

<sup>1</sup> Transcripts with high distal heritability mediate genetic effects on  
<sup>2</sup> complex traits

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<sup>7</sup> **Abstract**

<sup>8</sup> Gene expression is an important mediator of genetic effects on phenotype. Although many genes are subject  
<sup>9</sup> to simple, local regulation, recent evidence suggests that complex distal regulation may be more important  
<sup>10</sup> in mediating trait variability. To investigate this possibility, we combined two large, data sets modeling  
<sup>11</sup> diet-induced obesity and metabolic disease in genetically diverse mice. Using a novel high-dimensional  
<sup>12</sup> mediation analysis, we identified a heritable composite transcript that explained 30% of the variation across  
<sup>13</sup> all metabolic traits. The composite transcript was interpretable in terms of enriched biological processes  
<sup>14</sup> and predicted obesity status in an independent mouse cohort as well as in human cohorts with measured  
<sup>15</sup> gene expression. Transcripts contributing most strongly to this composite mediator tended to have complex,  
<sup>16</sup> distal regulation distributed throughout the genome. These results suggest that trait-relevant variation in  
<sup>17</sup> transcription is largely distally regulated, but is nonetheless identifiable, interpretable, and translatable across  
<sup>18</sup> species.

<sup>19</sup> **Introduction**

<sup>20</sup> In the quest to understand the genetic architecture of complex traits, gene expression is an important mediator  
<sup>21</sup> between genotype and phenotype. There is ample evidence from genome-wide association studies (GWAS)  
<sup>22</sup> that regulation of gene expression accounts for the bulk of the genetic effect on complex traits, as most  
<sup>23</sup> trait-associated variants lie in gene regulatory regions<sup>1–7</sup>. It is widely assumed that these variants influence  
<sup>24</sup> local transcription, and methods such as transcriptome-wide association studies (TWAS)<sup>8–11</sup>, summary  
<sup>25</sup> data-based Mendelian randomization (SMR)<sup>10</sup>, and others capitalize on this idea to identify genes associated

<sup>26</sup> with multiple disease traits<sup>12–15</sup>

<sup>27</sup> Despite the great promise of these methods, explaining trait effects with local gene regulation has been more  
<sup>28</sup> difficult than initially assumed<sup>16;17</sup>. Although trait-associated variants tend to lie in non-coding, regulatory  
<sup>29</sup> regions, they often do not have detectable effects on gene expression<sup>16</sup> and tend not to co-localize with  
<sup>30</sup> expression quantitative trait loci (eQTLs)<sup>17;18</sup>.

<sup>31</sup> One possible explanation for these observations is that gene expression is not being measured in the appropriate  
<sup>32</sup> cell types and thus local eQTLs influencing traits cannot be detected<sup>16</sup>. An alternative explanation that has  
<sup>33</sup> been discussed in recent years is that effects of these variants are mediated not through local regulation of  
<sup>34</sup> gene expression, but through distal regulation<sup>18–20;15</sup>.

<sup>35</sup> In this model, a gene's expression is influenced by many variants throughout the genome through their  
<sup>36</sup> cumulative effects on a broader regulatory network. In other words, the heritable component of the  
<sup>37</sup> transcriptome is an emergent state arising from the myriad molecular interactions defining and constraining  
<sup>38</sup> gene expression.

<sup>39</sup> To assess the role of wide-spread distal gene regulation on complex traits, we investigated diet-induced obesity  
<sup>40</sup> and metabolic disease as an archetypal example. Diet-induced obesity and metabolic disease are genetically  
<sup>41</sup> complex with hundreds of variants mapped through GWAS [REFS]. These variants are known to act through  
<sup>42</sup> multiple tissues that interact dynamically with each other [REFS], including adipose tissue, pancreatic  
<sup>43</sup> islets, liver, and skeletal muscle. The multi-system etiology of metabolic disease complicates mechanistic  
<sup>44</sup> dissection of the genetic architecture, requiring large, dedicated data sets that include high-dimensional,  
<sup>45</sup> clinically relevant phenotyping, dense genotyping in a highly recombined population, and transcriptome-wide  
<sup>46</sup> measurements of gene expression in multiple tissues.

<sup>47</sup> Measuring gene expression in multiple tissues is critical to adequately assess the extent to which local gene  
<sup>48</sup> regulation varies across the tissues and whether such variability might account for previous failed attempts to  
<sup>49</sup> identify trait-relevant local eQTL. Such data sets are extremely difficult to obtain in human populations,  
<sup>50</sup> particularly in the large numbers of subjects required for adequate statistical power. Thus, to further  
<sup>51</sup> investigate the role of local and distal gene regulation on complex traits, we generated two complementary  
<sup>52</sup> data sets: A discovery data set in a large population of diversity outbred (DO) mice<sup>21</sup>, and an independent  
<sup>53</sup> validation data set derived by crossing inbred strains from the Collaborative Cross (CC) mice<sup>22</sup> to form CC  
<sup>54</sup> F1 mice (CC-RIX). Both populations modeled diet-induced obesity and metabolic disease<sup>12</sup>

<sup>55</sup> Both the DO and CC mice were derived from eight inbred founder mouse strains, five classical lab strains,  
<sup>56</sup> and three strains more recently derived from wild mice<sup>21</sup>. They represent three subspecies of mouse *Mus*

57 *musculus domesticus*, *Mus musculus musculus*, and *Mus musculus castaneus*, and capture 90% of the known  
58 variation in laboratory mice<sup>23</sup>. The DO mice are maintained with a breeding scheme that ensures equal  
59 contributions from each founder across the genome thus rendering almost the whole genome visible to genetic  
60 inquiry<sup>21</sup>. The CC mice were initially outbred to recombine the genomes from all eight founders, and then  
61 inbred for at least 20 generations to generate multiple inbred lines.

62 In the DO population, we paired clinically relevant metabolic traits from 500 mice [REF], including body  
63 weight, plasma levels of insulin and glucose and plasma lipids, with transcriptome-wide gene expression in  
64 four tissues related to metabolic disease: adipose tissue, pancreatic islets, liver, and skeletal muscle. We  
65 measured similar metabolic traits in the CC-RIX and gene expression from three of the four tissues used  
66 in the DO: adipose tissue, liver, and skeletal muscle. Because the CC-RIX carry the same founder alleles  
67 as the DO, local gene regulation is expected to match between the populations, but because the alleles are  
68 recombined through the genome, distal effects are expected to vary from those in the DO, allowing us to  
69 directly assess the role of local gene regulation in driving trait-associated transcript variation. Together, these  
70 data enable a comprehensive view into the genetic architecture of metabolic disease.

## 71 Results

### 72 Genetic variation contributed to wide phenotypic variation

73 Although the environment was consistent across all animals, the genetic diversity present in this population  
74 resulted in widely varying distributions across physiological measurements (Fig. 1). For example, body  
75 weights of adult individuals varied from less than the average adult B6 body weight to several times the body  
76 weight of a B6 adult in both sexes (Males: 18.5 - 69.1g, Females: 16.0 - 54.8g) (Fig. 1A). Fasting blood  
77 glucose (FBG) also varied considerably (Fig. 1B) although few of the animals had FBG levels that would  
78 indicate pre-diabetes (19 animals, 3.8%), or diabetes (7 animals, 1.4%) according to previously developed  
79 cutoffs (pre-diabetes: FBG  $\geq$  250 mg/dL, diabetes: FBG  $\geq$  300, mg/dL)<sup>24</sup>. Males had higher FBG than  
80 females on average (Fig. 1C) as has been observed before suggesting either that males were more susceptible  
81 to metabolic disease on the high-fat diet, or that males and females may require different thresholds for  
82 pre-diabetes and diabetes.

83 Body weight was strongly positively correlated with food consumption (Fig. 1D  $R^2 = 0.51$ ,  $p < 2.2 \times 10^{-16}$ )  
84 and fasting blood glucose (FBG) (Fig. 1E,  $R^2 = 0.21$ ,  $p < 2.2 \times 10^{-16}$ ) suggesting a link between behavioral  
85 factors and metabolic disease. However, the heritability of this trait and others (Fig. 1F) indicates that  
86 background genetics contribute substantially to correlates of metabolic disease in this population.

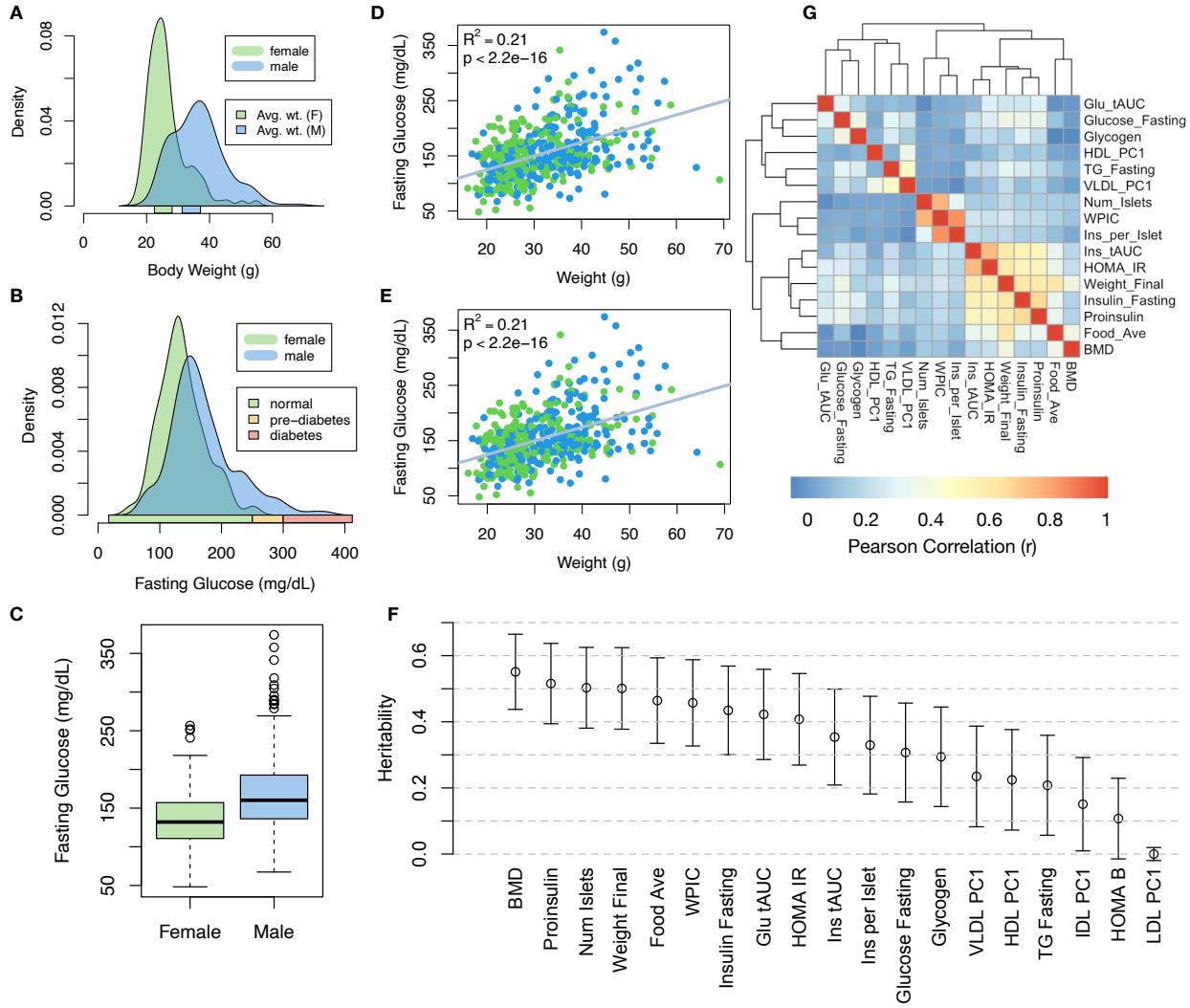


Figure 1: Clinical overview. **A.** Distributions of final body weight in the diversity outbred mice. Sex is indicated by color. The average B6 male and female adult weights at 24 weeks of age are indicated by blue and green bars on the x-axis. **B.** The distribution of final fasting glucose across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

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

91 **Distal Heritability Correlated with Phenotype Relevance**

92 We performed eQTL analysis using R/qtl2<sup>25</sup> (Methods) and identified both local and distal eQTLs for  
 93 transcripts in each of the four tissues (Supp. Fig 1). Significant local eQTLs far outnumbered distal eQTLs  
 94 (Supp. Fig. 1F) and tended to be shared across tissues (Supp. Fig. 1G) whereas the few significant distal  
 95 eQTLs we identified tended to be tissue-specific (Supp. Fig. 1H)

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

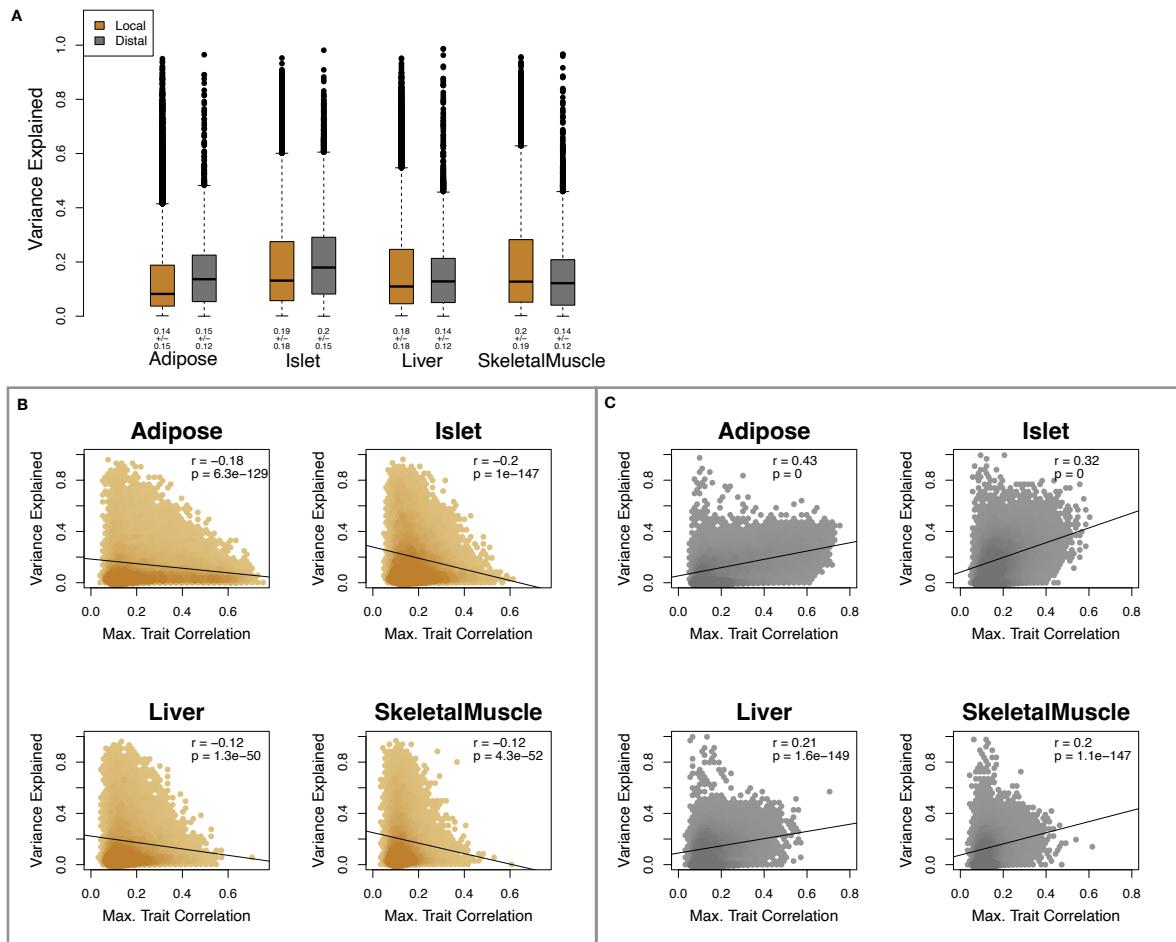


Figure 2: Transcript heritability and trait relevance. **A.** Distributions of distal and local heritability of transcripts across the four tissues. Overall local and distal factors contribute equally to transcript heritability. The relationship between **(B.)** local and **(C.)** distal heritability and trait relevance across all four tissues. Here trait relevance is defined as the maximum correlation between the transcript and all traits. Local heritability 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.

99 The local heritability of transcripts was negatively correlated with their trait relevance. We defined trait  
100 relevance as the maximum correlation of a transcript across all traits (Fig. 2B). This suggests that the more  
101 local genotype influenced transcript abundance, the less effect this variation had on the measured traits.  
102 Conversely, the distal heritability of transcripts was positively correlated with trait relevance (Fig. 2C). That  
103 is, transcripts that were more highly correlated with the measured traits tended to be distally, rather than  
104 locally, heritable. Importantly, this pattern was consistent across all tissues, strongly suggesting that this  
105 is a generic finding. This finding is consistent with previous observations that low-heritability transcripts  
106 explain more expression-mediated disease heritability than high-heritability transcripts<sup>19</sup>. However, the  
107 positive relationship between trait correlation and distal heritability demonstrated further that there are  
108 diffuse genetic effects throughout the genome converging on trait-related transcripts.

109 **High-Dimensional Mediation identified a high-heritability composite trait that was mediated  
110 by a composite transcript**

111 The above univariate analyses establish the importance of distal heritability for trait-relevant transcripts.  
112 However, the number of transcripts dramatically exceeds the number of degrees of freedom of the phenome.  
113 Thus, we expect the heritable, trait-relevant transcripts to be highly correlated and organized according  
114 to coherent, emergent biological processes representing the mediating endophenotypes driving clinical trait  
115 variation. To identify these endophenotypes in a theoretically principled way, we developed a novel dimension-  
116 reduction technique, HDMA, that uses the theory of causal graphical models to identify a transcriptomic  
117 signature that is simultaneously 1) highly heritable, 2) strongly correlated to the measured phenotypes, and  
118 3) conforms to the causal mediation hypothesis (Fig. 3). HDMA projects the high-dimensional scores—a  
119 composite genome score ( $G_C$ ), a composite transcriptome score ( $T_C$ ), and a composite phenome score  
120 ( $P_C$ )—and uses the univariate theory of mediation to constrain these projections to satisfy the hypotheses of  
121 perfect mediation. Specifically, perfect mediation implies that upon controlling for the transcriptomic score,  
122 the genome score is uncorrelated to the phenome score, which can also be viewed as a constraint on the  
123 correlation coefficients

$$\text{Corr}(G_C, P_C) = \text{Corr}(G_C, T_C)\text{Corr}(T_C, P_C),$$

124 which corresponds to the path coefficient in the mediation model [REF]. Operationally, HDMA is closely  
125 related to generalized canonical correlation analysis, for which provably convergent algorithms have recently  
126 been developed<sup>26</sup>. Implementation details for HDMA are available in **Supp. Methods XXX**.

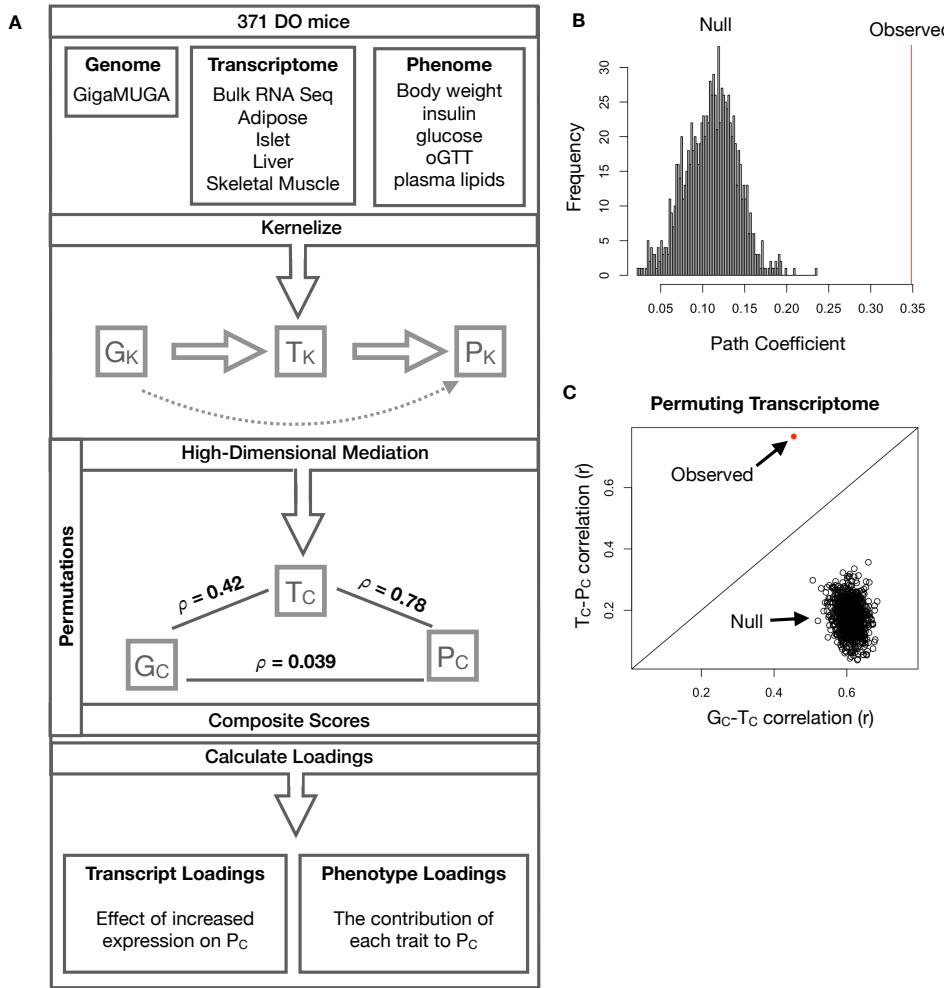


Figure 3: High-dimensional mediation. **A.** Workflow indicating major steps of high-dimensional mediation. The genotype, transcriptome, and phenotype matrices were independently normalized and converted to kernel matrices representing the pairwise relationships between individuals for each data modality ( $K_G$  = genome kernel,  $K_T$  = transcriptome kernel;  $K_P$  = 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  $\rho$  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).

127 We used high-dimensional mediation to identify the major axis of variation in the transcriptome that mediated  
 128 the effects of the genome on metabolic traits (Fig 3). Fig. 3A shows the partial correlations ( $\rho$ ) between  
 129 the pairs of these composite vectors. The partial correlation between  $G_C$  and  $T_C$  was 0.42, and the partial  
 130 correlation between  $T_C$  and  $P_C$  was 0.78. However, when the transcriptome was taken into account, the partial  
 131 correlation between  $G_C$  and  $P_C$  was effectively zero (0.039).  $P_C$  captured 30% of the overall trait variance,

132 and its estimated heritability was  $0.71 \pm 0.084$ , which was higher than any of the measured traits (Fig. 1F).  
133 Thus, HDMA identified a maximally heritable metabolic composite trait that was perfectly mediated by a  
134 highly heritable component of the transcriptome.

135 Standard CCA is prone to over-fitting because in any two large matrices it can be trivial to identify highly  
136 correlated composite vectors [REF]. To assess whether our implementation of HDMA was similarly prone to  
137 over-fitting in a high-dimensional space, we performed permutation testing. We permuted the individual  
138 labels on the transcriptome matrix 1000 times and recalculated the path coefficient, which is the partial  
139 correlation of  $G_C$  and  $T_C$  multiplied by the partial correlation of  $T_C$  and  $P_C$ . This represents the path  
140 from  $G_C$  to  $P_C$  that is mediated through  $T_C$ . The null distribution of the path coefficient is shown in Fig.  
141 3B, and the observed path coefficient from the original data is indicated by the red line. The observed  
142 path coefficient was well outside the null distribution generated by permutations ( $p < 10^{-16}$ ). Fig. 3C  
143 illustrates this observation in more detail. Although we identified high correlations between  $G_C$  and  $T_C$ , and  
144 modest correlations between  $T_C$  and  $P_C$  in the null data (Fig 3C), these two values could not be maximized  
145 simultaneously in the null data. In contrast, the red dot shows that in the real data both the  $G_C-T_C$   
146 correlation and the  $T_C-P_C$  correlation could be maximized simultaneously suggesting that the path from  
147 genotype to phenotype through transcriptome is highly non-trivial and identifiable in this case. These results  
148 suggest that these composite vectors represent genetically determined variation in phenotype that is mediated  
149 through genetically determined variation in transcription.

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

152 Each composite score is simply a weighted combination of the measured variables and the magnitude and  
153 sign of the weights, called loadings, correspond the relative importance and directionality of each variable in  
154 the composite score. The loadings of each measured trait onto  $P_C$  indicate how much each contributed to  
155 the composite phenotype. Final body weight contributed the most (Fig. 4), followed by homeostatic insulin  
156 resistance (HOMA\_IR) and fasting plasma insulin levels (Insulin\_Fasting). We can thus interpret  $P_C$  as  
157 an index of metabolic disease (Fig. 4B). Individuals with high values of  $P_C$  have a higher metabolic index  
158 and greater metabolic disease, including higher body weight and higher insulin resistance. We refer to  $P_C$  as  
159 the metabolic index going forward. Traits contributing the least to the metabolic index were measures of  
160 cholesterol and pancreas composition. Thus, when we interpret the transcriptomic signature identified by  
161 HDMA, we are explaining primarily the transcriptional mediation of body weight and insulin resistance, as  
162 opposed to cholesterol measurements.

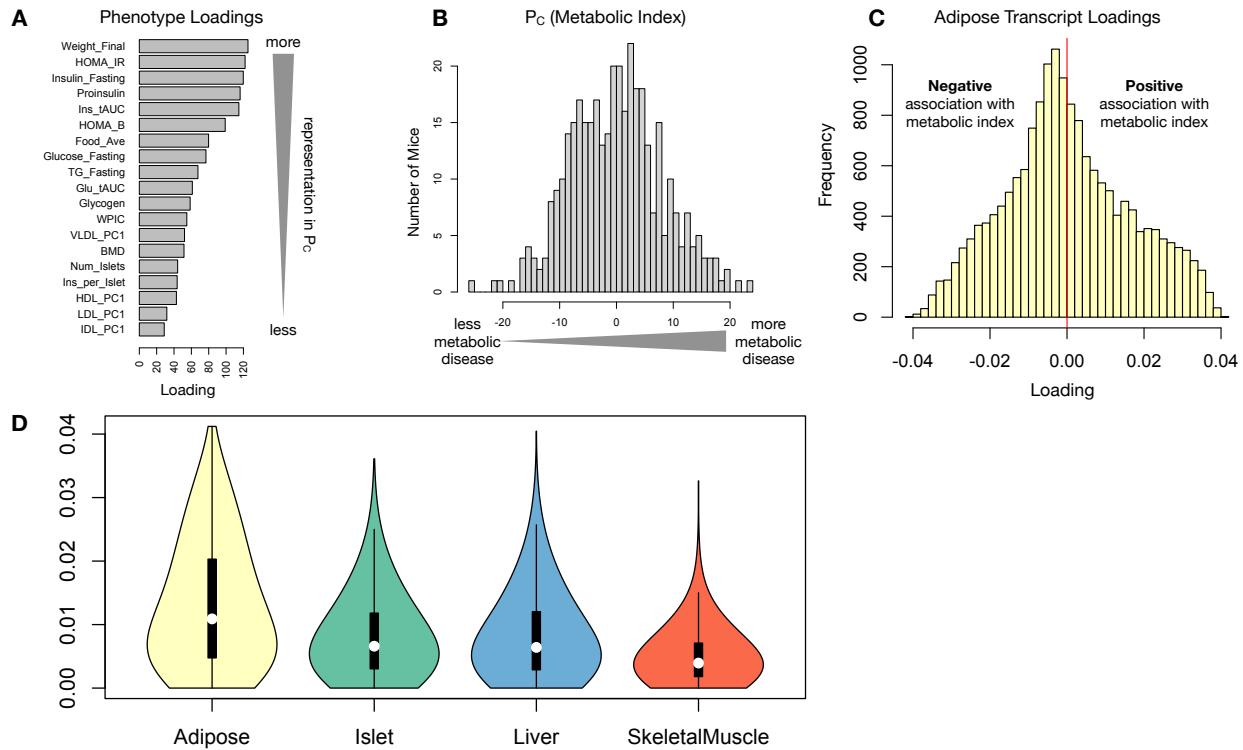


Figure 4: Interpretation of loadings. **A.** Loadings across traits. Body weight and insulin resistance contributed the most to the composite trait. **B.** Phenotype scores across individuals. Individuals with large positive phenotype scores had higher body weight and insulin resistance than average. 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 adipose tissue gene expression was a strong mediator of genotype on body weight and insulin resistance.

- 163 **High-loading transcripts have low local heritability, high distal heritability, and were linked**  
 164 **mechanistically to obesity**
- 165 We interpreted large loadings onto transcripts as indicating strong mediation of the effect of genetics on  
 166 metabolic index. Large positive loadings indicate that higher expression was associated with a higher  
 167 metabolic index (i.e. higher risk of obesity and metabolic disease on the high-fat diet) (Fig. 4C). Conversely,  
 168 large negative loadings indicate that high expression of these transcripts was associated with a lower metabolic  
 169 index (i.e. lower risk of obesity and metabolic disease on the high-fat diet) (Fig. 4C). We used gene set  
 170 enrichment analysis (GSEA)<sup>27;28</sup> to look for biological processes and pathways that were enriched at the top  
 171 and bottom of this list (Methods).
- 172 In adipose tissue, both GO processes and KEGG pathway enrichments pointed to an axis of inflammation

173 and metabolism (Supp. Fig. 2 and Fig. 11). GO terms and KEGG pathways associated with inflammation,  
174 particularly macrophage infiltration, were positively associated with metabolic index, indicating that increased  
175 expression in inflammatory pathways was associated with a higher metabolic index. It is well established that  
176 adipose tissue in obese individuals is inflamed [cite] and infiltrated by macrophages [cite], and the results  
177 here suggest that this may be a heritable component of metabolic disease.

178 The strongest negative enrichments in adipose tissue were related to mitochondrial activity in general, and  
179 thermogenesis in particular (Supp. Fig. 2 and Fig. 11). It has been shown mouse strains with greater  
180 thermogenic potential are also less susceptible to obesity on a high-fat diet [cite].

181 Transcripts associated with the citric acid (TCA) cycle as well as the catabolism of the branched-chain amino  
182 acids (BCAA) (valine, leucine, and isoleucine) were strongly enriched with negative loadings in adipose  
183 tissue (Supp. Fig. 3). Expression of genes in both pathways (for which there is some overlap) has been  
184 previously associated with insulin sensitivity<sup>12;29;30</sup>, suggesting that heritable variation in regulation of these  
185 pathways may influence risk of insulin resistance.

186 Looking at the 10 most positively and negatively loaded transcripts from each tissue, it is apparent that  
187 transcripts in the adipose tissue had the largest loadings, both positive and negative, of all tissues (Fig. 5A  
188 bar plot) This suggests that much of the effect of genetics on body weight and insulin resistance is mediated  
189 through gene expression in adipose tissue. The strongest loadings in liver and pancreas were comparable,  
190 and those in skeletal muscle were the weakest (Fig. 5A), suggesting that less of the genetic effects were  
191 mediated through transcription in skeletal muscle. Heritability analysis showed that transcripts with the  
192 largest loadings had higher distal heritability than local heritability (Fig. 5A heat map and box plot). This  
193 pattern contrasts with transcripts nominated by TWAS (Fig. 5B), which tended to have lower loadings,  
194 higher local heritability and lower distal heritability. Transcripts with the highest local heritability in each  
195 tissue (Fig. 5C) had the lowest loadings.

196 We performed a literature search for the genes in each of these groups along with the terms “diabetes”,  
197 “obesity”, and the name of the expressing tissue to determine whether any of these genes had previous  
198 associations with metabolic disease in the literature (Methods). Multiple genes in each group had been  
199 previously associated with obesity and diabetes (Fig. 5 bolded gene names). Genes with high loadings were  
200 most highly enriched for previous literature support. They were 2.375 more likely than TWAS hits and 3.8  
201 times more likely than genes with high local heritability to be previously associated with obesity or diabetes.

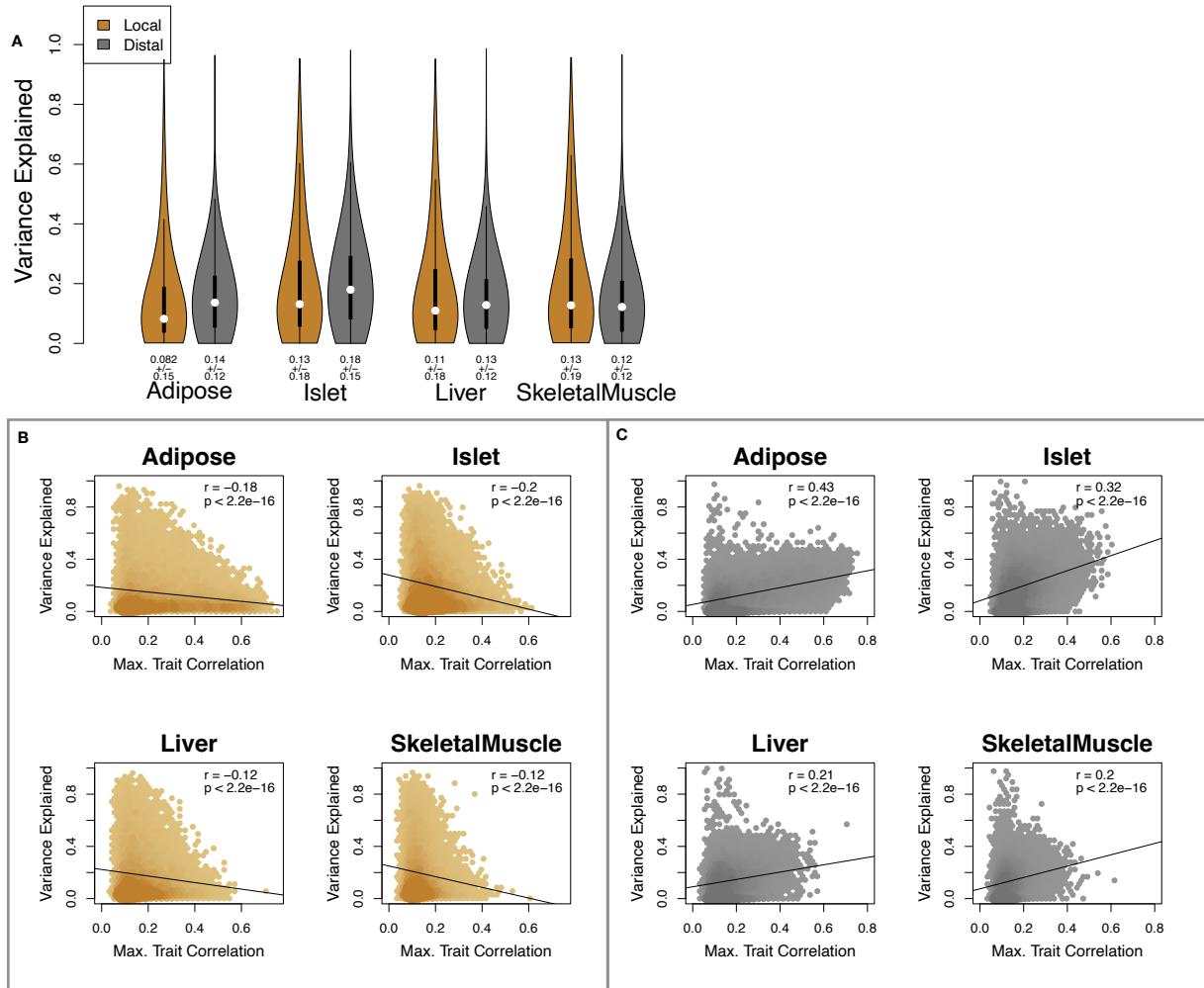


Figure 5: Transcripts with high loadings have high distal heritability and literature support. Each panel has a bar plot showing the loadings of transcripts selected by different criteria. Bar color indicates the tissue of origin. The heat map shows the local (L - left) and distal (D - right) heritability 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.

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

203 Clustering of transcripts with top loadings in each tissue showed tissue-specific functional modules associated  
 204 with obesity and insulin resistance (Fig. 6A) (Methods). The clustering highlights the importance of immune  
 205 activation particularly in adipose tissue. The “mitosis” cluster had large positive loadings in three of the  
 206 four tissues potentially suggesting system-wide hypertrophy. Otherwise, all clusters were strongly loaded in  
 207 only one or two tissues. For example, the lipid metabolism cluster was loaded most heavily in liver. The  
 208 positive loadings suggest that high expression of these genes particularly in the liver was associated with

increased metabolic disease. This cluster included the gene *Pparg*, whose primary role is in the adipose tissue where it is considered a master regulator of adipogenesis<sup>31</sup>. Agonists of *Pparg*, such as thiazolidinediones, are FDA-approved to treat type II diabetes, and reduce inflammation and adipose hypertrophy<sup>31</sup>. Consistent with this role, the loading for *Pparg* in adipose tissue was negative, suggesting that higher expression was associated with leaner mice (Fig. 6B). In contrast, *Pparg* had a large positive loading in liver, where it is known to play a role in the development of hepatic steatosis, or fatty liver. Mice that lack *Pparg* specifically in the liver, are protected from developing steatosis and show reduced expression of lipogenic genes<sup>32;33</sup>. Overexpression of *Pparg* in the livers of mice with a *Ppara* knockout, causes upregulation of genes involved in adipogenesis<sup>34</sup>. In the livers of both mice and humans high *Pparg* expression is associated with hepatocytes that accumulate large lipid droplets and have gene expression profiles similar to adipocytes<sup>35;36</sup>.

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

Gene lists for all clusters are available in Supplemental File XXX.

## Gene expression, but not local eQTLs, predicted body weight in an independent population

To test whether the transcript loadings identified in the DO could be translated to another population, we tested whether they could predict metabolic phenotype in an independent population of CC-RIX mice, which were F1 mice derived from multiple pairings of Collaborative Cross (CC) [cite] strains (Fig. 7) (Methods). We tested two questions. First, we asked whether the loadings identified in the DO mice were relevant to the relationship between the transcriptome and the phenotype in the CC-RIX. We predicted body weight (a surrogate for metabolic index) in each CC-RIX individual using measured gene expression in each tissue and the transcript loadings identified in the DO (Methods). The predicted body weight and actual body weight were highly correlated in all tissues (Fig. 7B left column). The best prediction was achieved for adipose tissue, which supports the observation in the DO that adipose expression was the strongest mediator of the genetic effect on metabolic index. This result also confirms the validity and translatability of the transcript loadings and their relationship to metabolic disease.

The second question related to the source of the relevant variation in gene expression. If local regulation was

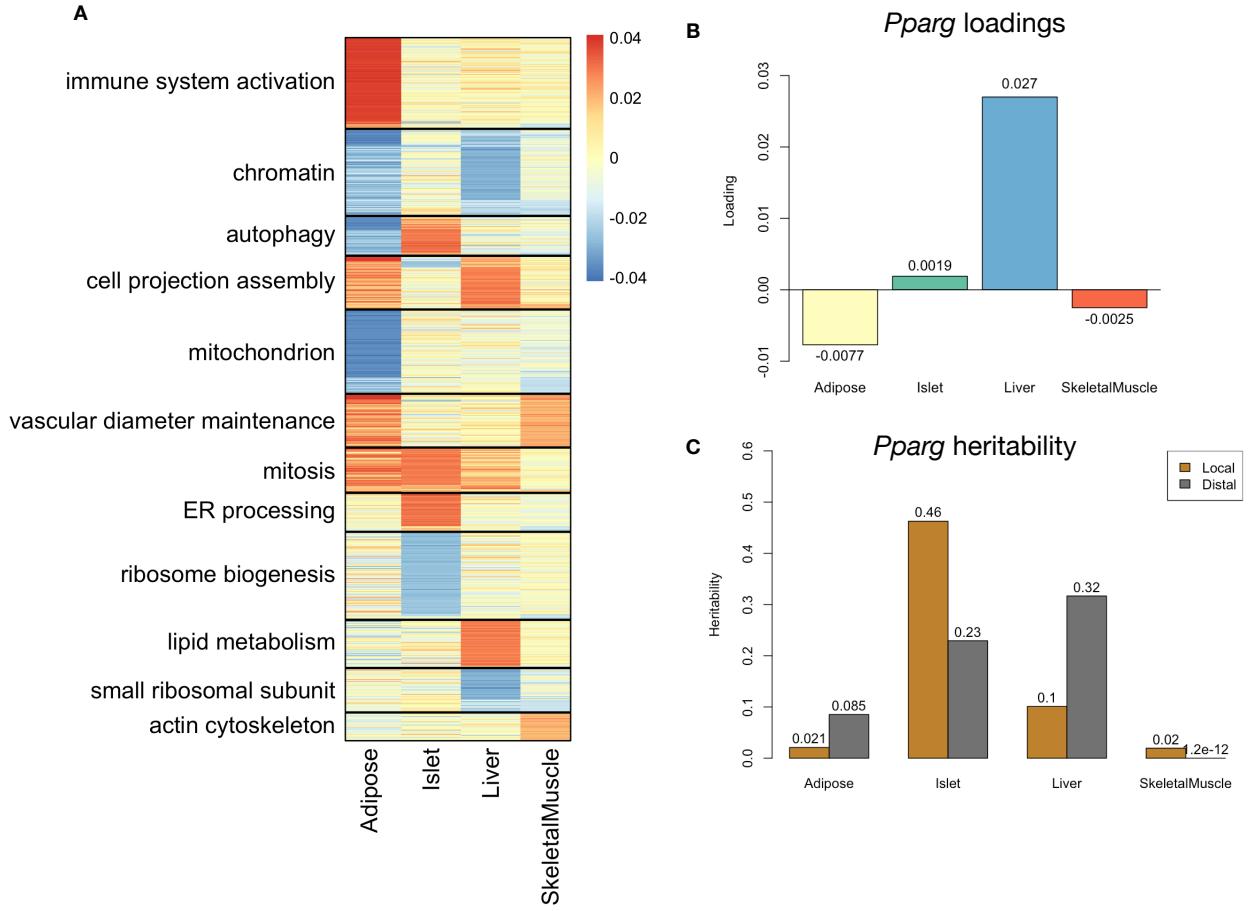


Figure 6: Tissue-specific transcriptional programs were associated with obesity and insulin resistance. **A** Heat map showing the loadings of all transcripts with loadings greater than 2.5 standard deviations from the mean in any tissue. The heat map was clustered using k medoid clustering. Functional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

the predominant factor influencing gene expression, we should be able to predict phenotype in the CC-RIX using transcripts imputed from local genotype (Fig. 7A). The DO and the CC-RIX were derived from the same eight founder strains and so carry the same alleles throughout the genome. We imputed gene expression in the CC-RIX using local genotype and were able to estimate variation in gene transcription robustly (Supp. Fig. 4). However, these imputed values failed to predict body weight in the CC-RIX when weighted with the loadings from HDMA. (Fig. 7B right column). This result suggests that local regulation of gene expression is not the primary factor driving heritability of complex traits, consistent with our findings in the DO population that distal heritability was a major driver of trait-relevant variation and that high-loading transcripts had comparatively high distal and low local heritability.

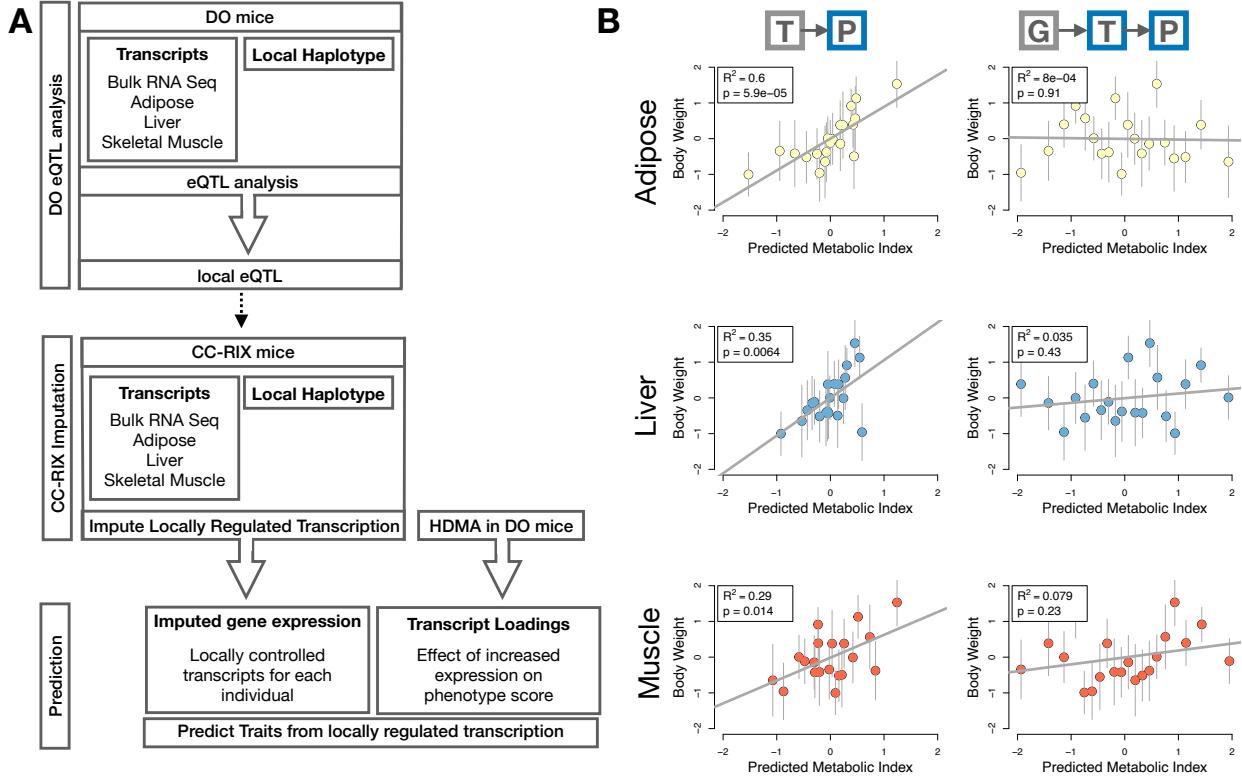


Figure 7: Transcription, but not local genotype, predicts phenotype in the CC-RIX. **A.** Workflow showing procedure for translating HDMA results to an independent population of mice. **B.** Relationships between the predicted metabolic index and measured body weight. The left column shows the predictions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

249 **Distally heritable transcriptomic signatures reflected variation in composition of adipose tissue  
250 and islets**

251 The interpretation of global genetic influences on gene expression and phenotype is potentially more challenging  
252 than the interpretation and translation of local genetic influences, as genetic effects cannot be localized to  
253 individual gene variants or transcripts. However, there are global patterns across the loadings that can  
254 inform mechanism. For example, heritable variation in cell type composition can be derived from transcript  
255 loadings. We observed above that immune activation in the adipose tissues was an important driver of obesity  
256 in the DO population. To determine whether this is reflected as an increase in macrophages in adipose  
257 tissue, we compared loadings of cell-type specific genes in adipose tissue (Methods). The mean loading  
258 of macrophage-specific genes was significantly greater than 0 (Fig. 8A), indicating that obese mice were  
259 genetically predisposed to have high levels of macrophage infiltration in adipose tissue in response to the  
260 high-fat, high-sugar diet.

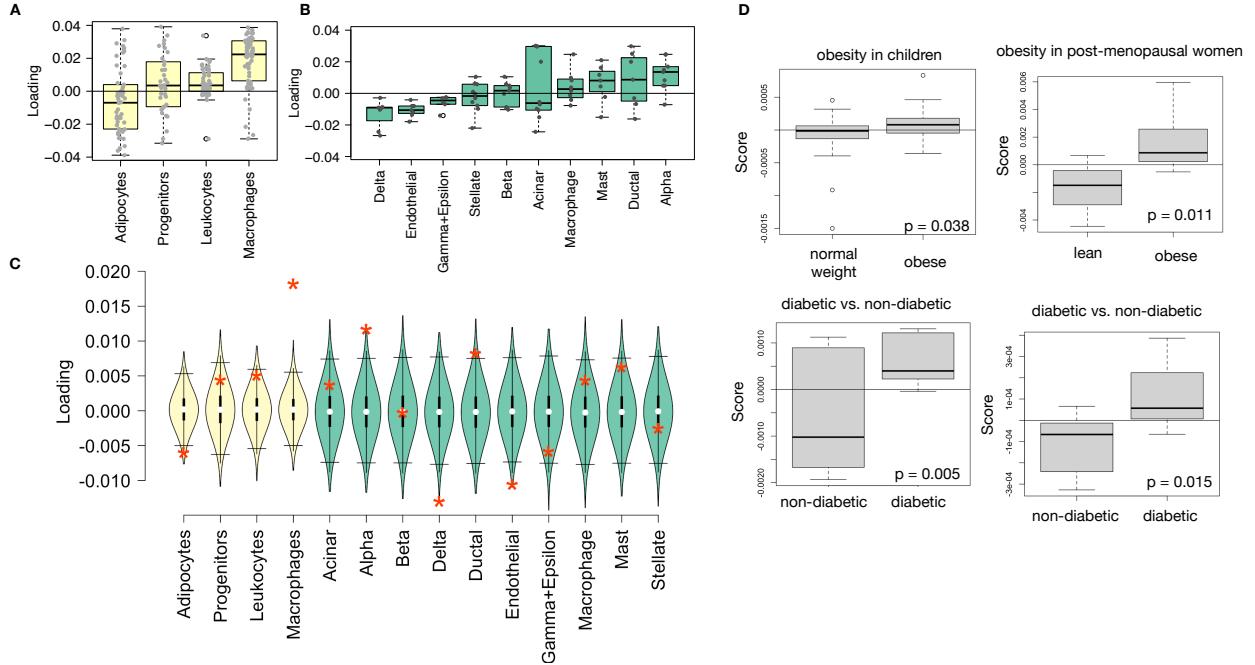


Figure 8: HDMA results translate to humans. **A.** Distribution of loadings for cell-type-specific transcripts in adipose tissue. **B.** Distribution of loadings for cell-type-specific transcripts in pancreatic islets (green). **C.** Null distributions for the mean loading of randomly selected transcripts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

261 We also compared loadings of cell-type specific transcripts in islet (Methods). The mean loadings for alpha-cell  
 262 specific transcripts were significantly greater than 0, while the mean loadings for delta- and endothelial-cell  
 263 specific genes were significantly less than 0 (Fig. 8B). These results suggest either that mice with higher  
 264 metabolic index had inherited a higher proportions of alpha cells, and lower proportions of endothelial and  
 265 delta cells in their pancreatic islets, that such compositional changes were induced by the HFHS diet in a  
 266 heritable way, or both. In either case, these results support the hypothesis that alterations in islet composition  
 267 drive variation in metabolic index.

268 Notably, the loadings for pancreatic beta cell-type specific loadings was not significantly different from zero.  
 269 This is not necessarily reflective of the function of the beta cells in the obese mice, but rather suggests that  
 270 any variation in the number of beta cells in these mice was unrelated to obesity and insulin resistance. This  
 271 is further consistent with the islet composition traits having small loadings in the phenotype score (Fig. 4).

272 **Heritable transcriptomic signatures translated to human disease**

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

278 We calculated a predicted obesity score for each individual in the human studies based on their adipose  
279 tissue gene expression (Methods) and compared the predicted scores for obese and non-obese groups as well  
280 as diabetic and non-diabetic groups. In all cases, the predicted obesity scores were higher on average for  
281 individuals in the obese and diabetic groups compared with the lean and non-diabetic groups (Fig. 8D).  
282 This indicates that the distally heritable signature of obesity identified in DO mice is relevant to obesity and  
283 diabetes in human subjects.

284 **Targeting gene signatures**

285 Another potential application of the transcript loading landscape is in ranking potential drug candidates  
286 for the treatment of metabolic disease. Although high-loading transcripts may be good candidates for  
287 understanding specific biology related to obesity, the transcriptome overall is highly interconnected and  
288 redundant, and focusing on individual transcripts for treatment may be less effective than using broader  
289 transcriptomic signatures that capture the emergent biology [cite or remove]. The ConnectivityMap (CMAP)  
290 database<sup>37</sup> developed by the Broad Institute allows us to query thousands of compounds that reverse or  
291 enhance the extreme ends of transcriptomic signatures in multiple different cell types. By identifying drugs  
292 that reverse pathogenic transcriptomic signatures, we can potentially identify compounds that have favorable  
293 effects on gene expression.

294 To test this hypothesis, we queried the CMAP database through the CLUE online query tool (<https://clue.io/query/>, version 1.1.1.43) (Methods). We identified top anti-correlated hits across all cell types. To  
295 get more tissue-specific results, we also looked at top results in cell types that most closely resembled our  
296 tissues. We looked at results in adipocytes (ASC) as well as pancreatic tumor cells (YAPC) regardless of *p*  
297 value (Supplemental Figure XXX and XXX).

298 Looking broadly across cell types, the notable top hits from the adipose tissue loadings included mTOR  
299 inhibitors and glucocorticoid agonists (Supplemental Figure XXX). It is thought that metformin, which  
300 is commonly used to improve glycemic control, acts, at least in part, by inhibiting mTOR signaling<sup>38;39</sup>.

302 However, long-term use of other mTOR inhibitors, such as rapamycin, are known to cause insulin resistance  
303 and  $\beta$ -cell toxicity<sup>39–41</sup>. Glucocorticoids are used to reduce inflammation, which was a prominent signature  
304 in the adipose tissues, but these drugs also promote hyperglycemia and diabetes<sup>42;43</sup>. Accute treatment  
305 with glucocorticoids has further been shown to reduce thermogenesis in rodent adipocytes<sup>44–46</sup>, but increase  
306 thermogenesis in human adipocytes<sup>47;48</sup>. Thus, the pathways identified by CMAP across all cell types were  
307 highly related to the transcript loading profiles, but the relationship was not a simple reversal.

308 The top hit for the adipose composite transcript in CMAP adipocytes was a PARP inhibitor (Supplemental  
309 Figure XXXB). PARPs play a role in lipid metabolism and are involved in the development of obesity and  
310 diabetes<sup>49</sup>. PARP1 inhibition increases mitochondrial biogenesis<sup>50</sup>. Inhibition of PARP1 activity can further  
311 prevent necrosis in favor of the less inflammatory apoptosis<sup>51</sup>, thereby potentially reducing inflammation in  
312 stressed adipocytes. Other notable hits among the top 20 were BTK inhibitors, which have been observed  
313 to suppress inflammation and improve insulin resistance<sup>52</sup> as well as to reduce insulin antibodies in type I  
314 diabetes<sup>53</sup>. IKK inhibitors have been shown to improve glucose control in type II diabetes<sup>54;55</sup>.

315 Among the top most significant hits for the transcript loadings from pancreatic islets (Fig. XXX), was  
316 suppression of T cell receptor signaling, which is known to be involved in Type 1 diabetes<sup>56</sup>, as well as  
317 TNFR1, which has been associated with mortality in diabetes patients<sup>57</sup>. Suppression of NOD1/2 signaling  
318 was also among the top hits. NOD1 and 2 sense ER stress<sup>58;59</sup>, which is associated with  $\beta$ -cell death in type  
319 1 and type 2 diabetes<sup>60</sup>. This cell death process is dependent on NOD1/2 signaling<sup>58</sup>, although the specifics  
320 have not yet been worked out.

321 We also looked specifically at hits in pancreatic tumor cells (YAPC) regardless of significance level to get a  
322 transcriptional response more specific to the pancreas. Hits in this list included widely used diabetes drugs,  
323 such as sulfonylureas, PPAR receptor agonists, and insulin sensitizers. Rosiglitazone is a PPAR- $\gamma$  agonist  
324 and was one of the most prescribed drugs for type 2 diabetes before its use was reduced due to cardiac  
325 side-effects<sup>61</sup>. Sulfonylureas are another commonly prescribed drug class for type 2 diabetes, but also have  
326 notable side effects including hypoglycemia and accellerated  $\beta$ -cell death<sup>62</sup>.

## 327 Discussion

328 Here we used a novel high-dimensional mediation analysis (HDMA) to investigate the relative contributions of  
329 local and distal gene regulation to heritable trait variation in a genetically diverse mouse model of diet-induced  
330 obesity and metabolic disease. We identified tissue-specific composite transcripts mediating the effect of  
331 genetic background on metabolic traits. Transcripts contributing most strongly to these composite transcripts

332 were distally heritable. These composite transcripts, but not local eQTL, were able to predict obesity in  
333 an independent mouse population with divergent allelic structure. Moreover, the composite transcript from  
334 adipose tissue predicted obesity and diabetes status in human cohorts with measured adipose gene expression.  
335 Taken together, these results support the hypothesis that gene expression mediating the effect of genetic  
336 background on phenotype is primarily distally regulated, and that the gene regulatory networks influencing  
337 metabolic disease are conserved across mice and humans.

338 It has frequently been assumed that gene regulation in *cis* is the primary driver of genetically associated  
339 trait variation, but attempts to use local gene regulation to explain phenotypic variation have had limited  
340 success<sup>16;17</sup>. In recent years, evidence has mounted that distal gene regulation may be an important mediator  
341 of trait heritability<sup>19;18;63</sup>. It has been observed that transcripts with high local heritability explain less  
342 expression-mediated disease heritability than transcripts with low local heritability<sup>19</sup>. Consistent with this  
343 observation, genes located near GWAS hits tend to be complexly regulated<sup>18</sup>. They also tend to be enriched  
344 with functional annotations, in contrast to genes with simple local regulation, which tend to be depleted  
345 of functional annotations suggesting they are less likely to be directly involved in disease traits<sup>18</sup>. These  
346 observations are consistent with principles of robustness in complex systems<sup>64–66</sup>. If a transcript were both  
347 important to a trait and subject to strong local regulation, a population would be susceptible to extremes  
348 in phenotype that might frequently cross the threshold to disease. Indeed, strong disruption of highly  
349 trait-relevant genes is the cause of Mendelian disease.

350 The composite transcripts we identified here supported the hypothesis that distally regulated gene expression  
351 is the dominant mediator of trait variation. Transcript loadings (the degree to which they contributed to  
352 the composite transcript) were negatively correlated with local heritability and positively correlated with  
353 distal heritability. The most strongly loaded transcripts were enriched for functional annotations associated  
354 with metabolic disease. These distally regulated composite transcripts were highly heritable and explained a  
355 high proportion of disease risk, further supporting their role as mediators. The composite transcripts were  
356 moreover able to predict obesity in an independent cohort of mice whereas models using local eQTL only  
357 could not. Together these observations suggest that distal gene regulation was the dominant mode through  
358 which gene expression mediated the effect of genetic background on complex metabolic traits.

359 Identification of this distally heritable signature depended on the high-dimensional approach we used. Because  
360 HDMA uses a kinship matrix rather than genotypes at individual loci, it allows for arbitrarily complex  
361 gene regulation, as well as the interconnectedness and redundancy of the transcriptome. This feature also  
362 means that HDMA assumes that traits are highly polygenic and distributed across the genome. In contrast,  
363 one-dimensional, univariate approaches assume a large, localized genetic effect. Thus, the HDMA approach

364 is consistent with the omnigenic model of complex traits which posits that complex traits are massively  
365 polygenic and that their heritability is spread out across the genome<sup>67</sup>. In the omnigenic model, genes  
366 are classified either as “core genes,” which directly impinge on the trait, or “peripheral genes,” which are  
367 not directly trait-related, but influence core genes through the complex gene regulatory network. HDMA  
368 explicitly models a central proposal of the omnigenic model which posits that once the expression of the  
369 core genes (i.e. trait-mediating genes) is accounted for, there should be no residual correlation between the  
370 genome and the phenotype. Here, when the composite transcript was taken into account there was no residual  
371 correlation between the composite genome and composite phenotype (Fig. 3A).

372 Thus, the composite transcript is essentially a weighted vector with larger weights (loadings) indicating higher  
373 “core-ness” of a transcript. There was no clear demarcation between the core and peripheral genes in loading  
374 magnitude, but we do not necessarily expect a clear separation given the complexity of gene regulation and  
375 the genotype-phenotype map<sup>68</sup>. Still, the transcripts with the largest loadings had high distal heritability,  
376 low local heritability, and were enriched for biological processes related to metabolic traits, as we would  
377 predict for core genes.

378 An extension of the omnigenic model proposed that most heritability of complex traits is driven by weak  
379 distal eQTLs<sup>63</sup>. This is consistent with what we observed here. The transcripts with the largest loadings  
380 were strongly distally regulated and only weakly locally regulated, suggesting that distal gene regulation  
381 plays a primary role in driving heritable trait variation. We saw further that the patterns of distal heritability  
382 were complex spread across the genome. Even for transcripts whose expression was strongly regulated by  
383 distal factors, these factors were multiple and spread across the genome. For example, *Nucb2*, was a strongly  
384 mediating transcript in islet and was also strongly distally regulated (66% distal heritability) (Fig. 5). This  
385 gene is expressed in pancreatic  $\beta$  cells and is involved in insulin and glucagon release<sup>69-71</sup>. Although its  
386 transcription was highly heritable in islets, that regulation was distributed across the genome, with no clear  
387 distal eQTL (Supp. Fig. 5). Thus, although distal regulation of some genes may be strong, this regulation is  
388 likely to be highly complex and not easily localized.

389 The composite transcripts identified by HDMA are richly interpretable in both tissue- and gene-specific  
390 manners. The transcripts with the strongest loadings were enriched in biological functions previously known  
391 to be involved in the pathogenesis of metabolic disease, such as inflammation in adipose tissue. That these  
392 processes were identified in this analysis suggests that they have a heritable component, and that some  
393 individuals are genetically susceptible to greater adipose inflammation on a high-fat, high-sugar diet.

394 Individual transcripts also demonstrated biologically interpretable, tissue-specific patterns. We highlighted

395 *Pparg*, which is known to be protective in adipose tissue<sup>31</sup> where it was negatively loaded, and harmful in the  
396 liver<sup>32–36</sup>, where it was positively loaded. Such granular patterns may be useful in generating hypotheses for  
397 further testing, and prioritizing genes as therapeutic targets. The tissue-specific nature of the loadings also  
398 may provide clues to tissue-specific effects, or side effects, of targeting particular genes system-wide, since  
399 antagonists of *Pparg* may reduce fatty liver disease, but exacerbate adipose tissue inflammation.

400 We showed further that these composite transcripts can be used as weighted vectors in multiple types of  
401 analysis, such as drug prioritization using gene set enrichment analysis (GSEA) and the CMAP database. In  
402 particular, the CMAP analysis identified drugs which have been demonstrated to reverse insulin resistance  
403 and other aspects of metabolic disease. This finding supports the causal role of these gene signatures in  
404 pathogenesis of metabolic disease and thus their utility in prioritizing drugs and gene targets as therapeutics.

405 Another useful application of the composite transcripts is to pair them with cell-type specific genes to generate  
406 hypotheses about cell composition in individual tissues. Combining the multi-tissue, transcriptome-wide  
407 weighted vectors with public databases and data sets thus provides a path for generating a wide range of  
408 testable hypotheses. Moreover, each data set presented here was derived from human tissues or cell lines,  
409 thus demonstrating the translatability of these results. That the mouse-derived adipose composite transcript  
410 was able to classify human adipose gene expression in terms of obesity and diabetes status further supports  
411 the direct translatability of these findings, the utility of HDMA, and the continued importance of mouse  
412 models of human disease in which it is possible to obtain complete transcriptomes in multiple tissues across  
413 large numbers of individuals.

414 In conclusion, we have shown that both tissue specificity and distal gene regulation are critically important to  
415 understanding the genetic architecture of complex traits. We identified important genes and gene signatures  
416 that were heritable, causal of disease, and translatable to other mouse populations and to humans. Finally,  
417 we have shown that by directly acknowledging the complexity of both gene regulation and the genotype-to-  
418 phenotype map, we can gain a new perspective on disease pathogenesis and develop actionable hypotheses  
419 about pathogenic mechanisms and potential treatments.

## 420 Data Availability

421 Here we tell people where to find the data

## 422 Acknowledgements

423 Here we thank people

424 **Supplemental Figures**

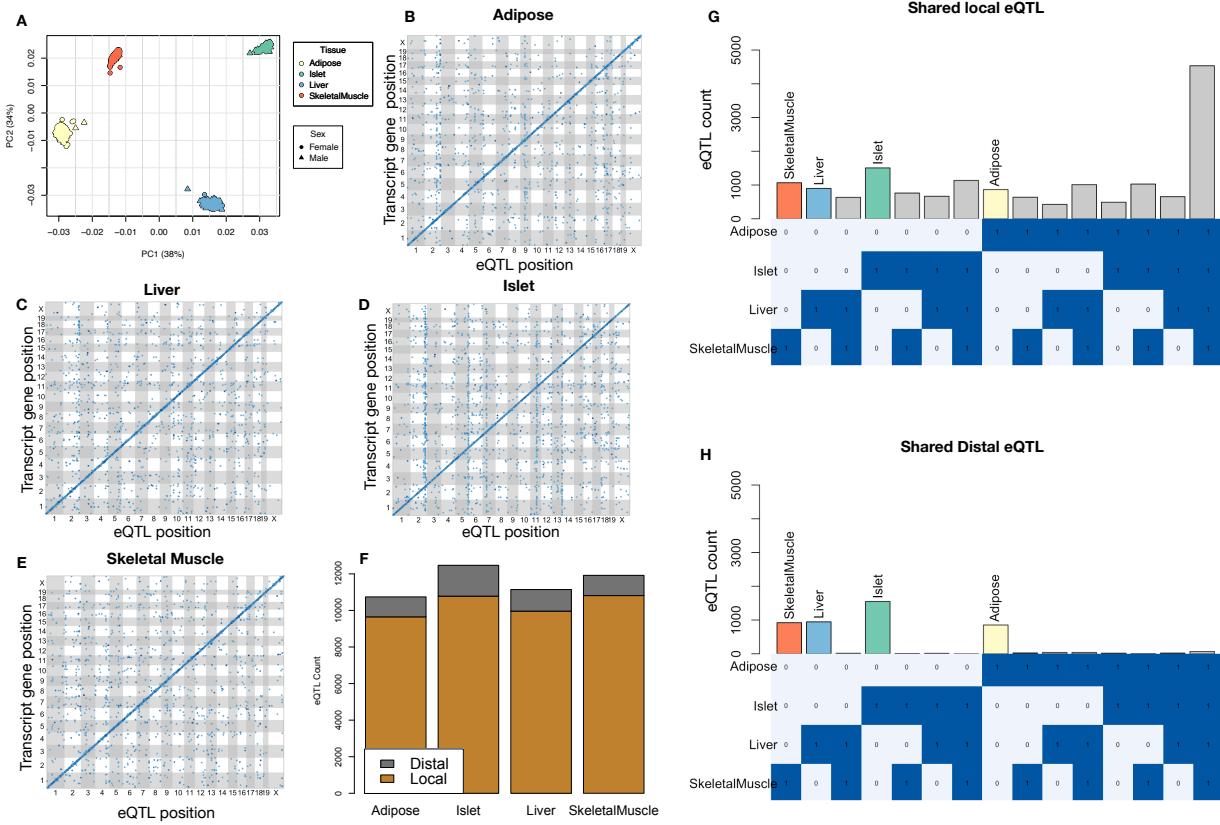


Figure 9: Overview of eQTL analysis in DO mice. **A.** RNA seq samples from the four different tissues clustered by tissue. **B.-E.** eQTL maps are shown for each tissue. The *x*-axis shows the position of the mapped eQTL, and the *y*-axis shows the physical position of the gene encoding each mapped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

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## KEGG pathway enrichments by GSEA

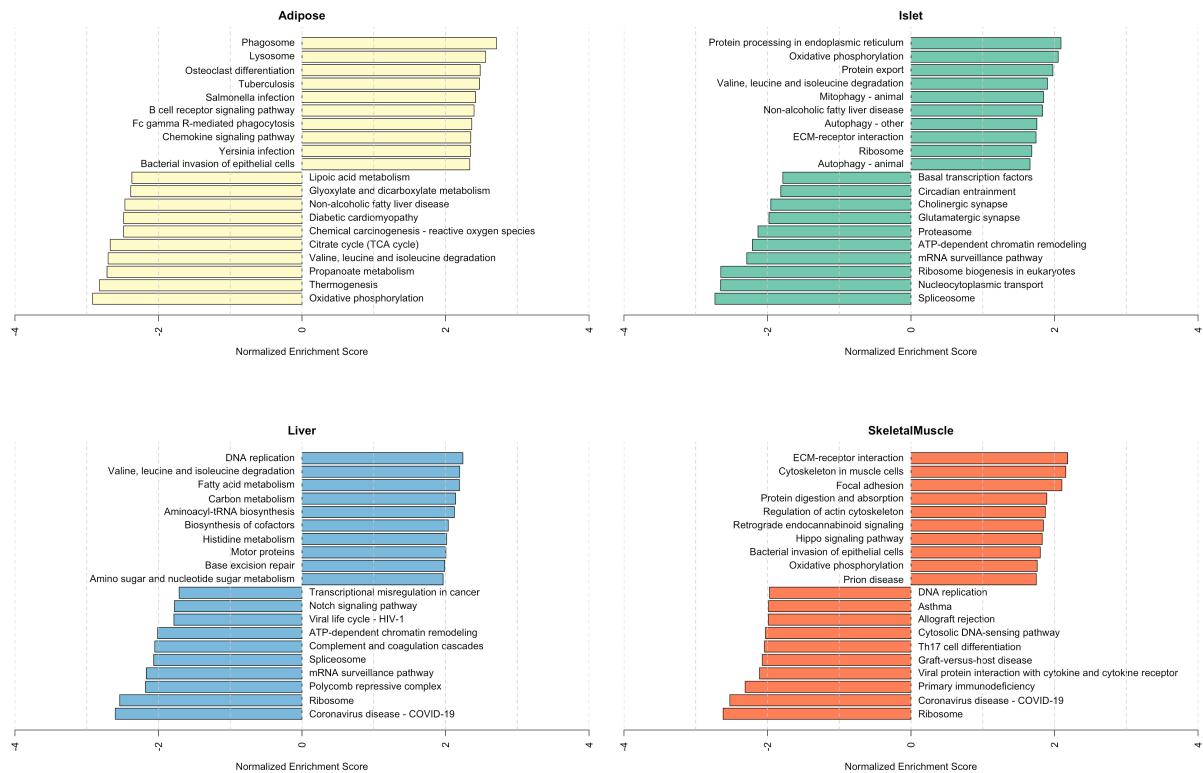


Figure 10: Bar plots showing normalized enrichment scores (NES) for KEGG pathways as determined by fast gene score enrichment analysis (fgsea). Only the top 10 positive and top 10 negative scores are shown. Colors indicate tissue. The name beside each bar shows the name of each enriched KEGG pathway.

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## Top GO term enrichments by GSEA

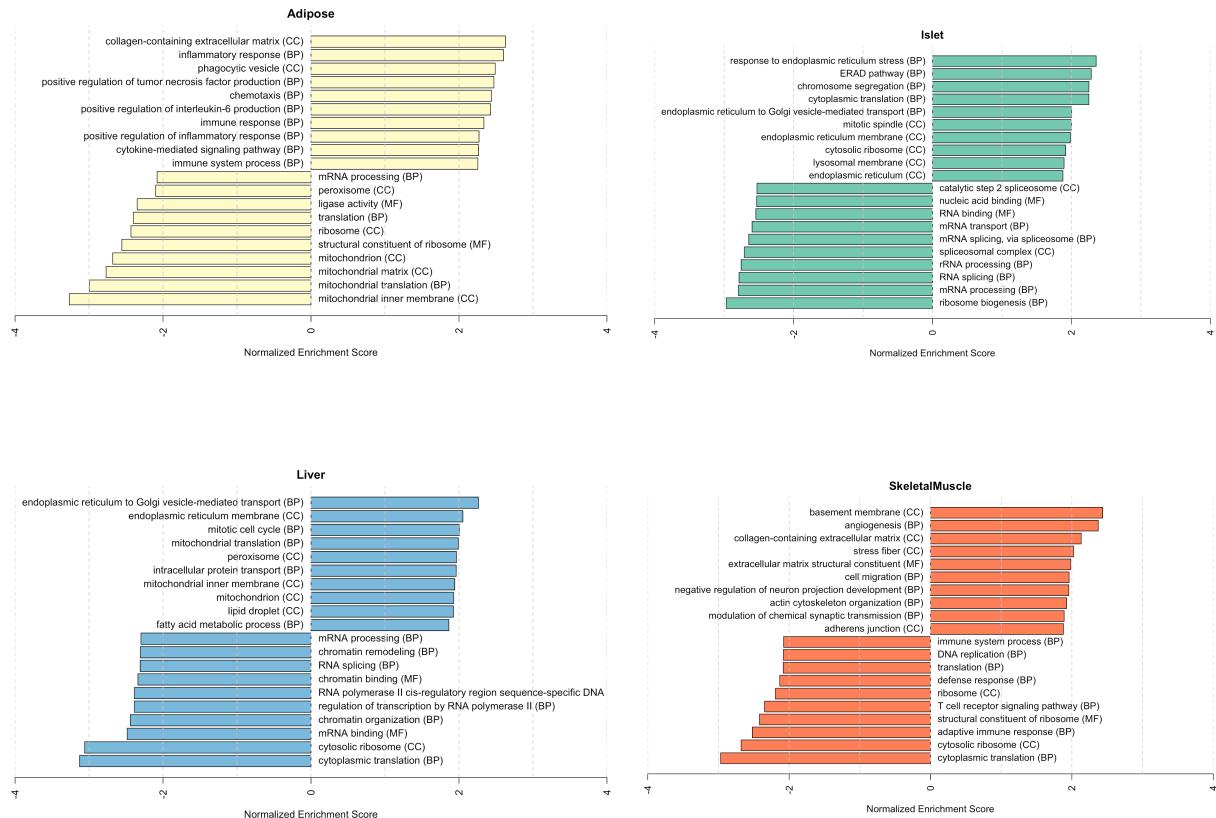


Figure 11: Bar plots showing normalized enrichment scores (NES) for GO terms as determined by fast gene score enrichment analysis (fgsea). Only the top 10 positive and top 10 negative scores are shown. Colors indicate tissue. The name beside each bar shows the name of each enriched GO term. The letters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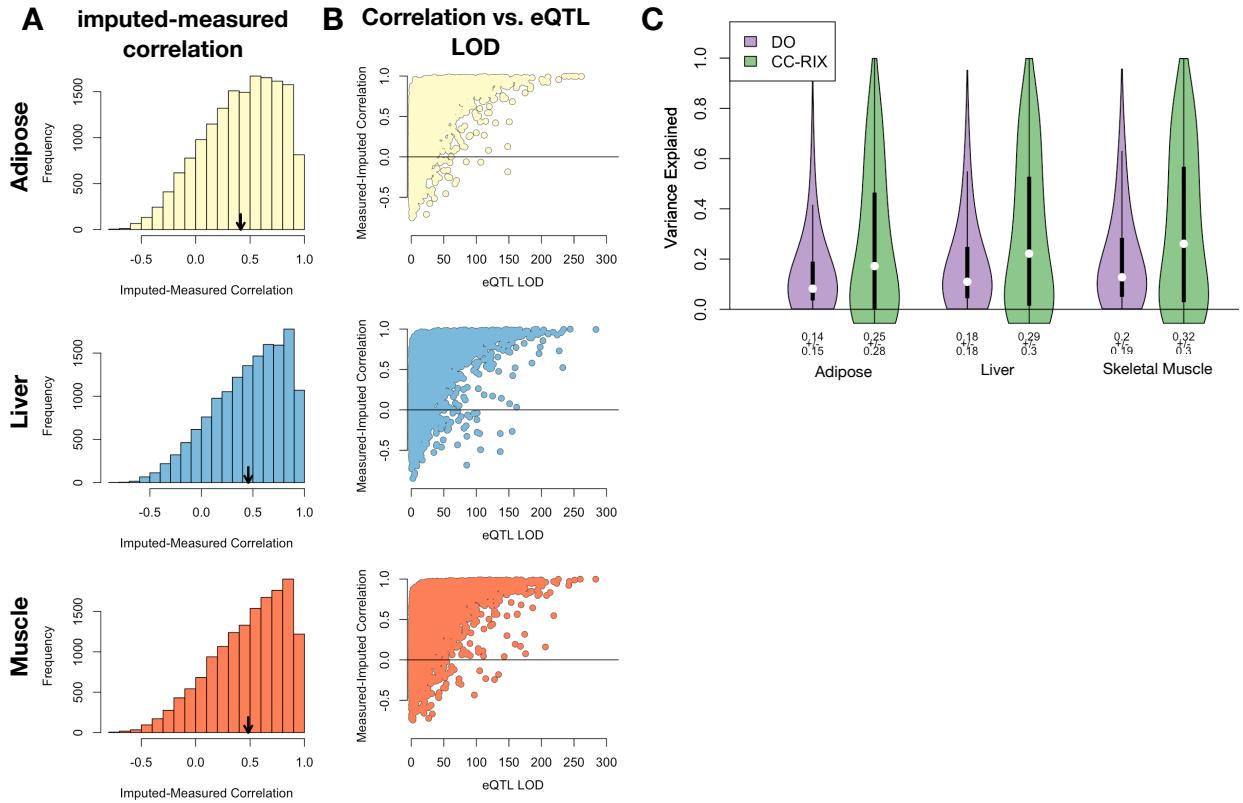


Figure 12: Validation of transcript imputation in the CC-RIX. **A.** Distributions of correlations between imputed and measured transcripts in the CC-RIX. The mean of each distribution is shown by the red line. All distributions were skewed toward positive correlations and had positive means near a Pearson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

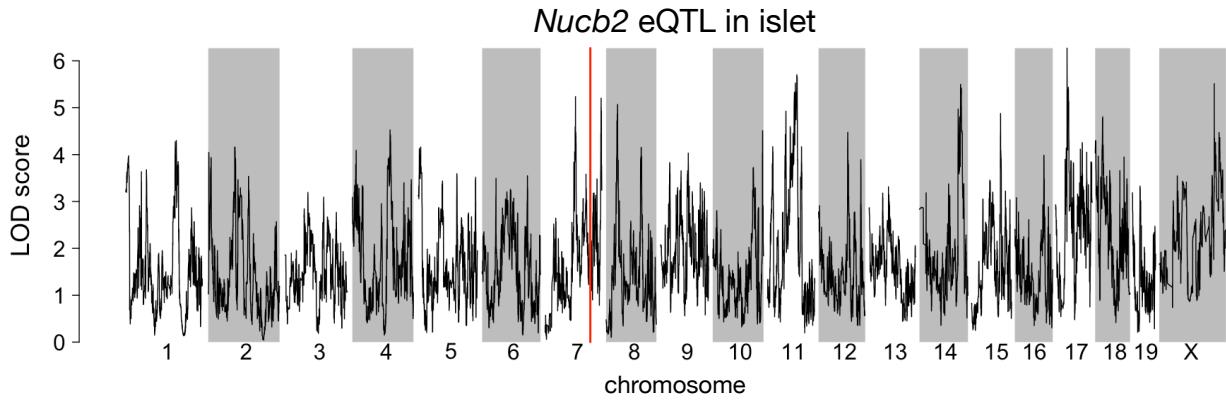


Figure 13: Regulation of *Nucb2* expression in islet. *Nucb2* is encoded on mouse chromosome 7 at 116.5 Mb (red line). In islets the heritability of *Nucb2* expression levels is 69% heritable. This LOD score trace shows that there is no local eQTL at that position, nor any strong distal eQTL anywhere else in the genome.

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