

1 Transcripts with high distal heritability mediate genetic effects on
2 complex traits

3

4 **Abstract**

5 The transcriptome is increasingly viewed as a bridge between genetic risk factors for complex disease and
6 their associated pathophysiology. Powerful insights into disease mechanism can be made by linking genetic
7 variants affecting gene expression (expression quantitative trait loci - eQTLs) to phenotypes.

8 **Introduction**

9 In the quest to understand the genetic architecture of complex traits, gene expression is an important bridge
10 between genotype and phenotype. By identifying mediating transcripts, we get one step closer to a molecular
11 understanding of how genetic variants influence traits. Moreover, there is evidence from genome-wide
12 association studies (GWAS) that regulation of gene expression accounts for the bulk of the genetic effect
13 on complex traits, as most trait-associated variants lie in gene regulatory regions [1, 2, 3, 4, 5, 6, 7]. It is
14 widely assumed that these variants influence local transcription, and methods such as transcriptome-wide
15 association studies (TWAS) [8, 9, 10, 11], summary data-based Mendelian randomization (SMR) [10], and
16 others have capitalized on this idea to identify genes associated with multiple disease traits [12, 13, 14, 15]

17 Despite the great promise of these methods, however, they have not been as widely successful as it seemed
18 they could have been, and the vast majority of complex trait heritability remains unexplained. Although
19 trait-associated variants tend to lie in non-coding, regulatory regions, they often do not have detectable effects
20 on gene expression [16] and tend not to co-localize with expression quantitative trait loci (eQTLs) [17, 18].

21 One possible explanation for these observations is that gene expression is not being measured in the appropriate
22 cell types and thus true eQTLs influencing traits cannot be detected [16]. An alternative explanation that
23 has been discussed in recent years is that effects of these variants are mediated not through local regulation
24 of gene expression, but through distal regulation [18, 19, 20, 15].

25 However, assessing the role of wide-spread distal gene regulation on complex traits requires large, dedicated data

26 sets that include high-dimensional, clinically relevant phenotyping, dense genotyping in a highly recombined
27 population, and transcriptome-wide measurements of gene expression in multiple tissues. Measuring gene
28 expression in multiple tissues is critical to adequately assess the extent to which local gene regulation varies
29 across multiple tissues and whether such variability might account for previous failed attempts to identify
30 trait-relevant local eQTL. Such data sets are extremely difficult to obtain in human populations, particularly
31 in the large numbers of subjects required for statistical testing. Thus, to investigate further the role of local
32 and distal gene regulation on complex traits, we have generated an appropriate data set in a large population
33 of diversity outbred (DO) mice [21] in a population model of diet-induced obesity and metabolic disease [12].

34 The DO mice were derived from eight inbred founder mouse strains, five classical lab strains, and three
35 strains more recently derived from wild mice [21]. They represent three subspecies of mouse *Mus musculus*
36 *domesticus*, *Mus musculus musculus*, and *Mus musculus castaneus*, and capture 90% of the known variation
37 in laboratory mice [cite]. They are maintained with a breeding scheme that ensures equal contributions from
38 each founder across the genome thus rendering almost the whole genome visible to genetic inquiry [21]. We
39 measured clinically relevant metabolic traits, including body weight, plasma levels of insulin and glucose,
40 and plasma lipids in 500 DO mice. We further measured transcriptome-wide gene expression in four tissues
41 related to metabolic disease: adipose tissue, pancreatic islets, liver, and skeletal muscle.

42 To assess the role of gene regulation in mediating variation in metabolic traits in this population, we propose
43 high-dimensional mediation (HDM). In univariate approaches, such as TWAS, SMR, and other Mendelian
44 randomization approaches, each transcript is tested independently for mediation of a local variant on a
45 trait. This process requires huge numbers of statistical tests, which is computationally expensive, requires
46 strict corrections for multiple testing, and assumes independence of genetic variants and transcripts. Such
47 methods are therefore limited to detecting only the largest statistical effects and are biased toward local gene
48 regulation. In contrast, with high-dimensional mediation we assessed broad relationships among the genome,
49 transcriptome, and phenotype as a whole and identified a highly heritable composite trait that was perfectly
50 mediated by a composite transcript. We show that composite transcripts were tissue-specific and highly
51 interpretable in terms of biological processes as well as cell type composition. Heritability analysis of the
52 transcripts showed that the strongest transcriptional mediators of metabolic disease had low local heritability
53 and high distal heritability. Finally, we show that the composite transcripts identified in the DO population
54 predicted obesity in an independent population of Collaborative Cross recombinant inbred (CC-RIX) mice
55 and in human subjects. In contrast, local eQTL were unable to predict obesity in the CC-RIX mice. Together
56 our results suggest that both the tissue used for gene expression analysis as well as distal gene regulation are
57 critically important in identifying transcriptional mediators of the genome on complex traits.

58 **Results**

59 **Genetic variation contributes to wide phenotypic variation**

60 A population of 500 diversity outbred mice (split evenly between male and female) from generates 18, 19,
61 and 21, was placed on a high-fat (44.6% kcal fat), high-sugar (34% carbohydrate), adequate protein (17.3
62 % protein) diet from Envigo Teklad (catalog number TD.08811) starting at four weeks of age as described
63 previously [12]. Each individual was assessed longitudinally for multiple metabolic measures including fasting
64 glucose levels, glucose tolerance, insulin levels, body weight, and blood lipid levels (Methods).

65 Although the environment was consistent across animals, the genetic diversity present in this population
66 resulted in widely varying distributions across physiological measurements (Fig. 1). For example, body
67 weights of adult individuals varied from less than the average adult B6 body weight to several times the body
68 weight of a B6 adult in both sexes (Fig. 1A). Fasting blood glucose (FBG) also varied considerably (Fig. 1B)
69 although few of the animals had FBG levels that would indicate pre-diabetes (animals,), or diabetes (7
70 animals, 1.4) according to previously developed cutoffs (pre-diabetes: $FBG \geq 250$ mg/dL, diabetes: $FBG \geq$
71 300, mg/dL) [22]. Males had higher FBG than females on average (Fig. 1C) as has been observed before
72 suggesting either that males were more susceptible to metabolic disease on the high-fat diet, or that males
73 and females may require different thresholds for pre-diabetes and diabetes.

74 Body weight was strongly positively correlated with food consumption (Fig. 1D $R^2 = 0.51, p = 1.5 \times 10^{-75}$)
75 and fasting blood glucose (FBG) (Fig. 1E, $R^2 = 0.25, p = 2 \times 10^{-32}$) suggesting a link between behavioral
76 factors and metabolic disease. However, the heritability of this trait and others (Fig. 1F) indicates that
77 background genetics contribute substantially to correlates of metabolic disease in this population.

78 The landscape of trait correlations (Fig. 1G) shows that most of the metabolic trait pairs were relatively
79 weakly correlated indicating complex relationships among the measured traits. This low level of redundancy
80 suggests a broad sampling of multiple heritable aspects of metabolic disease including overall body weight,
81 glucose homeostasis, pancreatic composition and liver function.

82 **Distal Heritability Correlates with Phenotype Relevance**

83 To elaborate the mechanistic details of genetic effects on metabolic phenotypes in the DO population, we
84 also measured gene expression in four tissues known to be involved in metabolic disease: adipose, pancreatic
85 islet, liver, and skeletal muscle. To confirm the heritability of transcript levels, we performed expression QTL
86 analysis using R/qt12 [cite] (Methods) and identified both local and distal eQTL for transcripts in each tissue
87 (Supp. Fig 9). Significant local eQTLs far outnumbered distal eQTLs (Supp. Fig. 9F) and tended to be

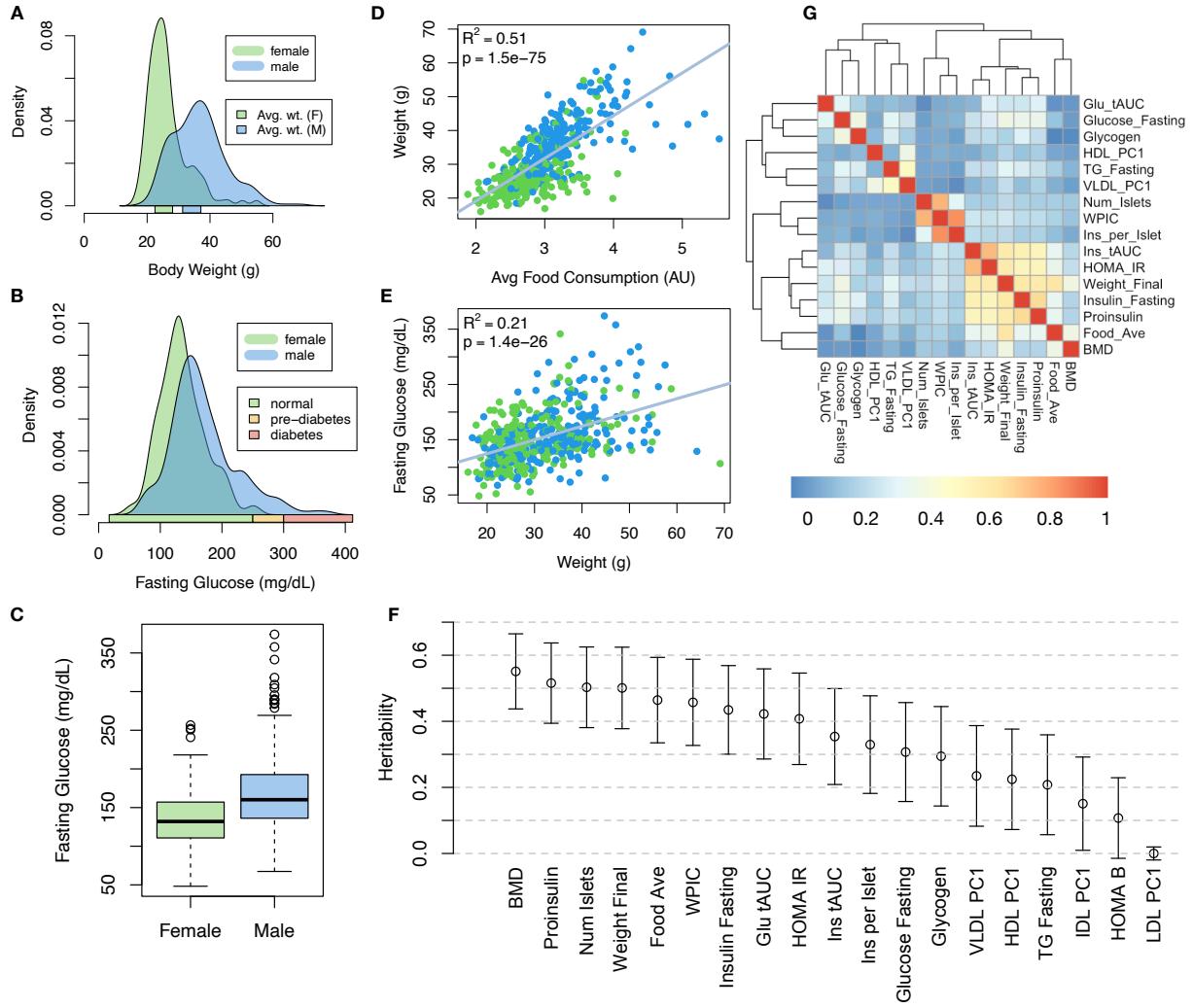


Figure 1: Clinical overview. **A.** Distributions of final body weight in the diversity outbred mice. Sex is indicated by color. The average B6 male and female adult weights at 24 weeks of age are indicated by blue and green bars on the x-axis. **B.** The distribution of final fasting glucose across the population split by sex. Normal, pre-diabetic, and diabetic fasting glucose levels for mice are shown by colored bars along the x-axis. **C.** Males had higher fasting blood glucose on average than females. **D.** The relationship between food consumption and body weight for both sexes. **E.** Relationship between body weight and fasting glucose for both sexes. **F.** Heritability estimates for each physiological trait. Bars show standard error of the estimate. **G.** Correlation structure between pairs of physiological traits.

shared across tissues (Supp. Fig. 9G) whereas the few significant distal eQTL we identified tended to be tissue-specific (Supp. Fig. 9H)

To better compare the relative contribution of local and distal genetics to transcript levels, we performed a heritability analysis for each transcript (Methods). Overall, local and distal factors contributed approximately equally to transcript abundance. In all tissues, both local and distal factors explained between 13 and 19% of the variance in the median transcript (Fig 2A).

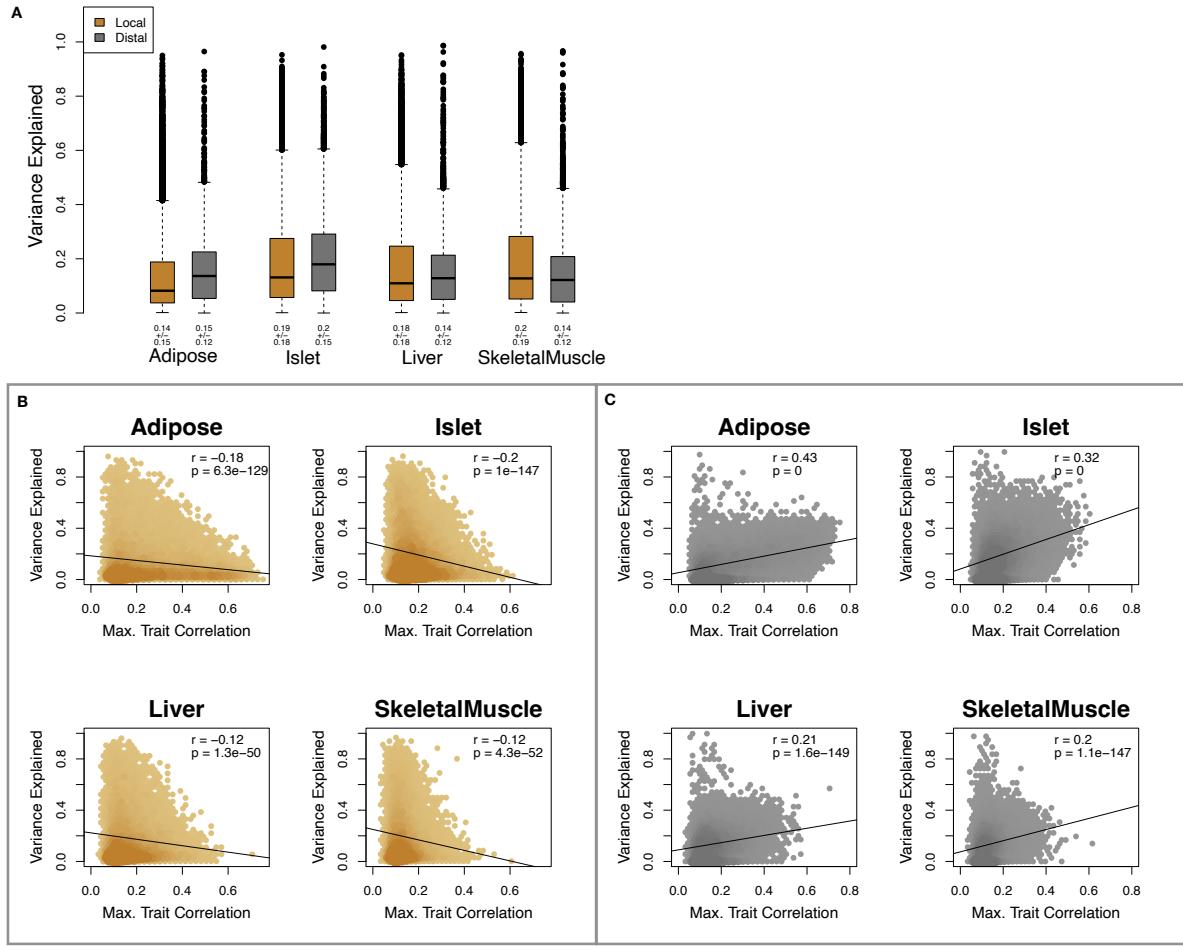


Figure 2: Transcript heritability and trait relevance. **A.** Distributions of distal and local heritability of transcripts across the four tissues. Overall local and distal factors contribute equally to transcript heritability. The relationship between **(B.)** local and **(C.)** distal heritability and trait relevance across all four tissues. Here trait relevance is defined as the maximum correlation between the transcript and all traits. Local heritability is negatively correlated with trait relevance, and distal heritability is positively correlated with trait relevance. Pearson (r) and p values for each correlation are shown in the upper-right of each panel.

94 Local heritability of transcripts was negatively correlated with their trait relevance, defined as the maximum
 95 correlation of a transcript across all traits (Fig. 2B). This suggests that the more local genotype influenced
 96 transcript abundance, the less effect variation in transcript abundance was related to the measured traits.
 97 Conversely, distal heritability of transcripts was positively correlated with trait relevance (Fig. 2C). That is,
 98 transcripts that were more highly correlated with the measured traits tended to be distally, rather than locally,
 99 heritable. That trait-correlated transcripts have low local heritability is consistent with previous observations
 100 that low-heritability transcripts explain more expression-mediated disease heritability than high-heritability
 101 transcripts [19]. However, the positive relationship between trait correlation and distal heritability suggests
 102 that there are alternative mechanisms through which genetic regulation of transcripts may influence traits.

103 **High-Dimensional Mediation identifies composite transcript that perfectly mediates composite
104 trait**

105 To identify mechanisms through which genetic regulation of transcripts influences heritable traits, we propose
106 high-dimensional mediation (HDM) (Fig. 3). In this process we kernelize each of the genome, transcriptome,
107 and phenotype, and perform regularized and sparse generalized canonical correlation analysis (RGCCA) [cite]
108 in which we explicitly model the mediation by the transcriptome of the effect of the genome on the phenotype
109 (Methods, Fig. 3). RGCCA is an extended form of canonical correlation analysis (CCA) [cite] in which
110 multiple data sets can be analyzed simultaneously with explicit relationships.

111 The result of this process is three vectors representing the composite genome (G_C), composite transcriptome
112 (T_C) and the composite phenotype (P_C) where T_C perfectly mediates the effect of G_C on P_C . Each vector is of
113 length n where n is the number of individual mice. Fig. 3A shows the partial correlations between all pairs of
114 composite vectors. The partial correlation r between G_C and T_S was 0.46, and the partial correlation between
115 T_S and P_S was 0.78. However, when the transcriptome was taken into account, the partial correlation between
116 G_S and P_S was effectively 0 (-0.01). The estimated heritability of the composite phenotype was heritability of
117 0.71 ± 0.08 , which was higher than any of the individual traits (Fig. 1F). Thus, we have identified a maximally
118 heritable metabolic trait that is perfectly mediated by a heritable component of the transcriptome.

119 Standard CCA is prone to over-fitting because in any two large matrices it can be trivial to identify
120 highly correlated composite vectors. To assess whether RGCCA was similarly prone to over-fitting in a
121 high-dimensional space, we performed permutation testing. We permuted the individual labels on the
122 transcriptome kernel matrix 1000 times and recalculated the path coefficient, which is the partial correlation
123 of G_C and T_C multiplied by the partial correlation of T_C and P_C . This represents the path from G_C to
124 P_C that is mediated through T_C . The null distribution of the path coefficient is shown in Fig. 3B, and the
125 observed path coefficient from the original data is indicated by the red line. The observed path coefficient
126 was well outside the null distribution generated by permutations. Fig. 3C illustrates this observation in more
127 detail. Although we identified high correlations between G_C and T_C , and modest correlations between T_C and
128 P_C in the null data (Fig 3C), these two values could not be maximized simultaneously. The red dot shows that
129 in the real data both the G_C - T_C correlation and the T_C - P_C correlation could be maximized simultaneously
130 suggesting that that path from genotype to phenotype through transcriptome is highly non-trivial and
131 identifiable in this case. These results suggest that these composite vectors represent genetically determined
132 variation in phenotype that is mediated through genetically determined variation in transcription.

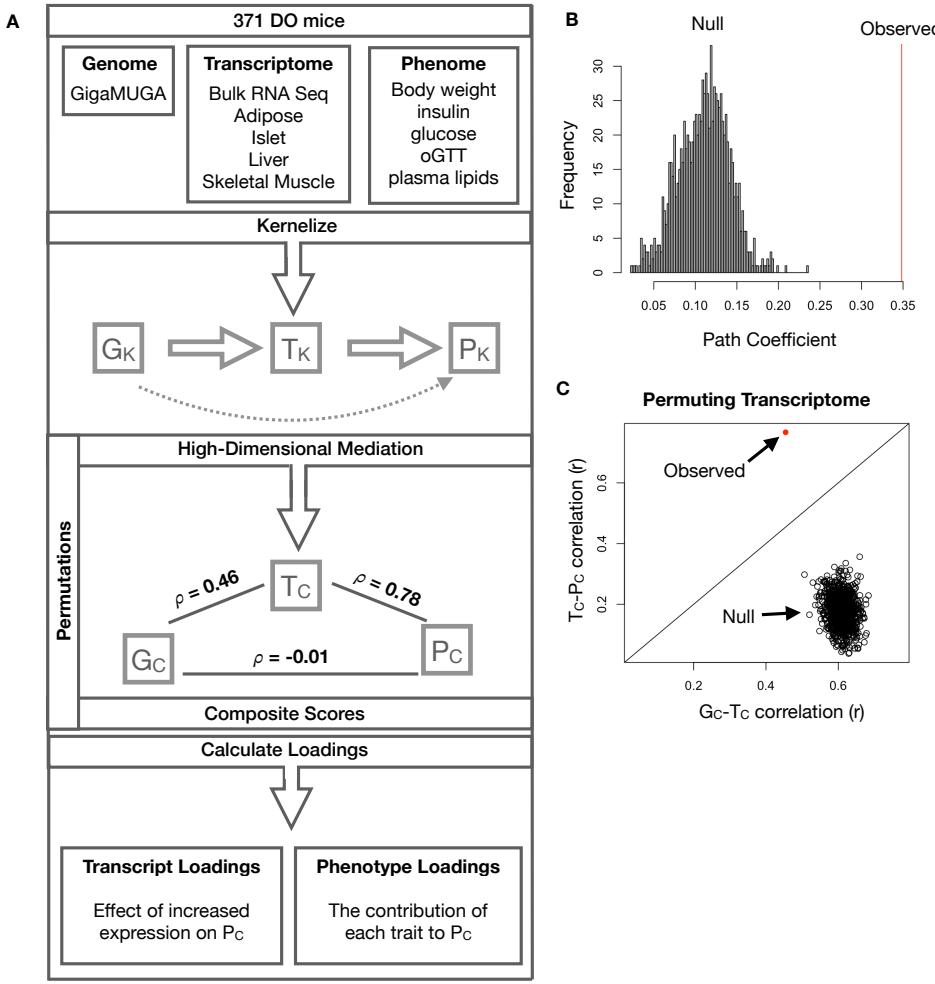


Figure 3: High-dimensional mediation. **A.** Workflow indicating major steps of high-dimensional mediation. The genotype, transcriptome, and phenotype matrices were kernelized to yield single matrices representing the relationships between all individuals for each data modality (G_K = genome kernel, T_K = transcriptome kernel; P_K = phenome kernel). High-dimensional mediation was applied to these matrices to maximize the direct path $G \rightarrow T \rightarrow P$, the mediating pathway (arrows), while simultaneously minimizing the direct $G \rightarrow P$ pathway (dotted line). The composite vectors that resulted from high-dimensional mediation were G_c , T_c , and P_c . The partial correlations ρ between these vectors indicated perfect mediation. Transcript and trait loadings were calculated as described in the methods. **B.** The null distribution of the path coefficient derived from 10,000 permutations compared to the observed path coefficient (red line). **C.** The null distribution of the G_c-T_c correlation vs. the T_c-P_c correlation compared with the observed value (red dot).

133 **Body weight and insulin resistance were highly represented in the expression-mediated com-**
 134 **posite trait**

135 The loadings of each measured trait onto P_c indicate how much each contributed to P_c . Final body weight
 136 contributed the most to P_c (Fig. 4), followed by homeostatic insulin resistance (HOMA_IR) and fasting
 137 plasma insulin levels (Insulin_Fasting). We can thus interpret P_c as an index of metabolic disease (Fig. 4B).
 138 Individuals with high values of P_c have a higher metabolic index and greater metabolic disease, including

139 higher body weight and higher insulin resistance. We refer to P_C as the metabolic index going forward. Traits
 140 contributing the least to the metabolic index were measures of cholesterol and pancreas composition. Thus,
 141 when we interpret the transcriptomic signature identified by HDM, we are explaining primarily transcriptional
 142 mediation of body weight and insulin resistance, as opposed to cholesterol measurements.

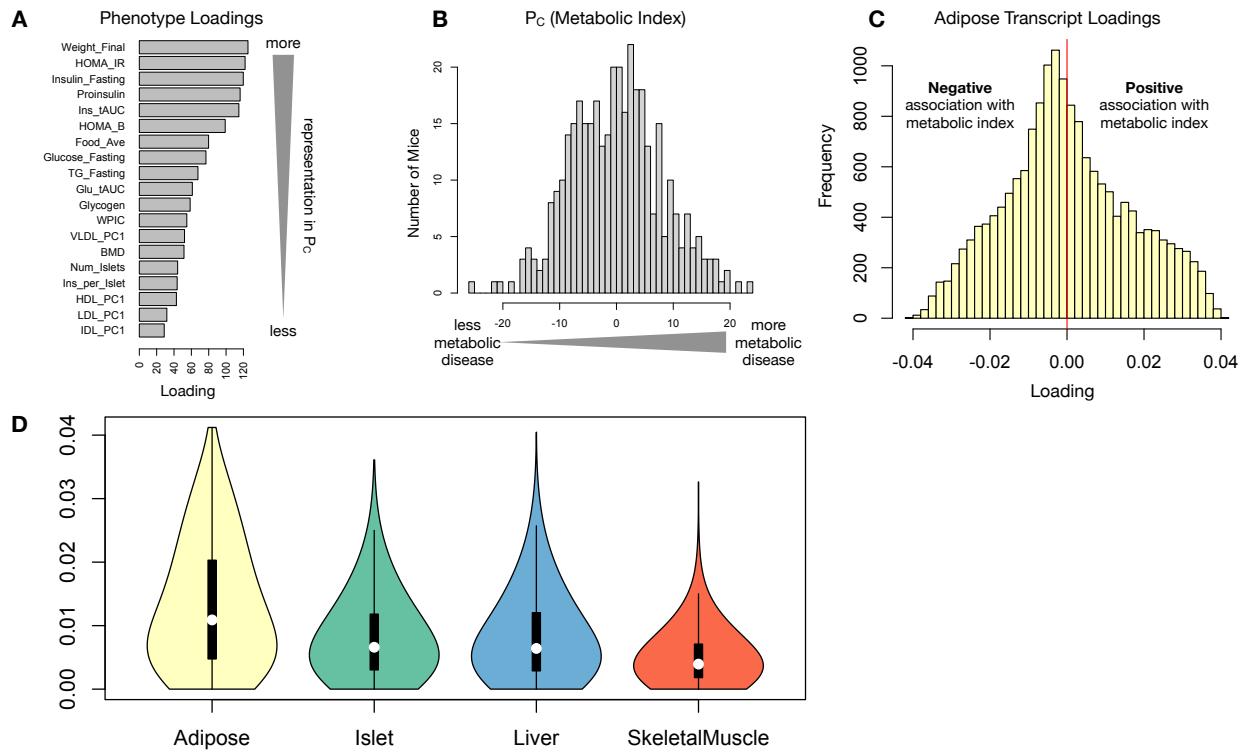


Figure 4: Interpretation of loadings. **A.** Loadings across traits. Body weight and insulin resistance contributed the most to the composite trait. **B.** Phenotype scores across individuals. Individuals with large positive phenotype scores had higher body weight and insulin resistance than average. Individuals with large negative phenotype scores had lower body weight and insulin resistance than average. **C.** Distribution of transcript loadings in adipose tissue. For transcripts with large positive loadings, higher expression was associated with higher phenotype scores. For transcripts with large negative loadings, higher expression was associated with lower phenotype scores. **D.** Distribution of absolute value of transcript loadings across tissues. Transcripts in adipose tissue had the largest loadings indicating that transcripts in adipose tissue were the best mediators of the genetic effects on body weight and insulin resistance.

143 **High-loading transcripts have low local heritability, high distal heritability, and are linked
 144 mechanistically to obesity**

145 We interpreted large loadings onto transcripts as indicating strong mediation of the effect of genetics on
 146 metabolic index. Large positive loadings indicate that inheriting higher expression was associated with a
 147 higher metabolic index (i.e. higher risk of obesity and metabolic disease on the high-fat diet) (Fig. 4C).

148 Conversely, large negative loadings indicate that inheriting lower expression of these transcripts was associated

¹⁴⁹ with a lower metabolic index (i.e. lower risk of obesity and metabolic disease on the high-fat diet) (Fig. 4C).
¹⁵⁰ We used GSEA to look for biological processes and pathways that were enriched at the top and bottom of
¹⁵¹ this list (Methods).

¹⁵² In adipose tissue, both GO processes and KEGG pathway enrichments pointed to an axis of inflammation
¹⁵³ and metabolism (Supp. Fig. 10 and 11). Processes and pathways associated with inflammation, particularly
¹⁵⁴ macrophage infiltration were positively associated with metabolic index, indicating that increased expression
¹⁵⁵ in inflammatory pathways was associated with a higher metabolic index. It is well established that adipose
¹⁵⁶ tissue in obese individuals is highly inflamed [cite] and infiltrated by macrophages [cite], and the results here
¹⁵⁷ suggest that this may be a heritable component of metabolic disease.

¹⁵⁸ The strongest negative enrichments in adipose tissue were related to mitochondrial activity in general, and
¹⁵⁹ thermogenesis in particular (Supp. Fig. 10 and 11). It has been shown mouse strains with greater thermogenic
¹⁶⁰ potential are also less susceptible to obesity on a high-fat diet.

¹⁶¹ Transcripts associated with the citric acid (TCA) cycle as well as the catabolism of branched-chain amino acids
¹⁶² (BCAA), valine, leucine, and isoleucine also had strong negative enrichment in the adipose tissue (Supp. Fig.
¹⁶³ XXX). Expression of genes in both pathways (for which there is some overlap) has been previously associated
¹⁶⁴ with insulin sensitivity [12, 23, 24], suggesting that impairment in these pathways may be associated with
¹⁶⁵ insulin resistance. Selective PPAR γ modulation by insulin-sensitizing thiazolidinedione drugs has further
¹⁶⁶ been shown to influence both inflammation and BCAA metabolism in obese rats suggesting a relationship
¹⁶⁷ between these pathways and insulin resistance [25]. BCAA levels are also related to insulin resistance in
¹⁶⁸ human subjects and are elevated in insulin-resistant obese individuals relative to weight-matched non-insulin
¹⁶⁹ resistant individuals [26]. In the DO mice studied here, inheriting increased expression of genes involved in
¹⁷⁰ BCAA catabolism was associated with reduced body weight and insulin resistance.

¹⁷¹ Transcripts in the adipose tissue had the largest loadings, both positive and negative, of all tissues, suggesting
¹⁷² that much of the effect of genetics on body weight and insulin resistance is mediated through gene expression
¹⁷³ in adipose tissue (Fig. 5A). The loadings in liver and pancreas were comparable, and those in skeletal muscle
¹⁷⁴ were the weakest (Fig. 5A), suggesting that less of the genetic effects were mediated through transcription in
¹⁷⁵ skeletal muscle. Across all tissues, transcripts with the largest loadings tended to have relatively high distal
¹⁷⁶ heritability compared with local heritability (Fig. 5A). Transcripts with the highest local heritability tended
¹⁷⁷ to have very weak loadings and were 3.6 times less likely to be associated with diabetes and obesity in the
¹⁷⁸ literature than transcripts with high loadings (Fig. fig:loading_heritabilityB, Methods). TWAS-nominated
¹⁷⁹ transcripts also had relatively weak loadings and high local heritability (Fig. 4C). They were half as likely as

180 transcripts with the highest loadings to be associated with diabetes and obesity in the literature (Fig. 4C).

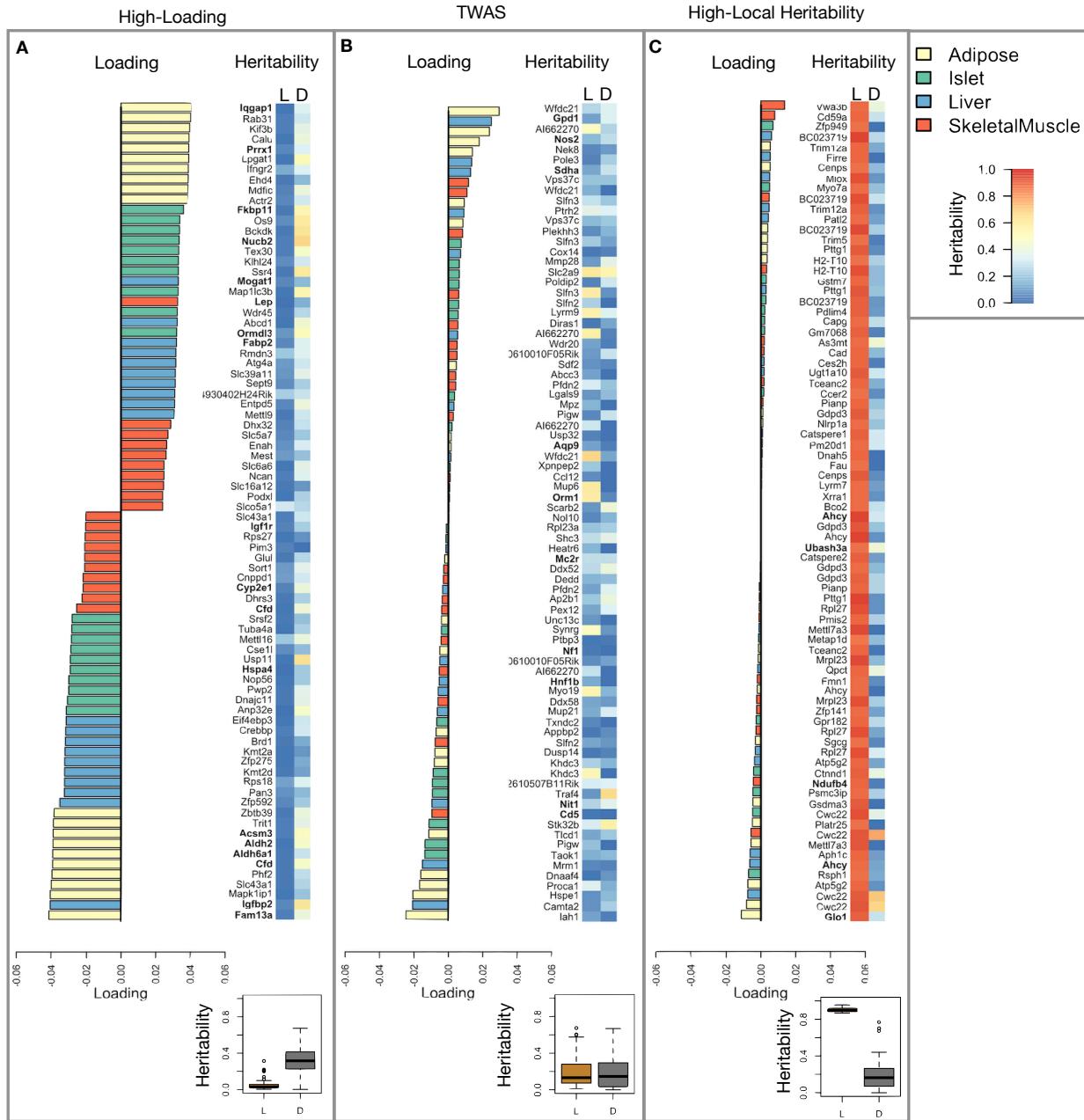


Figure 5: Transcripts with high loadings have high distal heritability and literature support. Each panel has a bar plot showing the loadings of transcripts selected by different criteria. Bar color indicates the tissue of origin. The heat map shows the local (L - left) and distal (D - right) heritability of each transcript. **A.** Loadings for the 10 transcripts with the largest positive loadings and the 10 transcripts with the largest negative loadings for each tissue. **B.** Loadings of TWAS candidates with the 10 largest positive correlations with traits and the largest negative correlations with traits across all four tissues. **C.** The transcripts with the largest local heritability (top 20) across all four tissues.

181 **Tissue-specific transcriptional programs were associated with metabolic traits**

182 Clustering of transcripts with top loadings in each tissue showed tissue-specific functional modules associated
183 with obesity and insulin resistance in the DO population (Fig. 6A). In this figure, the importance of immune
184 activation specifically in the adipose tissue is apparent. There are also other tissue-specific processes. Positive
185 loadings on lipid metabolism in liver suggest that inheriting high liver expression of genes in this cluster is
186 positively associated with metabolic disease. This cluster included the gene *Pparg*, whose primary role is in
187 the adipose tissue where it is considered a master regulator of adipogenesis [27]. Agonists of *Pparg*, such
188 as Thiazolidinediones, which are FDA-approved to treat type II diabetes, reduce inflammation and adipose
189 hypertrophy [27]. Consistent with this role, the loading for *Pparg* in adipose tissue is slightly negative,
190 suggesting that upregulation is associated with leaner mice (Fig. 6B). In contrast, *Pparg* has a large positive
191 loading in liver, where it plays a role in the development of hepatic steatosis, or fatty liver. Mice that lack
192 *Pparg* specifically in the liver, are protected from developing steatosis and show reduced expression of lipogenic
193 genes [28, 29]. Overexpression of *Pparg* in the livers of mice with a *Ppara* knockout, causes upregulation of
194 genes involved in adipogenesis [30]. In the livers of both mice and humans [31, 32] High *Pparg* expression is
195 associated with hepatocytes that accumulate large lipid droplets and have gene expression profiles similar to
196 adipocytes.

197 The local and distal heritability of *Pparg* is low in adipose tissue suggesting its expression in this tissue is
198 highly constrained in the population (Fig. 6B). However, the distal heritability of *Pparg* in liver is relatively
199 high suggesting it is complexly regulated and has sufficient variation in this population to drive variation
200 in phenotype. Both local and distal heritability of *Pparg* in the islet are fairly high, but the loading is
201 low, suggesting that variability of expression in the islet does not drive phenotypic variation. These results
202 highlight the importance of tissue context when investigating the role of heritable transcript variability in
203 driving phenotype.

204 Gene lists for all clusters are available in Supplemental Files XXX.

205 **Gene expression, but not local eQTLs, predict body weight in an independent population**

206 The loading of each transcript indicates how inherited expression levels influence metabolic phenotypes.
207 If local regulation is the predominant factor influencing gene expression, we should be able to predict an
208 individual's phenotype based on their genotypes across all local eQTLs. We tested this hypothesis in an
209 independent population of F1 mice generated through multiple pairings of Collaborative Cross (CC) [cite]
210 strains (Fig. 7A) (Methods).

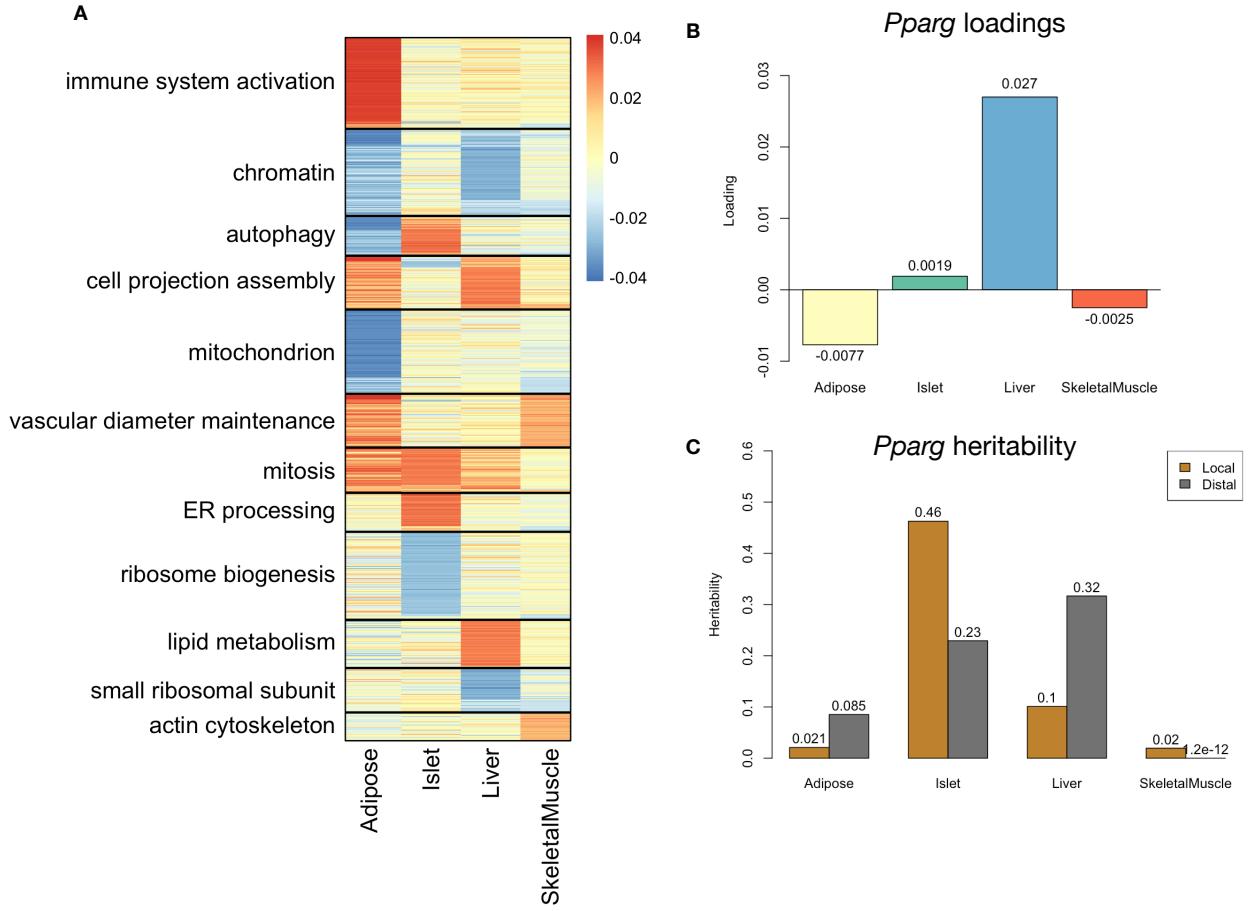


Figure 6: Tissue-specific transcriptional programs were associated with obesity and insulin resistance. **A** Heat map showing the loadings of all transcripts with loadings greater than 2.5 standard deviations from the mean in any tissue. The heat map was clustered using k medoid clustering. Functional enrichments of each cluster are indicated along the left margin. **B** Loadings for *Pparg* in different tissues. **C** Local and distal of *Pparg* expression in different tissues.

211 We first tested whether the transcript loadings derived from HDM in the DO were relevant to the relationship
 212 between the transcriptome and the phenotype in the CC-RIX. To do this, we multiplied the transcript loadings
 213 derived from HDM in the DO mice by transcript measurements in the CC-RIX standardized across individuals.
 214 This created a transcript vector weighted by importance to metabolic disease as determined in the DO.
 215 The mean of this vector was the predicted metabolic index for the animal based on its transcription in
 216 either adipose tissue, liver, or skeletal muscle. Across all three tissues, weighted transcription values were
 217 significantly correlated with metabolic index in the CC-RIX population measured as body weight (Fig. 7B left
 218 column). Adipose tissue transcription yielded the most accurate prediction (stats). This result confirms the
 219 validity and translatability of the transcript loadings determined in the DO population and their relationship
 220 to metabolic disease. It also supports the observation that transcription in adipose tissue is the strongest

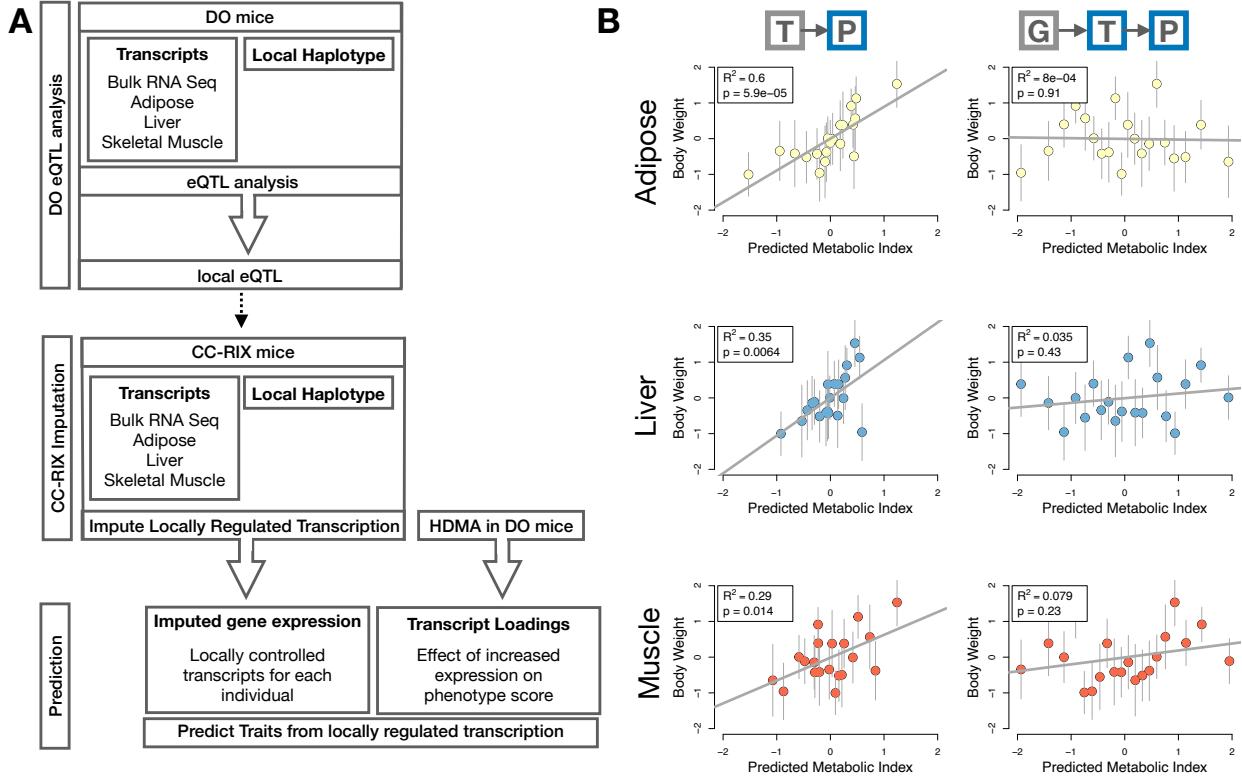


Figure 7: Transcription, but not local genotype, predicts phenotype in the CC-RIX. **A.** Workflow showing procedure for translating HDM results to an independent population of mice. **B.** Relationships between the predicted metabolic index and measured body weight. The left column shows the predictions using measured transcripts. The right column shows the prediction using transcript levels imputed from local genotype. Gray boxes indicate measured quantities, and blue boxes indicate calculated quantities. The dots in each panel represent individual CC-RIX strains. The gray lines show the standard deviation on body weight for the strain.

mediator of genetic effects on metabolic index.
 We then tested whether this mediation signal was encoded by local genotype. To do this, we imputed gene expression in the CC-RIX using local genotype. We were able to estimate variation in gene transcription robustly. The correlation between measured gene expression and imputed gene expression across all tissues was close to $R = 0.5$, and the variance explained by local genotype was comparable in the DO and CC-RIX (Supp. Fig. 12). However, when weighted with the loadings derived from HDM in the DO population, these imputed transcripts across all tissues failed to predict metabolic index in the CC-RIX (Fig. 7B right column). Taken together, these results support the hypothesis that distal, rather than local genetic factors are primarily driving complex-trait related variation in gene expression.

230 **Distally heritable transcriptomic signatures reflect variation in composition of adipose tissue
231 and islets**

232 Interpretation of global distal genetic influences on gene expression and phenotype is potentially more
233 challenging than interpretation and translation of local genetic influences. Effects can not be located to
234 individual gene variants or transcripts, but because we have a measure of importance across all transcripts in
235 multiple tissues, we can look at global patterns. We noted earlier that functional enrichments of transcripts
236 with large positive loadings in the adipose tissue, suggested that the obese mice in the population had a
237 genetic predisposition toward elevated macrophage infiltration into the adipose tissue. This suggests heritabl
238 variability in cell-type composition of the adipose tissue. We investigated this further bioinformatically
239 by comparing the loadings of cell-type-specific transcripts (Methods). For adipose tissue we used a list of
240 cell-type specific genes identified in human adipose tissue

241 In adipose tissue, the mean loading of macrophage-specific genes was substantially greater than 0 (Fig. 8A),
242 indicating that obese mice were genetically predisposed to have high levels of macrophage infiltration in
243 adipose tissue in response to the high-fat, high-sugar diet.

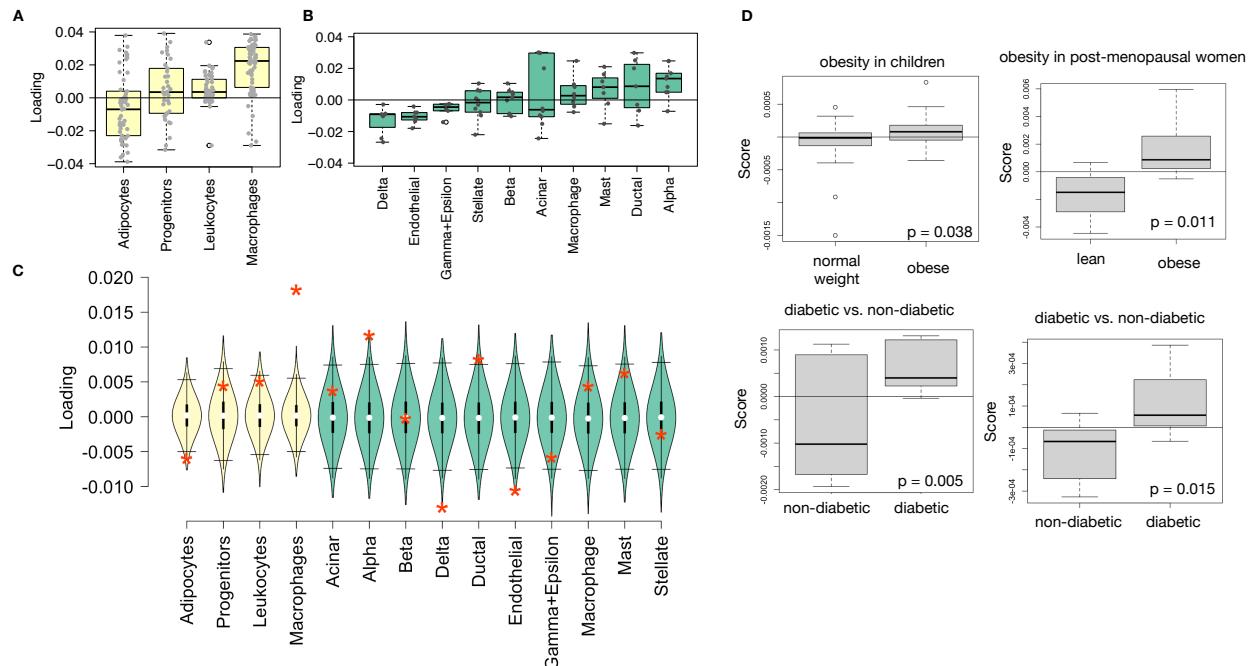


Figure 8: HDM results translate to humans. **A.** Distribution of loadings for cell-type-specific transcripts in adipose tissue. **B.** Distribution of loadings for cell-type-specific transcripts in pancreatic islets (green). **C.** Null distributions for the mean loading of randomly selected transcripts in each cell type compared with the observed mean loading of each group of transcripts (red asterisk). **D.** Predictions of metabolic phenotypes in four adipose transcription data sets downloaded from GEO. In each study the obese/diabetic patients were predicted to have greater metabolic disease than the lean/non-diabetic patients based on the HDM results from DO mice.

²⁴⁴ In islet, the mean loadings for alpha-cell specific transcripts were significantly positive, while the mean
²⁴⁵ loadings for delta- and endothelial-cell specific genes were significantly negative (Fig. 8B). These results
²⁴⁶ suggest that obese mice had inherited higher proportions of alpha cells, and lower proportions of endothelial
²⁴⁷ and delta cells in their pancreatic islets.

²⁴⁸ The loadings for pancreatic beta cell-type specific loadings was not significantly different from zero. This
²⁴⁹ does not reflect on the function of the beta cells in the obese mice, but rather suggests that mice prone to
²⁵⁰ obesity were not obese because they inherited fewer beta cells than non-obese mice.

²⁵¹ Biological interpretation of alpha, endothelial, delta cells??

²⁵² **Distally heritable transcriptomic signatures translate to human disease**

²⁵³ Ultimately, the distally heritable transcriptomic signatures that we identified in DO mice will be useful if
²⁵⁴ they inform pathogenicity and treatment of human disease. To investigate the potential for translation of the
²⁵⁵ gene signatures identified in DO mice, we compared them to transcriptional profiles in obese and non-obese
²⁵⁶ human subjects (Methods). We limited our analysis to adipose tissue because the adipose tissue signature
²⁵⁷ had the strongest relationship to obesity and insulin resistance in the DO.

²⁵⁸ We calculated a predicted obesity score for each individual in the human studies based on their adipose
²⁵⁹ tissue gene expression (Methods) and compared the predicted scores for obese and non-obese groups as well
²⁶⁰ as diabetic and non-diabetic groups. In all cases, the predicted obesity scores were higher on average for
²⁶¹ individuals in the obese and diabetic groups compared with the lean and non-diabetic groups, indicating that
²⁶² the distally heritable signature of obesity identified in DO mice is relevant to obesity and diabetes in human
²⁶³ subjects.

²⁶⁴ **Targeting gene signatures**

²⁶⁵ Although high-loading transcripts are likely good candidates for understanding specific biology related to
²⁶⁶ obesity, we emphasize that the transcriptome overall is highly interconnected and redundant, and that
²⁶⁷ focusing on individual transcripts for treatment may be less effective than using a broader transcriptomic
²⁶⁸ signature. The ConnectivityMap (CMAP) database [cite] developed by the Broad Institute allows us to query
²⁶⁹ thousands of compounds that reverse or enhance transcriptomic signatures as a whole in multiple different
²⁷⁰ cell types. By identifying drugs that reverse pathogenic transcriptomic signatures as a whole rather than
²⁷¹ targeting individual genes, we can potentially increase efficacy of tested compounds.

²⁷² We thus queried the CMAP database through the CLUE online query tool developed by The Broad Institute

273 [cite] (Methods).

274 Alternatively, we can target the gene signature as a whole using CMAP. Identifying drugs to target gene
275 signatures is possible through CMAP. We put our loadings from islet into CMAP. The top hit was PPAR
276 receptor agonist. Rosiglitazone, a widely used diabetes drug, is a PPAR receptor agonist. Another class of
277 drugs on the list was sulfonylureas, which are another major class of drugs for type 2 diabetes.

278 • **Supplemental Table** results from CMAP

279 Discussion

280 Yao *et al.* [19] observed that genes with low local heritability explained more expression-mediated disease
281 heritability than genes with high local heritability. This observation is consistent with principles of robustness
282 in complex systems. If a transcript were both important to a trait and subject to strong local regulation,
283 a population would be susceptible to extremes in phenotype that might frequently cross the threshold to
284 disease. Indeed, strong disruption of highly trait-relevant genes is the cause of Mendelian disease.

285 Rather, observations suggest that genes near GWAS hits and have obvious functional relevance to a trait
286 tend to have highly complex regulatory landscapes under strong selection pressures [18]. In contrast, genes
287 with strong local regulation tend to be depleted of functional annotations and are under looser selection
288 constraints [18]. These observations and others led Liu *et al.* [33] to suggest that most heritability of complex
289 traits is driven by weak trans-eQTLs. They proposed a framework of understanding heritability of complex
290 traits in which massive polygenicity is distributed across common variants in both functional “core genes”,
291 as well as more peripheral genes that may not seem obviously related to the trait.

292 We developed high-dimension mediation to test the omnigenic model with a more holistic approach. This
293 model posits that once the expression of the core genes (i.e. trait-mediating genes) is accounted for, there
294 should be no residual correlation between the genome and the phenotype. This hypothesis lends itself well to
295 systems approaches that can account for arbitrarily complex gene regulation, as well as the interconnectedness
296 and redundancy of the transcriptome without explicitly modeling them. The HDM approach we propose here
297 tests the hypothesis of the omnigenic model

298 • distal heritability correlates with phenotype relevance

299 • others who use local eQTL to associate genotype with traits often say “we nominated this gene” even
300 though other nearby genes have higher eQTL LOD scores (27019110, 31465442) Our method supports
301 the idea that the transcripts with the strongest local regulation are less likely to be functionally related
302 to the trait

303 **Data Availability**

304 Here we tell people where to find the data

305 **Acknowledgements**

306 Here we thank people

307 **Supplemental Figures**

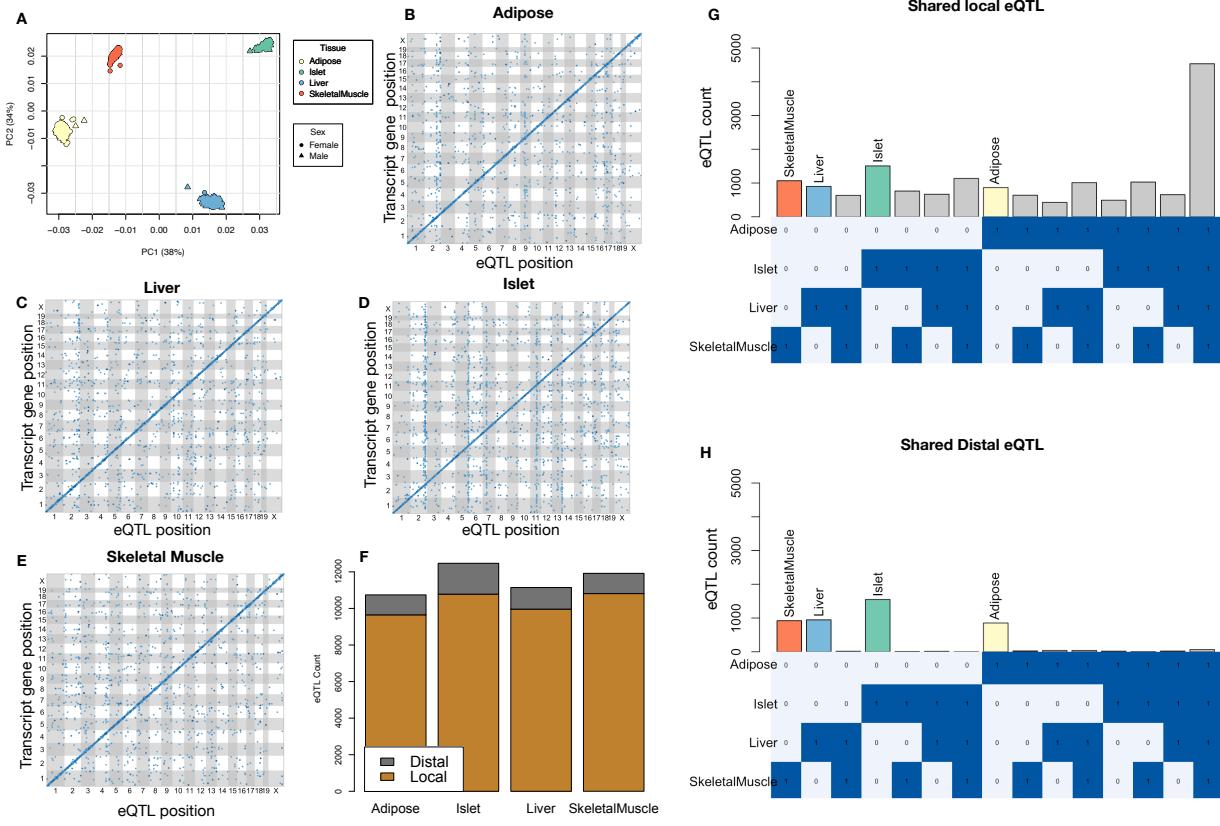


Figure 9: Overview of eQTL analysis in DO mice. **A.** RNA seq samples from the four different tissues clustered by tissue. **B.-E.** eQTL maps are shown for each tissue. The *x*-axis shows the position of the mapped eQTL, and the *y*-axis shows the physical position of the gene encoding each mapped transcript. Each dot represents an eQTL with a minimum LOD score of 8. The dots on the diagonal are locally regulated eQTL for which the mapped eQTL is at the within 4Mb of the encoding gene. Dots off the diagonal are distally regulated eQTL for which the mapped eQTL is distant from the gene encoding the transcript. **F.** Comparison of the total number of local and distal eQTL with a minimum LOD score of 8 in each tissue. All tissues have comparable numbers of eQTL. Local eQTL are much more numerous than distal eQTL. **G.** Counts of transcripts with local eQTL shared across multiple tissues. The majority of local eQTL were shared across all four tissues. **H.** Counts of transcripts with distal eQTL shared across multiple tissues. The majority of distal eQTL were tissue-specific and not shared across multiple tissues. For both G and H, eQTL for a given transcript were considered shared in two tissues if they were within 4Mb of each other. Colored bars indicate the counts for individual tissues for easy of visualization.

KEGG pathway enrichments by GSEA

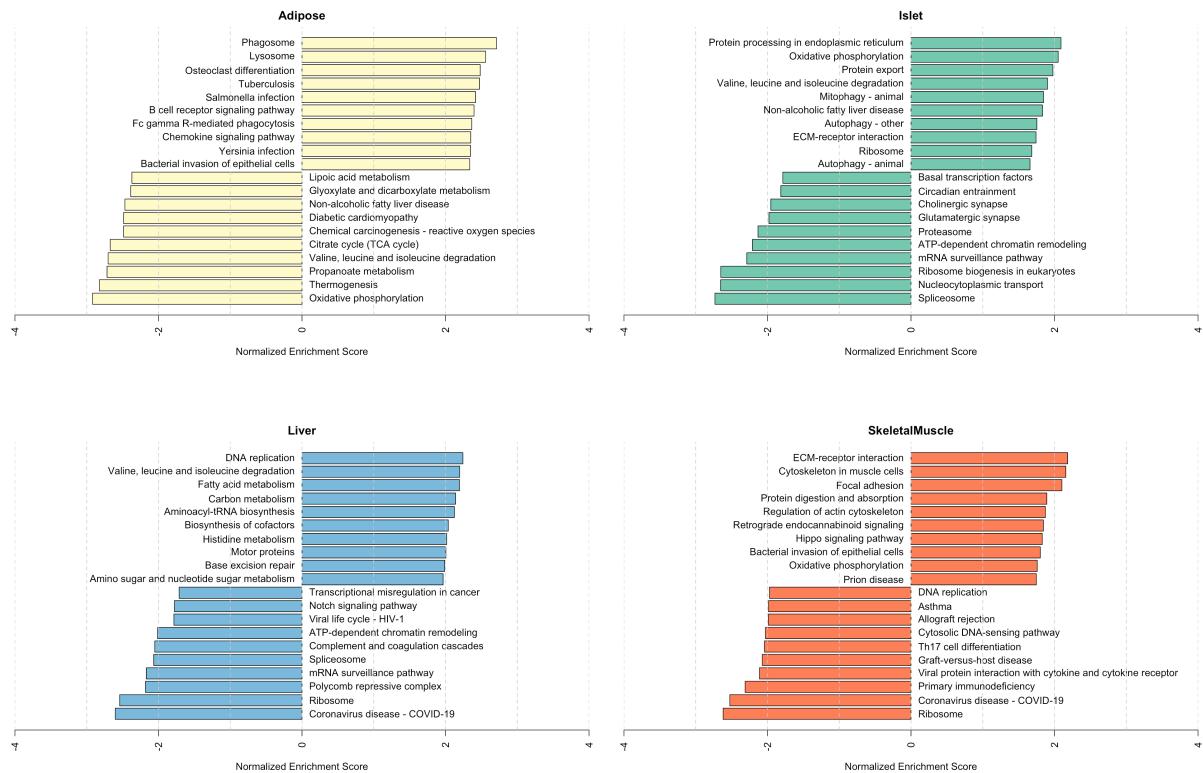


Figure 10: Bar plots showing normalized enrichment scores (NES) for KEGG pathways as determined by fast gene score enrichment analysis (fgsea). Only the top 10 positive and top 10 negative scores are shown. Colors indicate tissue. The name beside each bar shows the name of each enriched KEGG pathway.

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Top GO term enrichments by GSEA

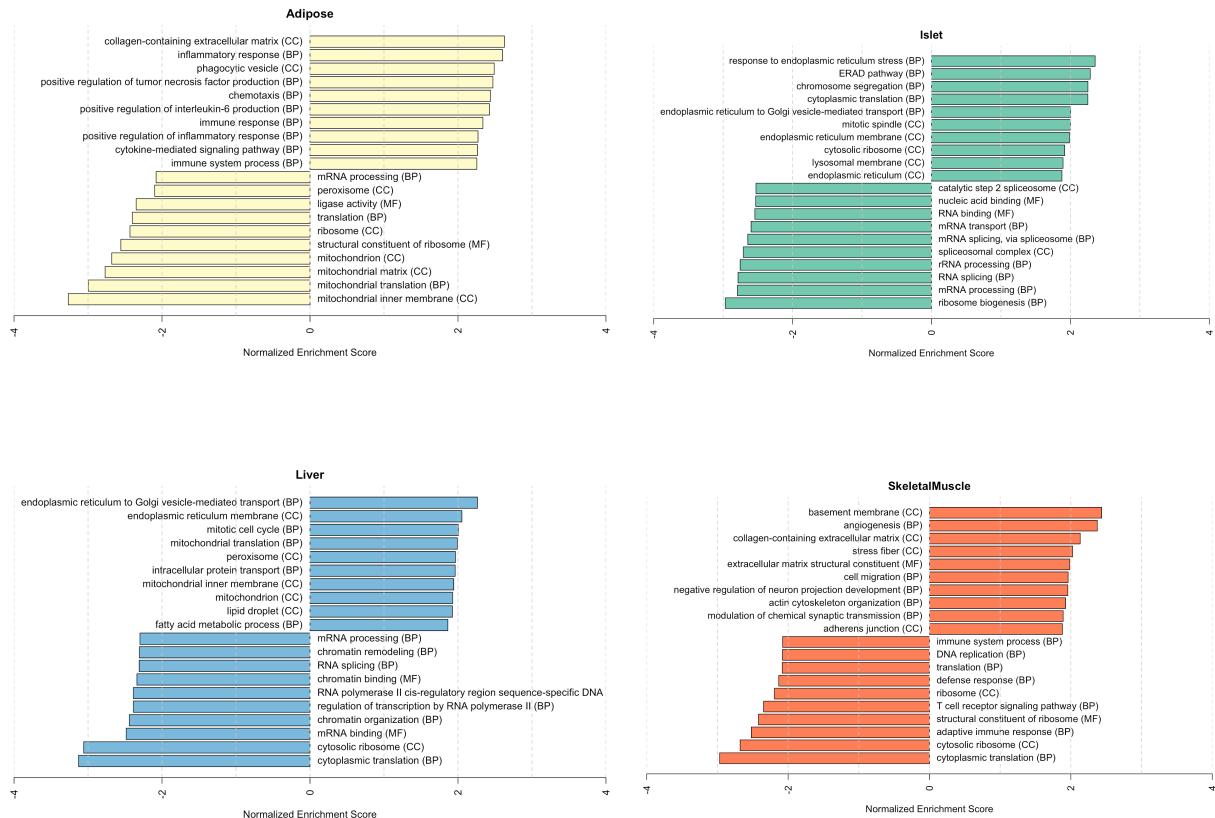


Figure 11: Bar plots showing normalized enrichment scores (NES) for GO terms as determined by fast gene score enrichment analysis (fgsea). Only the top 10 positive and top 10 negative scores are shown. Colors indicate tissue. The name beside each bar shows the name of each enriched GO term. The letters in parentheses indicate whether the term is from the biological process ontology (BP), the molecular function ontology (MF), or the cellular compartment ontology (CC).

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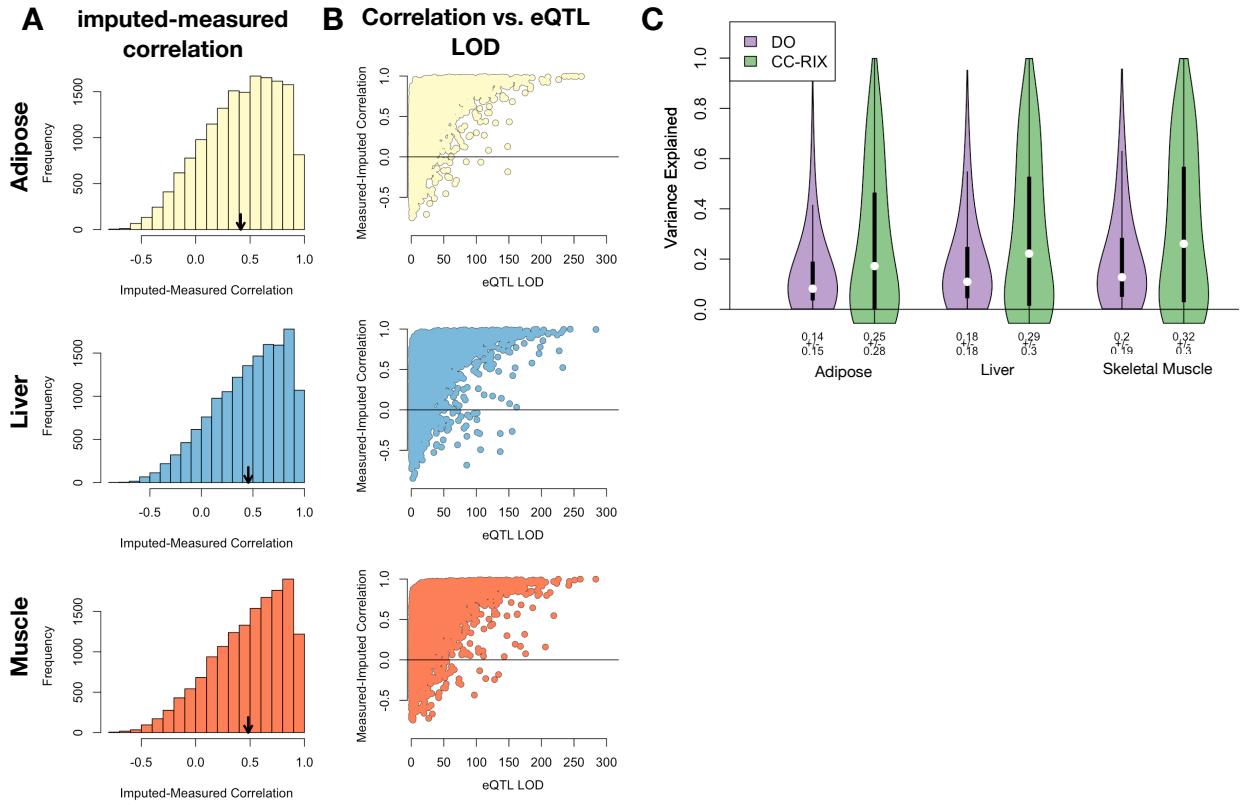


Figure 12: Validation of transcript imputation in the CC-RIX. **A.** Distributions of correlations between imputed and measured transcripts in the CC-RIX. The mean of each distribution is shown by the red line. All distributions were skewed toward positive correlations and had positive means near a Pearson correlation (r) of 0.5. **B.** The relationship between the correlation between measured and imputed expression in the CC-RIX (x-axis) and eQTL LOD score. As expected, imputations are more accurate for transcripts with strong local eQTL. **C.** Variance explained by local genotype in the DO and CC-RIX.

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