

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

69 Body weight was strongly positively correlated with food consumption (Fig. 1D  $R^2 = 0.51, p = 1.5 \times 10^{-75}$ )  
70 and fasting blood glucose (FBG) (Fig. 1E,  $R^2 = 0.21, p = 1.4 \times 10^{-26}$ ) suggesting a link between behavioral  
71 factors and metabolic disease. However, the heritability of this trait and others (Fig. 1F) indicates that  
72 background genetics contribute substantially to correlates of metabolic disease in this population.

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

77 **Distal Heritability Correlates with Phenotype Relevance**

78 We performed eQTL analysis using R/qltl2 [23] (Methods) and identified both local and distal eQTL for  
79 transcripts in each of the four tissues (Supp. Fig 9). Significant local eQTLs far outnumbered distal eQTLs  
80 (Supp. Fig. 9F) and tended to be shared across tissues (Supp. Fig. 9G) whereas the few significant distal  
81 eQTL we identified tended to be tissue-specific (Supp. Fig. 9H)

82 We calculated the heritability of each transcript in terms of local and distal genetic factors (Methods). Overall,  
83 local and distal genetic factors contributed approximately equally to transcript abundance. In all tissues,  
84 both local and distal factors explained between 8 and 18% of the variance in the median transcript (Fig 2A).

85 Local heritability of transcripts was negatively correlated with their trait relevance, defined as the maximum  
86 correlation of a transcript across all traits (Fig. 2B). This suggests that the more local genotype influenced  
87 transcript abundance, the less effect variation in transcript abundance had on the measured traits. Conversely,

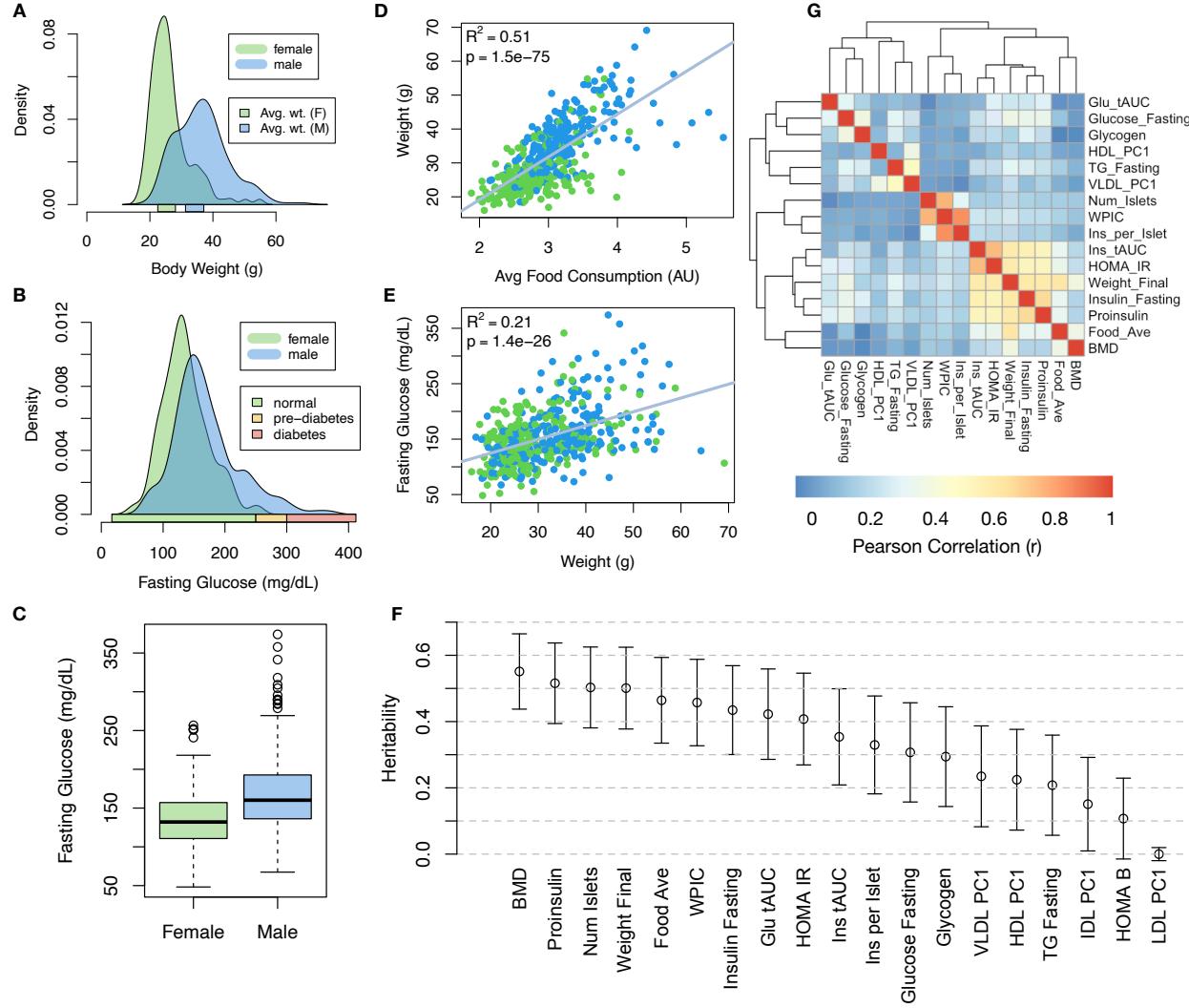


Figure 1: Clinical overview. **A.** Distributions of final body weight in the diversity outbred mice. Sex is indicated by color. The average B6 male and female adult weights at 24 weeks of age are indicated by blue and green bars on the x-axis. **B.** The distribution of final fasting glucose across 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.

distal heritability of transcripts was positively correlated with trait relevance (Fig. 2C). That is, transcripts that were more highly correlated with the measured traits tended to be distally, rather than locally, heritable. That trait-correlated transcripts have low local heritability is consistent with previous observations that low-heritability transcripts explain more expression-mediated disease heritability than high-heritability transcripts [19]. However, the positive relationship between trait correlation and distal heritability suggests that there are alternative mechanisms through which genetic regulation of transcripts may influence traits.

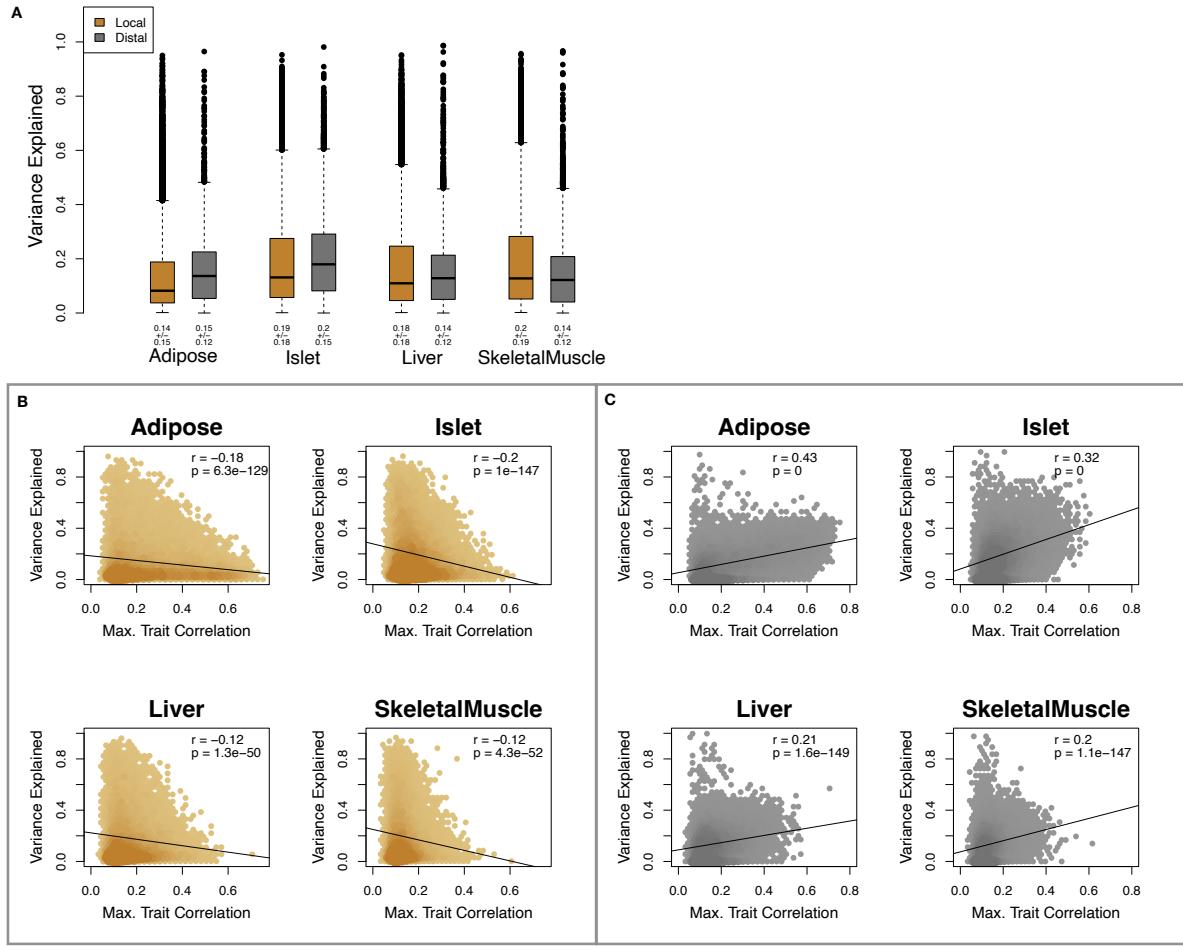


Figure 2: Transcript heritability and trait relevance. **A.** Distributions of distal and local heritability of transcripts across the four tissues. Overall local and distal factors contribute equally to transcript heritability. The relationship between **(B.)** local and **(C.)** distal heritability and trait relevance across all four tissues. Here trait relevance is defined as the maximum correlation between the transcript and all traits. Local heritability was 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 **High-Dimensional Mediation identifies composite transcript that perfectly mediates composite  
95 trait**

96 We used high-dimensional mediation to identify the major axis of variation in the transcriptome that mediated  
97 the effects of the genome on metabolic traits (Fig. 3). We kernelized the genome, phenome, and transcriptome  
98 matrices and used generalized canonical correlation analysis (RGCCA) [24] to identify a composite transcript  
99 ( $T_C$ ) that perfectly mediated the effect of the composite genome ( $G_C$ ) on the composite phenome ( $P_C$ ).

100 Fig. 3A shows the partial correlations ( $\rho$ ) between the pairs of these composite vectors. The partial correlation  
101 between  $G_C$  and  $T_S$  was 0.42, and the partial correlation between  $T_S$  and  $P_S$  was 0.78. However, when the

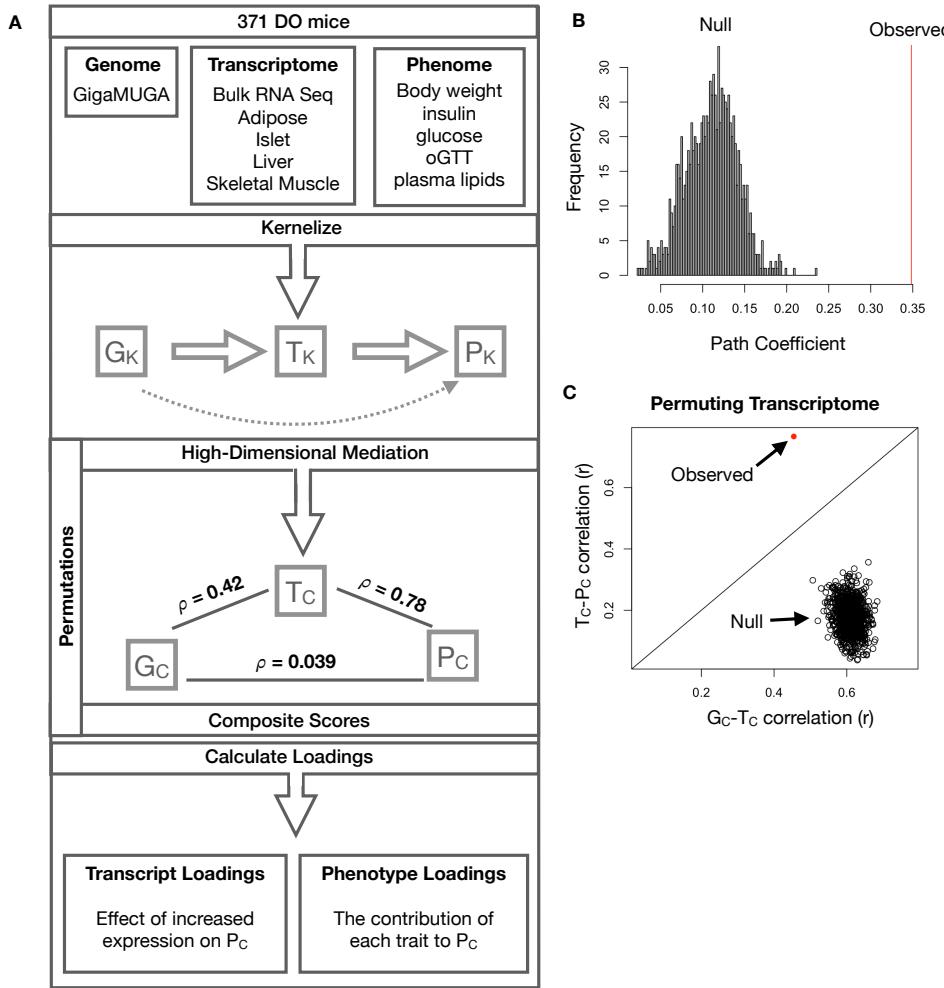


Figure 3: High-dimensional mediation. **A.** Workflow indicating major steps of high-dimensional mediation. The genotype, transcriptome, and phenotype matrices were kernelized to yield single matrices representing the relationships between all individuals for each data modality ( $G_K$  = genome kernel,  $T_K$  = transcriptome kernel;  $P_K$  = phenotype 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  $\rho$  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).

- 102 transcriptome was taken into account, the partial correlation between  $G_S$  and  $P_S$  was effectively 0 (0.039).
- 103 The estimated heritability of the composite phenotype was heritability of  $0.71 \pm 0.084$ , which was higher than
- 104 any of the individual traits (Fig. 1F). Thus, we have identified a maximally heritable metabolic trait that is
- 105 perfectly mediated by a heritable component of the transcriptome.
- 106 Standard CCA is prone to over-fitting because in any two large matrices it can be trivial to identify
- 107 highly correlated composite vectors. To assess whether RGCCA was similarly prone to over-fitting in

108 a high-dimensional space, we performed permutation testing. We permuted the individual labels on the  
109 transcriptome kernel matrix 1000 times and recalculated the path coefficient, which is the partial correlation of  
110  $G_C$  and  $T_C$  multiplied by the partial correlation of  $T_C$  and  $P_C$ . This represents the path from  $G_C$  to  $P_C$  that is  
111 mediated through  $T_C$ . The null distribution of the path coefficient is shown in Fig. 3B, and the observed path  
112 coefficient from the original data is indicated by the red line. The observed path coefficient was well outside  
113 the null distribution generated by permutations. Fig. 3C illustrates this observation in more detail. Although  
114 we identified high correlations between  $G_C$  and  $T_C$ , and modest correlations between  $T_C$  and  $P_C$  in the null  
115 data (Fig 3C), these two values could not be maximized simultaneously. The red dot shows that in the real  
116 data both the  $G_C$ - $T_C$  correlation and the  $T_C$ - $P_C$  correlation could be maximized simultaneously suggesting  
117 that the path from genotype to phenotype through transcriptome is highly non-trivial and identifiable in  
118 this case. These results suggest that these composite vectors represent genetically determined variation in  
119 phenotype that is mediated through genetically determined variation in transcription.

120 **Body weight and insulin resistance were highly represented in the expression-mediated composite trait**

122 The loadings of each measured trait onto  $P_C$  indicate how much each contributed to the composite phenotype.  
123 Final body weight contributed the most (Fig. 4), followed by homeostatic insulin resistance (HOMA\_IR) and  
124 fasting plasma insulin levels (Insulin\_Fasting). We can thus interpret  $P_C$  as an index of metabolic disease (Fig.  
125 4B). Individuals with high values of  $P_C$  have a higher metabolic index and greater metabolic disease, including  
126 higher body weight and higher insulin resistance. We refer to  $P_C$  as the metabolic index going forward. Traits  
127 contributing the least to the metabolic index were measures of cholesterol and pancreas composition. Thus,  
128 when we interpret the transcriptomic signature identified by HDM, we are explaining primarily transcriptional  
129 mediation of body weight and insulin resistance, as opposed to cholesterol measurements.

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

132 We interpreted large loadings onto transcripts as indicating strong mediation of the effect of genetics on  
133 metabolic index. Large positive loadings indicate that inheriting higher expression was associated with a  
134 higher metabolic index (i.e. higher risk of obesity and metabolic disease on the high-fat diet) (Fig. 4C).  
135 Conversely, large negative loadings indicate that inheriting lower expression of these transcripts was associated  
136 with a lower metabolic index (i.e. lower risk of obesity and metabolic disease on the high-fat diet) (Fig. 4C).  
137 We used GSEA to look for biological processes and pathways that were enriched at the top and bottom of  
138 this list (Methods).

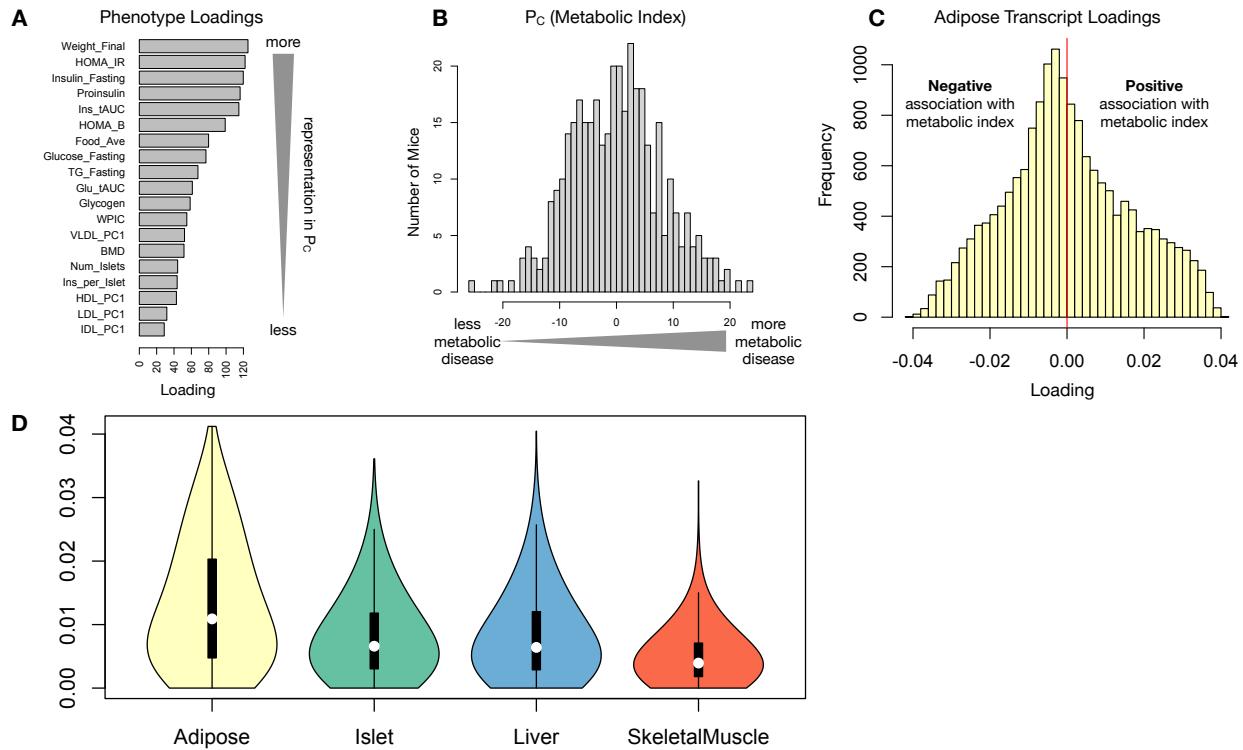


Figure 4: Interpretation of loadings. **A.** Loadings across traits. Body weight and insulin resistance contributed the most to the composite trait. **B.** Phenotype scores across individuals. Individuals with large positive phenotype scores had higher body weight and insulin resistance than average. 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.

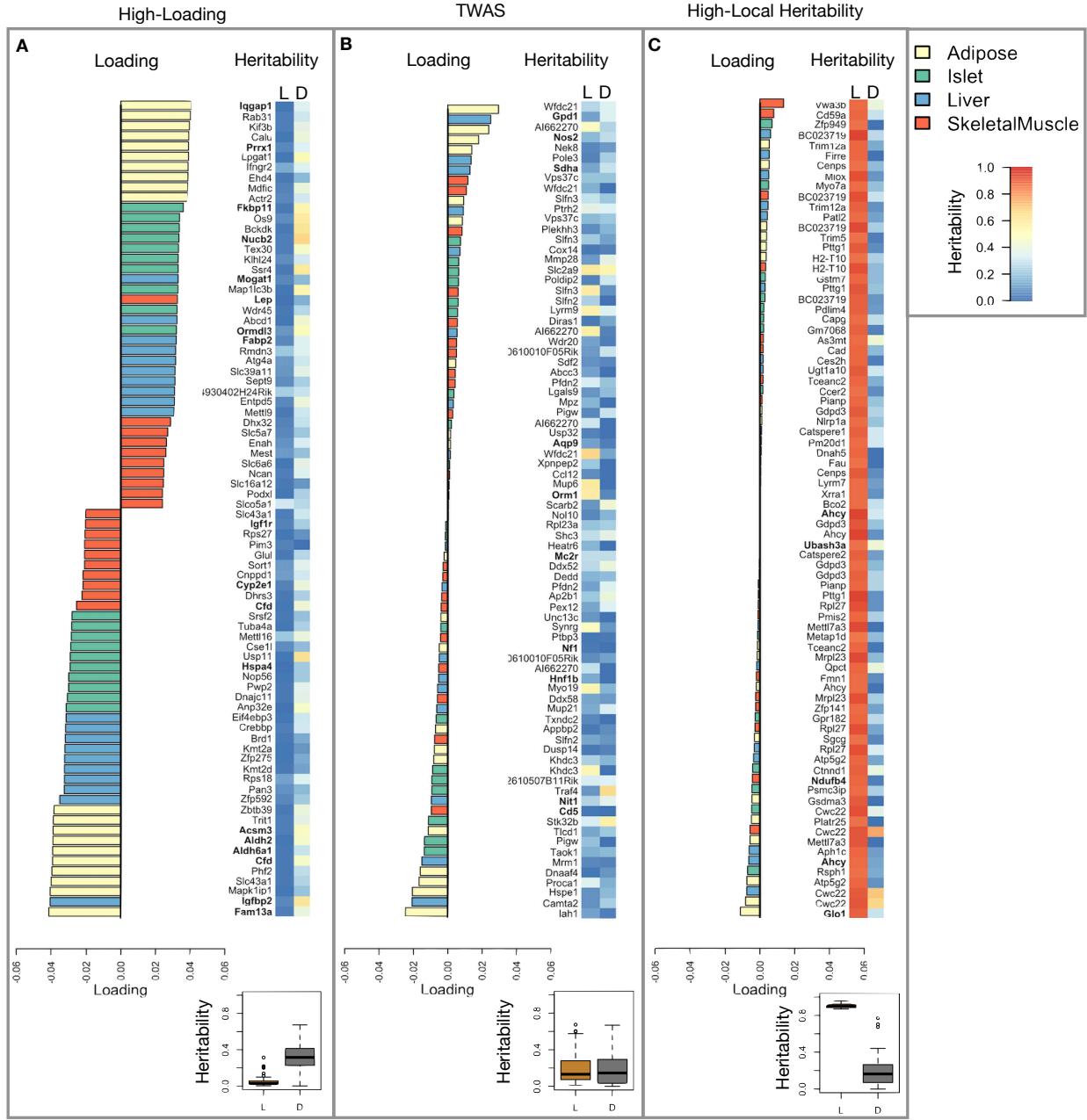
- 139 In adipose tissue, both GO processes and KEGG pathway enrichments pointed to an axis of inflammation  
 140 and metabolism (Supp. Fig. 10 and 11). Processes and pathways associated with inflammation, particularly  
 141 macrophage infiltration were positively associated with metabolic index, indicating that increased expression  
 142 in inflammatory pathways was associated with a higher metabolic index. It is well established that adipose  
 143 tissue in obese individuals is highly inflamed [cite] and infiltrated by macrophages [cite], and the results here  
 144 suggest that this may be a heritable component of metabolic disease.
- 145 The strongest negative enrichments in adipose tissue were related to mitochondrial activity in general, and  
 146 thermogenesis in particular (Supp. Fig. 10 and 11). It has been shown mouse strains with greater thermogenic  
 147 potential are also less susceptible to obesity on a high-fat diet.
- 148 Transcripts associated with the citric acid (TCA) cycle as well as the catabolism of branched-chain amino acids

149 (BCAA), valine, leucine, and isoleucine also had strong negative enrichment in the adipose tissue (Supp. Fig.  
150 XXX). Expression of genes in both pathways (for which there is some overlap) has been previously associated  
151 with insulin sensitivity [12, 25, 26], suggesting that impairment in these pathways may be associated with  
152 insulin resistance. Selective PPAR $\gamma$  modulation by insulin-sensitizing thiazolidinedione drugs has further  
153 been shown to influence both inflammation and BCAA metabolism in obese rats suggesting a relationship  
154 between these pathways and insulin resistance [27]. BCAA levels are also related to insulin resistance in  
155 human subjects and are elevated in insulin-resistant obese individuals relative to weight-matched non-insulin  
156 resistant individuals [28]. In the DO mice studied here, inheriting increased expression of genes involved in  
157 BCAA catabolism was associated with reduced body weight and insulin resistance.

158 Transcripts in the adipose tissue had the largest loadings, both positive and negative, of all tissues, suggesting  
159 that much of the effect of genetics on body weight and insulin resistance is mediated through gene expression  
160 in adipose tissue (Fig. 5A). The loadings in liver and pancreas were comparable, and those in skeletal muscle  
161 were the weakest (Fig. 5A), suggesting that less of the genetic effects were mediated through transcription in  
162 skeletal muscle. Across all tissues, transcripts with the largest loadings tended to have relatively high distal  
163 heritability compared with local heritability (Fig. 5A). Transcripts with the highest local heritability tended  
164 to have very weak loadings and were 3.6 times less likely to be associated with diabetes and obesity in the  
165 literature than transcripts with high loadings (Fig. fig:loading\_heritabilityB, Methods). TWAS-nominated  
166 transcripts also had relatively weak loadings and high local heritability (Fig. 4C). They were half as likely as  
167 transcripts with the highest loadings to be associated with diabetes and obesity in the literature (Fig. 4C).

#### 168 **Tissue-specific transcriptional programs were associated with metabolic traits**

169 Clustering of transcripts with top loadings in each tissue showed tissue-specific functional modules associated  
170 with obesity and insulin resistance in the DO population (Fig. 6A). In this figure, the importance of immune  
171 activation specifically in the adipose tissue is apparent. There are also other tissue-specific processes. Positive  
172 loadings on lipid metabolism in liver suggest that inheriting high liver expression of genes in this cluster is  
173 positively associated with metabolic disease. This cluster included the gene *Pparg*, whose primary role is in  
174 the adipose tissue where it is considered a master regulator of adipogenesis [29]. Agonists of *Pparg*, such  
175 as Thiazolidinediones, which are FDA-approved to treat type II diabetes, reduce inflammation and adipose  
176 hypertrophy [29]. Consistent with this role, the loading for *Pparg* in adipose tissue is slightly negative,  
177 suggesting that upregulation is associated with leaner mice (Fig. 6B). In contrast, *Pparg* has a large positive  
178 loading in liver, where it plays a role in the development of hepatic steatosis, or fatty liver. Mice that lack  
179 *Pparg* specifically in the liver, are protected from developing steatosis and show reduced expression of lipogenic



183 adipocytes.

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

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

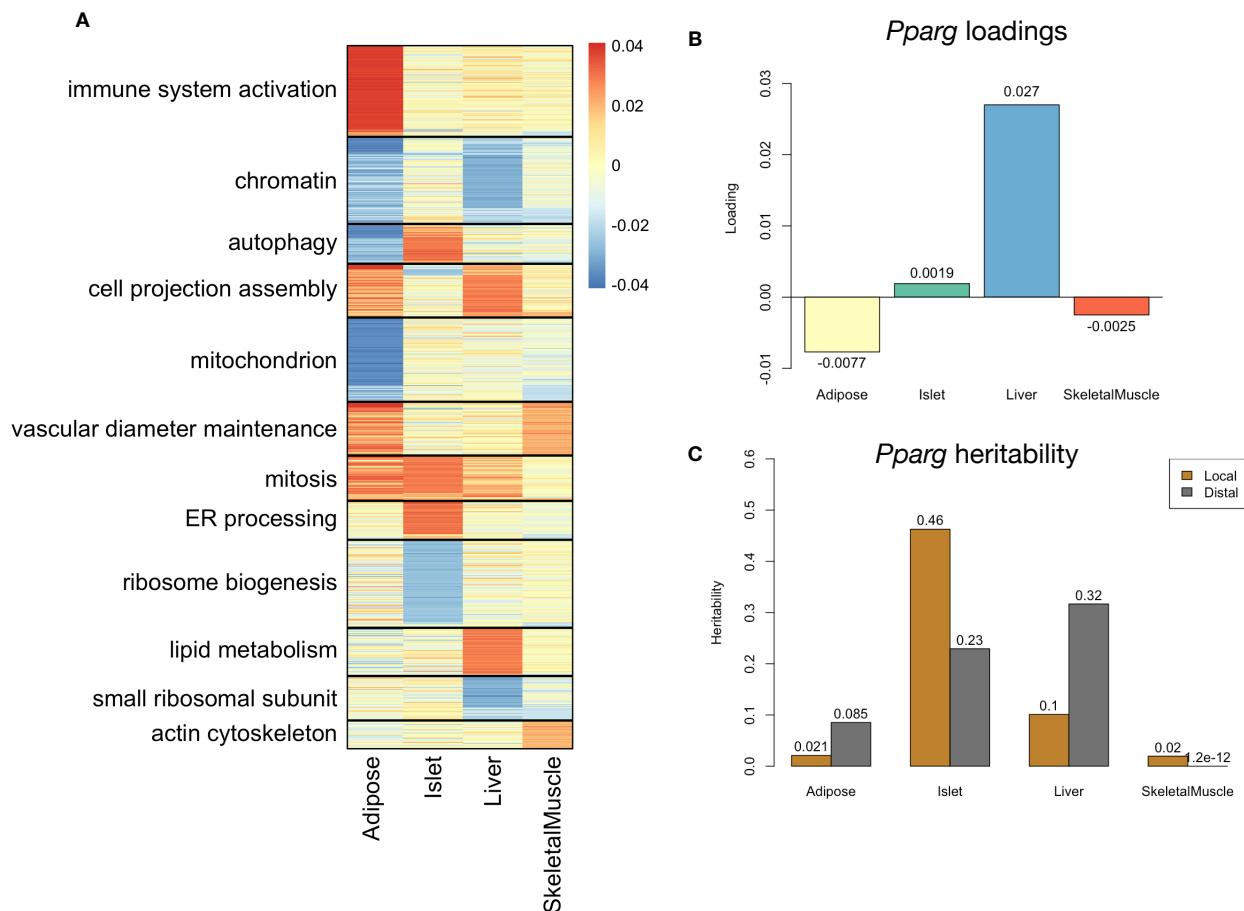


Figure 6: Tissue-specific transcriptional programs were associated with obesity and insulin resistance. **A** Heat map showing the loadings of all transcripts with loadings greater than 2.5 standard deviations from the mean in any tissue. The heat map was clustered using k medoid clustering. Functional 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.

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

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

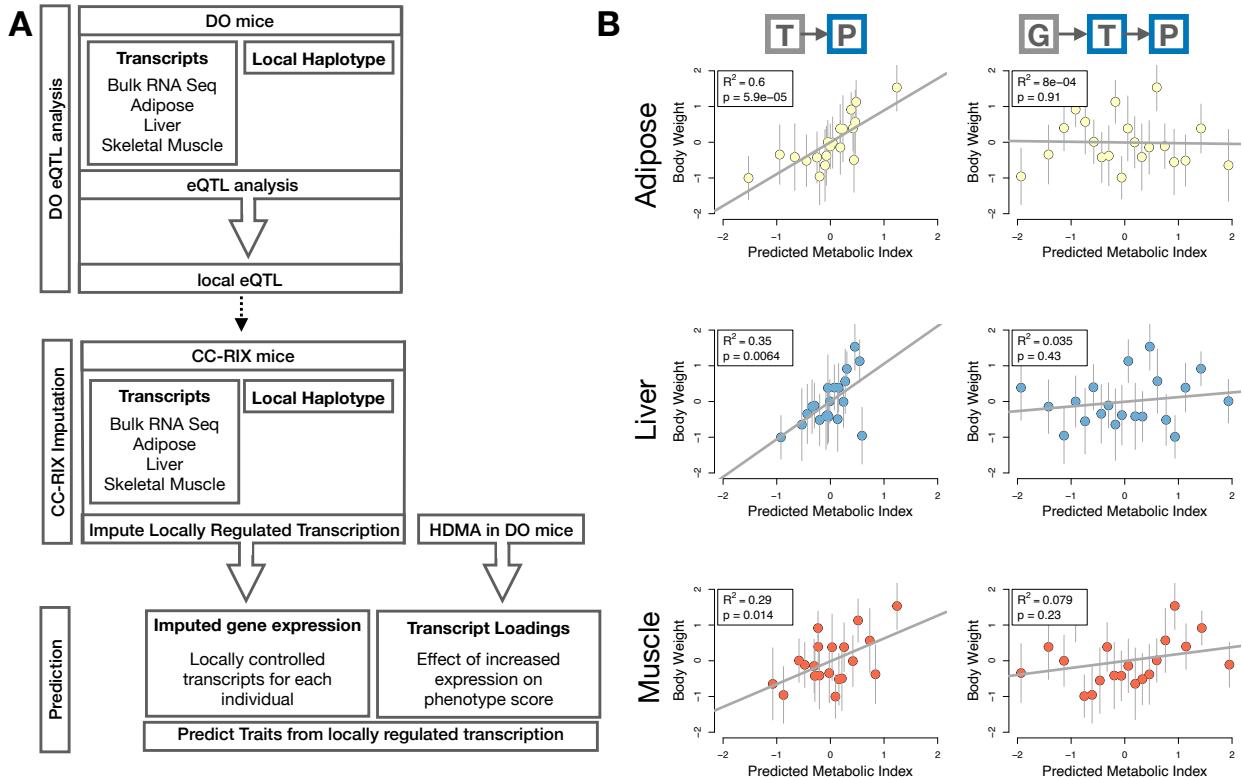


Figure 7: Transcription, but not local genotype, predicts phenotype in the CC-RIX. **A.** Workflow showing procedure for translating HDM results to an independent population of mice. **B.** Relationships between the predicted metabolic index and measured body weight. The left column shows the predictions 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.

198 We first tested whether the transcript loadings derived from HDM in the DO were relevant to the relationship  
 199 between the transcriptome and the phenotype in the CC-RIX. To do this, we multiplied the transcript loadings  
 200 derived from HDM in the DO mice by transcript measurements in the CC-RIX standardized across individuals.  
 201 This created a transcript vector weighted by importance to metabolic disease as determined in the DO.  
 202 The mean of this vector was the predicted metabolic index for the animal based on its transcription in  
 203 either adipose tissue, liver, or skeletal muscle. Across all three tissues, weighted transcription values were

204 significantly correlated with metabolic index in the CC-RIX population measured as body weight (Fig. 7B left  
205 column). Adipose tissue transcription yielded the most accurate prediction (stats). This result confirms the  
206 validity and translatability of the transcript loadings determined in the DO population and their relationship  
207 to metabolic disease. It also supports the observation that transcription in adipose tissue is the strongest  
208 mediator of genetic effects on metabolic index.

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

217 **Distally heritable transcriptomic signatures reflect variation in composition of adipose tissue  
218 and islets**

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

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

231 In islet, the mean loadings for alpha-cell specific transcripts were significantly positive, while the mean  
232 loadings for delta- and endothelial-cell specific genes were significantly negative (Fig. 8B). These results  
233 suggest that obese mice had inherited higher proportions of alpha cells, and lower proportions of endothelial

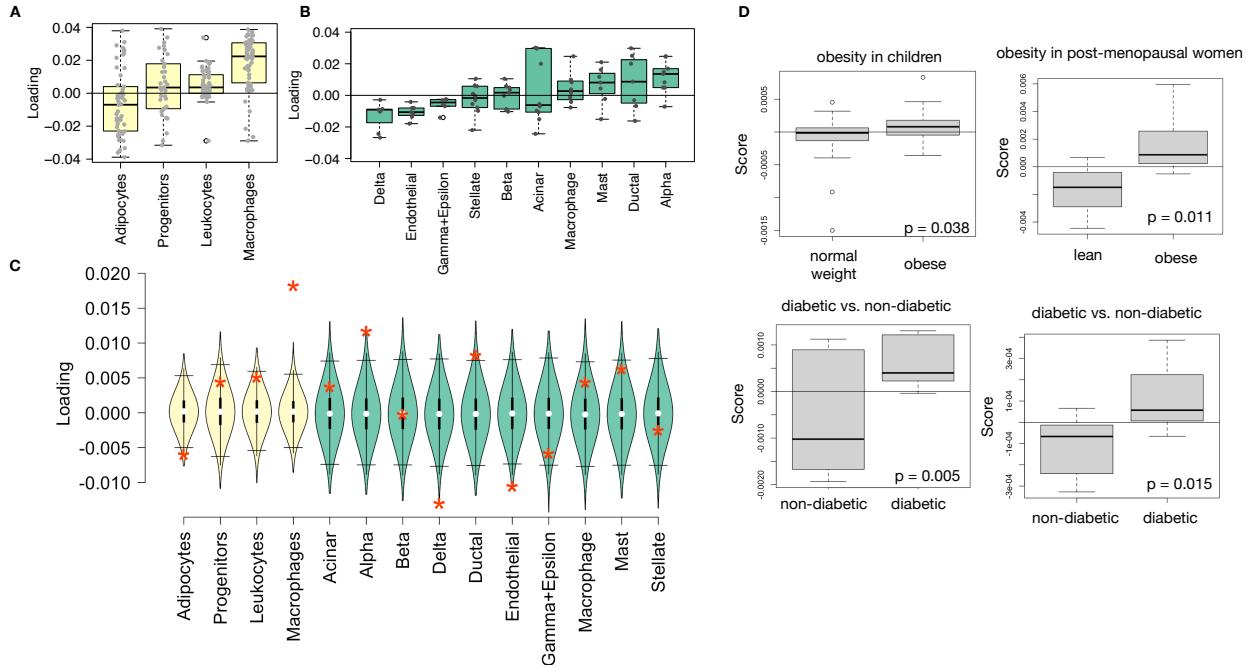


Figure 8: HDM results translate to humans. **A.** Distribution of loadings for cell-type-specific transcripts in adipose tissue. **B.** Distribution of loadings for cell-type-specific transcripts in pancreatic islets (green). **C.** Null distributions for the mean loading of randomly selected transcripts 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.

234 and delta cells in their pancreatic islets.

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

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

### 239 Distally heritable transcriptomic signatures translate to human disease

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

245 We calculated a predicted obesity score for each individual in the human studies based on their adipose

246 tissue gene expression (Methods) and compared the predicted scores for obese and non-obese groups as well  
247 as diabetic and non-diabetic groups. In all cases, the predicted obesity scores were higher on average for  
248 individuals in the obese and diabetic groups compared with the lean and non-diabetic groups, indicating that  
249 the distally heritable signature of obesity identified in DO mice is relevant to obesity and diabetes in human  
250 subjects.

251 **Targeting gene signatures**

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

259 We thus queried the CMAP database through the CLUE online query tool developed by The Broad Institute  
260 [cite] (Methods).

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

265 • **Supplemental Table** results from CMAP

266 **Discussion**

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

272 Rather, observations suggest that genes near GWAS hits and have obvious functional relevance to a trait  
273 tend to have highly complex regulatory landscapes under strong selection pressures [18]. In contrast, genes  
274 with strong local regulation tend to be depleted of functional annotations and are under looser selection

275 constraints [18]. These observations and others led Liu et al. [35] to suggest that most heritability of complex  
276 traits is driven by weak trans-eQTLs. They proposed a framework of understanding heritability of complex  
277 traits in which massive polygenicity is distributed across common variants in both functional “core genes”,  
278 as well as more peripheral genes that may not seem obviously related to the trait.

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

- 285 • distal heritability correlates with phenotype relevance  
286 • others who use local eQTL to associate genotype with traits often say “we nominated this gene” even  
287 though other nearby genes have higher eQTL LOD scores (27019110, 31465442) Our method supports  
288 the idea that the transcripts with the strongest local regulation are less likely to be functionally related  
289 to the trait

## 290 Data Availability

291 Here we tell people where to find the data

## 292 Acknowledgements

293 Here we thank people

294 Supplemental Figures

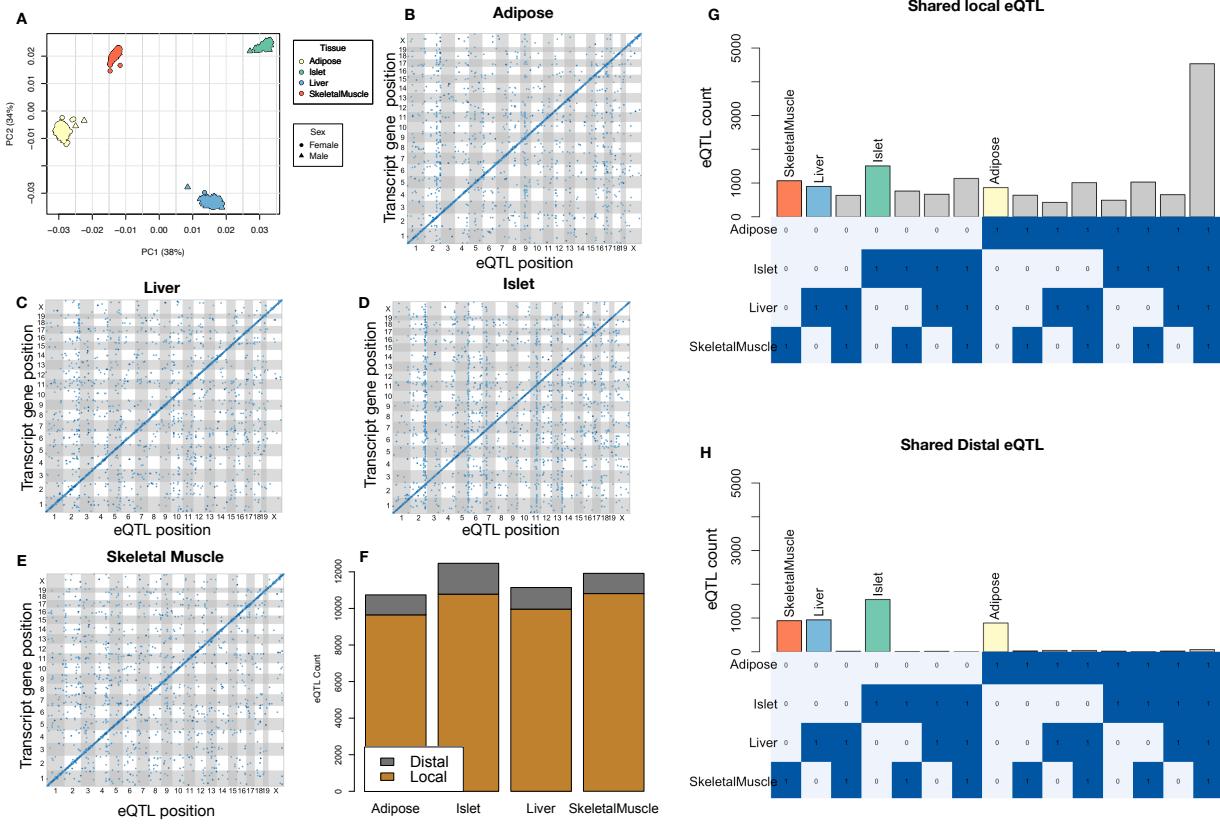


Figure 9: Overview of eQTL analysis in DO mice. **A.** RNA seq samples from the four different tissues clustered by tissue. **B.-E.** eQTL maps are shown for each tissue. The *x*-axis shows the position of the mapped eQTL, and the *y*-axis shows the physical position of the gene encoding each mapped 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

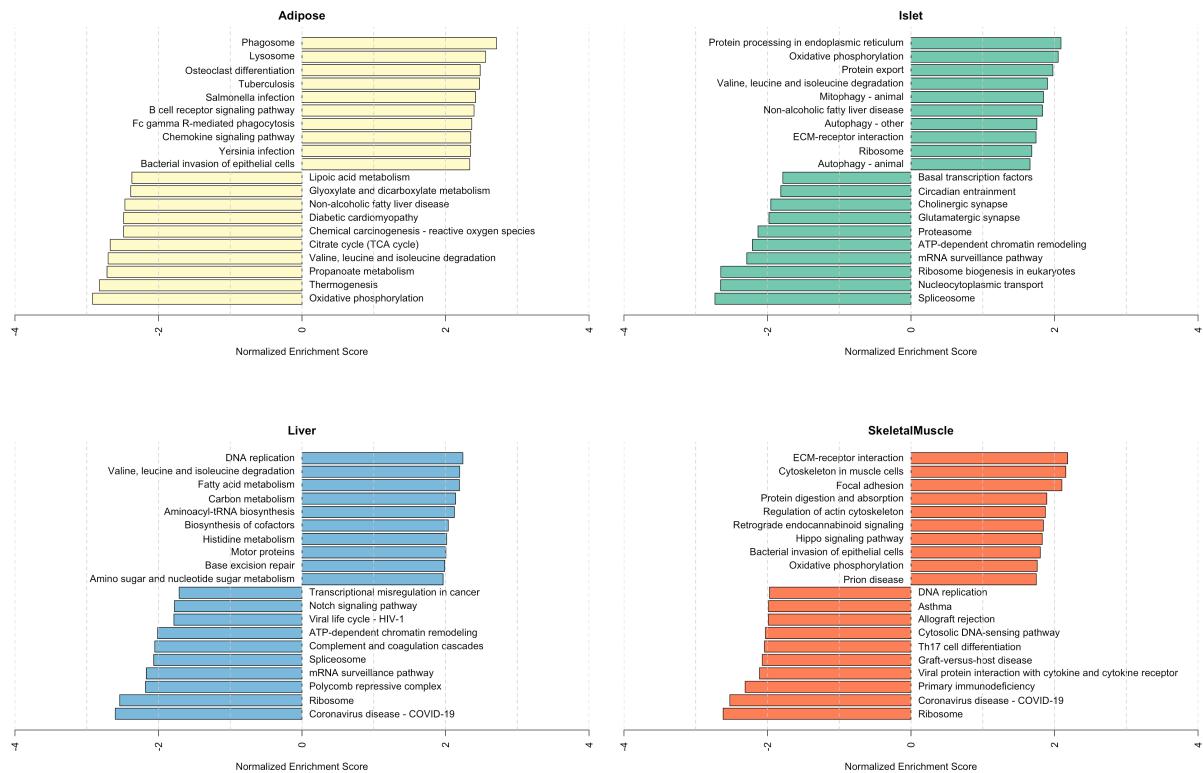


Figure 10: Bar plots showing normalized enrichment scores (NES) for KEGG pathways as determined by fast gene score enrichment analysis (fgsea). Only the top 10 positive and top 10 negative scores are shown. Colors indicate tissue. The name beside each bar shows the name of each enriched KEGG pathway.

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## Top GO term enrichments by GSEA

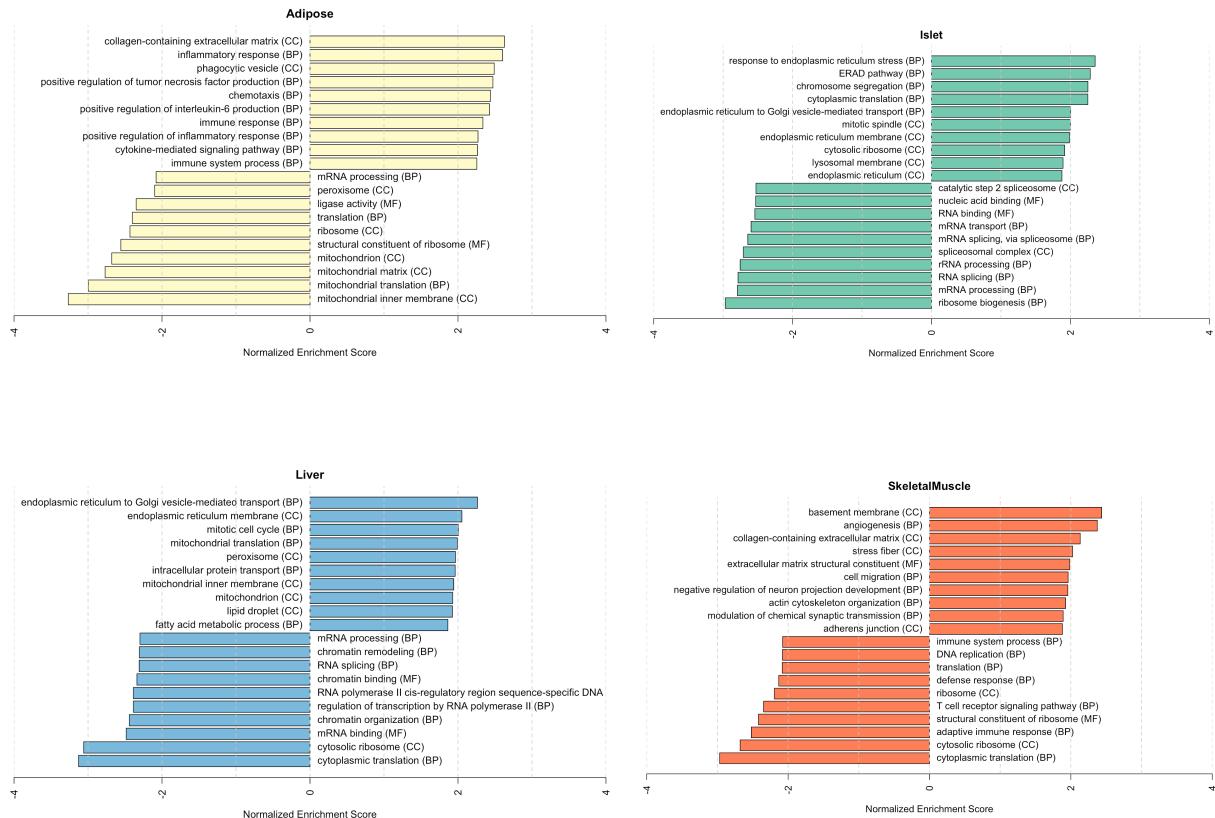


Figure 11: Bar plots showing normalized enrichment scores (NES) for GO terms as determined by fast gene score enrichment analysis (fgsea). Only the top 10 positive and top 10 negative scores are shown. Colors indicate tissue. The name beside each bar shows the name of each enriched GO term. The letters 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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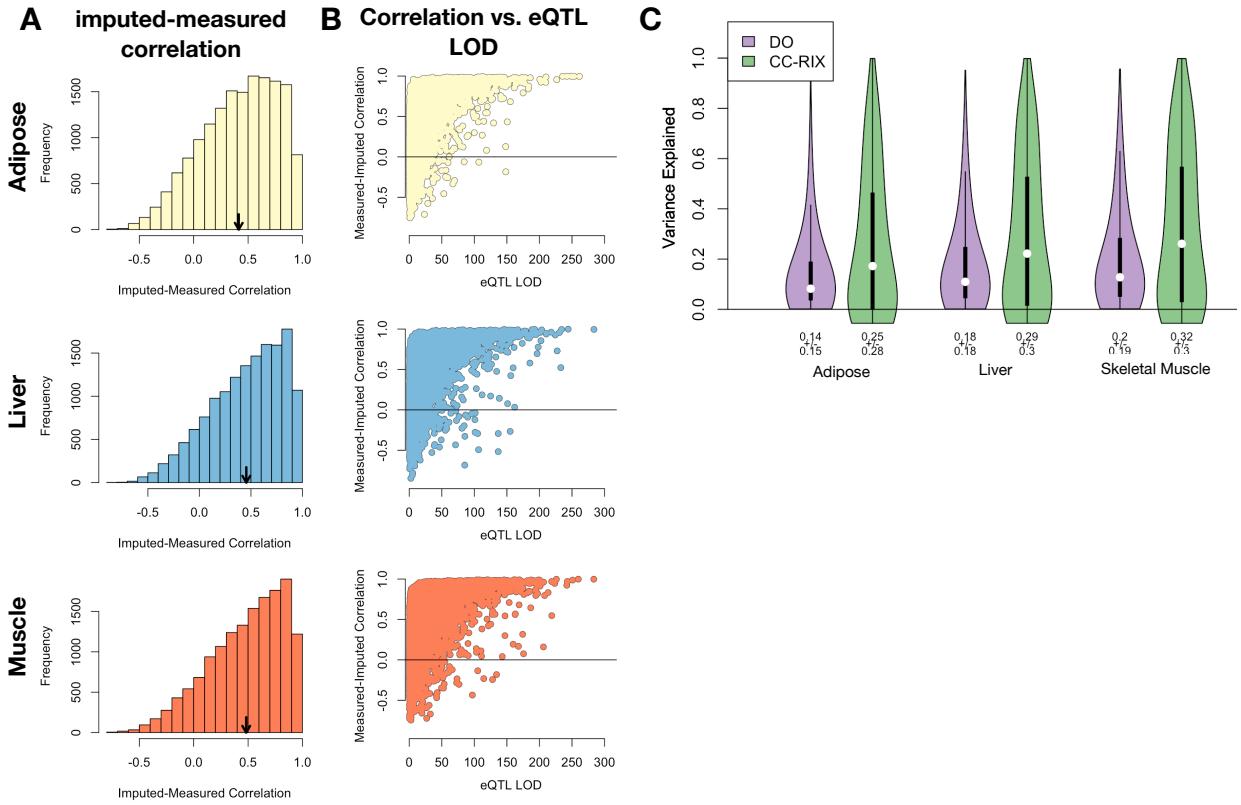


Figure 12: Validation of transcript imputation in the CC-RIX. **A.** Distributions of correlations between imputed and measured transcripts in the CC-RIX. The mean of each distribution is shown by the red line. All distributions were skewed toward positive correlations and had positive means near a Pearson 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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