysis (**Table 2**,
622 **Supplementary Data 1-6**, **Supplementary Fig. 6**). For BMI, 2 novel loci were identified by Approach 1,
623 including 1 near *EPHA3* and 1 near *INADL*. For WCadjBMI, 2 novel loci were identified near *RAI14* and
624 *PRNP*. For WHRadjBMI, five novel loci were identified in secondary meta-analyses near *BBX, TRBI1*,
625 *EHMT2*, *SMIM2* and *EYA4*. A comprehensive summary of nearby genes for all novel loci and their
626 potential biological relevance is available in **Supplementary Note 2**.
627
628 **Figure 3** presents analytical power for Approaches 1 and 2 while **Supplementary Table 8** and
629 **Supplementary Fig. 7** present simulation results to evaluate type 1 error (**Methods)**. A heat map cross-
630 tabulates P-values for Approaches 1 and 2 along with Approach 3 examining interaction only

(**Supplementary Fig 8**). We demonstrate that the two approaches yield valid type 1 error rates and that Approach 1 can be more powerful to find associations given zero or negligible quantitative interactions, whereas Approach 2 is more efficient in finding associations when interaction exists.

Modification of Genetic Predisposition by Smoking

Approach 3 directly evaluated GxSMK interaction (SNPint) (**Table 3, Supplementary Data 1-6**, **Figure 2**, **Supplementary Fig. 9-10)**. For primary meta-analysis of BMI, two loci reached GWS including a previously identified GxSMK interaction locus near *CHRNB4*[3], and a novel locus near *INPP4B*. Both loci exhibit GWS effects on BMI in smokers and no effects in nonsmokers. For *CHRNB4* (cholinergic nicotine receptor B4), the variant minor allele (G) exhibits a decreasing effect on BMI in current smokers (βsmk = - 0.047) but no effect in nonsmokers (βnonsmk = 0.002). Previous studies identified nearby SNPs in high LD associated with smoking (nonsynonymous, rs16969968 in *CHRNA5*)[3] and arterial calcification (rs3825807, a missense variant in *ADAMTS7)*[18]. Conditioning on these variants attenuated our interaction effect but did not eliminate it (**Supplementary Table 7**), suggesting a complex relationship between smoking, obesity, heart disease, and genetic variants in this region. Importantly, the *CHRNA5-CHRNA3-CHRNB4* gene cluster has been associated with lower BMI in current smokers[3], but with higher BMI in never smokers[3], evidence supporting the lack of association in nonsmokers as well as a lack of previous GWAS findings on 15q25 (**Supplementary Data 8**)[1]. The *CHRNA5-CHRNA3-CHRNB4* genes encode the nicotinic acetylcholine receptor (nAChR) subunits α3, α5 and β4, which are expressed in the central nervous system[19]. Nicotine has differing effects on the body and brain, causing changes in metabolism and feeding behaviors[20]. These findings suggest smoking exposure may modify genetic effects on 15q24-25 to influence smoking-related diseases, such as obesity, through distinct pathways.

In primary meta-analyses of WCadjBMI, one novel GWS locus (near *GRIN2A*) with opposite effect directions by smoking status was identified for Approach 3 (SNPint) (**Table 3, Supplementary Data 2, Figure 2, Supplementary Fig. 9-10**). The T allele of rs4141488 increases WCadjBMI in current smokers and decreases it in nonsmokers (βsmk = 0.037, βnonsmk = -0.015). In secondary meta-analysis of European women-only, we identified an interaction between rs6076699, near *PRNP*, and SMK on WCadjBMI (**Table 4**, **Supplementary Data 5**, **Supplementary Fig. 6**), a locus also identified in Approach 2 (SNPjoint) for European women. The major allele, A, has a positive effect on current smokers as compared to a weaker and negative effect on WC in nonsmokers (βsmk = 0.169, βnonsmk = -0.070), suggesting why this variant remained undetected in previous GWAS of WCadjBMI (**Supplementary Data 8**).

Approach 4 (SNPscreen) (**Figure 1**, **Methods**) evaluated GxSMK interactions after screening SNPadjSMK results (from Approach 1) using Bonferroni-correction (**Methods**, **Tables 3-4**, **Supplementary Data 1-6**). We identified two SNPs, near *LYPLAL1* and *RSPO3*, with significant interaction; both have previously published main effects on anthropometric traits. These loci exhibit effects on WHRadjBMI in nonsmokers, but not in smokers (**Figure 2**). In secondary meta-analyses, we identified three known loci with significant GxSMK interaction effects on WHRadjBMI near *MAP3K1*, *HOXC4-HOXC6*, and *JUND* (**Table 4**, **Supplementary Data 3 and 6**). We identified rs1809420, near *CHRNA5-CHRNA3-CHRNB4*, for BMI in the men-only, combined-ancestries meta-analysis (**Supplementary Data 1**).

Power calculations demonstrate that Approach 4 has increased power to identify SNPs that show (i) an effect in one stratum (smokers or nonsmokers) and a less pronounced but concordant effect in the other stratum, or (ii) an effect in the larger nonsmoker stratum and no effect in smokers (**Figure 3**). In contrast, Approach 3 has increased power for SNPs that show (i) an effect in the smaller smoker stratum

and no effect in nonsmokers, or (ii) an opposite effect between smokers and nonsmokers (**Figure 3**). Our findings for both approaches agree with these power predictions, supporting usingboth analytical approaches to identify GxSMK interactions.

Enrichment of Genetic Effects by Smoking Status

When examining the smoking specific effects for BMI and WCadjBMI loci in our meta-analyses, no significant enrichment of genetic effects by smoking status were noted. (**Figure 2**, **Supplementary Fig. 11-12**). However, our results for WHRadjBMI were enriched for loci with a stronger effect in nonsmokers as compared to smokers, with 35 of 45 loci displaying numerically larger effects in nonsmokers ($P_{binomial}=1.2x10^{-4}$).

We calculated the variance explained by subsets of SNPs selected on 15 significance thresholds for Approach 1 from $P_{SNPadjSMK}=1x10^{-8}$ to $P_{SNPadjSMK}=0.1$ (**Supplementary Table 9**, **Figure 4**). Differences in variance explained between smokers and nonsmokers were significant (P<0.003=0.05/15, Bonferroni-corrected for 15 thresholds) for BMI at each threshold, with more variance explained in smokers. For WCadjBMI, the difference was significant for SNP sets beginning with $P_{SNPadjSMK}<3.16x10^{-4}$, and for WHRadjBMI at $P_{SNPadjSMK}<1x10^{-6}$. In contrast to BMI, SNPs from Approach 1 explained a greater proportion of the variance in nonsmokers for WHRadjBMI. Differences in variance explained were greatest for BMI (differences ranged from 1.8% - 21% for smokers) and lowest for WHRadjBMI (ranging from 0.3% to 8.8% for nonsmokers).

These results suggest that smoking may increase genetic susceptibility to overall adiposity, but attenuate genetic effects on body fat distribution. This contrast is concordant with phenotypic observations of higher overall adiposity and lower central adiposity in smokers[4, 5, 7, 8, 9]. Additionally,

smoking increases oxidative stress and general inflammation in the body[21] and may exacerbate weight gain[22]. Many genes implicated in BMI are involved in appetite regulation and feeding behavior[1]. For waist traits, our results adjusted for BMI likely highlight distinct pathways through which smoking alters genetic susceptibility to body fat distribution. Overall, our results indicate that more loci remain to be discovered as more variance in the trait can be explained as we drop the threshold for significance.

Functional or Biological Role of Novel Loci

We conducted thorough searches of the literature and publicly available bioinformatics databases to understand the functional role of all genes within 500 kb of our lead SNPs. We systematically explored the potential role of our novel loci in affecting gene expression both with and without accounting for the influence of smoking behavior (**Methods**, **Supplementary Note 3, Supplementary Tables 10-12**).

We found the majority of novel loci are near strong candidate genes with biological functions similar to previously identified adiposity-related loci, including regulation of body fat/weight, angiogenesis/adipogenesis, glucose and lipid homeostasis, general growth and development. (**Supplementary Notes 2** and **3**).

We identified rs17396340 for WCadjBMI (Approaches 1 and 2), an intronic variant in the *KIF1B* gene. This variant is associated with expression of *KIF1B* in whole blood with and without accounting for SMK (GTeX and **Supplementary Tables 10** and **12**) and is highly expressed in the brain[23]. Knockout and mutant forms of *KIF1B* in mice resulted in multiple brain abnormalities, including hippocampus morphology[24], a region involved in (food) memory and cognition[25]. Variant rs17396340 is associated with expression levels of *ARSA* in LCL tissue. Human adipocytes express functional *ARSA*, which turns

dopamine sulfate into active dopamine. Dopamine regulates appetite through leptin and adiponectin levels, suggesting a role for *ARSA* in regulating appetite[26].

Expression of *CD47* (CD47 molecule), near rs670752 for WHRadjBMI (Approach 1, women-only), is significantly decreased in obese individuals and negatively correlated with BMI, WC, and Hip circumference[27]. Conversely, in mouse models, CD47 deficient mice show decreased weight gain on high fat diets, increased energy expenditure, improved glucose profile, and decreased inflammation[28].

Several novel loci harbor genes involved in unique biological functions and pathways including addictive behaviors and response to oxidative stress. These potential candidate genes near our association signals are highly expressed in relevant tissues for regulation of adiposity and smoking behavior (e.g. brain, adipose tissue, liver, lung, muscle) (**Supplementary Note 2**, **Supplementary Table 10**).

The *CHRNA5-CHRNA3-CHRNB4* cluster is involved in the eNOS signaling pathway (Ingenuity KnowledgeBase, http://www.ingenuity.com) that is key for neutralizing reactive oxygen species introduced by tobacco smoke and obesity[29, 30]. Disruption of this pathway has been associated with dysregulation of adiponectin in adipocytes of obese mice, implicating this pathway in downstream effects on weight regulation[30, 31]. This finding is especially important due to the compounded stress adiposity places on the body as it increases chronic oxidative stress itself[31]. *INPP4B* has been implicated in the regulation of the PI3K/Akt signaling pathway[32] that is important for cellular growth and proliferation, but also eNOS signaling, carbohydrate metabolism, and angiogenesis[33].

GRIN2A, near rs4141488, controls long-term memory and learning through regulation and efficiency of synaptic transmission[34] and has been associated with heroin addiction[35]. Nicotine increases the

752 expression of *GRIN2A* in the prefrontal cortex in murine models[36]. There are no established relationships
753 between *GRIN2A* and obesity-related phenotypes in the literature, yet memantine and ketamine,
754 pharmacological antagonists of GRIN2A activity[37, 38, 39, 40], are implicated in treatment for obesity-
755 associated disorders, including binge-eating disorders and morbid obesity (ClinicalTrials.gov identifiers:
756 NCT00330655, NCT02334059, NCT01997515, NCT01724983). Memantine is under clinical investigation
757 for treatment of nicotine dependence (ClinicalTrials.gov identifiers: NCT01535040, NCT00136786,
758 NCT00136747). While our lead SNP is not within a characterized gene, rs4141488 and variants in high LD
759 (r^2>0.7) are within active enhancer regions for several tissues, including liver, fetal leg muscle, smooth
760 stomach and intestinal muscle, cortex, and several embryonic and pluripotent cell types
761 (**Supplementary Note 2**), and therefore may represent an important regulatory region for nearby genes
762 like *GRIN2A*.
763
764 In secondary meta-analysis of European women-only, we identified a significant GxSMK interaction for
765 rs6076699 on WCadjBMI (**Table 4**, **Supplementary Data 4**, **Supplementary Fig. 6**). This SNP is 100kb
766 upstream of *PRNP* (prion protein), a signaling transducer involved in multiple biological processes
767 related to the nervous system, immune system, and other cellular functions (**Supplementary Note 2**)[41].
768 Alternate forms of the oligomers may form in response to oxidative stress caused by copper exposure[42].
769 Copper is present in cigarette smoke and elevated in the serum of smokers, but is within safe ranges[43,
770 44]. Another gene near rs6076699, *SLC23A2* (Solute Carrier Family 23 [Ascorbic Acid Transporter],
771 Member 2), is essential for the uptake and transport of Vitamin C, an important nutrient for DNA and
772 cellular repair in response to oxidative stress both directly and through supporting the repair of Vitamin
773 E after exposure to oxidative agents[45, 46]. SLC23A2 is present in the adrenal glands and murine models
774 indicate that it plays an important role in regulating dopamine levels[47]. This region is associated with
775 success in smoking cessation and is implicated in addictive behaviors in general[48, 49]. Our tag SNP is

776 located within an active enhancer region (marked by open chromatin marks, DNAse hypersentivity, and
777 transcription factor binding motifs); this regulatory activity appears tissue specific (sex-specific tissues
778 and lungs) [HaploReg and UCSC Genome Browser].
779
780 Nicotinamide mononucleotide adenylyltransferease (*NMNAT1*), upstream of WCadjBMI variant
781 rs17396340, is responsible for the synthesis of NAD from ATP and NMN[50, 51]. NAD is necessary for
782 cellular repair following oxidative stress. Upregulation of *NMNAT* protects against damage caused by
783 reactive oxygen species in the brain, specifically the hippocampus[52, 53]. Also for WCadjBMI, both *CDK6*,
784 near SNP rs10269774, and *FAM49B*, near SNP rs6470765, are targets of the *BACH1* transcription factor,
785 involved in cellular response to oxidative stress and management of the cell cycle[54].
786
787 **Influence of Novel Loci on Related Traits**
788
789 In a look-up in existing GWAS of smoking behaviors (Ever/Never, Current/Not-Current, Smoking
790 Quantity [SQ])[55] (**Supplementary Data 8**), eight of our 26 SNPs were nominally associated with at least
791 one smoking trait. After multiple test correction ($P<0.05/26=0.0019$), only one SNP remains significant:
792 rs12902602, identified for Approaches 2 (SNPjoint) and 3 (SNPint) for BMI, showed association with SQ
793 ($P=1.45x10^{-9}$).
794
795 We conducted a search in the NHGRI-EBI GWAS Catalog[56, 57] to determine if any of our newly identified
796 loci are in high LD with variants associated with related cardiometabolic and behavioral traits or
797 diseases. Of the seven novel BMI SNPs, only rs12902602 was in high LD ($r^2>0.7$) with SNPs previously
798 associated with smoking-related traits (e.g. nicotine dependence), lung cancer, and cardiovascular
799 diseases (e.g. coronary heart disease) (**Supplementary Table 13**). Of the 12 novel WCadjBMI SNPs, five
800 were in high LD with previously-reported GWAS variants for mean platelet volume, height, infant length,

and melanoma. Of the six novel WHRadjBMI SNPs, three were near several previously associated variants, including cardiometabolic traits (e.g. LDL cholesterol, triglycerides, and measures of renal function).

Given high phenotypic correlation between WC and WHR with height, and established shared genetic associations that overlap our adiposity traits and height[1, 2, 58] we expect cross-trait associations between our novel loci and height. Therefore, we conducted a look-up of all of our novel SNPs to identify overlapping association signals (**Supplementary Data 8**). No novel BMI loci were significantly associated with height (P<0.002[0.05/24] SNPs). However, there are additional variants that may be associated with height, but not previously reported in GWAS examining height, including 2 for WHRadjBMI near *EYA4* and *TRIB1*, and 2 for WCadjBMI near *KIF1B* and *HDLBP* (P<0.002).

Lastly, as smoking has a negative (weight decreasing) effect on BMI, it is likely that smoking associated genetic variants have an effect on BMI in current smokers. Therefore, we expected that smoking associated SNPs exhibit some interaction with smoking on BMI. We looked up published smoking behavior SNPs[56, 57], 10 variants in 6 loci, in our own results. Two variants reached nominal significance (P<0.05) for GxSMK interaction on BMI (**Supplementary Table 14**), but only one reached Bonferroni-corrected significance (P<0.005). No smoking-associated SNPs exhibited GxSMK interaction. Therefore, we did not see a strong enrichment for low interaction P-values among previously identified smoking loci.

Validation of Novel Loci

We pursued validation of our novel and interaction SNPs in an independent study sample of up to 119,644 European adults from the UK Biobank study (**Tables 1-4**, **Supplementary Table 15,**

826 **Supplementary Fig 9**). We found consistent directions of effects in smoking strata (for Approaches 2 and
827 3) and in SNPadjSMK results (Approach 1) for each locus examined (**Supplementary Fig. 13**). For BMI, 3
828 SNPs were not GWS (P>5E-8) following meta-analysis with our GIANT results: rs12629427 near *EPAH3*
829 (Approach 1); rs1809420 within a known locus near *ADAMTS7* i(Approach 4) remained significant for
830 interaction, but not for SNPadjSMK; and rs336396 near *INPP4B* (Approach 3). For WCadjBMI, 3 SNPs
831 were not GWS (P>5E-8) following meta-analysis with our results: rs1545348 near *RAI14* (Approach 1);
832 rs4141488 near *GRIN2A* (Approach 3); and rs6012558 near *PRNP* (Approach 3). For WHRadjBMI, only 1
833 SNP from Approach 4 was not significant following meta-analysis with our results: rs12608504 near
834 *JUND* remained GWS for SNPadjSMK, but was only nominally significant for interaction (P_{int}=0.013).
835
836 **Challenges in Accounting for Environmental Exposures in GWAS**
837
838 A possible limitation of our study may be the definition and harmonization of smoking status. We chose
839 to stratify on current smoking status without consideration of type of smoking (e.g. cigarette, pipe) for
840 two reasons. First, focusing on weight alone, former smokers tend to return to their expected weight
841 quickly following smoking cessation[9, 15, 59]. Second, this definition allowed us to maximize sample size, as
842 many participating studies only had current smoking status available. However, WC and WHR may not
843 behave in the same manner as weight and BMI with former smokers retaining excess fat around their
844 waist[60]. Thus, results may differ with alternative harmonization of smoking exposure.
845
846 Another limitation may be potential bias in our effect estimates when adjusting for a correlated
847 covariate (e.g. collider bias)[61, 62]. This phenomenon is of particular concern when the correlation
848 between the outcome and the covariate is high and when significant genetic associations occur with
849 both traits in opposite directions. IOur analyses adjusted both WC and WHR for BMI. WHR has a
850 correlation of 0.49 with BMI, while WC has a correlation of 0.85[62]. Using previously published results for

BMI, WCadjBMI and WHRadjBMI, we find three novel loci for WCadjBMI (near *DOCK3, ARFGEF2, TMEM38B*) and two for WHRadjBMI (near *EHMT2, HLA-C*) (**Supplementary Data 8**) with nominally significant associations with BMI and opposite directions of effect. At these loci, the genetic effect estimates should be interpreted with caution. Additionally, we adjusted for SMK in Approach 1 (SNPadjSMK). However binary smoking status, as we used, has a low correlation to BMI, WC, and WHR, as estimated in the ARIC study's European descent participants (-0.13, 0.08, and 0.12 respectively) and in the Framingham Heart Study (-0.05, 0.08, 0.16). Additionally, there are no loci identified in Approach 1 (SNPadjSMK) that are associated with any smoking behavior trait and that exhibit an opposite direction of effect from that identified in our adiposity traits (**Supplementary Data 8**). We therefore preclude potential collider bias and postulate true gain in power through SMK-adjustment at these loci.

To assess how much additional information is provided by accounting for SMK and GxSMK in GWAS for obesity traits, we compared genetic risk scores (GRSs) based on various subsets of lead SNP genotypes in various regression models (**Methods**). While any GRS was associated with its obesity trait ($P<1.6 \times 10^{-7}$, **Supplementary Table 16**), adding SMK and GxSMK terms to the regression model along with novel variants to the GRSs substantially increased variance explained. For example, variance explained increased by 38% for BMI (from 1.53% to 2.11%, $P=4.3\times10^{-5}$), by 27% for WCadjBMI (from 2.59% to 3.29%, $P=3.9\times10^{-6}$) and by 168% for WHRadjBMI (from 0.82% to 2.20%, $P=3.2\times10^{-11}$). Therefore, despite potential limitations, there is much to be gained by accounting for environmental exposures in GWAS studies.

DISCUSSION

To better understand the effects of smoking on genetic susceptibility to obesity, we conducted meta-analyses to uncover genetic variants that may be masked when the environmental influence of smoking is not considered, and to discover genetic loci that interact with smoking on adiposity-related traits. We identified 161 loci in total, including 23 novel loci (6 for BMI, 11 for WCadjBMI, and 6 for WHRadjBMI). While many of our newly identified loci support the hypothesis that smoking may influence weight fluctuations through appetite regulation, these novel loci also have highlighted new biological processes and pathways implicated in the pathogenesis of obesity.

Importantly, we identified nine loci with convincing evidence of GxSMK interaction on obesity-related traits. We were able to replicate the previous GxSMK interaction with BMI within the *CHRNA5-CHRNA3-CHRNB4* gene cluster. One novel BMI-associated locus near *INPP4B* and two novel WCadjBMI-associated loci near *GRIN2A* and *PRNP* displayed significant GxSMK interaction. We were also able to identify significant GxSMK interaction for one known BMI-associated locus near *ADAMTS7* and for five known WHRadjBMI-associated loci near *LYPLAL1*, *RSPO3*, *MAP3K1*, *HOXC4-HOXC6* and *JUND*. The majority of these loci harbor strong candidate genes for adiposity with a possible role for the modulation of effects through tobacco use.

We identified 18 new loci in Approach 1 ($P_{SNPadjSMK}$) by adjusting for current smoking status. Our analyses did not allow us to determine whether these discoveries are due to different subsets of subjects included in the analyses compared to previous studies[1, 2] or due only to adjusting for current smoking. Adjustment for current smoking in our analyses, however, did reveal novel associations. Specifically after accounting for smoking in our analyses, all novel BMI loci exhibit P-values that are at least one order of magnitude lower than in previous GIANT investigations, despite smaller samples in the current analysis[2]. While sample sizes for both WCadjBMI and WHRadjBMI are comparable with previous GIANT

investigations, our p-values for variants identified in Approach 1 are at least two orders of magnitude lower than previous findings. Thus, adjustment for smoking may have indeed revealed new loci. Further, loci identified in Approach 2, including 9 novel loci, suggest that accounting for interaction improves our ability to detect these loci even in the presence of only modest evidence of GxSMK interaction.

There are several challenges in validating genetic associations that account for environmental exposure. In addition to exposure harmonization and potential bias due to adjustment for smoking exposure, differences in trait distribution, environmental exposure frequency, ancestry-specific LD patterns and allele frequency across studies may lead to difficulties in replication, especially for gene-by-environment studies[63, 64]. Further, the "winner's curse" (inflated discovery effects estimates) requires larger sample sizes for adequate power in replication studies[65]. Despite these challenges, we were able to detect consistent direction of effect in an independent sample for all novel loci. Some results that did not remain GWS in the GIANT + UKBB meta-analysis had results that were just under the threshold for significance, suggesting that a larger sample may be needed to confirm these results, and thus the associations near *INPP4B*, *GRIN2A*, *RAI14*, *PRNP*, and *JUND* should be interpreted with caution.

While we found that effects were not significantly enriched in smokers for BMI, there is a greater proportion of variance in BMI explained by variants that are significant for Approach 1 (SNPadjSMK), which may be expected given that there are a greater number of variants with higher effect estimates in smokers. For WCadjBMI, there was no enrichment for stronger effects in one stratum compared to the other for our significant loci; however, there was a greater proportion of explained variance in WCadjBMI for loci identified in Approach 1 (SNPadjSMK) in nonsmokers. For WHRadjBMI, there were significantly more loci that exhibit greater effects in nonsmokers, and this pattern was mirrored in the variance explained analysis. The large difference between effects in smokers and nonsmokers likely

explains the sub-GWS levels of our loci in previous GIANT investigations[2]. For example, the T allele of rs7697556, 81kb from the *ADAMTS3* gene, was associated with increased WCadjBMI and exhibits a six-fold greater effect in nonsmokers compared to smokers, although the interaction effect was only nominal; in previous GWAS this variant was nearly GWS. These differences in effect estimates between smokers and nonsmokers may help explain inconsistent findings in previous analyses that show central adiposity increases with increased smoking, but is associated with decreased weight and BMI[6, 11, 12].

Our results support previous findings that implicate genes involved in transcription and gene expression, appetite regulation, macronutrient metabolism, and glucose homeostasis. Several of our novel loci have candidate genes within 500 kb of our tag variants that are highly expressed and/or active in brain tissue (*BBX*, *KIF1B*, *SOX11*, and *EPHA3*) and, like other obesity-associated genes, may be involved in previously-identified pathways linked to neuronal regulation of appetite (*KIF1B*, *GRIN2A*, and *SLC23A2*), adipo/angiogenesis (*ANGPTL3* and *TNF*) and glucose, lipid and energy homeostasis (*CD47*, *STK25*, *STK19*, *RAGE*, *AIF1*, *LYPLAL1*, *HDLBP*, *ANGPTL3*, *DOCK7*, *KIF1B*, *PREX1*, and *RPS12*).

Many our newly identified loci highlight novel biological functions and pathways where dysregulation may lead to increased susceptibility to obesity, including response to oxidative stress, addictive behavior, and newly identified regulatory functions. There is a growing body of evidence that supports the notion that exposure to oxidative stress leads to increased adiposity, risk of obesity, and poor cardiometabolic outcomes[30, 66, 67]. Our results for BMI and WCadjBMI, specifically associations identified near *CHRNA5-CHRNA3-CHRNB4, PRNP, SLC23A2, BACH1, and NMNAT1,* highlight new biological pathways and processes for future examination and may lead to a greater understanding of how oxidative stress leads to changes in obesity phenotypes and downstream cardiometabolic risk.

By considering current smoking, we were able to identify 6 novel loci for BMI, 11 for WCadjBMI, and 6 for WHRadjBMI, and highlight novel biological processes and regulatory functions for genes implicated in increased obesity risk. Eighteen of these remained significant in our validation with the UK Biobank sample. We confirmed most established loci in our analyses after adjustment for smoking status in smaller samples than were needed in previous discovery analyses. A typical approach in large-scale GWAS meta-analyses is not to adjust for covariates such as current smoking; our findings highlight the importance of accounting for environmental exposures in genetic analyses.

METHODS

Study Design Overview

We applied four approaches to identify genetic loci that influence adiposity traits by accounting for current tobacco smoking status (**Figure 1**). We defined smokers as those who responded that they were currently smoking; not current smokers were those that responded "no" to currently smoking. We evaluated three traits: body mass index (BMI), waist circumference adjusted for BMI (WCadjBMI), and waist-to-hip ratio adjusted for BMI (WHRadjBMI). Our first two meta-analytical approaches were aimed at determining whether there are novel genetic variants that affect adiposity traits by adjusting for SMK (SNPadjSMK), or by jointly accounting for SMK and for interaction with SMK (SNPjoint); while Approaches 3 and 4 aimed to determine whether there are genetic variants that affect adiposity traits through interaction with SMK (SNPint and SNPscreen) (**Figure 1**). Our ***primary meta-analyses*** focused on results from all ancestries, sexes combined. ***Secondary meta-analyses*** were performed using the European-descent populations only, as well as stratified by sex (men-only and women-only) in all ancestries and in European-descent study populations.

Cohort Descriptions and Sample Sizes

The GIANT consortium was formed by an international group of researchers interested in understanding the genetic architecture of anthropometric traits (**Supplemental Tables 1-4** for study sample sizes and descriptive statistics). In total, we included up to 79 studies comprising up to 241,258 individuals for BMI (51,080 smokers, 190,178 nonsmokers), 208,176 for WCadjBMI (43,226 smokers, 164,950 nonsmokers), and 189,180 for WHRadjBMI (40,543 smokers, 148,637 nonsmokers) with HapMap II imputed genome-wide chip data (up to 2.8M SNPs in association analyses), and/or with genotyped MetaboChip data

(~195K SNPs in association analyses)[68]. In instances where studies submitted both Metabochip and GWAS data, these were for non-overlapping individuals. Each study's Institutional Review Board has approved this research and all study participants have provided written informed consent.

Phenotype descriptions

Our study highlights three traits of interest: BMI, WCadjBMI and WHRadjBMI. Height and weight, used to calculate BMI (kg/m^2), were measured in all studies; waist and hip circumferences were measured in the vast majority. For each sex, traits were adjusted using linear regression for age and age^2 (as well as for BMI for WCadjBMI and WHRadjBMI), and (when appropriate) for study site and principal components to account for ancestry. Family studies used linear mixed effects models to account for familial relationships and also conducted analyses for men and women combined including sex in the model. Phenotype residuals were obtained from the adjustment models and were inverse normally transformed subsequently to facilitate comparability across studies and with previously published analyses. The trait transformation was conducted separately for smokers and nonsmokers for the SMK-stratified model and using all individuals for the SMK-adjusted model.

Defining Smokers

The participating studies have varying levels of information on smoking, some with a simple binary variable and others with repeated, precise data. Since the effects of smoking cessation on adiposity appear to be immediate[9, 10, 59], a binary smoking trait (current smoker vs. not current smoker) is used for the analyses as most studies can readily derive this variable. We did not use a variable of 'ever smoker vs. never' as it increases heterogeneity across studies, thus adding noise; also this definition would make harmonization across studies difficult.

Genotype Identification and Imputation

Studies with GWAS array data or Metabochip array data contributed to the results. Each study applied study-specific standard exclusions for sample call rate, gender checks, sample heterogeneity and ethnic group outliers (**Supplementary Table 2**). For most studies (except those that employed directly typed MetaboChip genotypes), genome-wide chip data was imputed to the HapMap II reference data set via MACH[69], IMPUTE[70], BimBam[71] or Beagle[72].

Study Level Analyses

To obtain study-specific summary statistics used in subsequent meta-analyses, the following linear models (or linear mixed effects models for studies with families/related individuals) were run separately for men and women and separately for cases and controls for case-control studies using phenotype residuals from the models described above. Studies with family data also conducted analyses with these models for men and women combined after accounting for dependency among family members as a function of their kinship correlations. We assumed an additive genetic model.

SMK-adjusted: $TRAIT = \beta_0 + \beta_1 SNP + \beta_2 SMK$

SMK-stratified: $TRAIT = \beta_0 + \beta_1 SNP$ (run in current smokers and nonsmokers separately)

The analyses were run using various GWAS software, including MACH2QTL [73], SNPTEST [74], ProbABEL[75], GenABEL[76], Merlin[77], PLINK[78] or QUICKTEST[79].

Quality control of study-specific summary statistics

The aggregated summary statistics were quality-controlled according to a standardized protocol[80]. These included checks for issues with trait transformations, allele frequencies and strand. Low quality SNPs in

each study were excluded for the following criteria: (i) SNPs with low minor allele count (MAC <= 5, MAC = MAF * N) and monomorphic SNPs, (ii) genotyped SNPs with low SNP call-rate (< 95%) or low Hardy-Weinberg equilibrium test P-Value (< 10^{-6}), (iii) imputed SNPs with low imputation quality (MACH-Rsq or OEVAR<0.3, or information score <0.4 for SNPTEST/IMPUTE/IMPUTE2, or <0.8 for PLINK). To test for issues with relatedness or overlapping samples and to correct for potential population stratification, the study-specific standard errors and association P-Values were genomic control (GC) corrected using lambda factors[81] (**Supplementary Fig. 1**). GC correction for GWAS data used all SNPs, but GC correction for MetaboChip data were restricted to chip QT interval SNPs only as the chip was enriched for associations with obesity-related traits. Any study-level GWAS file with a lambda > 1.5 was removed from further analyses. While we established this criterion, no study results were removed for this reason.

Meta-analyses

Meta-analyses used study-specific summary statistics for the phenotype associations for each of the above models. We used a fixed-effects inverse variance weighted method for the SNP main effect analyses. All meta-analyses were run in METAL[82]. As study results came in two separate batches (Stage 1 and Stage 2), meta-analyses from the two stages were further meta-analyzed (Stage 1 + Stage 2). A second GC correction was applied to all SNPs when combining Stage 1 and Stage 2 meta-analyses in the final meta-analysis. First, Hapmap-imputed GWAS data were meta-analyzed together, as were Metabochip studies. This step was followed by a combined GWAS + Metabochip meta-analysis. For primary analyses, we conducted meta-analyses across ancestries and sexes. For secondary meta-analyses, we conducted meta-analyses in European-descent studies alone, and sex-specific meta-analyses. There were two reasons for conducting secondary meta-analyses. First, both WCadjBMI and WHRadjBMI have been shown to display sex-specific genetic effects[2, 83, 84]. Second, by including

populations from multiple ancestries in our primary meta-analyses, we may be introducing heterogeneity due to differences in effect sizes, allele frequencies, and patterns of linkage disequilibrium across ancestries, potentially decreasing power to detect genetic effects. See **Supplementary Fig. 1** for a summary of the primary meta-analysis study design. The obtained SMK-stratified summary statistics were later used to calculate summary SNPjoint and SNPint statistics using EasyStrata[85]. Briefly, this software implements a two-sample, large sample test of equal regression parameters between smokers and nonsmokers as described by Randall et al[83] for SNPint and the two degree of freedom test of main and interaction effects for SNPjoint as described by Aschard et al[16].

Lead SNP selection

Before selecting a lead SNP for each locus, SNPs with high heterogeneity $I^2 \geq 0.75$ or a minimum sample size below 50% of the maximum N for each strata (e.g. N> max[N Women Smokers]/2) were excluded. Lead SNPs that met significance criteria were selected based on distance (+/- 500 kb), and we defined the SNP with the lowest P-value as the top SNP for a locus. SNPs that reached genome-wide significance (GWS), but had no other SNPs within 500 kb with a P<1E-5 (lonely SNPs), were excluded from the SNP selection process. Two variants were excluded from Approach 2 based on this criterion, rs2149656 for WCadjBMI and rs2362267 for WHRadjBMI.

Approaches

Figure 1 outlines the four approaches that we used to identify novel SNPs. The left side of Figure 1 focuses on the first hypothesis that examines the effect of SNPs on adiposity traits. *Approach 1* considered a linear regression model that includes the SNP and SMK, thus adjusting for SMK (SNPadjSMK). Summary SNPadjSMK results were obtained from the SMK-adjusted meta-analysis. *Approach 2* used summary SMK-stratified meta-analysis results as described by Aschard et al.[16] to

consider the joint hypothesis that a genetic variant has main and/or interaction effects on outcomes as a 2 degree of freedom test (SNPjoint). For this approach, the null hypothesis was that there is no main and no interaction effect on the outcome. Thus, rejection of this hypothesis could be due to either a main effect or an interaction effect or to both.

The right side of Figure 1 focuses on our second hypothesis, testing for interaction of a variant with SMK on adiposity traits as outcomes. *Approach 3* used the SMK-stratified results to directly contrast the regression coefficients for a test of interaction (SNPint)[83]. *Approach 4* used a screening strategy to evaluate interaction, whereby the SMK-adjusted main effect results (Approach 1) were screened for variants significant at the $P<5x10^{-8}$ level. These variants were then carried forward for a test of interaction, comparing the SMK-stratified specific regression coefficients in the second step (SNPscreen).

In *Approaches 1-3* variants significant at $P<5x10^{-8}$ were considered GWS. In *Approach 4* (SNPscreen) variants for which the p-value of the test of interaction is less than 0.05 divided by the number of variants carried forward were considered significant for interaction. We performed analytical power computations to demonstrate the usefulness and characteristic of the two interaction Approaches.

LocusZoom Plots

Regional association plots were generated for novel loci using the program Locuszoom[86]. For each plot, LD was calculated using a multiethnic sample of the 1000 Genomes Phase I reference panels[87], including EUR, AFR, EAS, and AMR. Previous SNP-trait associations highlighted within the plots include traits of interest (e.g. cardiometabolic, addiction, behavior, anthropometrics) found in the NHGRI-EMI GWAS Catalog and supplemented with recent GWAS studies from the literature[1, 2, 58, 84].

Conditional Analyses

To determine if multiple association signals were present within a single locus, we used GCTA[17] to perform approximate joint conditional analyses on the SNPadjSMK and SMK- stratified data. The following criteria were used to select candidate loci for conditional analyses: nearby SNP (+/- 500kb) with an R^2>0.4 and an association P<1E-5 for any of our primary analyses. GCTA uses associations from our meta-analyses and LD estimates from reference data sets containing individual-level genotypic data to perform the conditional analyses. To calculate the LD structure, we used two U.S. cohorts, the Atherosclerosis Risk in Communities (ARIC) study consisting of 9,713 individuals of European descent and 580 individuals of African American descent, and the Framingham Heart Study (FramHS) consisting of 8,481 individuals of European ancestry, both studies imputed to HapMap r22. However, because our primary analyses were conducted in multiple ancestries, each study supplemented the genetic data using HapMap reference populations so that the final reference panel was composed of about 1-3% Asians (CHB + JPT) and 4-6% Africans (YRI for the FramHS) for the entire reference sample. We extracted each 1 MB region surrounding our candidate SNPs, performed joint approximate conditional analyses, and then repeated the steps for the appropriate Approach to identify additional association signals.

Many of the SNPs identified in the current analyses were nearby SNPs previously associated with related anthropometric and obesity traits (e.g. height, visceral adipose tissue). For all lead SNPs near a SNP previously associated with these traits, GCTA was also used to perform approximate conditional analyses on the SNPadjSMK and SMK-stratified data in order to determine if the loci identified here are independent of the previously identified SNP-trait associations.

Power and Type I Error

In order to illustrate the validity of the approaches with regards to type 1 error, we conducted simulations. For two MAF, we assumed standardized stratum-specific outcomes for 50,000 smokers and 180,000 nonsmokers and generated 10,000 simulated stratum-specific effect sizes under the stratum-specific null hypotheses of "no stratum-specific effects". We applied the four approaches to the simulated stratum-specific association results and inferred type 1 error of each approach by visually examining QQ plots and by calculating type 1 error rates. The type 1 error rates shown reflect the proportion of nominally significant simulation results for the respective approach. Analytical power calculations to identify effects for various combinations of SMK- and NonSMK-specific effects by the Approaches 1-4 again assumed 50,000 smokers and 180,000 nonsmokers. We first assumed three different fixed effect estimates in smokers that were small (R^2_{SMK}=0.01%, similar to the realistic *NUDT3* effect on BMI), medium (R^2_{SMK}=0.07%, similar to the realistic *BDNF* effect on BMI) or large (R^2_{SMK}=0.34%, similar to the realistic *FTO* effect on BMI) genetic effects, and varied the effect in nonsmokers. Second, we assumed fixed (small, medium and large) effects in nonsmokers and varied the effect in smokers.

Biological Summaries

To identify genes that may be implicated in the association between our lead SNPs (Tables 1-3) and BMI, WHRadjBMI, and WCadjBMI, and to shed light on the complex relationship between genetic variants, SMK and adiposity, we performed in-depth literature searches on nearby candidate genes. Snipper v1.2 (http://csg.sph.umich.edu/boehnke/snipper/) was used to identify any genes and cis- or trans-eQTLs within 500kb of our lead SNPs. All genes identified by Snipper were manually curated and examined for evidence of relationship with smoking and/or adiposity. To explore any potential regulatory or function role of the association regions, loci were also examined using several bioinformatic tools/databases, including HaploReg v4.1[88], UCSC Genome Browser[89] (available at http://genome.ucsc.edu/), GTeX Portal[90], and RegulomeDB[91].

eQTL Analyses

We used two approaches to systematically explore the role of novel loci in regulating gene expression. First, to gain a general overview of the regulatory role of newly identified GWAS regions, we conducted an eQTL lookup using >50 eQTL studies[92], with specific citations for >100 datasets included in the current query for blood cell related eQTL studies and relevant non-blood cell tissue eQTLs (e.g. adipose and brain tissues). Additional eQTL data was integrated from online sources including ScanDB, the Broad Institute GTEx Portal, and the Pritchard Lab (eqtl.uchicago.edu). Additional details on the methods, including study references can be found in **Supplementary Note 3**. Only significant cis-eQTLS in high LD with our novel lead SNPs (r2>0.9, calculated in the CEU+YRI+CHB+JPT 1000 Genomes reference panel), or proxy SNPs, were retained for consideration.

Second, since public databases with eQTL data do not have information available on current smoking status, we also conducted a cis-eQTL association analysis using expression results derived from fasting peripheral whole blood using the Human Exon 1.0 ST Array (Affymetrix, Inc., Santa Clara, CA). The raw expression data were quantile-normalized, log2 transformed, followed by summarization using Robust Multi-array Average[93] and further adjusted for technical covariates, including the first principal component of the expression data, batch effect, the all-probeset-mean residual, blood cell counts, and cohort membership. We evaluated all transcripts +/- 1MB around each novel variant in the Framingham Heart Study while accounting for current smoking status, using the following four approaches similar to those used in our primary analyses of our traits: 1) eQTL adjusted for SMK, 2) eQTL stratified by SMK, 3) eQTL x SMK interaction, and 4) joint main + eQTLxSMK interaction). Significance level was evaluated by FDR < 5% per eQTL analysis and across all loci identified for that model in the primary meta-analysis. Additional details can be found in **Supplementary Note 3**.

Variance-explained estimates

We estimated the phenotypic variance in smokers and nonsmokers explained by the association signals using a method previously described by Kutalik et al.[94] For each associated region, we selected subsets of SNPs within 500 kb of our lead SNPs and based on varying P value thresholds (ranging from $1x10^{-8}$ to 0.1) from Approach 1 (SNPadjSMK model). First, each subset of SNPs was clumped into independent regions to identify the lead SNP for each region. The variance explained by each subset of SNPs in the SMK and nonSMK strata was estimated by summing the variance explained by the individual lead SNPs.

Smoking Behavior Lookups

In order to determine if any of the loci identified in the current study are associated with smoking behavior, we conducted a look-up of all lead SNPs from novel loci and Approach 3 in existing GWAS of smoking behavior[3]. The analysis consists of phasing study-specific GWAS samples contributing to the smoking behavior meta-analysis, imputation, association testing and meta-analysis. To ensure that all SNPs of interest were available in the smoking GWAS, the program SHAPEIT2[95] was used to phase a region 500Kb either side of each lead SNP, and imputation was carried out using IMPUTE2[96] with the 1000 Genomes Phase 3 dataset as a reference panel.

Each region was analyzed for 3 smoking related phenotypes: (i) Ever vs Never smokers, (ii) Current vs Non-current smokers, and (iii) a categorical measure of smoking quantity[55]. The smoking quantity levels were 0 (defined as 1-10 cigarettes per day [CPD]), 1 (11-20 CPD), 2 (21-30 CPD) and 3 (31 or more CPD). Each increment represents an increase in smoking quantity of 10 cigarettes per day. There were 10,058 Never smokers, 13,418 Ever smokers, 11,796 Non-current smokers, 6,966 Current smokers and 11,436 samples with the SQ phenotypes. SNPMETA[55] was used to perform an inverse-variance weighted fixed

effects meta-analysis across cohorts at all SNPs in each region, and included a single GC correction. At each SNP, only those cohorts that had an imputation info score > 0.5 were included in the meta-analysis.

Main Effects Lookup in Previous GIANT Investigations

To better understand why our novel variants remained undiscovered in previous investigations that did not take SMK into account, we also conducted a lookup of our novel variants in published GWAS results examining genetic main effects on BMI, WC, WCadjBMI, WHR, WHRadjBMI, and height[1, 2, 58].

GWAS Catalog Lookups

To further investigate the identified genetic variants in this study and to gain additional insight into their functionality and possible effects on related cardiometabolic traits, we searched for previous SNP-trait associations nearby our lead SNPs. PLINK was used to find all SNPs within 500 kb of any of our lead SNPs and calculate r^2 values using a combined ancestry (AMR, AFR, EUR, ASN) 1000 Genomes Phase 1 reference panel[87] to allow for LD calculation for SNPs on the Illumina Metabochip and to best estimate LD in our multiethnic GWAS. All SNPs within the specified regions were compared with the NHGRI-EBI (National Human Genome Research Institute, European Bioinformatics Institute) GWAS Catalog, version 1.0 (www.ebi.ac.uk/gwas)[56, 57] for overlap, and distances between the two SNPs were calculated using STATA v14, for the chromosome and base pair positions based on human genome reference build 19. All previous associations within 500 kb and with an R^2>0.5 with our lead SNP were retained for further interrogation.

Genetic risk score calculation

We calculated several unweighted genetic risk scores (GRSs) for each individual in the population-based KORA-S3 and KORA-S4 studies (total N = 3,457). We compared GRSs limited to previously known lead

SNPs (see **Supplementary Data 7** for lists of previously known lead SNPs) with GRSs based on previously known and novel lead SNPs from the current study (see **Tables 1-4** for lists of novel lead SNPs). Risk scores were tested for association with the obesity trait using the following linear regression models: The unadjusted GRS model (TRAIT = $\beta_0 + \beta_1$GRS), the adjusted GRS model (TRAIT = $\beta_0 + \beta_1$GRS + β_2SMK) and the GRSxSMK interaction model (TRAIT = $\beta_0 + \beta_1$GRS + β_2SMK + β_3GRSxSMK).

DATA AVAILABILITY

Summary statistics of all analyses are available at https://www.broadinstitute.org/collaboration/giant/.

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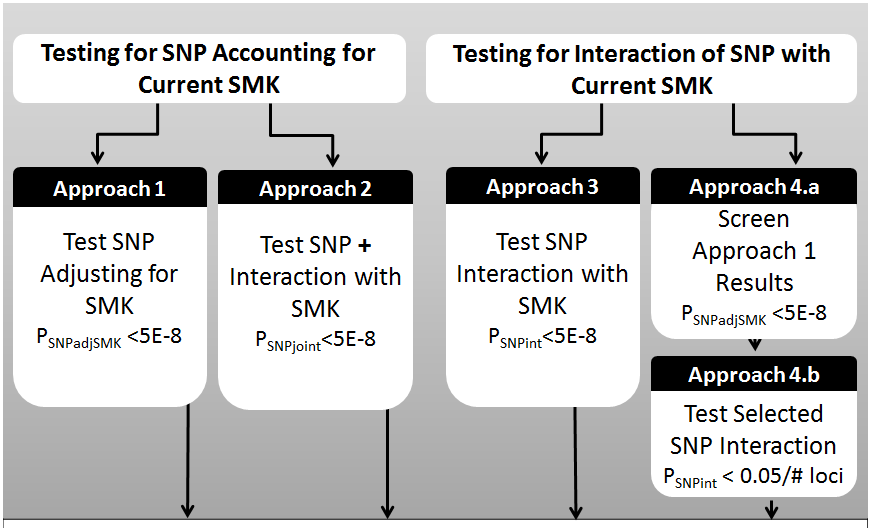
1673
1674 **COMPETING FINANCIAL INTERESTS**
1675 Bruce Psaty serves on the DSMB for a clinical trial funded by the device manufacturer (Zoll LifeCor) and
1676 on the Steering Committee of the Yale Open Data Access Project funded by Johnson & Johnson.

Figure 1. **Summary of study design and results**. Approach 1 uses both SNP and SMK in the association model. Approaches 2 and 3 use the SMK-stratified meta-analyses. Approach 4 screens loci based on Approach 1, then uses SMK-stratified results to identify loci with significant interaction effects (**Methods**).



Total Number of Significant Loci/Number of Novel

	Effect of SNP Accounting for Current SMK		Interaction of SNP with Current SMK	
Trait	Approach 1	Approach 2	Approach 3	Approach 4
BMI	65 / 4	57 / 2	2 / 1	1 / 0
WCadjBMI	72 / 9	66 / 5	2 / 2	0
WHRadjBMI	44 / 5	24 / 2	0	5 / 0

Total Non-Overlapping Loci

BMI: 68 / 6 **WCadjBMI: 76 / 11** **WHRadjBMI: 45 / 6**

Figure 2. **Forest plot for novel and GxSMK loci stratified by smoking status**. Estimated effect estimates (β ± 95% CI) per risk allele for **a**) BMI, **b**) WCadjBMI, and **c**) WHRadjBMI for novel loci from Approaches 1 and 2 (SNPadjSMK and SNPjoint, respectively) and all loci from Approaches 3 and 4 (SNPint and SNPscreen) identified in the primary meta-analyses. Loci are ordered by greater magnitude of effect in smokers compared to nonsmokers and labeled with the nearest gene. For the locus near *TMEM38B,* rs9409082 was used for effect estimates in this plot. (¥ loci identified for Approach 4, *loci identified for Approach 3).

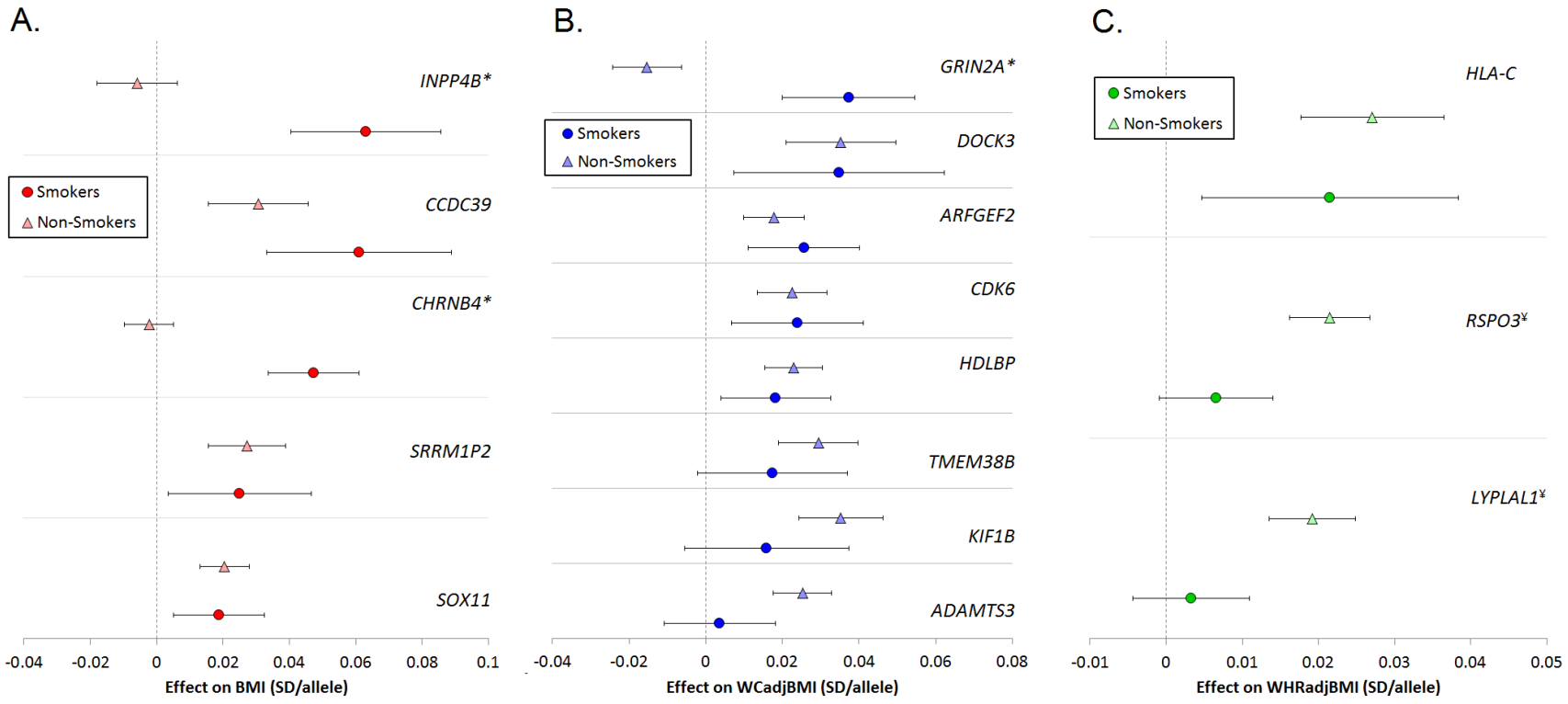
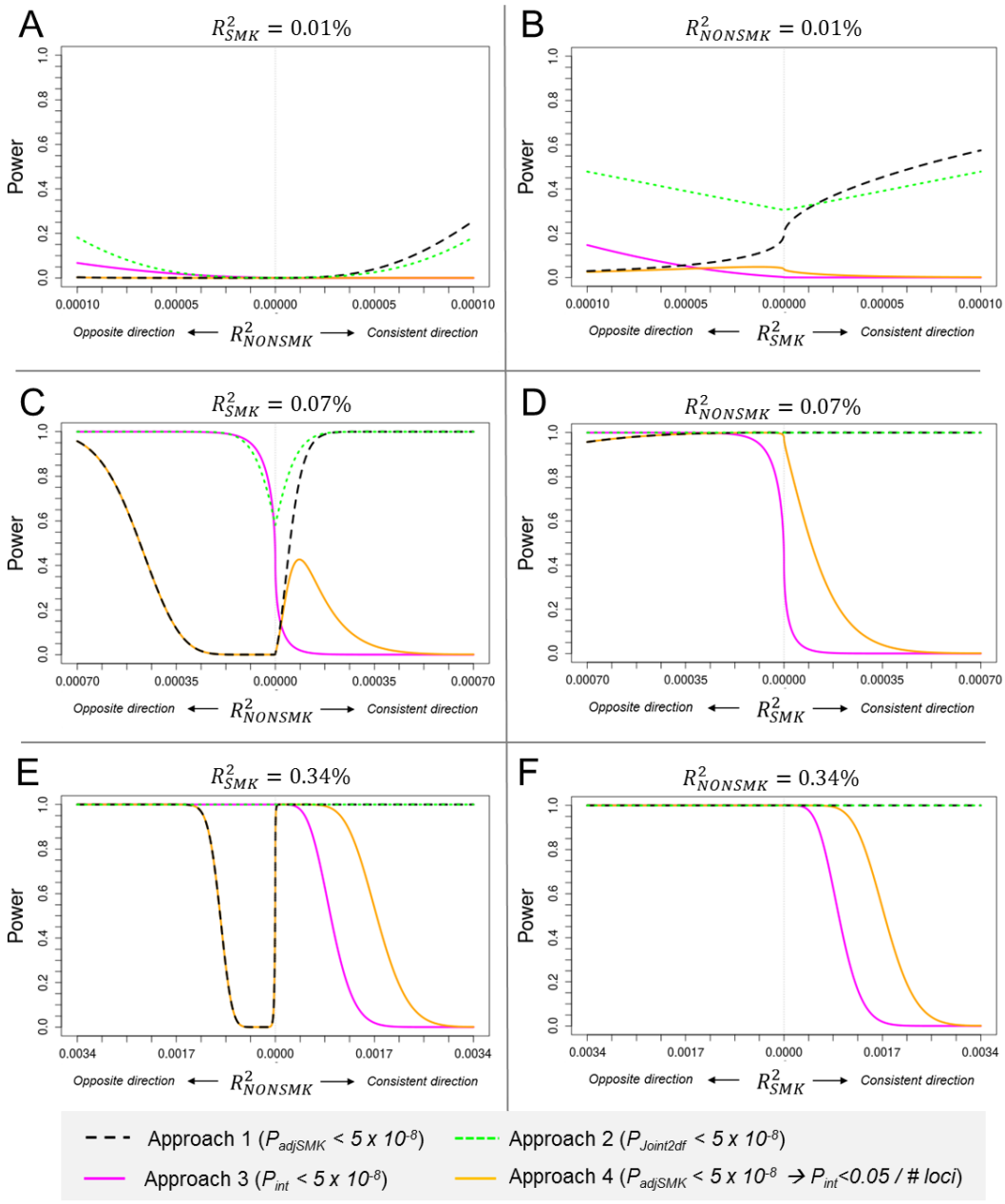
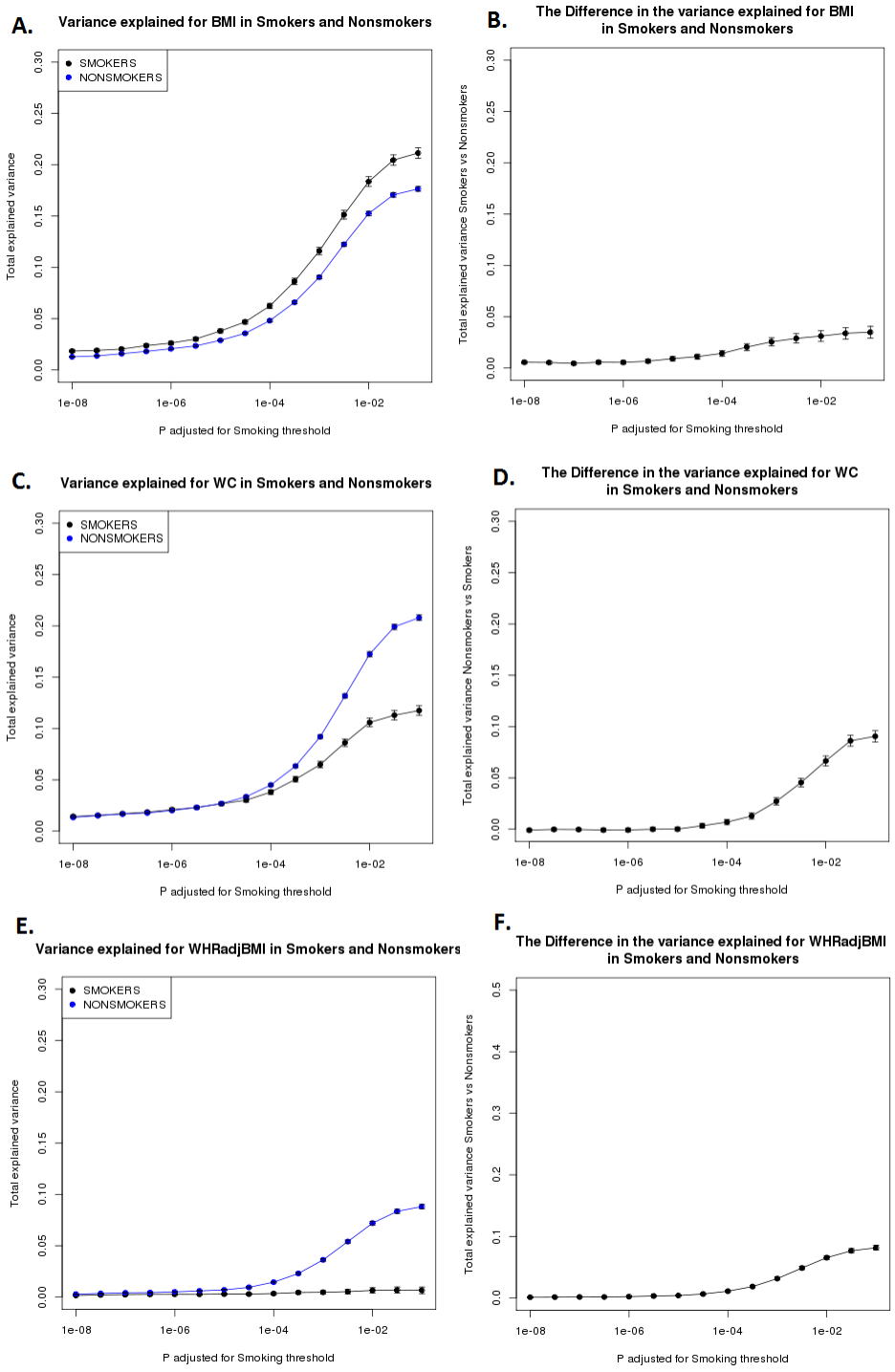


Figure 3. Power comparison across Approaches. Shown is the power to identify adjusted (Approach 1, dashed black lines), joint (Approach 2, dotted green lines) and interaction (Approach 3 and 4, solid magenta and orange lines) effects for various combinations of SMK- and NonSMK-specific effects and assuming 50,000 smokers and 180,000 nonsmokers. For Figures **a**, **c** and **e**, the effect in smokers was fixed at a small (R^2_{SMK}=0.01%, similar to the realistic *NUDT3* effect on BMI), medium (R^2_{SMK}=0.07%, similar to the realistic *BDNF* effect on BMI) or large (R^2_{SMK}=0.34%, similar to the realistic *FTO* effect on BMI) genetic effect, respectively, and varied in nonsmokers. For Figures **b**, **d** and **f**, the effect in nonsmokers was fixed to the small, medium and large BMI effects, respectively, and varied in smokers.


A
$R^2_{SMK} = 0.01\%$
B
$R^2_{NONSMK} = 0.01\%$
C
$R^2_{SMK} = 0.07\%$
D
$R^2_{NONSMK} = 0.07\%$
E
$R^2_{SMK} = 0.34\%$
F
$R^2_{NONSMK} = 0.34\%$
Power
Opposite direction
R^2_{NONSMK}
Consistent direction
R^2_{SMK}
Approach 1 ($P_{adjSMK} < 5 \times 10^{-8}$)
Approach 2 ($P_{Joint2df} < 5 \times 10^{-8}$)
Approach 3 ($P_{int} < 5 \times 10^{-8}$)
Approach 4 ($P_{adjSMK} < 5 \times 10^{-8} \rightarrow P_{int} < 0.05 / \#\ loci$)

1699
1700

Figure 4. **Stratum specific estimates of variance explained**. Total smoking status-specific explained variance (+/- SE) by SNPs meeting varying thresholds of overall association in Approach 1 (SNPadjSMK) and the difference between the proportion of variance explained between smokers and nonsmokers for these same sets of SNPs in BMI (**a,b**), WCadjBMI (**c,d**), and for WHRadjBMI (**e,f**).


A.
Variance explained for BMI in Smokers and Nonsmokers
SMOKERS
NONSMOKERS
Total explained variance
P adjusted for Smoking threshold
B.
The Difference in the variance explained for BMI in Smokers and Nonsmokers
Total explained variance Smokers vs Nonsmokers
P adjusted for Smoking threshold
C.
Variance explained for WC in Smokers and Nonsmokers
SMOKERS
NONSMOKERS
Total explained variance
P adjusted for Smoking threshold
D.
The Difference in the variance explained for WC in Smokers and Nonsmokers
Total explained variance Nonsmokers vs Smokers
P adjusted for Smoking threshold
E.
Variance explained for WHRadjBMI in Smokers and Nonsmokers
SMOKERS
NONSMOKERS
Total explained variance
P adjusted for Smoking threshold
F.
The Difference in the variance explained for WHRadjBMI in Smokers and Nonsmokers
Total explained variance Smokers vs Nonsmokers
P adjusted for Smoking threshold

1705
1706

Table 1. Summary of association results for novel loci reaching genome-wide significance in Approach (App) 1 ($P_{SNPadjSMK}$<5E-8) or Approach 2 ($P_{SNPjoint}$ <5E-8) for our primary meta-analysis in combined ancestries and combined sexes.

App	Marker	Chr:Pos (hg19)	Nearest Gene	N	EAF	Alleles E/O	SMOKERS β	SMOKERS P	NON-SMOKERS β	NON-SMOKERS P	Main and Interaction Effects β_{adj}	Main and Interaction Effects $P_{SNPadjSMK}$	Main and Interaction Effects P_{SNPint}	Main and Interaction Effects $P_{SNPjoint}$	GIANT + UKBB $P_{SNPadjSMK}$	GIANT + UKBB P_{SNPint}	GIANT + UKBB $P_{SNPjoint}$
BMI																	
1,2	rs10929925	2:6155557	*SOX11*	225,067	0.55	C/A	0.019	7.80E-03	0.02	8.40E-08	0.020	**1.1E-09**	8.2E-01	**1.6E-08**	**1.5E-13**	4.5E-01	**9.8E-13**
1	rs6794880	3:84451512	*SRRM1P2*	186,968	0.85	A/G	0.025	2.30E-02	0.027	3.90E-06	0.028	**4.3E-08**	8.5E-01	1.8E-06	**4.9E-09**	4.5E-01	9.7E-08
2	rs13069244	3:180441172	*CCDC39*	233,776	0.08	A/G	0.061	1.80E-05	0.031	6.60E-05	0.035	1.2E-07	4.6E-02	**3.5E-08**	**6.1E-10**	1.1E-02	**9.6E-11**
WCadjBMI																	
1,2	rs17396340	1:10286176	*KIF1B*	206,485	0.14	A/G	0.016	1.40E-01	0.035	**4.70E-10**	0.028	**3.0E-08**	9.8E-02	**9.1E-10**	**1.0E-11**	2.9E-02	**1.5E-13**
1,2	rs6743226	2:242236972	*HDLBP*	200,666	0.53	C/T	0.018	1.30E-02	0.023	**2.60E-09**	0.022	**1.2E-10**	5.5E-01	**5.8E-10**	**6.7E-12**	7.0E-01	**2.8E-11**
1	rs4378999	3:51208646	*DOCK3*	156,566	0.13	T/A	0.035	1.30E-02	0.035	1.30E-06	0.036	**4.1E-08**	9.7E-01	4.1E-07	**7.6E-11**	5.3E-01	**3.2E-10**
1,2	rs7697556	4:73515313	*ADAMTS3*	206,017	0.49	T/C	0.004	6.30E-01	0.025	**7.30E-11**	0.021	**5.2E-09**	6.7E-03	**7.6E-10**	**5.4E-19**	1.9E-02	**2.7E-19**
1	rs10269774	7:92253972	*CDK6*	157,552	0.34	A/G	0.024	6.60E-03	0.023	1.10E-06	0.023	**2.9E-08**	8.8E-01	1.6E-07	**2.9E-10**	7.7E-01	**2.1E-09**
1	rs6470765	8:130736697	*GSDMC*	157,450	0.76	A/C	0.032	1.90E-03	0.023	1.70E-05	0.026	**4.8E-08**	4.3E-01	9.5E-07	**2.5E-12**	8.9E-01	**9.0E-11**
2	rs9408815	9:108890521	*TMEM38B*	156,427	0.75	C/G	0.012	2.30E-01	0.03	**4.20E-09**	0.026	**2.3E-08**	8.5E-02	**1.7E-08**	**1.2E-11**	3.0E-01	**2.8E-11**
1	rs9409082	9:108901049		157,785	0.76	C/T	0.017	8.10E-02	0.029	**2.60E-08**	0.027	**1.5E-08**	2.7E-01	**4.6E-08**	**9.5E-12**	6.6E-01	**6.5E-11**
1	rs6012558	20:47531286	*ARFGEF2*	208,004	0.41	A/G	0.026	5.40E-04	0.018	6.50E-06	0.020	**1.9E-08**	3.3E-01	1.3E-07	**1.5E-09**	7.0E-02	**3.0E-09**
WHRadjBMI																	
1,2	rs1049281	6:31236567	*HLA-C*	149,285	0.66	C/T	0.022	1.30E-02	0.027	**2.00E-08**	0.025	**2.2E-09**	5.6E-01	**5.3E-09**	**1.2E-18**	8.3E-01	**1.8E-10**

Abbreviations: Chr- chromosome; Pos- position (bp); E/O- effect/other; EAF- effect allele frequency; adj- adjusted for smoking; int- interaction; App- Approach.

Table 2. Novel loci showing significant association in Approaches 1 (SNPadjSMK), 2 (SNPjoint), 3 (SNPint), and 4 (SNPscreen) for loci identified in secondary analysis samples, which were not identified in primary meta-analyses. All estimates are from the stratum specified in the Approach:Sample column (E-European-only, A- all ancestries, C- combined sexes, W-women only, M- men only). * This locus was filtered from approaches 2-4 due to low sample size in the SMK strata, and only p-values for Approach 1 are considered significant.

Approach: Strata	Marker	Chr:Pos (hg19)	Nearest Gene	N	EAF	Alleles E/O	SMOKERS β	SMOKERS P	NON-SMOKERS β	NON-SMOKERS P	Main and Interaction Effects β_{adj}	P_{adj}	P_{int}	P_{joint}	GIANT + UKBB $P_{SNPadjSMK}$	P_{SNPint}	$P_{SNPjoint}$
BMI																	
1:EC	rs2481665	1:62594677	*INADL*	209,453	0.56	T/C	0.015	4.60E-02	0.021	8.90E-08	0.019	**3.50E-08**	4.00E-01	6.70E-08	**3.3E-11**	7.8E-01	**2.0E-08**
1:AW	rs12629427	3:89145340	*EPHA3*	137,961	0.26	C/T	0.025	2.10E-02	0.028	3.60E-07	0.027	**4.80E-08**	8.00E-01	2.00E-07	7.7E-08	9.1E-01	3.0E-07
1:EW	rs2173039	3:89142175		117,942	0.26	C/G	0.024	3.10E-02	0.032	8.90E-08	0.031	**7.30E-09**	5.70E-01	6.50E-08	**2.4E-09**	9.3E-01	2.2E-07
WCadjBMI																	
1:EM	rs1545348	5:34718343	*RAI14*	77,677	0.73	T/G	0.044	3.10E-04	0.03	1.90E-05	0.034	**1.80E-08**	3.20E-01	1.70E-07	1.2E-07	1.2E-01	4.8E-07
2:EW	rs6076699	20:4566688	*PRNP*	76,930	0.97	A/G	0.169	1.40E-05	-0.07	1.20E-04	-0.034	3.50E-02	**1.40E-08**	**4.80E-08**	4.2E-02	2.3E-06	3.4E-06
WHRadjBMI																	
1:AW	rs670752	3:107312980	*BBX*	107,568	0.32	A/G	0.012	5.50E-02	0.009	1.50E-02	0.027	**4.90E-08**	6.80E-01	7.80E-03	**3.1E-10**	3.8E-01	9.5E-05
1:EC	rs589428	6:31848220	*EHMT2*	162,918	0.66	G/T	0.006	1.20E-01	0.011	4.10E-04	0.022	**2.80E-08**	3.50E-01	7.00E-04	**1.1E-17**	8.4E-02	**1.6E-10**
2:EC	rs1856293	6:133480940	*EYA4*	127,431	0.52	A/C	0.006	5.30E-01	-0.028	9.10E-09	-0.019	6.50E-06	5.40E-04	**4.70E-08**	9.6E-08	1.3E-02	**1.5E-08**
1:AW	rs2001945	8:126477978	*TRIB1*	103,446	0.4	G/C	0.009	1.20E-01	0.013	1.00E-04	0.025	**4.70E-08**	5.90E-01	1.30E-04	**1.1E-09**	3.0E-01	1.4E-06
1:EC	rs17065323	13:44627788	*SMIM2**	69,968	0.01	T/C	0.154	1.90E-01	-0.23	1.20E-10	-0.181	**9.20E-09**	1.40E-03	3.90E-10	**9.6E-09**	3.6E-03	**1.3E-09**

Abbreviations: Chr- chromosome, Pos- position (bp), E/O- effect/other, EAF- effect allele frequency, Padj- adjusted for smoking, int- interaction.

Table 3. Summary of association results for loci showing significance for interaction with smoking in Approach (App) 3 (SNPint) and/or Approach 4 (SNPscreen) in our primary meta-analyses of combined ancestries and combined sexes. Ł - known locus.

App	Marker	Chr:Pos (hg19)	Nearest Gene	N	EAF	Alleles E/O	SMOKERS β	SMOKERS P	NON-SMOKERS β	NON-SMOKERS P	Main and Interaction Effects β_{adj}	P_{adj}	P_{int}	P_{joint}	GIANT + UKBB $P_{SNPadjSMK}$	P_{SNPint}	$P_{SNPjoint}$
BMI																	
3	rs336396	4:143062811	*INPP4B*	169,646	0.18	T/C	0.063	**4.8E-08**	-0.006	3.4E-01	0.007	2.3E-01	**2.1E-08**	1.9E-07	7.4E-01	2.7E-06	1.3E-05
3	rs12902602 Ł	15:78967401	*CHRNB4*	240,135	0.62	A/G	0.047	**1.8E-11**	-0.002	5.5E-01	0.009	8.6E-03	**4.1E-11**	**1.1E-10**	1.1E-01	**6.0E-13**	**1.6E-12**
WCadjBMI																	
3	rs4141488	16:9629067	*GRIN2A*	153,892	0.5	T/C	0.037	2.2E-05	-0.015	9.6E-04	-0.003	4.4E-01	**2.7E-08**	5.0E-07	9.5E-01	1.8E-06	1.1E-05
WHRadjBMI																	
4	rs765751 Ł	1:219669226	*LYPLAL1*	189,028	0.64	C/T	0.003	3.9E-01	0.019	**3.1E-11**	0.029	**3.1E-16**	*7.3E-04*	**2.1E-10**	**9.1E-31**	*1.4E-04*	**7.8E-22**
4	rs7766106 Ł	6:127455138	*RSPO3*	188,174	0.48	T/C	0.007	7.9E-02	0.022	**2.2E-15**	0.037	**3.7E-27**	*9.7E-04*	**3.8E-15**	**4.4E-51**	*1.0E-05*	**3.4E-34**

Abbreviations: Chr- chromosome; Pos- position (bp); E/O- effect/other; EAF- effect allele frequency; adj- adjusted for smoking; int- interaction; App- Approach.

Table 4. Summary of association results for loci showing significance for interaction with smoking in Approach 3 (SNPint) and/or Approach 4 (SNPscreen) in our secondary meta-analyses not identified in primary meta-analyses. All estimates are from the stratum specified in the Approach:Sample column (E-European-only, A- all ancestries, C- combined sexes, W-women only, M- men only). Ł - known locus. The R^2 between the *ADAMTS7* (rs1809420) and *CHRNB4* variant (rs1290362) in **Table 3** is 0.72 (HapMap 2, CEU). Additionally, the *PRNP* variant (rs6076699) is the same as the variant that came up from Approach 2 (**Table 2**).

Approach: Strata	Marker	Chr:Pos (hg19)	Nearest Gene	N	EAF	Alleles E/O	SMOKERS β	SMOKERS P	NON-SMOKERS β	NON-SMOKERS P	Main and Interaction Effects β_{adj}	P_{adj}	P_{int}	P_{joint}	GIANT + UKBB $P_{SNPadjSMK}$	P_{SNPint}	$P_{SNPjoint}$
BMI																	
4:AM	rs1809420 Ł	15:79056769	*ADAMTS7*	57,081	0.59	T/C	0.074	**9.8E-08**	0.023	2.0E-03	0.036	**4.9E-08**	*9.4E-04*	**5.6E-09**	9.8E-05	*3.3E-05*	1.9E-07
WCadjBMI																	
3:EW	rs6076699	20:4566688	*PRNP*	76,930	0.97	A/G	0.169	1.4E-05	-0.07	1.2E-04	-0.034	3.5E-02	**1.4E-08**	**4.8E-08**	4.2E-02	2.3E-06	3.4E-06
WHRadjBMI																	
4:EM	rs30000 Ł	5:55803533	*MAP3K1*	71,424	0.27	G/A	0.002	7.8E-01	0.031	**3.7E-08**	0.04	**1.7E-10**	*1.6E-04*	2.7E-07	**2.7E-17**	*3.2E-07*	**3.8E-15**
4:AM	rs459193 Ł	5:55806751		80,852	0.27	A/G	0.004	5.0E-01	0.034	**4.1E-10**	0.043	**2.3E-13**	*6.8E-05*	**2.2E-09**	**3.5E-20**	*2.5E-07*	**1.6E-17**
4:AM	rs2071449 Ł	12:54428011	*HOXC4-*	70,868	0.37	A/C	0.003	6.0E-01	0.026	1.0E-06	0.034	**9.1E-09**	*1.1E-03*	5.7E-06	**2.7E-12**	8.0E-04	**2.8E-09**
4:EM	rs754133 Ł	12:54418920	*HOXC6*	71,136	0.36	A/G	0.003	6.2E-01	0.026	8.2E-07	0.034	**3.0E-09**	*1.1E-03*	4.0E-06	**2.1E-12**	*9.7E-04*	**4.0E-09**
4:AM	rs12608504 Ł	19:18389135	*JUND*	80,087	0.37	A/G	0.006	2.6E-01	0.025	5.0E-07	0.032	**4.7E-09**	*5.5E-03*	1.8E-06	**2.9E-11**	1.3E-02	**1.6E-08**

Abbreviations: E/O- effect/other, EAF- effect allele frequency, SE- standard error; Chr- chromosome; Pos- position (bp); adj- adjusted for smoking; int- interaction; App- Approach.