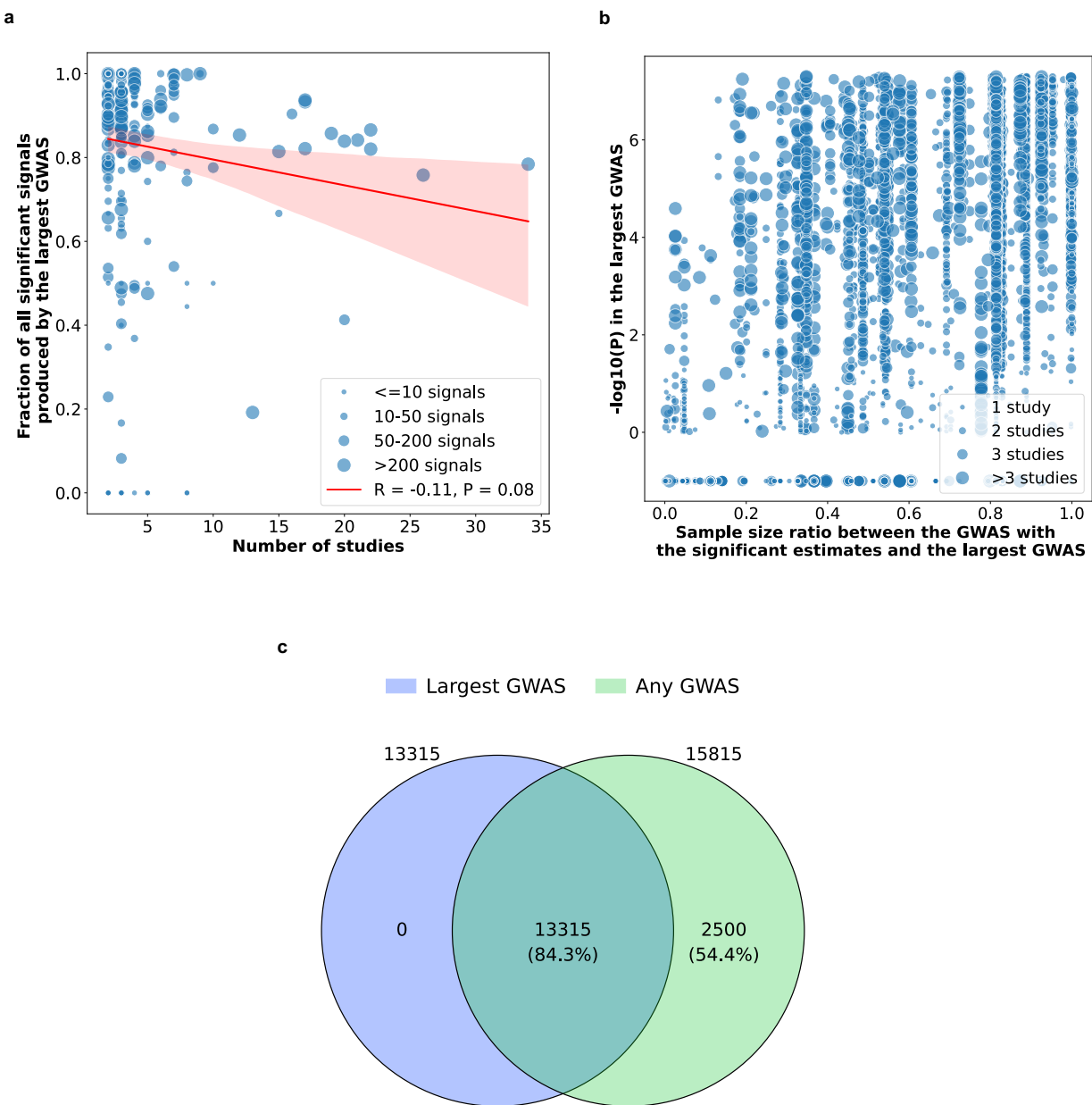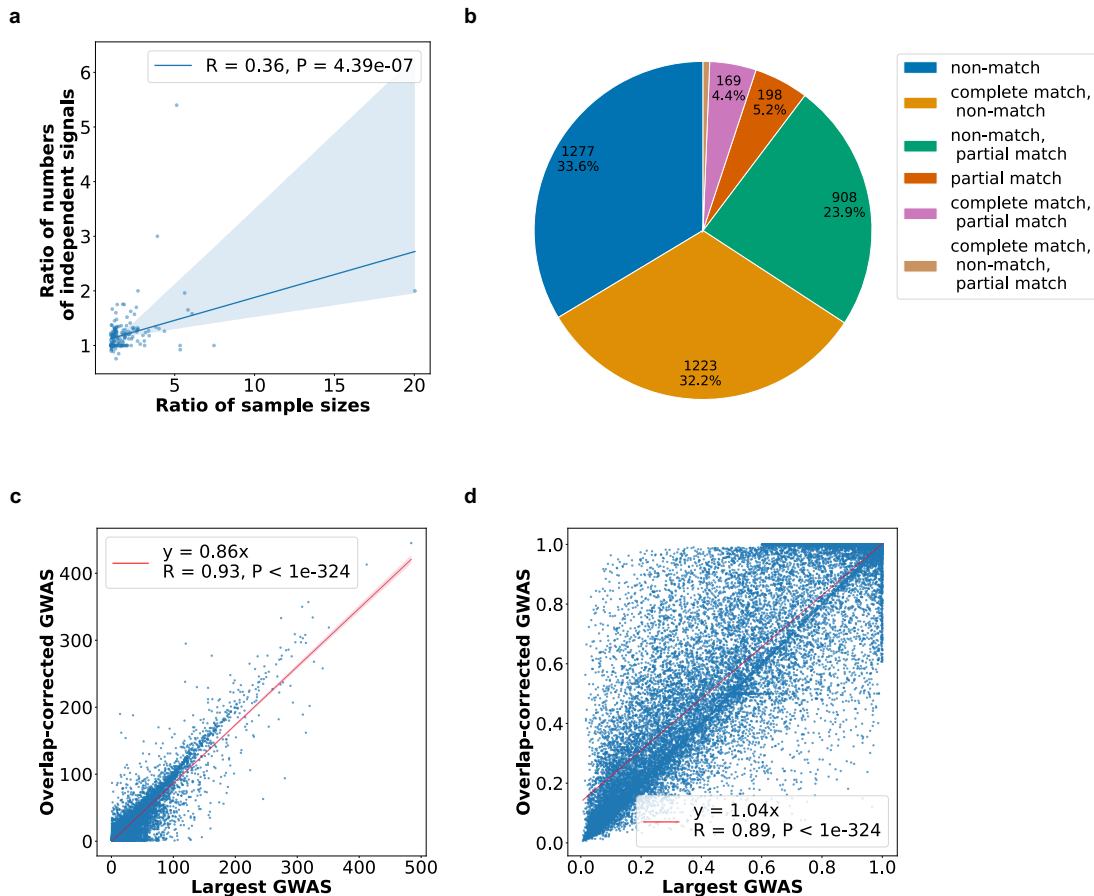1   **Supplementary Figure 1. Additional analyses to compare the association signals produced by the**
2   **largest GWAS and any GWAS. (a)** Number of studies vs. the fraction of significant signals produced by
3   the largest GWAS out of all significant signals produced by any GWAS. Sizes of dots represent the
4   number of significant signals produced by any GWAS. **(b)** Sample size ratio between the GWAS that
5   produced the most significant estimates and the largest GWAS, plotted against -log10(P) produced by the
6   largest GWAS across variants not significant in the largest GWAS but in another GWAS. Dots at the
7   bottom represent variants absent from the largest GWAS. Sizes of dots represent number of studies
8   where the signal was nominally significant (P < 0.05). **(c)** Overlap of association signals significant in the
9   largest GWAS (blue, left) and any GWAS (green, right) across 97 trait-ancestry pairs in the validation
10   analysis. Percentages represent the proportions of signals replicated in the gold-standard GWAS.

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12 **Supplementary Figure 2. Additional results from the conditional and fine-mapping analyses in**
13 **COJO**. **(a)** Ratio of the number of independent signals regressed on the ratio of sample sizes between
14 the overlap-aware GWAS and the largest GWAS. **(b)** Fraction of shared association regions with one
15 credible set produced by one GWAS and more than one credible set produced by the other GWAS with
16 different cases of matched credible sets. **(c)** Number of variants in completely matched credible sets
17 produced by the largest GWAS versus the overlap-aware GWAS. **(d)** Highest PIPs in completely matched
18 credible sets produced by the largest GWAS versus the overlap-aware GWAS.

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20   **Supplementary Figure 3. Additional results from LDSC and MAGMA.** QQ plots between the p-values
21   produced from the largest GWAS and the overlap-aware GWAS for trait heritability estimates **(a)**, genetic
22   correlations **(b)**, tissue-specific functional enrichment **(c)**, gene-level associations **(d)**, and gene set
23   enrichment **(e)**. **(f)** Spearman's correlation coefficients between gene set enrichment produced by the
24   overlap-aware GWAS and the largest GWAS for 159 trait-ancestry pairs.

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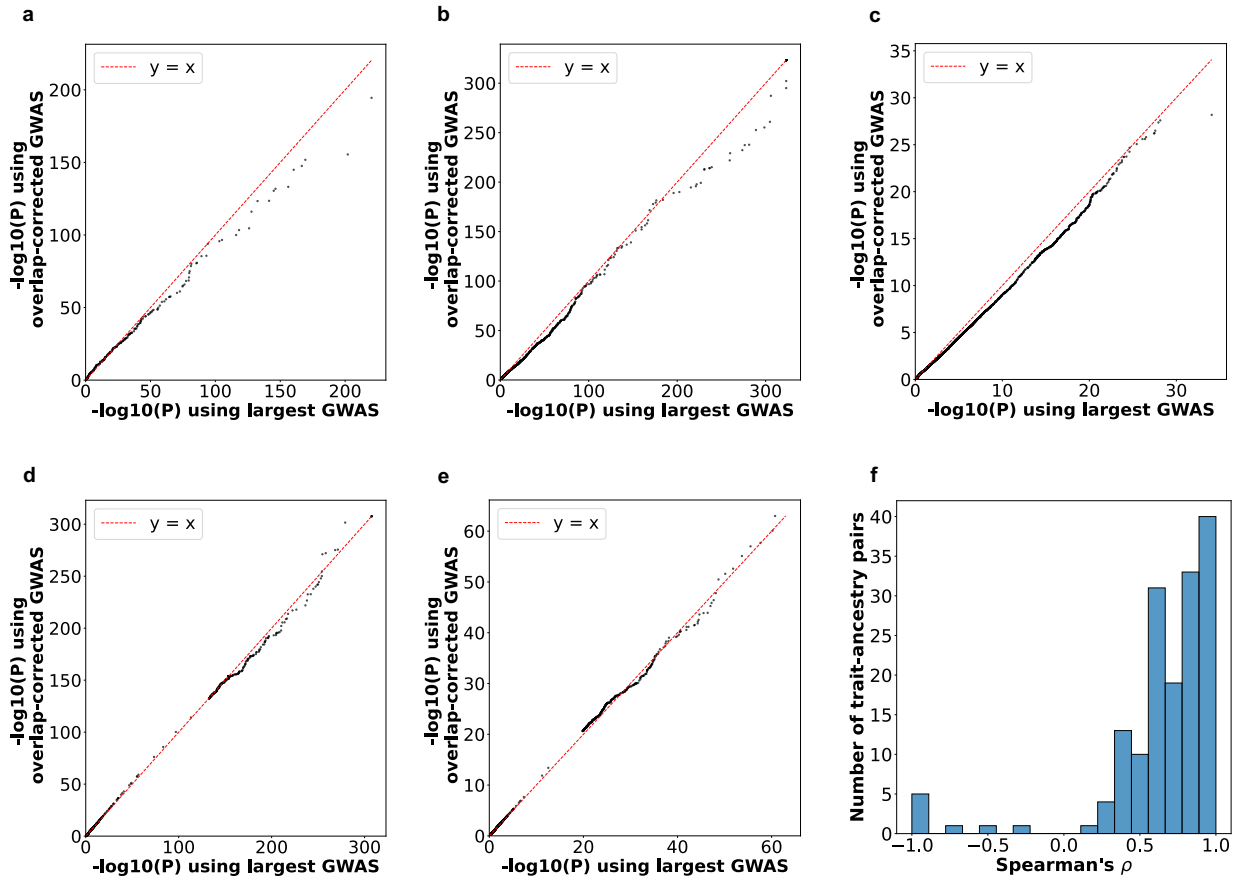
26   **Supplementary Figure 4. Trans-ancestry analyses. (a)** Overlap of association signals (clumped using
27   merged LD reference panels from individual ancestries) significant in the largest published trans-ancestry
28   GWAS (red, left) and the meta-analyzed trans-ancestry GWAS (green, right) across 131 traits. **(b)**
29   Overlap of association signals (clumped using European LD reference panel) significant in the largest
30   published trans-ancestry GWAS (red, left) and the meta-analyzed trans-ancestry GWAS (green, right)
31   across 131 traits. **(c)** Overlap of association signals significant in the largest published trans-ancestry
32   GWAS (green, right), the fixed-effects meta-analyzed trans-ancestry GWAS (red, left), and the random-
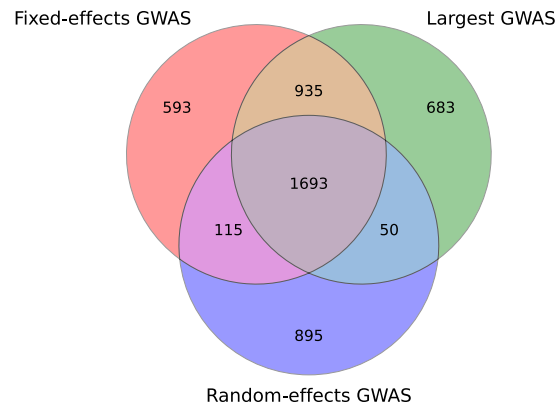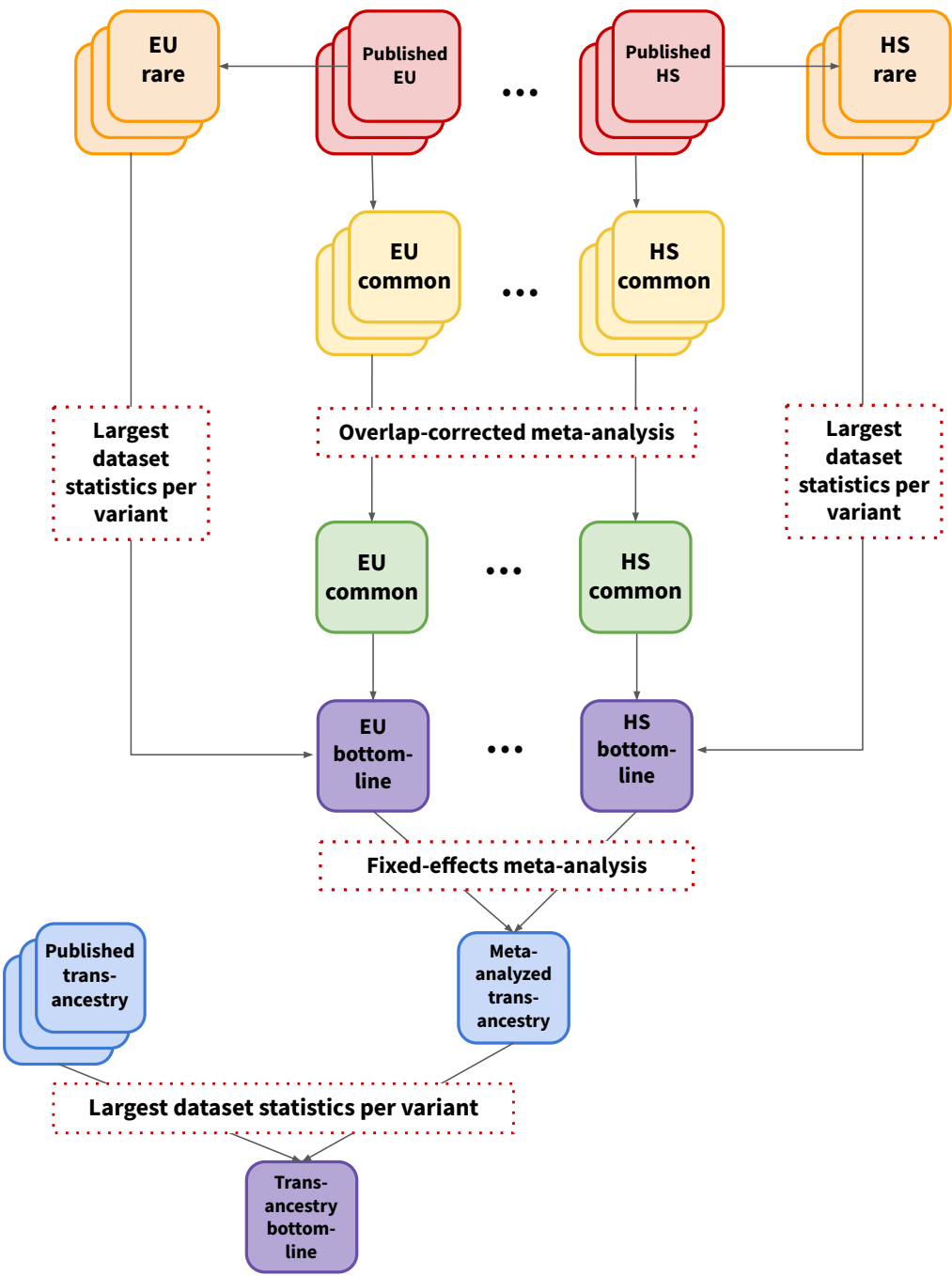33   effects meta-analyzed trans-ancestry GWAS (blue, bottom) across 48 "gold-standard" traits.

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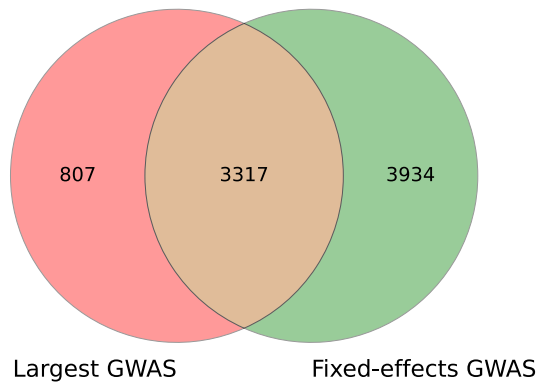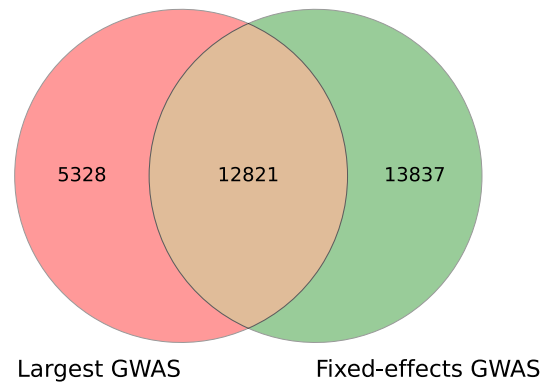
36 **Supplementary Figure 5. Bottom-line procedure to produce consensus GWAS.** EU (European) and
37 HS (Hispanic and Latin American) are two example ancestries.

38 **Supplementary Figure 6. Number of traits and studies across disease systems and ancestries in**
39 **the A2FKP as of July 2025. (a)** Number of traits (blue) and studies (orange) available in each of 11
40 disease systems. **(b)** Number of traits (blue) and studies (orange) available in each of 8 single ancestries
41 and trans-ancestry.
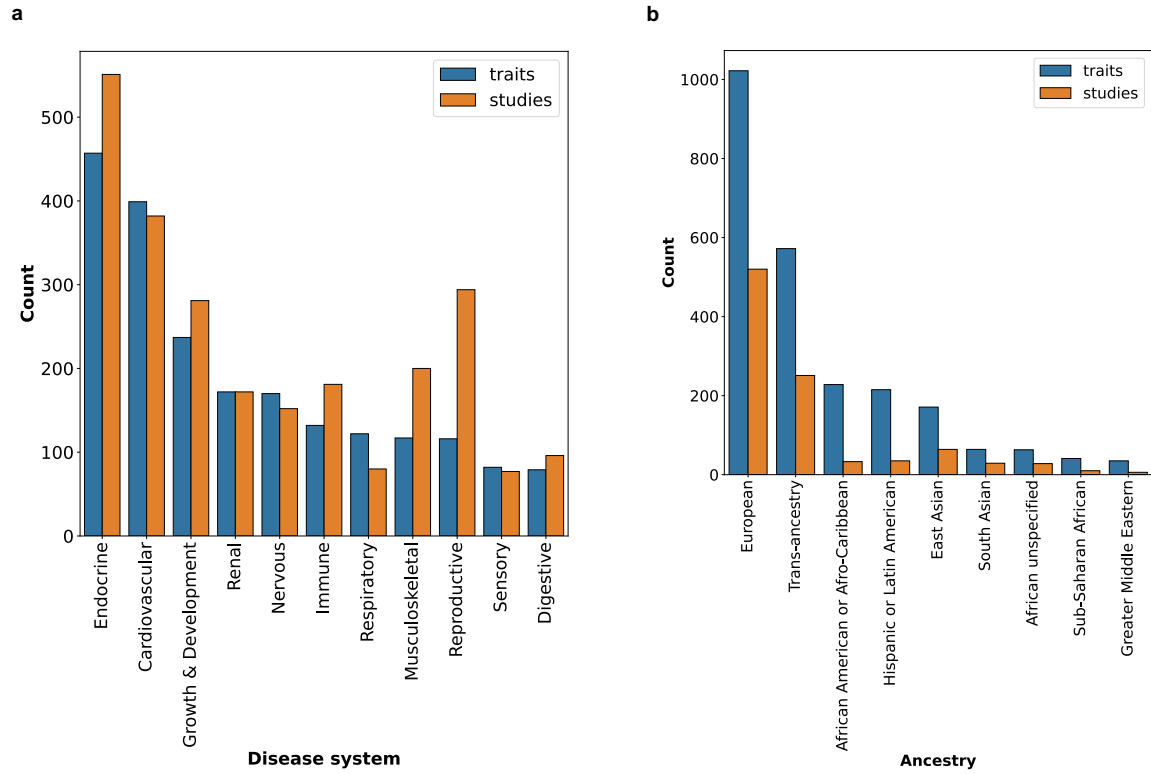
Supplementary Figure 7. Single-cell RNA analyses of *LDB3* in heart tissue. (a) UMAP plot showing the log-normalized expression values of all cells. **(b)** UMAP plot showing the annotated cell types of all cells. **(c)** Log fold change of expression in each cell type over expression of all cell types.