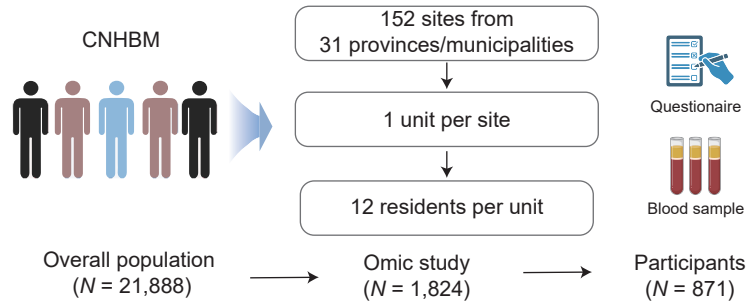
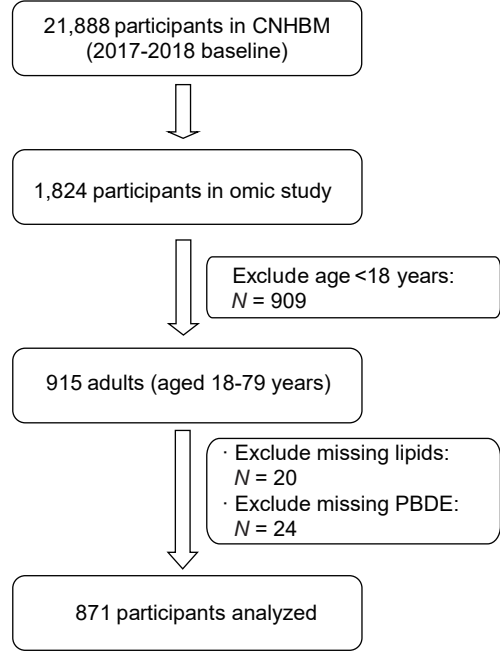
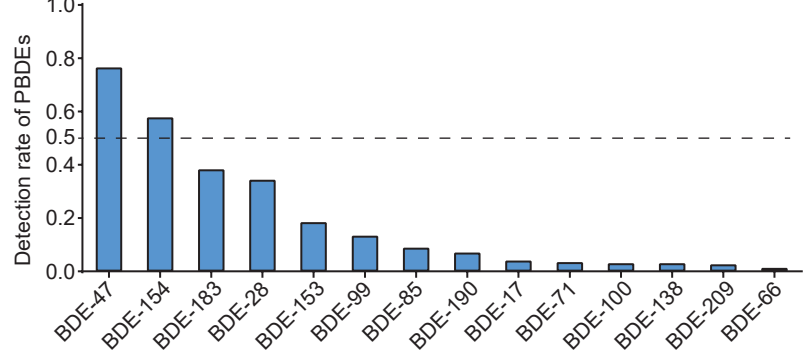
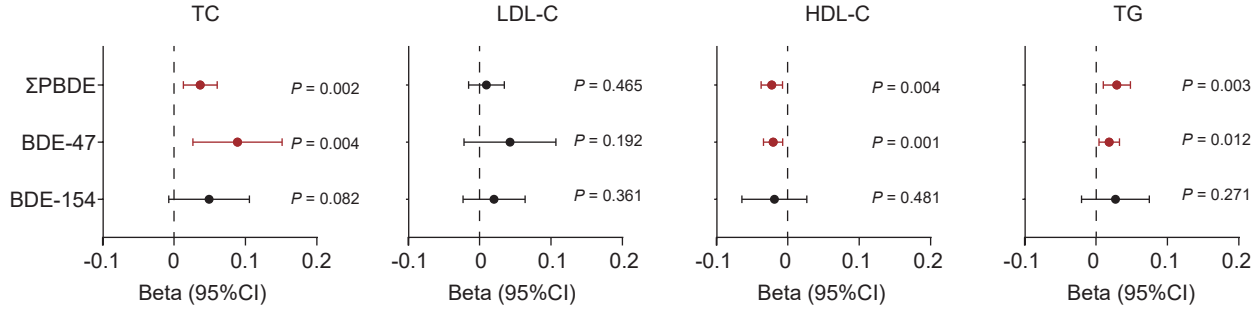


a**b****c****d**

Supplementary Fig. 1. Study design, PBDE detection, and lipid profile associations in the CNHBM cohort.

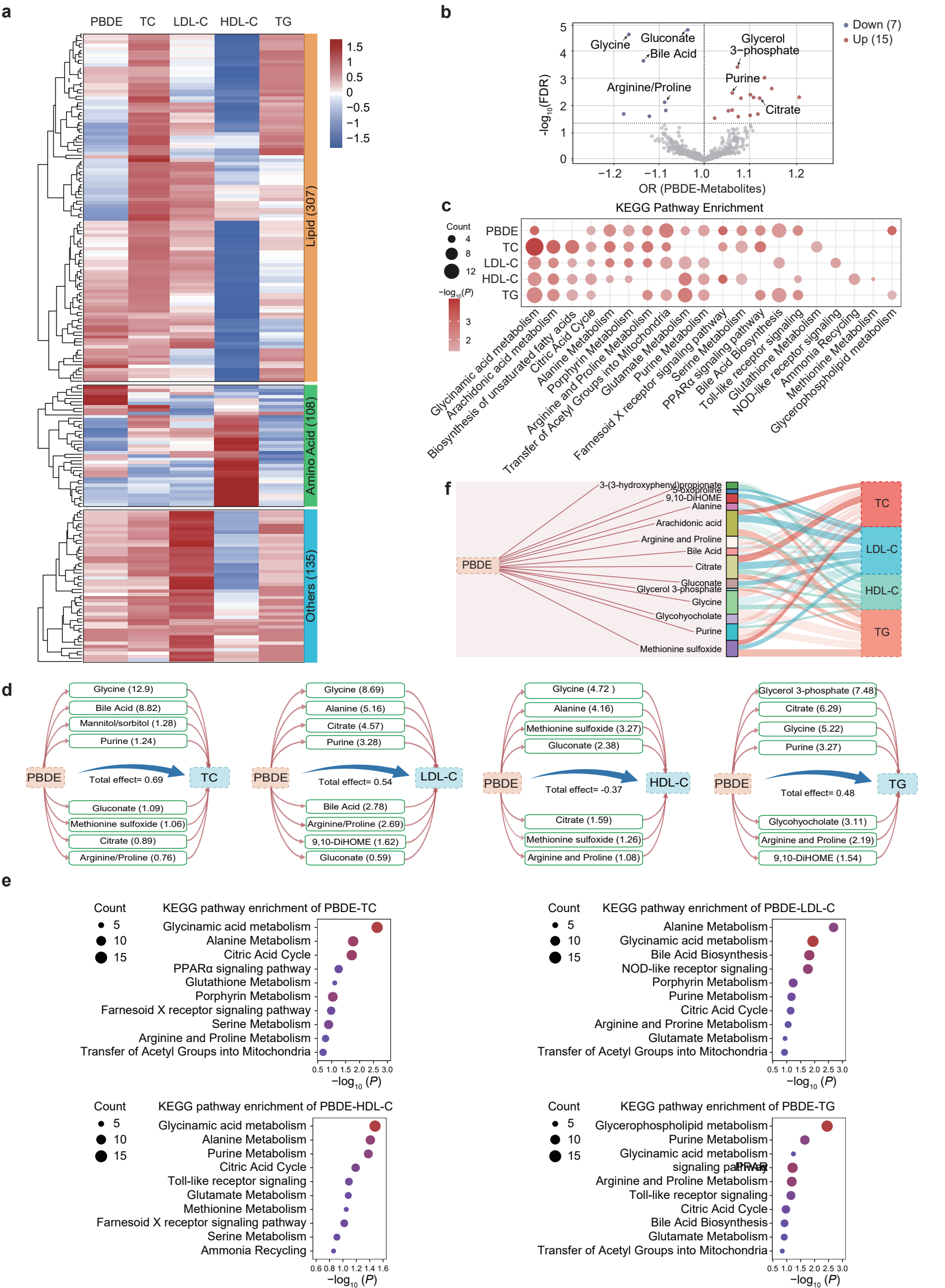
a, Schematic diagram of CNHBM study design. The total population ($N = 21,888$) was recruited from 152 sites across 31 provinces/municipalities, with 12 residents per site. Omics analyses ($N = 1,824$) were conducted in a subset from secondary sampling. The final analytic dataset, including questionnaire surveys and blood samples for omics detection, comprised 871 participants. Created in BioRender. Hu, N. (2026)

<https://BioRender.com/c75ezjr>.

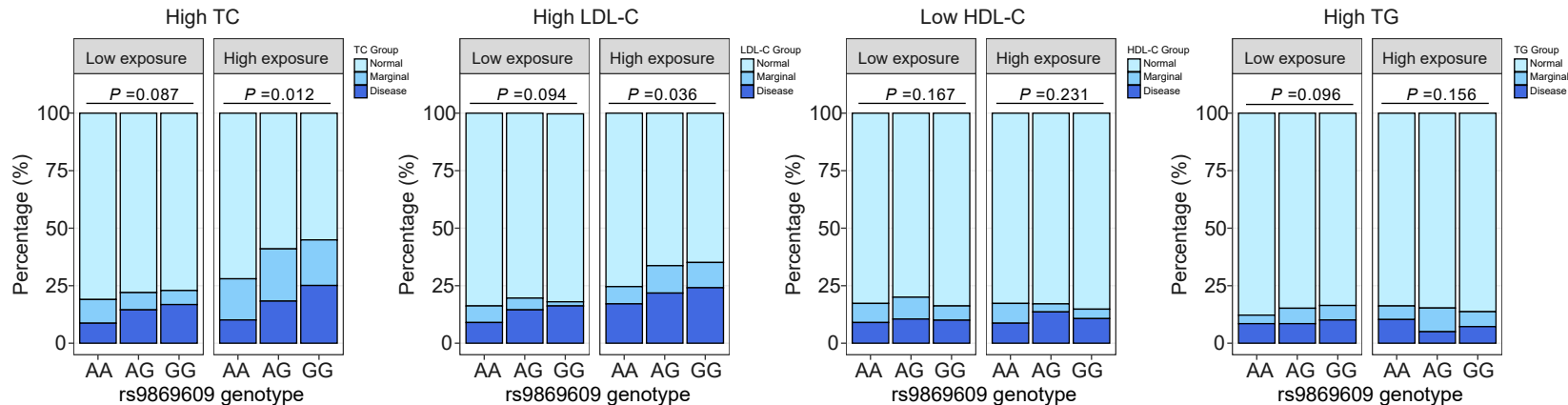
b, Flowchart of participant selection. From the subcohort for omics study, individuals aged <18 years ($N = 909$), those with missing lipid data ($N = 20$), and those with missing PBDE data ($N = 24$) were excluded, yielding 871 participants for final analysis.

c, Detection rates of PBDE congeners.

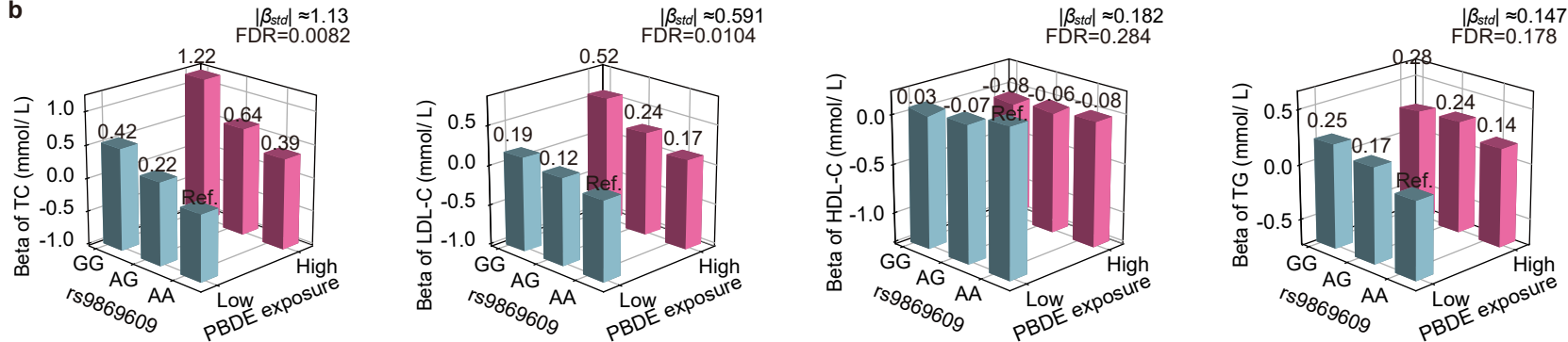
d, Associations between PBDEs (Σ PBDEs, BDE-47, BDE-154) and lipid profiles (TC, LDL-C, HDL-C, TG), expressed as beta coefficients (95% confidence intervals).



a



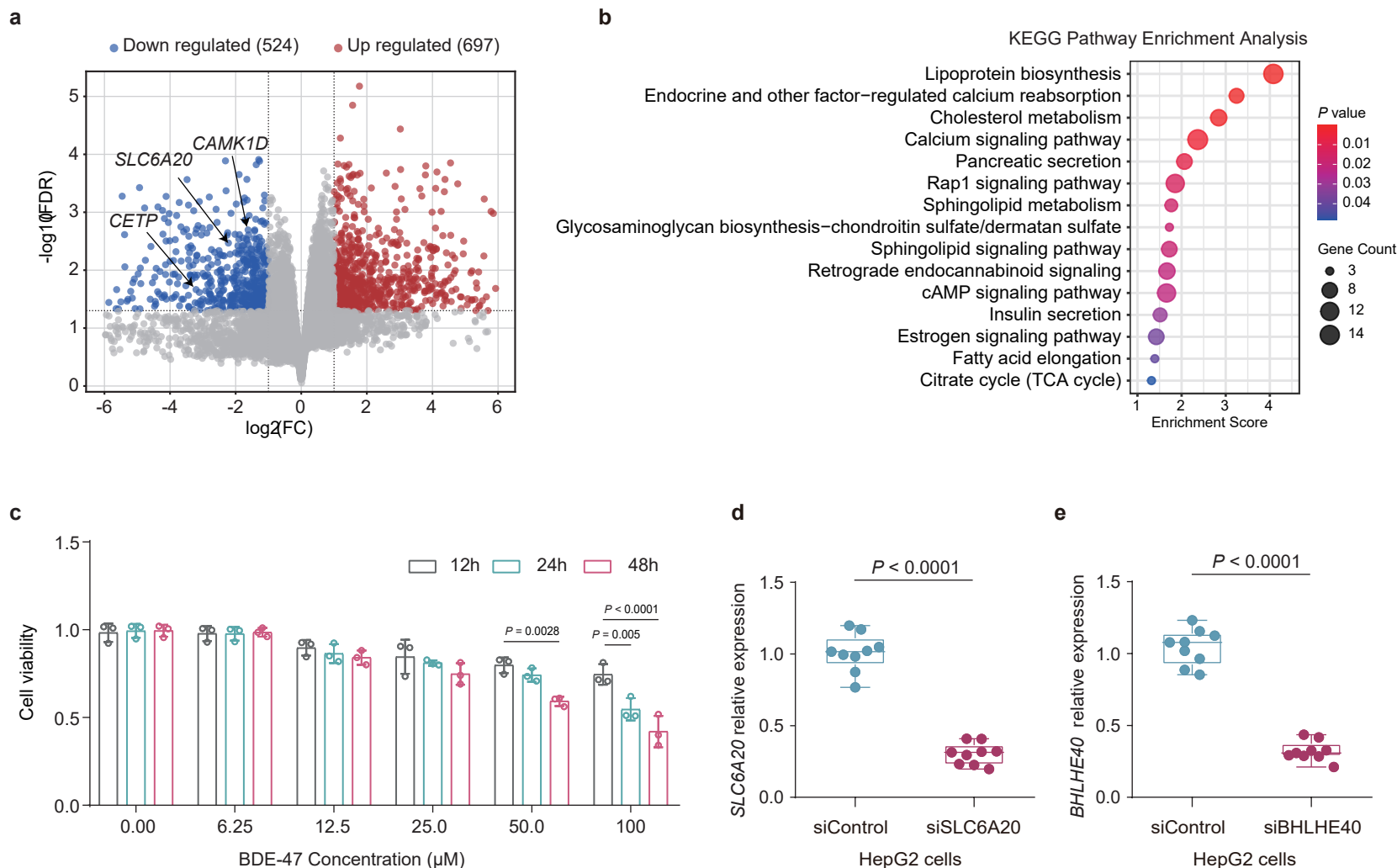
b



Supplementary Fig. 3. PBDE exposure, genetic variation, and their impacts on lipid metabolism

a, Cumulative distributions of lipid phenotypes (TC, LDL-C, HDL-C, TG) by rs9869609 genotype and exposure level ($n=871$).

b, Stratified risk analysis of the rs9869609 in lipid phenotypes (TC, LDL-C, HDL-C, TG) ($n=871$). Abbreviations: $|\beta_{std}|$, absolute standardized β .



Supplementary Fig. 4. Transcriptome Analysis, cytotoxic effects and gene expression modulation by BDE-47 exposure in HepG2 cells.

a, Volcano plot of $\log_2(\text{FC})$ for Differentially expressed genes (DEG) versus false discovery rate ($-\log_{10}(\text{FDR})$). red/blue dots = up/downregulated DEGs ($\text{FDR} < 0.05$); $n = 3$.

b, KEGG pathway enrichment analysis for DEG; Dot color and size represent P -values and gene counts, respectively.

c, HepG2 cell viability after 12 h (gray), 24 h (cyan), and 48 h (pink) treatment with increasing BDE-47 concentrations. $n = 3$. Statistical test: Two-way analysis of variance (ANOVA) (to assess effects of time, concentration, and their interaction) followed by Tukey's Honestly Significant Difference (HSD) post-hoc test.

d, Relative expression of SLC6A20 in HepG2 cells. The siSLC6A20 group (knockdown) showed significantly reduced expression compared to siControl ($P < 0.0001$). $n = 3$ independent experiments (each with 3 technical replicates). Statistical test: Two-sided Student's t-test.

e, Relative expression of BHLHE40 in HepG2 cells. The siBHLHE40 group (knockdown) exhibited markedly decreased expression compared to siControl ($P < 0.0001$). $n = 3$ independent experiments (each with 3 technical replicates). Statistical test: Two-sided Student's t-test.