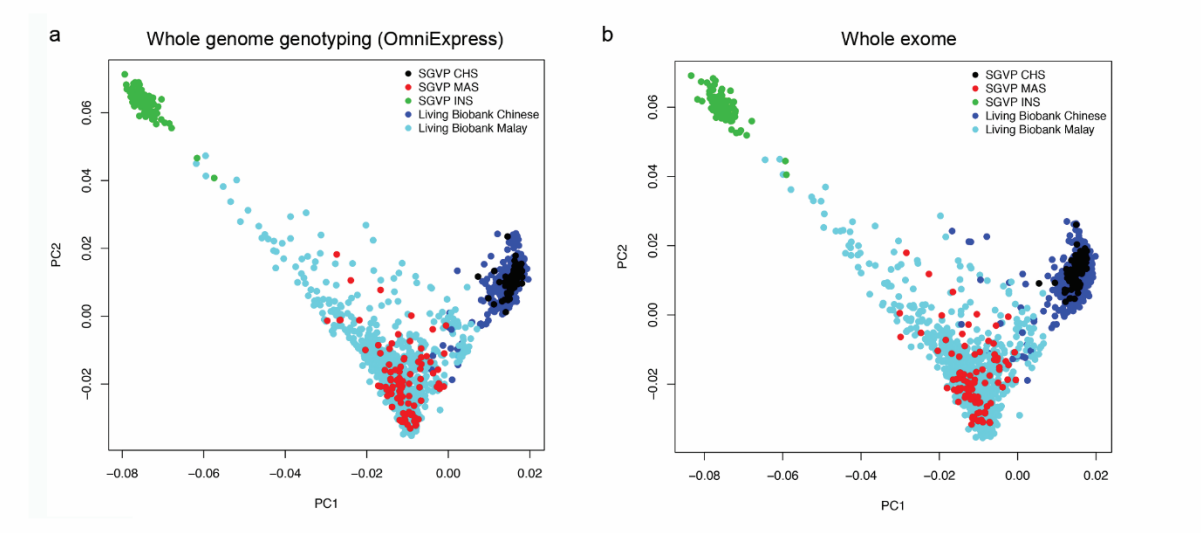
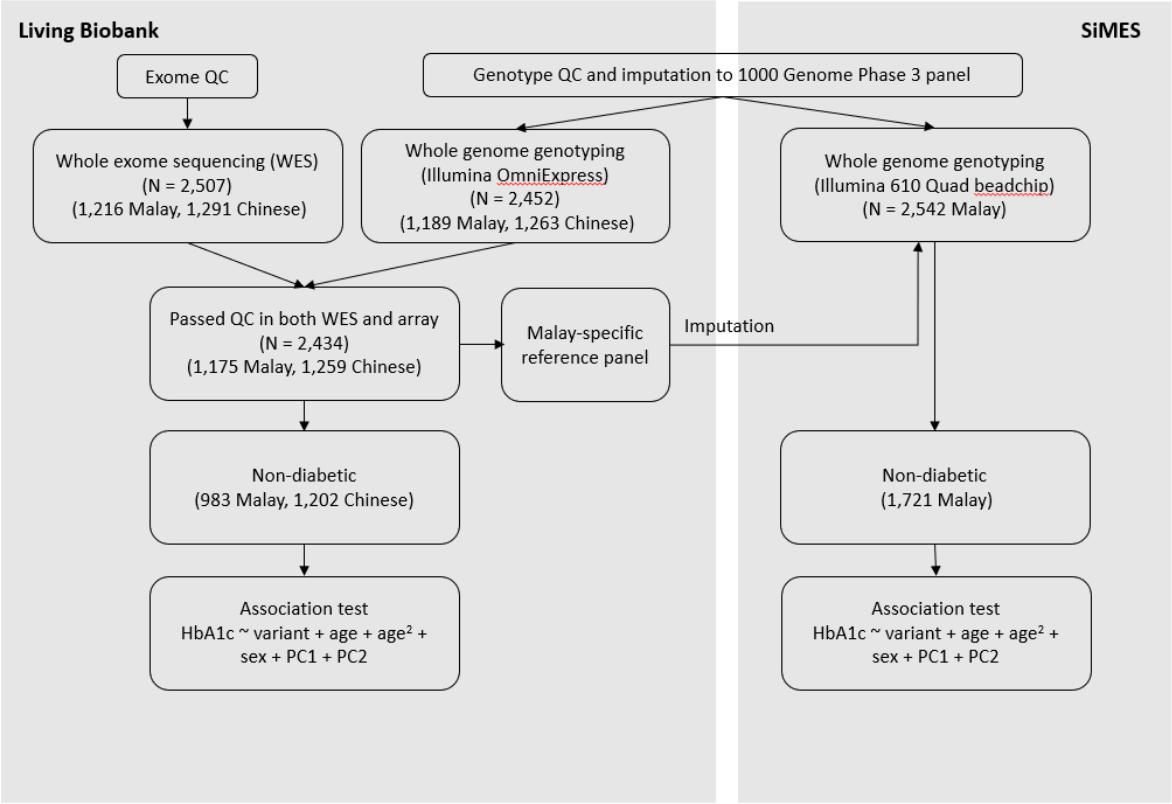
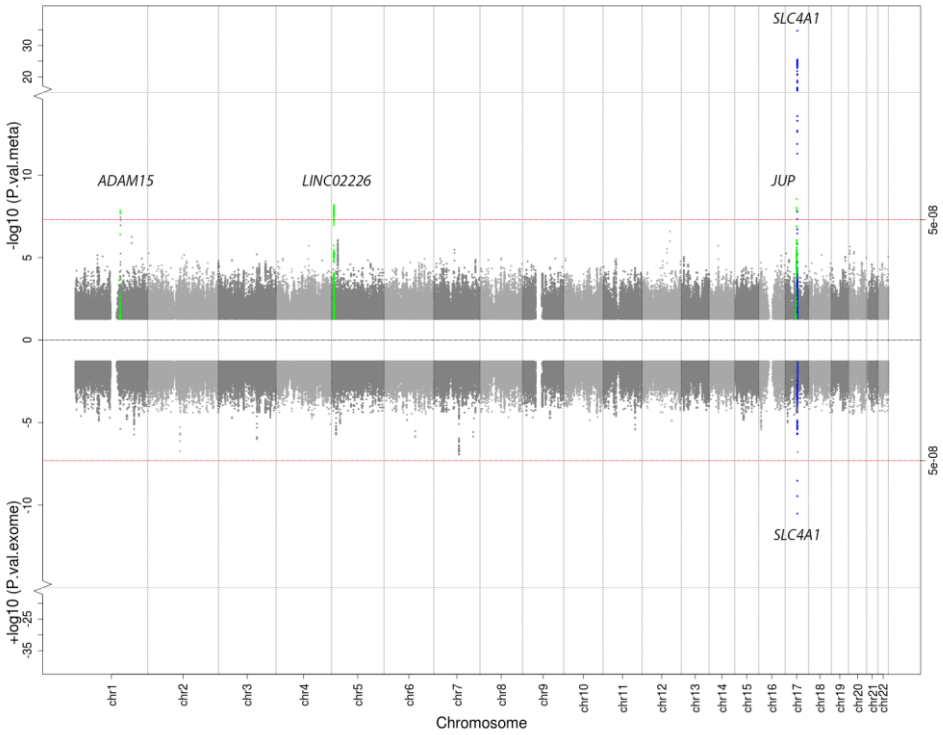
**Supplementary Figure 1.** Principal component analysis (PCA) of 268 samples from Singapore Genome Variation Project (SGVP) with Living Biobank study using (a) whole genome array (Illumina OmniExpress) data, and (b) whole exome sequence data. For each plot, the second principal component (PC) was plotted against the first PC.
CHS, Chinese; MAS, Malay; INS, Indian.



**Supplementary Figure 2.** Workflow showing genetic data processing for the Living Biobank study and the Singapore Malay Eye Study (SiMES).
QC, quality control; N, sample size.

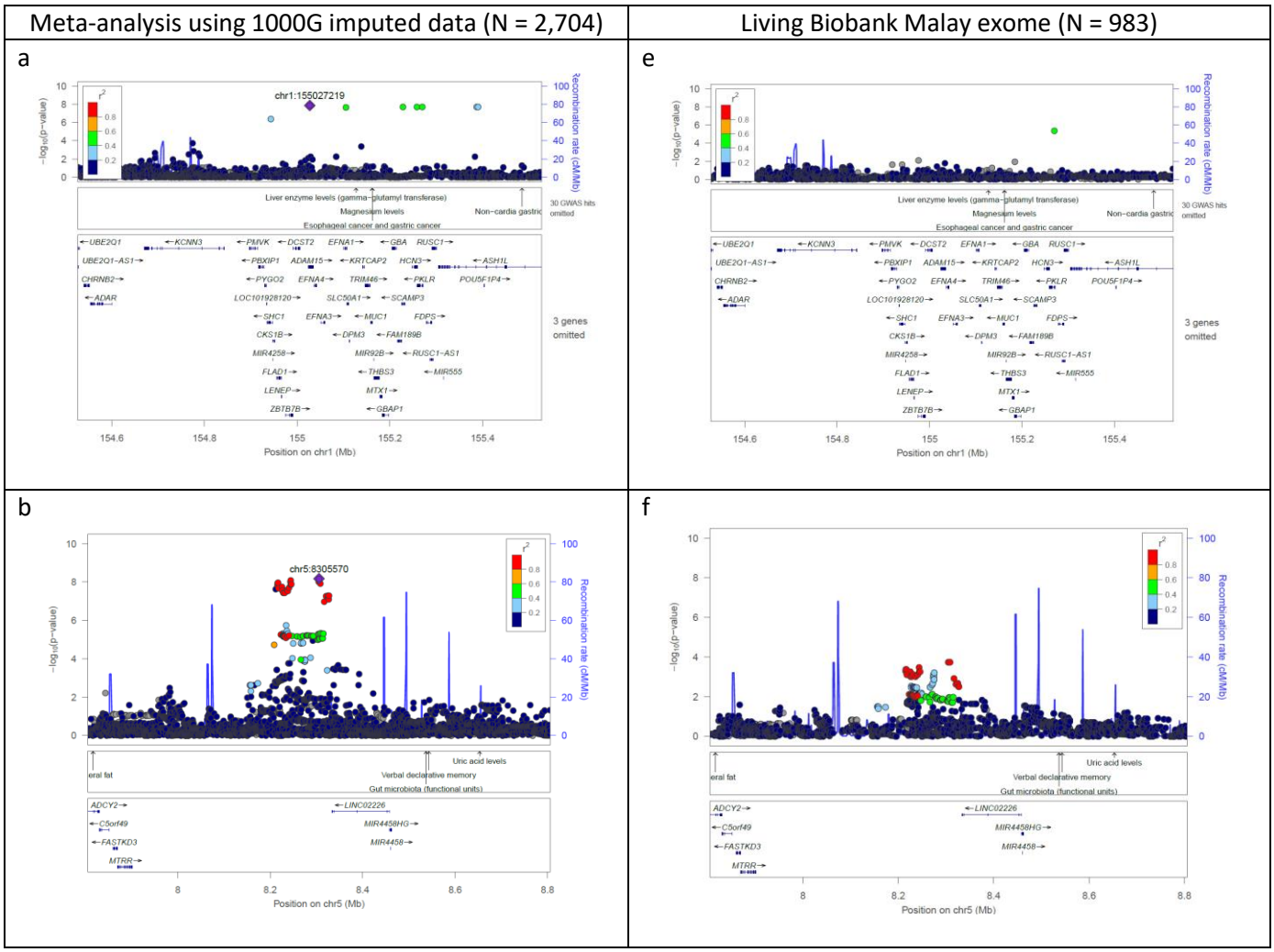


**Supplementary Figure 3**. Miami plot showing genome-wide associations with HbA1c. Upper panel represents association results from meta-analysis of Living Biobank Malay and SiMES using 1000 Genomes imputed data. Lower panel represents association results from Living Biobank Malay exome sequence data. Genome-wide significance was defined at $5x10^{-8}$. Each significant locus was labelled with a gene name. Locus coloured in green represents novel loci. Locus coloured in blue represents known HbA1c loci.

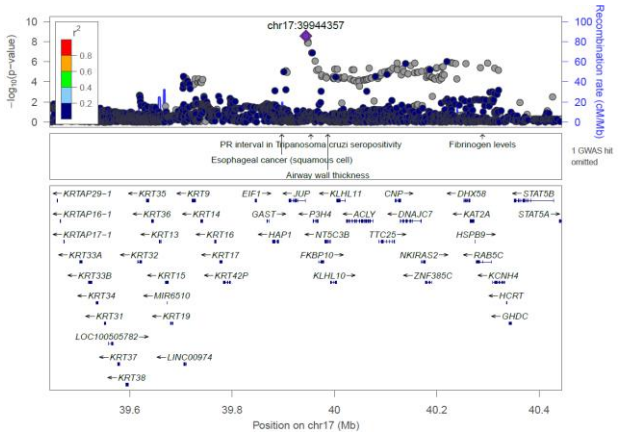


**Supplementary Figure 4.** Regional association plots at four loci that reached genome-wide significance ($P$ <5x10$^{-8}$) for HbA1c associations in the meta-analysis using 1000 Genomes imputed data. Left panel shows associations at the four loci for imputed variants, right panel shows associations at the four loci for exome variants. All plots were centred at the lead variants identified from meta-analysis using the 1000 Genomes imputed data. (a, e) *ADAM15* locus on chromosome 1, (b, f) *LINC02226* locus on chromosome 5, (c, g) *JUP* locus on chromosome 17, and (d) *SLC4A1* locus on chromosome 17.

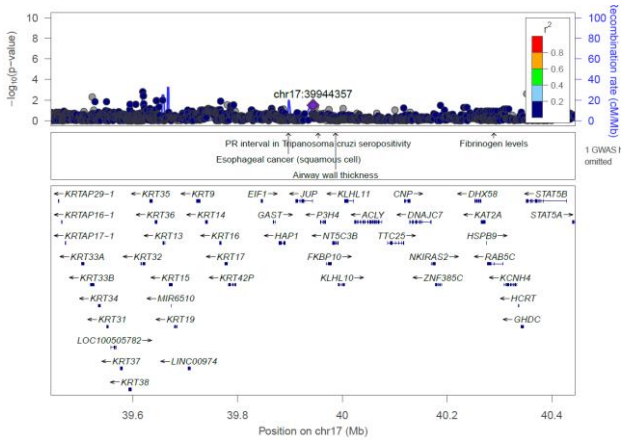
Purple diamond indicated the lead variant. Variants in each locus were colored based on 1000 Genomes East Asians LD with the lead variant. Variants coloured in grey indicates no LD information was available.



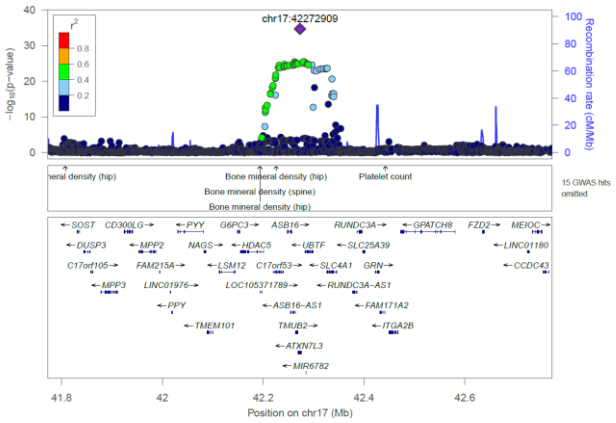
c


chr17:39944357
−log10(p−value)
Recombination rate (cM/Mb)
PR interval in Trypanosoma cruzi seropositivity
Fibrinogen levels
Esophageal cancer (squamous cell)
Airway wall thickness
1 GWAS hit omitted
Position on chr17 (Mb)

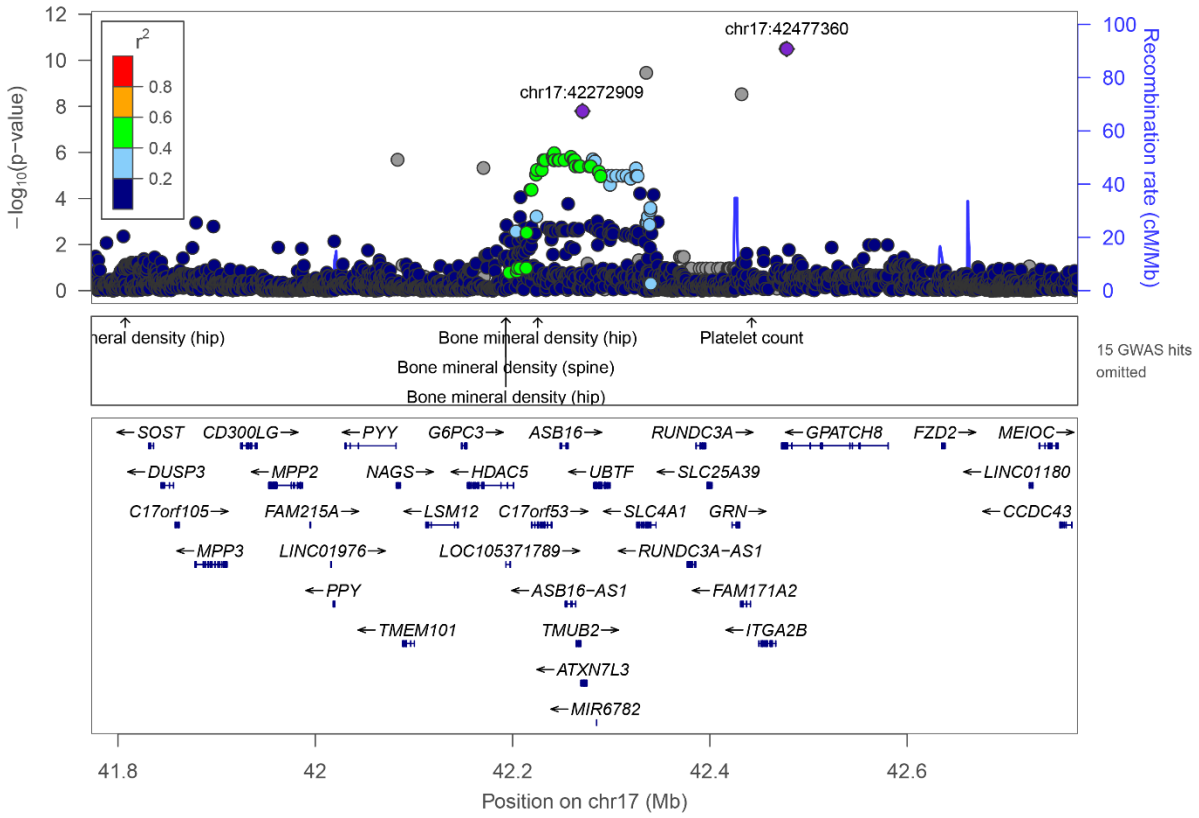
g


chr17:39944357
−log10(p−value)
Recombination rate (cM/Mb)
PR interval in Trypanosoma cruzi seropositivity
Fibrinogen levels
Esophageal cancer (squamous cell)
Airway wall thickness
1 GWAS hit omitted
Position on chr17 (Mb)

d

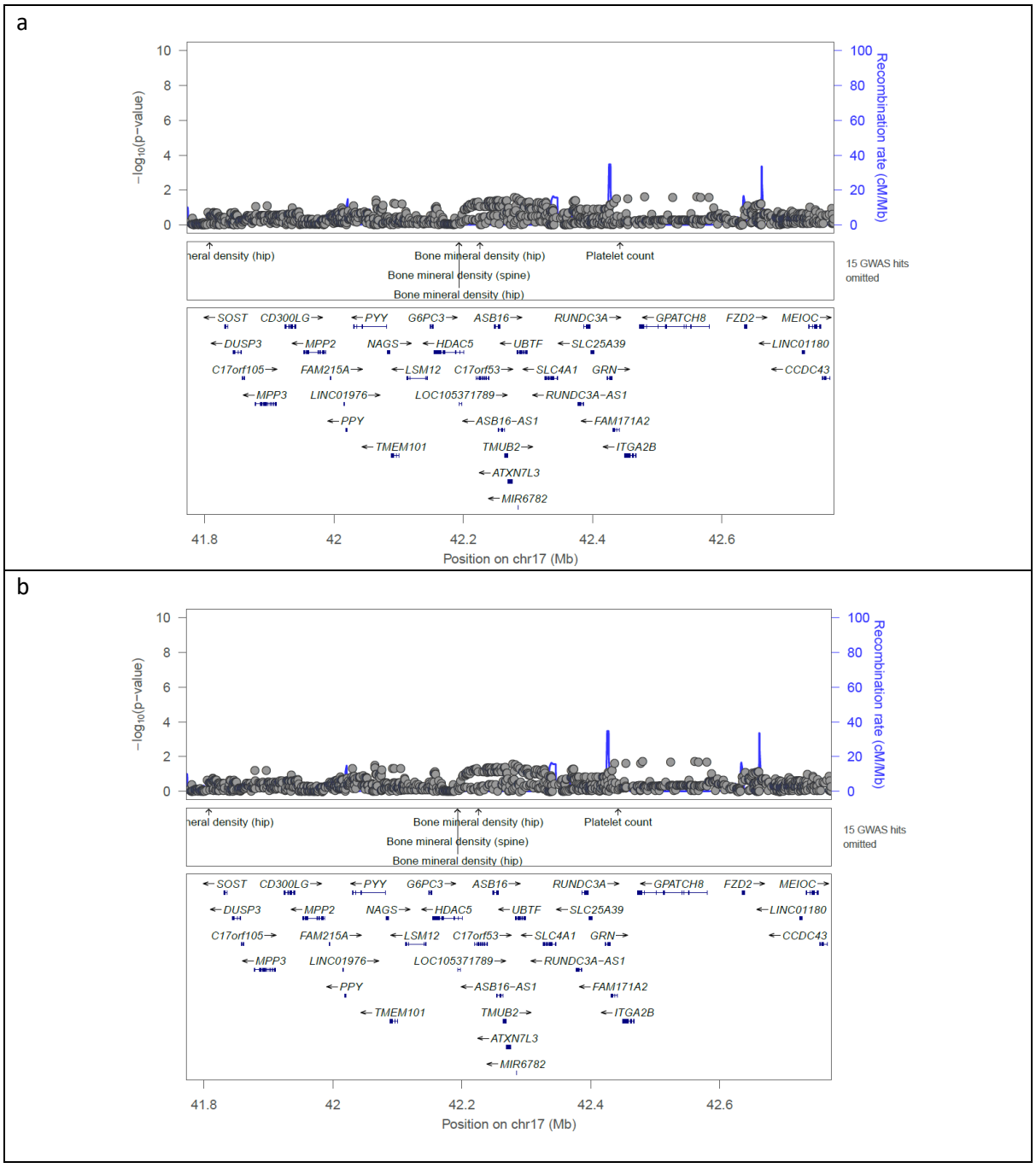

chr17:42272909
−log10(p−value)
Recombination rate (cM/Mb)
Bone mineral density (hip)
Platelet count
Bone mineral density (spine)
Bone mineral density (hip)
15 GWAS hits omitted
Position on chr17 (Mb)

**Supplementary Figure 5**. Regional association plot at *SLC4A1* locus on chromosome 17 showing combined HbA1c association results from Living Biobank array imputed to 1000G and exome data. Purple diamond indicated the lead variants: rs2285951 (chr17:42272909) from the analysis using the 1000 Genomes imputed data, and rs369762319 (chr17:42477360) from analysis using the exome data. Variants were coloured based on 1000 Genomes East Asians LD with the rs2285951 as rs369762319 is absent in 1000 Genomes reference panel. Variants coloured in grey indicates no LD information was available.

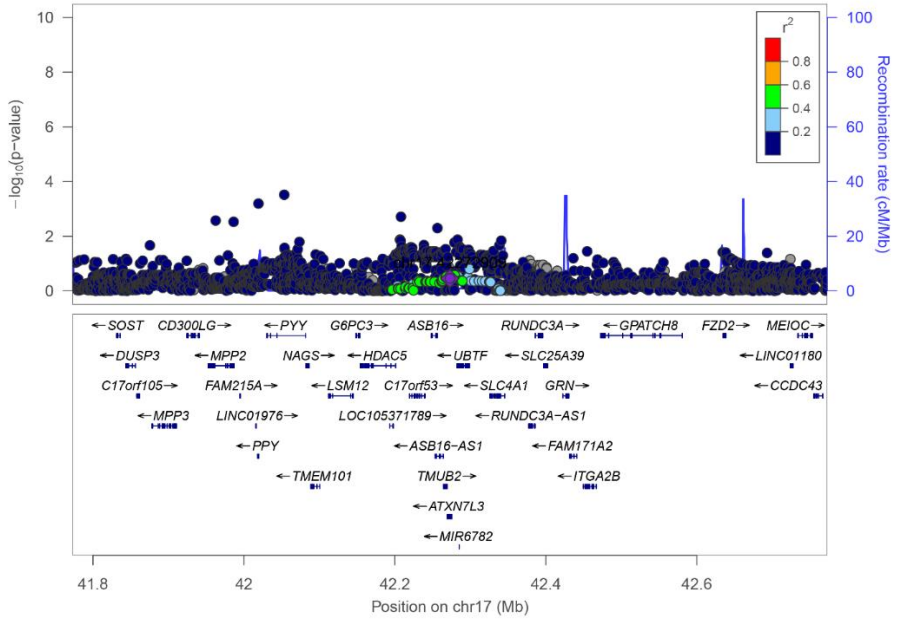


**Supplementary Figure 6.** Regional association plot showing conditional associations with HbA1c at *SLC4A1* locus on chromosome 17 in the Living Biobank Malay individuals (a) in the exome data after conditioning on the lead variant rs369762319, (b) in the exome data after conditioning on the *SLC4A1* 27bp deletion rs769664228, and (c) in the 1000 Genomes imputed data after conditioning on the *SLC4A1* 27bp deletion rs769664228.

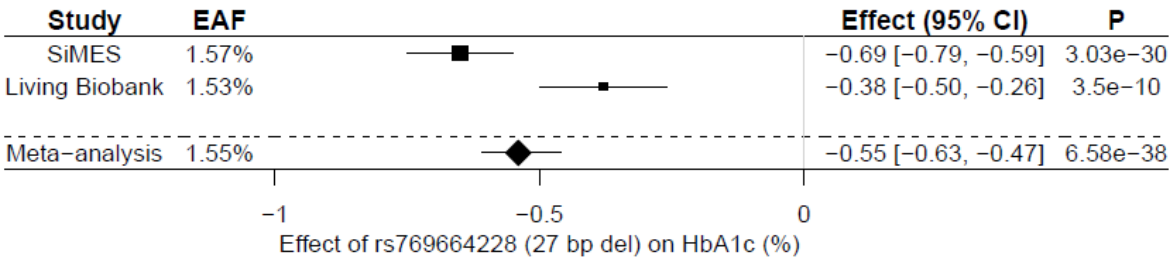
Purple diamond indicated the conditioned variant. Variants in the locus were colored based on 1000G East Asians LD with the conditioned variant. Variants coloured in grey indicates no LD information was available.

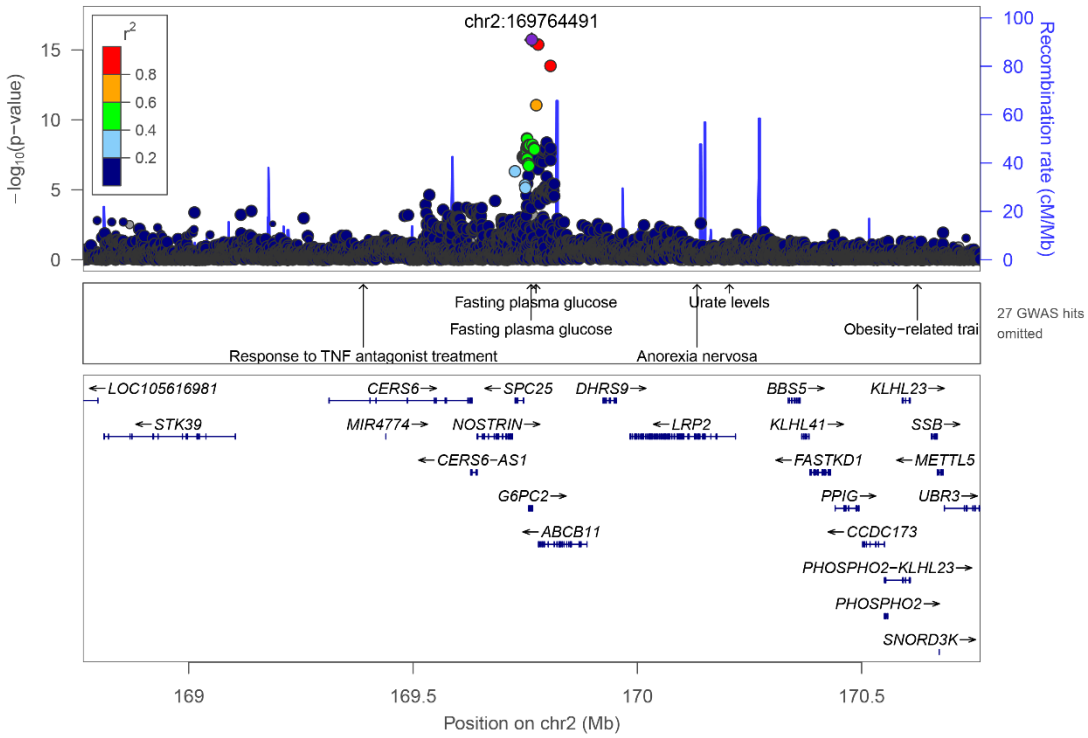


C


−log10(p−value)
Recombination rate (cM/Mb)
r2
0.8
0.6
0.4
0.2
SOST
CD300LG
PYY
G6PC3
ASB16
RUNDC3A
GPATCH8
FZD2
MEIOC
DUSP3
MPP2
NAGS
HDAC5
UBTF
SLC25A39
LINC01180
C17orf105
FAM215A
LSM12
C17orf53
SLC4A1
GRN
CCDC43
MPP3
LINC01976
LOC105371789
RUNDC3A−AS1
PPY
ASB16−AS1
FAM171A2
TMEM101
TMUB2
ITGA2B
ATXN7L3
MIR6782
Position on chr17 (Mb)

**Supplementary Figure 7.** Forest plot for lead variant rs769664228 at the *SLC4A1* locus in SiMES imputed into the Malay-specific reference panel (N=1,721), Living Biobank Malay exome (N=983), and meta-analysis (N=2,704). Effect reflected per allele effect of variants on untransformed HbA1c values. *P*-values were obtained from sample-size weighted fixed-effect meta-analysis on inverse-transformed HbA1c values.
EAF, effect allele frequency; CI, confidence interval; P, *P*-value.




Heterogeneity $I^2$ = 93.4%, $\chi^2$ = 15.08, $P$ = 1.03x$10^{-4}$

**Supplementary Figure 8.** Regional association plot at *G6PC2* for fasting glucose (FG) associations using 1000G imputed data in East Asians meta-analysis (Living Biobank Chinese + Living Biobank Malay + SiMES). Purple diamond indicated the lead variant in the locus. Variants in each locus were colored based on 1000G East Asians LD with the lead variant.