Supplementary Data Set 1 | Manhattan, quantile-quantile, and LD score plots for the 58 quantitative traits.

a, quantile-quantile (QQ) plot. b, LD score plot. c, Manhattan plot. GWAS was conducted using a linear regression model under the assumption of additive allelic effects of the SNP dosages. Novel loci are colored in blue, whereas known loci are colored in red. The dotted line represents a genome-wide significance threshold ($P = 5.0 \times 10^{-8}$).

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</table>
1.1 TC \((n = 128,305)\)
1.2 HDL-C \( (n = 70,657) \)

![Graphs showing HDL-C distribution and LD score bin means.](image)
1.3 LDL-C \( (n = 72,866) \)

![Graphs and diagrams showing statistical data and genetic loci distribution.](image-url)
1.4 TG \( (n = 105,597) \)

![Graph a](image)

![Graph b](image)

**c**

- **Novel loci \( (n = 4) \)**
- **Previously reported loci \( (n = 22) \)**
1.5 BS (n = 93,146)

![Graph a](image1.png)

![Graph b](image2.png)

![Graph c](image3.png)
1.6 HbA1c \((n = 42,790)\)

![Graph a: Observed vs Expected \(-\log_{10}(P)\)]

![Graph b: Mean \(\chi^2\) vs LD score bin]

![Graph c: Distribution of loci across chromosomes]

- **Novel loci** \((n = 16)\)
- Previously reported loci \((n = 10)\)
1.7 TP \((n = 113,509)\)

![Diagram a](image1)

![Diagram b](image2)

![Diagram c](image3)
1.8 Alb ($n = 102,223$)

![Graph a](image1.png)

![Graph b](image2.png)

![Graph c](image3.png)
1.9 NAP \( (n = 98,538) \)

\[ \text{Novel loci (n = 46)} \]
\[ \text{Previously reported loci (n = 2)} \]
1.10 A/G \((n = 98,626)\)

(a) Observed \(-\log_{10}(P)\) vs. Expected \(-\log_{10}(P)\)

(b) LD score bin vs. Mean \(\chi^2\)

(c) Novel loci \((n = 40)\)

- Previously reported loci \((n = 2)\)
1.11 BUN \( (n = 139,818) \)
### 1.12 sCr \((n = 142,097)\)

#### (a)

Observed \(-\log_{10}(P)\) vs. Expected \(-\log_{10}(P)\)

#### (b)

Mean \(\chi^2\) vs. LD score bin

#### (c)

- **Novel loci \((n = 51)\)**
- **Previously reported loci \((n = 15)\)**
1.13 eGFR (n = 143,658)

a

b

LD score bin

Mean χ²

0 25 50 75 100

1.0

1.5

2.0

2.5

Novel loci (n = 48)

Previously reported loci (n = 21)
1.14 UA \( (n = 109,029) \)

![Graph a](image1)

![Graph b](image2)

![Graph c](image3)
1.15 Na ($n = 127,304$)

(a) Observed $-\log_{10}(P)$ vs. Expected $-\log_{10}(P)$

(b) Mean $\chi^2$ vs. LD score bin

(c) Novel loci ($n = 14$)
1.16 K \( (n = 132,938) \)

(a) Observed \(-\log_{10}(P)\) vs. Expected \(-\log_{10}(P)\)

(b) Mean \(\chi^2\) vs. LD score bin

(c) Novel loci \((n = 14)\)
1.17 CI \( (n = 126,402) \)

![Graph of Observed vs. Expected -log10(P)](image)

![Scatter plot of Mean \( \chi^2 \) vs. LD score bin](image)

![Dot plot of Novel loci \( (n = 19) \)](image)
1.18 **Ca** \( (n = 71,701) \)

![Graph a](image1.png)

![Graph b](image2.png)

![Graph c](image3.png)
1.19 $P$ \((n = 42,793)\)

![Graph a](image1)

![Graph b](image2)

![Graph c](image3)
1.20 T Bil \( (n = 110,207) \)

---

**a**

Observed \(-\log_{10}(P)\)

Expected \(-\log_{10}(P)\)

---

**b**

Mean \(\chi^2\)

LD score bin

---

**c**

Novel loci \((n = 9)\)

Previously reported loci \((n = 2)\)
1.21 ZTT \((n = 12,303)\)

![Graph a](image1)

![Graph b](image2)

![Graph c](image3)
1.22 AST \((n=134,154)\)

\[\begin{align*}
\text{Novel loci} \quad (n=22) \\
\text{Previously reported loci} \quad (n=3)
\end{align*}\]
1.23 ALT \((n = 134,182)\)

(a) Observed \(-\log_{10}(\text{P})\) vs. Expected \(-\log_{10}(\text{P})\)

(b) Mean \(\chi^2\) vs. LD score bin

(c) Novel loci \((n = 23)\)

Previously reported loci \((n = 4)\)
1.24 ALP  \((n = 105,030)\)
1.25 GGT ($n = 118,309$)

c
Novel loci ($n = 24$)
Previously reported loci ($n = 18$)
1.26 APTT \((n = 37,767)\)
1.27 PT \((n = 58,110)\)

![Graph a](image1.png)

![Graph b](image2.png)

![Graph c](image3.png)
1.28 Fbg \( (n = 18,348) \)

\( a \)

\( b \)

Previously reported loci \((n = 1)\)
1.29 CK \( (n = 106,080) \)

**a**

![Graph showing observed vs. expected \(-\log_{10}(P)\) values.]

**b**

![Graph showing Mean \(\chi^2\) vs. LD score bin.]

**c**

![Scatter plot of \(-\log_{10}(P)\) vs. chromosome.]

Novel loci \( (n = 31) \)

Previously reported loci \( (n = 5) \)
1.30 LDH \( (n = 126,319) \)

\begin{itemize}
  \item \textbf{a} \hspace{1cm} \textbf{b} \hspace{1cm} \textbf{c}
\end{itemize}

\begin{itemize}
  \item \textbf{a} \hspace{1cm} \textbf{b} \hspace{1cm} \textbf{c}
\end{itemize}

\begin{itemize}
  \item \textbf{c}
\end{itemize}

\textbf{c}

\textbf{Novel loci} \((n = 5)\)

\textbf{Previously reported loci} \((n = 5)\)
1.31 CRP ($n = 75,391$)

(a) Observed $-\log_{10}(P)$ vs. Expected $-\log_{10}(P)$

(b) Mean $\chi^2$ vs. LD score bin

(c) Novel loci ($n = 1$) and Previously reported loci ($n = 6$)
1.32 WBC ($n = 107,964$)

(a) Observed $-\log_{10}(P)$ vs. Expected $-\log_{10}(P)$

(b) Mean $\chi^2$ vs. LD score bin

(c) Distribution of $-\log_{10}(P)$ across chromosomes

- Novel loci ($n = 7$)
- Previously reported loci ($n = 29$)
1.33 Neutro \( (n = 62,076) \)

![Graphs and plots showing statistical data and distributions related to Neutro, including LD score bin and observed vs expected values.](image-url)
1.34 Eosino \( (n = 62,076) \)
1.35 Baso \((n = 62,076)\)
1.36 Mono \( (n = 62,076) \)

![Graph a](image1)

**Graph a:** Observed \(-\log_{10}(P)\) vs. Expected \(-\log_{10}(P)\)

![Graph b](image2)

**Graph b:** Mean $\chi^2$ vs. LD score bin

![Graph c](image3)

**Graph c:** -log\(_{10}(P)\) vs. Chromosome

- Novel loci \( (n = 2) \)
- Previously reported loci \( (n = 39) \)
1.37 Lym \( (n = 62,076) \)

(a) Observed \(-\log_{10}(P)\) vs Expected \(-\log_{10}(P)\).

(b) Mean \(\chi^2\) vs LD score bin.

(c) Distribution of \(-\log_{10}(P)\) across chromosomes for novel and previously reported loci.
1.38 RBC (n = 108,794)
1.39 Hb (n = 108,769)
1.40 Ht \((n = 108,757)\)

(a) Observed \(-\log_{10}(P)\) vs. Expected \(-\log_{10}(P)\).

(b) Mean \(\chi^2\) vs. LD score bin.

(c) Novel loci \((n = 8)\) and Previously reported loci \((n = 14)\).
1.41 MCV \((n = 108,256)\)

\[\text{Novel loci (}\ n = 17)\]

\[\text{Previously reported loci (}\ n = 74)\]
1.42 MCH \( (n = 108,054) \)

(a) Observed \(-\log_10(P)\) vs. Expected \(-\log_10(P)\)

(b) Mean \(\chi^2\) vs. LD score bin

(c) Novel loci \( (n = 10) \) vs. Previously reported loci \( (n = 77) \)
1.43 MCHC \((n = 108,728)\)
1.44 Plt \( (n = 108,208) \)

![Graph a](image1)

![Graph b](image2)

![Graph c](image3)
1.45 SBP (n = 136,597)

(a) Observed $-\log_{10}(P)$ vs. Expected $-\log_{10}(P)$

(b) Mean $\chi^2$ vs. LD score bin

(c) Chromosome distribution of SBP loci:
- Novel loci (n = 4)
- Previously reported loci (n = 19)
1.46 DBP \((n = 136,615)\)

(a) Observed \(-\log_{10}(P)\) vs. Expected \(-\log_{10}(P)\)

(b) Mean \(\chi^2\) vs. LD score bin

(c) Novel loci \((n = 3)\) and Previously reported loci \((n = 15)\)
1.47 MAP \((n = 136,482)\)
1.48 PP ($n = 136,249$)

![Image](image_url)

(a) Observed $-\log_{10}(P)$ vs Expected $-\log_{10}(P)$

(b) Mean $\chi^2$ vs LD score bin

(c) Novel loci ($n = 8$) and Previously reported loci ($n = 9$)
1.49 IVS \((n = 19,318)\)
1.50 PW \( (n = 19,373) \)
1.51 LVDd \((n = 19,676)\)

![Image a](image1.png)

![Image b](image2.png)

![Image c](image3.png)

Novel loci \((n = 3)\)
1.52 LVDs \( (n = 19,586) \)

**a**

- Observed \(-\log_{10}(P)\) vs. Expected \(-\log_{10}(P)\)

**b**

- Mean \(\chi^2\) vs. LD score bin

**c**

- Novel loci \( (n = 4) \)
1.53 LVM \( (n = 19,076) \)
1.54 LVMi \((n = 17,837)\)
a.  

b.  

c. Novel loci ($n = 1$)
1.56 FS \( (n = 19,580) \)

**a**

![Graph a](image)

**b**

![Graph b](image)

**c**

![Graph c](image)
1.57  EF  \((n = 19,516)\)

**a**

![Image of observed vs expected \(-\log_{10}(P)\) plot]

**b**

![Image of mean \(\chi^2\) vs LD score bin plot]

**c**

![Image of \(-\log_{10}(P)\) vs Chromosome plot with novel loci marked]

Novel loci \((n = 3)\)
1.58  E/A  \( (n = 8,600) \)