

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

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⁴ Anna L Tyler, J Matthew Mahoney, Mark P Keller, Candice N. Baker, Margaret Gaca, Anuj Srivastava,
⁵ Isabela Gerdes Gyuricza, Madeleine Braun, Nadia A Rosenthal, Alan D Attie, Gary A Churchill and Gregory
⁶ W Carter

⁷ **Abstract**

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

¹⁹ **Introduction**

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

26 with multiple disease traits^{12–15}

27 Despite the great promise of these methods, explaining trait effects with local gene regulation has been more
28 difficult than initially assumed^{16;17}. Although trait-associated variants tend to lie in non-coding, regulatory
29 regions, they often do not have detectable effects on gene expression¹⁶ and tend not to co-localize with
30 expression quantitative trait loci (eQTLs)^{17;18}.

31 One possible explanation for these observations is that gene expression is not being measured in the appropriate
32 cell types and thus local eQTLs influencing traits cannot be detected¹⁶. An alternative explanation that has
33 been discussed in recent years is that effects of these variants are mediated not through local regulation of
34 gene expression, but through distal regulation^{18–20;15}.

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

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

47 Measuring gene expression in multiple tissues is critical to adequately assess the extent to which local gene
48 regulation varies across the tissues and whether such variability might account for previous failed attempts to
49 identify trait-relevant local eQTL. Such data sets are extremely difficult to obtain in human populations,
50 particularly in the large numbers of subjects required for adequate statistical power. Thus, to further
51 investigate the role of local and distal gene regulation on complex traits, we generated two complementary
52 data sets: A discovery data set in a large population of diversity outbred (DO) mice²¹, and an independent
53 validation data set derived by crossing inbred strains from the Collaborative Cross (CC) mice²² to form CC
54 F1 mice (CC-RIX). Both populations modeled diet-induced obesity and metabolic disease¹²

55 The DO population and CC recombinant inbred lines were derived from the same eight inbred founder mouse
56 strains, five classical lab strains, and three strains more recently derived from wild mice²¹. They represent

57 three subspecies of mouse *Mus musculus domesticus*, *Mus musculus musculus*, and *Mus musculus castaneus*,
58 and capture 90% of the known variation in laboratory mice²³. The DO mice are maintained with a breeding
59 scheme that ensures equal contributions from each founder across the genome thus rendering almost the
60 whole genome visible to genetic inquiry²¹. The CC mice were initially outcrossed to recombine the genomes
61 from all eight founders, and then inbred for at least 20 generations to generate multiple inbred lines. Because
62 these two populations have common ancestral haplotypes we could directly and unambiguously compare
63 the local genetic effects on gene expression at the whole-transcriptome level while varying the population
64 structure driving distal regulation.

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

74 Results

75 To comprehensively assess the genetic control of gene expression in metabolic disease in mice, we assayed
76 metabolic traits and multi-tissue gene expression in DO mice.

77 Genetic variation contributed to wide phenotypic variation

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

87 pre-diabetes and diabetes.

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

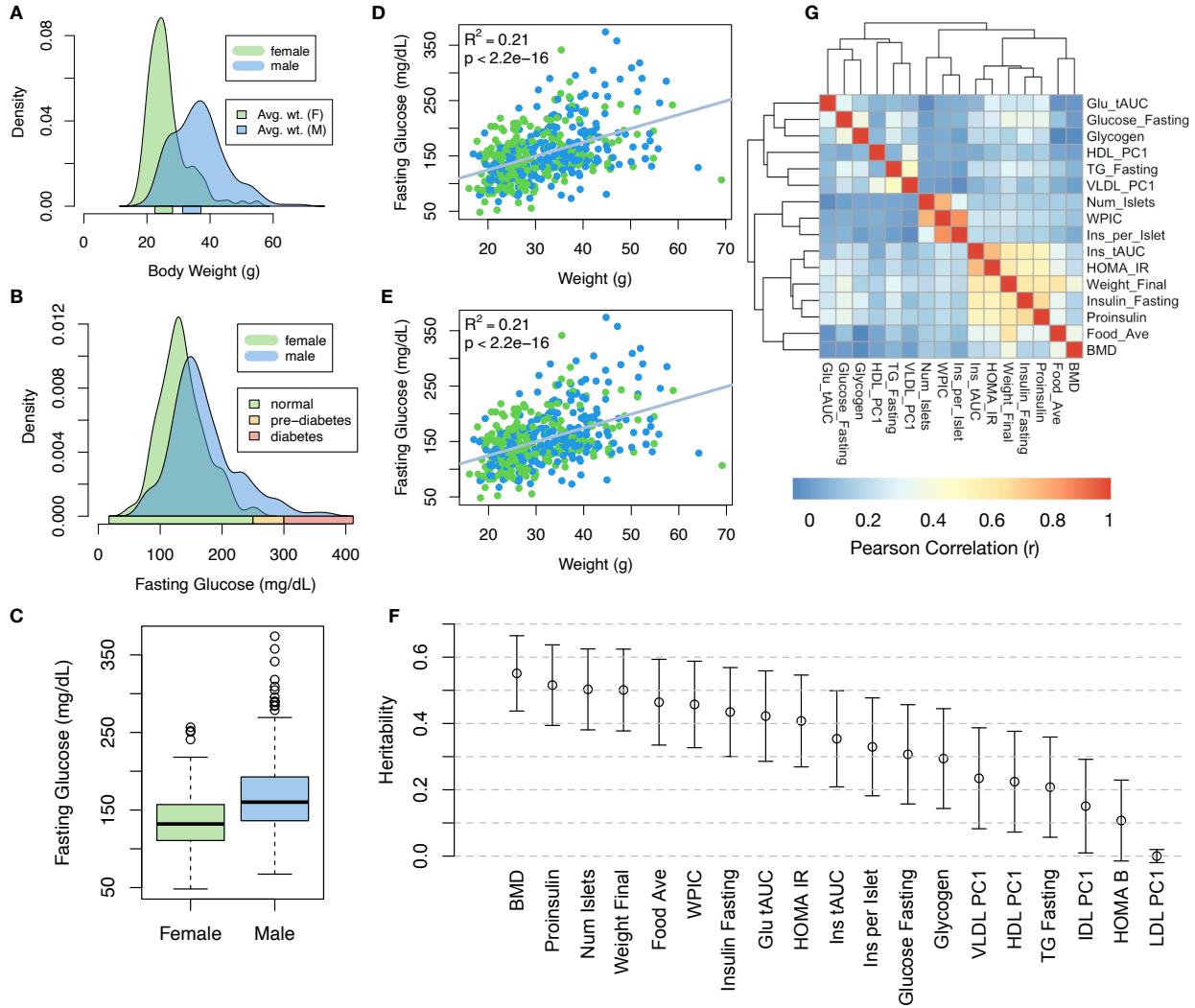


Figure 1: Clinical overview. **A.** Distributions of final body weight in the diversity outbred mice. Sex is indicated by color. The average B6 male and female adult weights at 24 weeks of age are indicated by blue and green bars on the x-axis. **B.** The distribution of final fasting glucose across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

92 The trait correlations (Fig. 1G) showed that most of the metabolic trait pairs were only modestly correlated

93 indicating complex relationships among the measured traits. This low level of redundancy suggests a broad
94 sampling of multiple heritable aspects of metabolic disease including overall body weight, glucose homeostasis,
95 pancreatic composition and liver function.

96 **Distal Heritability Correlated with Phenotype Relevance**

97 To comprehensively assess the genetic control of gene expression in metabolic disease we assayed adipose, islet,
98 liver, and skeletal muscle gene expression in the DO cohort. We performed eQTL analysis using R/qltl²⁵
99 (Methods) and identified both local and distal eQTLs for transcripts in each of the four tissues (Fig. S1).
100 Significant local eQTLs far outnumbered distal eQTLs (Fig. S1F) and tended to be shared across tissues
101 (Fig. S1G) whereas the few significant distal eQTLs we identified tended to be tissue-specific (Fig. S1H)
102 We calculated the heritability of each transcript in terms of local and distal genetic factors (Methods). Overall,
103 local and distal genetic factors contributed approximately equally to transcript abundance. In all tissues,
104 both local and distal factors explained between 8 and 18% of the variance in the median transcript (Fig 2A).
105 To assess the importance of genetic regulation transcript levels to organism-level traits, we compared the
106 local and distal heritabilities of transcripts to their trait relevance, defined as the maximum correlation
107 of a transcript across all traits. The local heritability of transcripts was negatively correlated with their
108 trait relevance (Fig. 2B), suggesting that the more local genotype influenced transcript abundance, the
109 less effect this variation had on the measured traits. Conversely, the distal heritability of transcripts was
110 positively correlated with trait relevance (Fig. 2C). That is, transcripts that were more highly correlated
111 with the measured traits tended to be distally, rather than locally, heritable. Importantly, this pattern was
112 consistent across all tissues, strongly suggesting that this is a generic finding. This finding is consistent with
113 previous observations that low-heritability transcripts explain more expression-mediated disease heritability
114 than high-heritability transcripts¹⁹. However, the positive relationship between trait correlation and distal
115 heritability demonstrated further that there are diffuse genetic effects throughout the genome converging on
116 trait-related transcripts.

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

119 The above univariate analyses establish the importance of distal heritability for trait-relevant transcripts.
120 However, the number of transcripts dramatically exceeds the number of phenotypes. Thus, we expect the
121 heritable, trait-relevant transcripts to be highly correlated and organized according to coherent, emergent
122 biological processes representing the mediating endophenotypes driving clinical trait variation. To identify

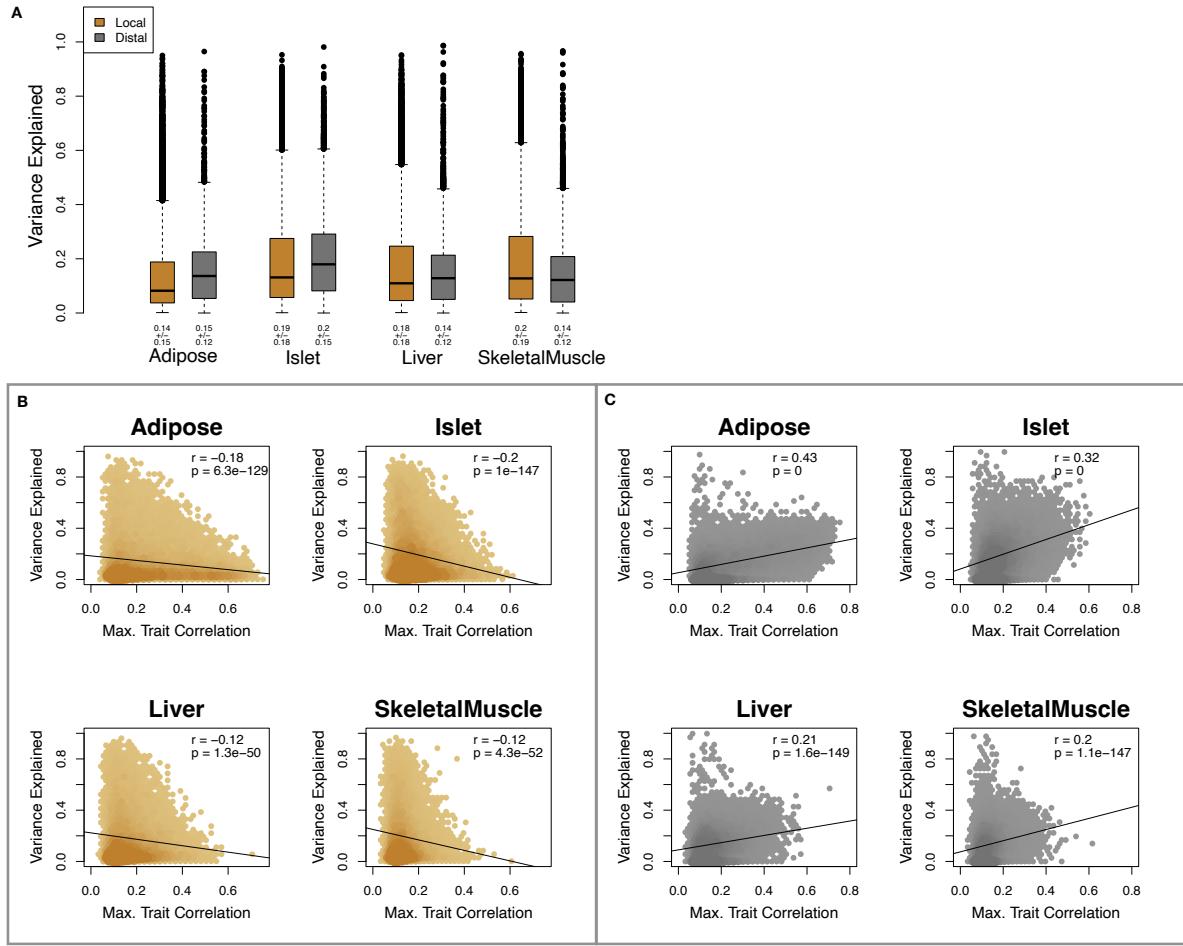


Figure 2: Transcript heritability and trait relevance. **A.** Distributions of distal and local heritability of transcripts across the four tissues. Overall local and distal factors contribute equally to transcript heritability. The relationship between **(B.)** local and **(C.)** distal heritability 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.

these endophenotypes in a theoretically principled way, we developed a novel dimension-reduction technique, HDMA, that uses the theory of causal graphical models to identify a transcriptomic signature that is simultaneously 1) highly heritable, 2) strongly correlated to the measured phenotypes, and 3) conforms to the causal mediation hypothesis (Fig. 3). HDMA projects the high-dimensional scores—a composite genome score (G_C), a composite transcriptome score (T_C), and a composite phenotype score (P_C)—and uses the univariate theory of mediation to constrain these projections to satisfy the hypotheses of perfect mediation, namely that upon controlling for the transcriptomic score, the genome score is uncorrelated to the phenotype score. Formally, perfect mediation implies a constraint on the correlation coefficients among scores as

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

which is equivalent to the partial correlation of G_C and P_C after controlling for T_C being zero. The value $\text{Corr}(G_C, T_C)\text{Corr}(T_C, P_C)$ is called the path coefficient of the mediation model. The projections of the high-dimensional data matrices in HDMA are designed to satisfy this constraint, and thus conform to the perfect mediation hypothesis, as closely as possible. We stress, however, that validating any causal assertion requires direct experimentation and, thus, that the output of HDMA are scores that are consistent with causal mediation. Thus, HDMA is a strategy for causal hypothesis generation, where the causal mediator is a complex endophenotype learned from a high-dimensional readout.

Operationally, HDMA is closely related to generalized canonical correlation analysis (CCA), for which provably convergent algorithms have recently been developed²⁶. A complete mathematical derivation and implementation details for HDMA are available in **Supp. Methods XXX**.

We used HDMA to identify the major axis of variation in the transcriptome was consistent with mediating the effects of the genome on metabolic traits (Fig 3). Fig. 3A shows the partial correlations (ρ) between the pairs of these composite vectors. The partial correlation between G_C and T_C was 0.42, and the partial correlation between T_C and P_C was 0.78. However, when the transcriptome was taken into account, the partial correlation between G_C and P_C was effectively zero (0.039). P_C captured 30% of the overall trait variance, and its estimated heritability was 0.71 ± 0.084 , which was higher than any of the measured traits (Fig. 1F). Thus, HDMA identified a maximally heritable metabolic composite trait and a highly heritable component of the transcriptome that are correlated as expected in the perfectly mediated model.

As discussed in Supp. Methods XXX, HDMA is related to a generalized form of CCA. Standard CCA is prone to over-fitting because in any two large matrices it can be trivial to identify highly correlated composite vectors [REF]. To assess whether our implementation of HDMA was similarly prone to over-fitting in a high-dimensional space, we performed permutation testing. We permuted the individual labels on the transcriptome matrix 1000 times and recalculated the path coefficient, which is the partial correlation of G_C and T_C multiplied by the partial correlation of T_C and P_C . This represents the strength of the path from G_C to P_C that is putatively mediated through T_C . The null distribution of the path coefficient is shown in Fig. 3B, and the observed path coefficient from the original data is indicated by a red line. The observed path coefficient was well outside the null distribution generated by permutations ($p < 10^{-16}$). Fig. 3C illustrates this observation in more detail. Although we identified high correlations between G_C and T_C , and modest correlations between T_C and P_C in the null data (Fig 3C), these two values could not be

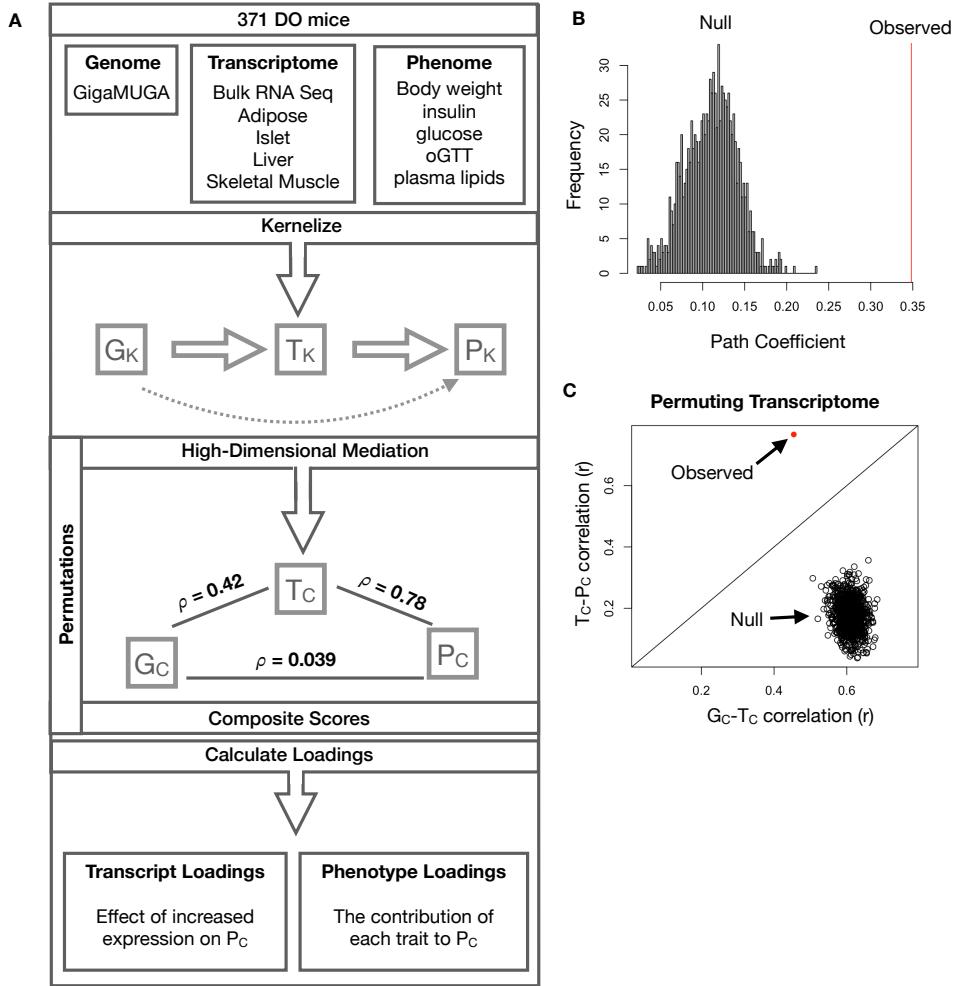


Figure 3: High-dimensional mediation. **A.** Workflow indicating major steps of high-dimensional mediation. The genotype, transcriptome, and phenotype matrices were independently normalized and converted to kernel matrices representing the pairwise relationships between individuals for each data modality (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 ρ between these vectors indicated perfect mediation. Transcript and trait loadings were calculated as described in the methods. **B.** The null distribution of the path coefficient derived from 10,000 permutations compared to the observed path coefficient (red line). **C.** The null distribution of the G_C-T_C correlation vs. the T_C-P_C correlation compared with the observed value (red dot).

160 maximized simultaneously in the null data. In contrast, the red dot shows that in the real data both the
 161 G_C-T_C correlation and the T_C-P_C correlation could be maximized simultaneously suggesting that the path
 162 from genotype to phenotype through transcriptome is highly non-trivial and identifiable in this case. These
 163 results suggest that these composite vectors represent genetically determined variation in phenotype that is
 164 mediated through genetically determined variation in transcription.

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

167 Each composite score is simply a weighted combination of the measured variables and the magnitude and
168 sign of the weights, called loadings, correspond the relative importance and directionality of each variable in
169 the composite score. The loadings of each measured trait onto P_C indicate how much each contributed to
170 the composite phenotype. Final body weight contributed the most (Fig. 4), followed by homeostatic insulin
171 resistance (HOMA_IR) and fasting plasma insulin levels (Insulin_Fasting). We can thus interpret P_C as
172 an index of metabolic disease (Fig. 4B). Individuals with high values of P_C have a higher metabolic index
173 and greater metabolic disease, including higher body weight and higher insulin resistance. We refer to P_C
174 as the metabolic index going forward. Traits contributing the least to the metabolic index were measures
175 of cholesterol and pancreas composition. Thus, when we interpret the transcriptomic signature identified
176 by HDMA, we are explaining primarily the putative transcriptional mediation of body weight and insulin
177 resistance, as opposed to cholesterol measurements.

178 **High-loading transcripts have low local heritability, high distal heritability, and were linked
179 mechanistically to obesity**

180 We interpreted large loadings onto transcripts as indicating strong mediation of the effect of genetics on
181 metabolic index. Large positive loadings indicate that higher expression was associated with a higher
182 metabolic index (i.e. higher risk of obesity and metabolic disease on the high-fat diet) (Fig. 4C). Conversely,
183 large negative loadings indicate that high expression of these transcripts was associated with a lower metabolic
184 index (i.e. lower risk of obesity and metabolic disease on the high-fat diet) (Fig. 4C). We used gene set
185 enrichment analysis (GSEA)^{27;28} to look for biological processes and pathways that were enriched at the top
186 and bottom of this list (Methods).

187 In adipose tissue, both GO processes and KEGG pathway enrichments pointed to an axis of inflammation and
188 metabolism (Figs. S2 and S3). GO terms and KEGG pathways associated with inflammation, particularly
189 macrophage infiltration, were positively associated with metabolic index, indicating that increased expression
190 in inflammatory pathways was associated with a higher metabolic index. It is well established that adipose
191 tissue in obese individuals is inflamed [cite] and infiltrated by macrophages [cite], and the results here suggest
192 that this may be a dominant heritable component of metabolic disease.

193 The strongest negative enrichments in adipose tissue were related to mitochondrial activity in general, and
194 thermogenesis in particular (Figs. S2 and S2). Genes in the KEGG oxidative phosphorylation pathway in
195 mice were almost universally negatively loaded in adipose tissue, suggesting that increased expression of these

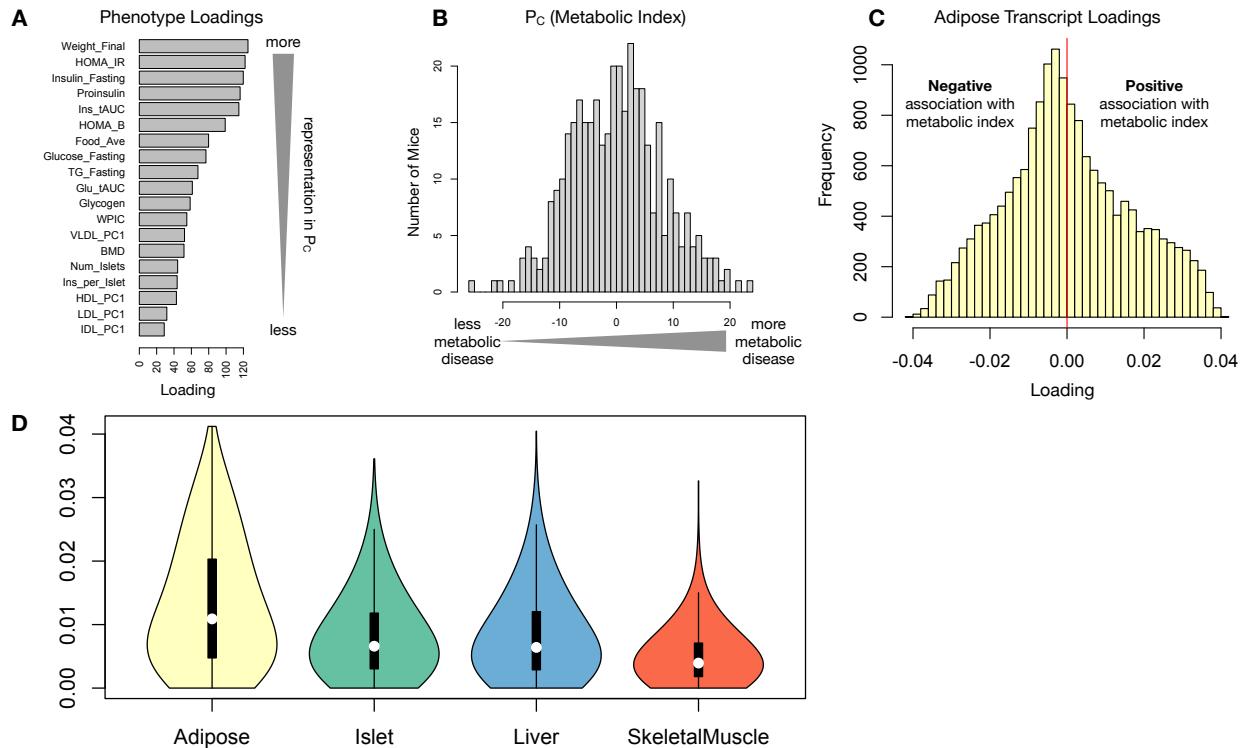


Figure 4: Interpretation of loadings. **A.** Loadings across traits. Body weight and insulin resistance contributed the most to the composite trait. **B.** Phenotype scores across individuals. Individuals with large positive phenotype scores had higher body weight and insulin resistance than average.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

196 genes was associated with reduced metabolic index (Supp. Fig. S4). Consistent with this observations, it
 197 has been shown previously that mouse strains with greater thermogenic potential are also less susceptible to
 198 obesity on a high-fat diet²⁹.

199 Transcripts associated with the citric acid (TCA) cycle as well as the catabolism of the branched-chain amino
 200 acids (BCAA) (valine, leucine, and isoleucine) were strongly enriched with negative loadings in adipose
 201 tissue (Supp. Figs. S2, S5 and S6). Expression of genes in both pathways (for which there is some overlap)
 202 has been previously associated with insulin sensitivity^{12;30;31}, suggesting that heritable variation in regulation
 203 of these pathways may influence risk of insulin resistance.

204 Looking a the 10 most positively and negatively loaded transcripts from each tissue, it is apparent that
 205 transcripts in the adipose tissue had the largest loadings, both positive and negative, of all tissues (Fig. 5A

206 bar plot) This suggests that much of the effect of genetics on body weight and insulin resistance is mediated
207 through gene expression in adipose tissue. The strongest loadings in liver and pancreas were comparable,
208 and those in skeletal muscle were the weakest (Fig. 5A), suggesting that less of the genetic effects were
209 mediated through transcription in skeletal muscle. Heritability analysis showed that transcripts with the
210 largest loadings had higher distal heritability than local heritability (Fig. 5A heat map and box plot). This
211 pattern contrasts with transcripts nominated by TWAS (Fig. 5B), which tended to have lower loadings,
212 higher local heritability and lower distal heritability. Transcripts with the highest local heritability in each
213 tissue (Fig. 5C) had the lowest loadings, consistent with our findings above (Fig. 2B).

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

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

221 Clustering of transcripts with top loadings in each tissue showed tissue-specific functional modules associated
222 with obesity and insulin resistance (Fig. 6A) (Methods). The clustering highlights the importance of immune
223 activation particularly in adipose tissue. The “mitosis” cluster had large positive loadings in three of the
224 four tissues potentially suggesting system-wide hypertrophy. Otherwise, all clusters were strongly loaded in
225 only one or two tissues. For example, the lipid metabolism cluster was loaded most heavily in liver. The
226 positive loadings suggest that high expression of these genes particularly in the liver was associated with
227 increased metabolic disease. This cluster included the gene *Pparg*, whose primary role is in the adipose tissue
228 where it is considered a master regulator of adipogenesis³². Agonists of *Pparg*, such as thiazolidinediones, are
229 FDA-approved to treat type II diabetes, and reduce inflammation and adipose hypertrophy³². Consistent
230 with this role, the loading for *Pparg* in adipose tissue was negative, suggesting that higher expression was
231 associated with leaner mice (Fig. 6B). In contrast, *Pparg* had a large positive loading in liver, where it is
232 known to play a role in the development of hepatic steatosis, or fatty liver. Mice that lack *Pparg* specifically
233 in the liver, are protected from developing steatosis and show reduced expression of lipogenic genes^{33;34}.
234 Overexpression of *Pparg* in the livers of mice with a *Ppara* knockout, causes upregulation of genes involved in
235 adipogenesis³⁵. In the livers of both mice and humans high *Pparg* expression is associated with hepatocytes
236 that accumulate large lipid droplets and have gene expression profiles similar to that of adipocytes^{36;37}.

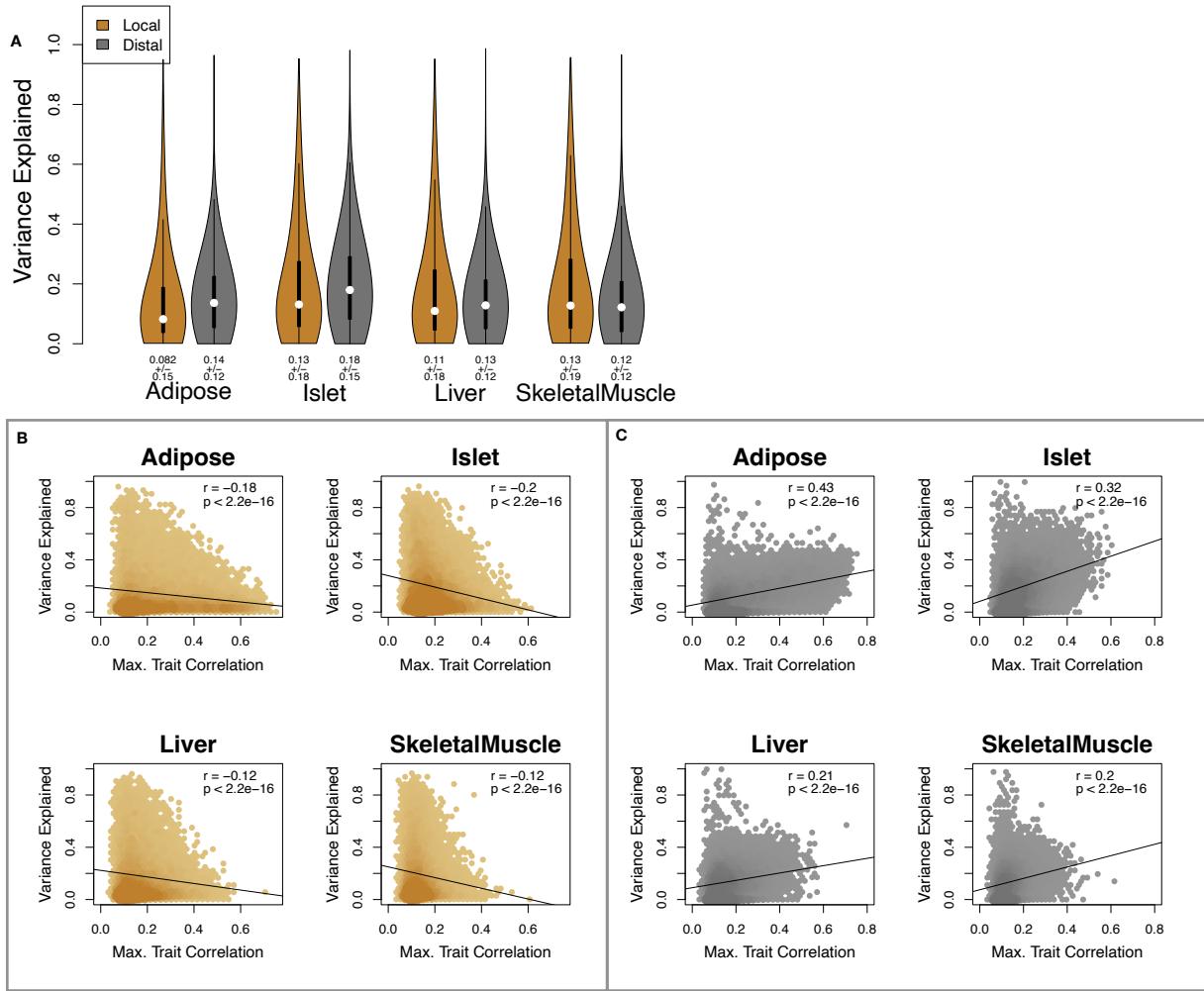


Figure 5: Transcripts with high loadings have high distal heritability and literature support. Each panel has a bar plot showing the loadings of transcripts selected by different criteria. Bar color indicates the tissue of origin. The heat map shows the local (L - left) and distal (D - right) heritability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

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

²⁴⁴ Gene lists for all clusters are available in Supplemental File XXX.

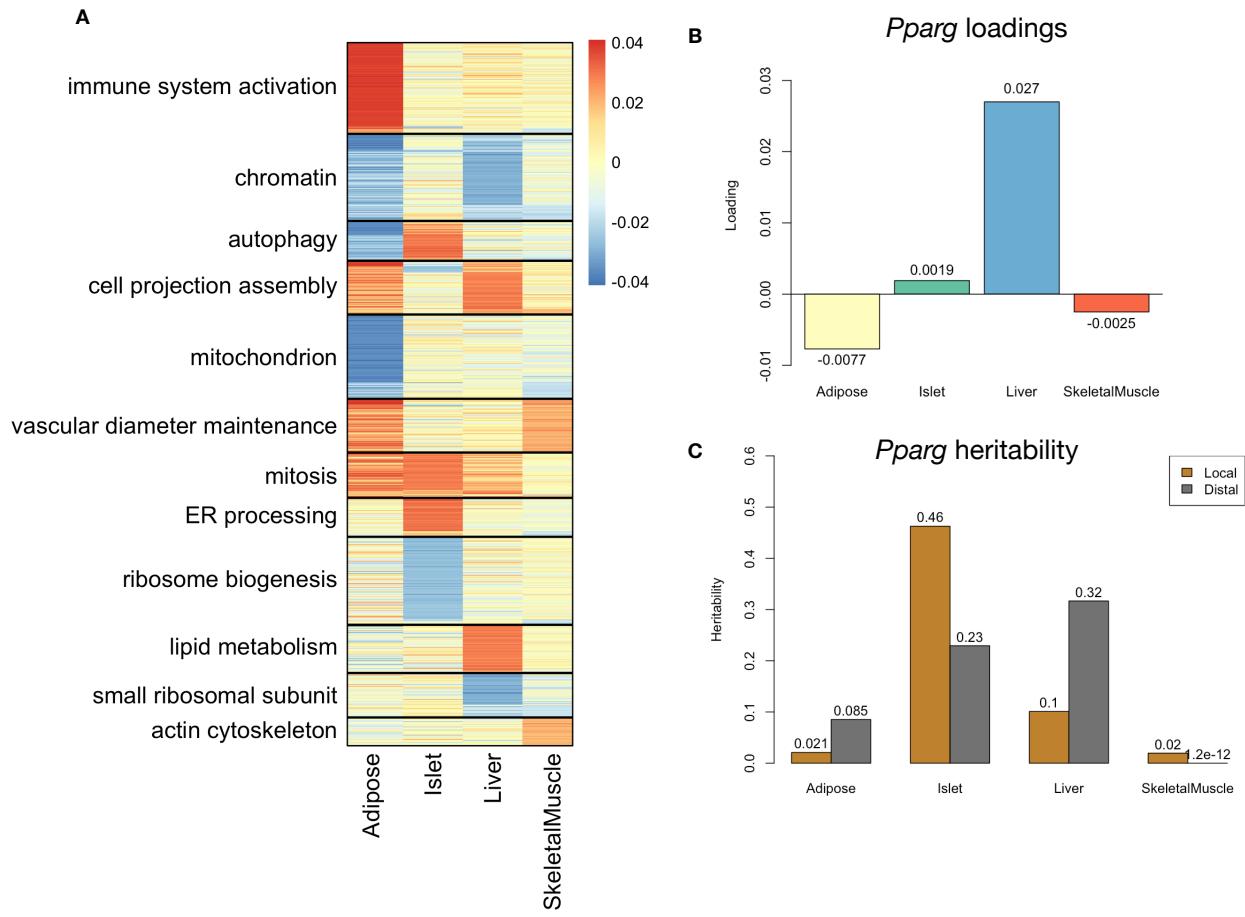


Figure 6: Tissue-specific transcriptional programs were associated with obesity and insulin resistance. **A** Heat map showing the loadings of all transcripts with loadings greater than 2.5 standard deviations from the mean in any tissue. The heat map was clustered using k medoid clustering. Functional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

²⁴⁵ Gene expression, but not local eQTLs, predicted body weight in an independent population

²⁴⁶ To test whether the transcript loadings identified in the DO could be translated to another population, we
²⁴⁷ tested whether they could predict metabolic phenotype in an independent population of CC-RIX mice, which
²⁴⁸ were F1 mice derived from multiple pairings of Collaborative Cross (CC) [cite] strains (Fig. 7) (Methods).
²⁴⁹ We tested two questions. First, we asked whether the loadings identified in the DO mice were relevant to
²⁵⁰ the relationship between the transcriptome and the phenotype in the CC-RIX. We predicted body weight (a
²⁵¹ surrogate for metabolic index) in each CC-RIX individual using measured gene expression in each tissue and
²⁵² the transcript loadings identified in the DO (Methods). The predicted body weight and actual body weight
²⁵³ 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.

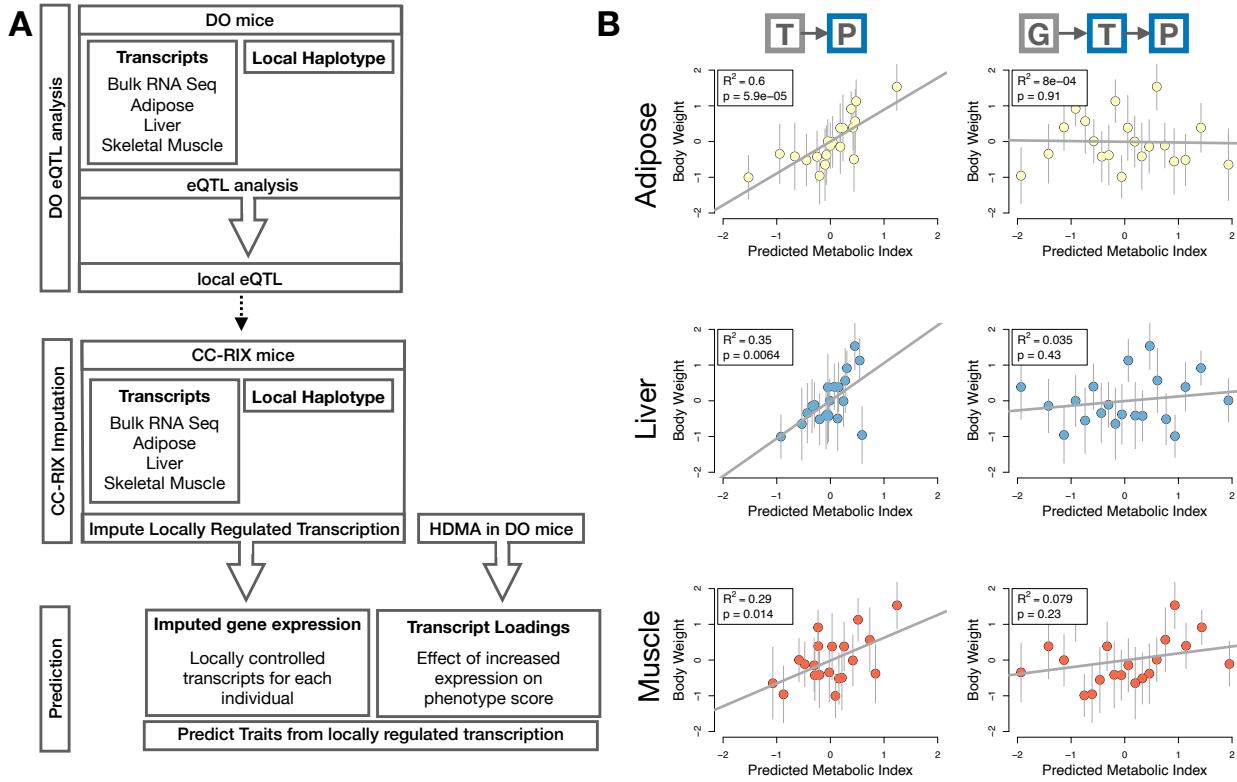


Figure 7: Transcription, but not local genotype, predicts phenotype in the CC-RIX. **A.** Workflow showing procedure for translating HDMA results to an independent population of mice. **B.** Relationships between the predicted metabolic index and measured body weight. The left column shows the predictions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

The second question related to the source of the relevant variation in gene expression. If local regulation was 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. 5). 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

266 comparatively high distal and low local heritability.

267 **Distally heritable transcriptomic signatures reflected variation in composition of adipose tissue
268 and islets**

269 The interpretation of global genetic influences on gene expression and phenotype is potentially more challenging
270 than the interpretation and translation of local genetic influences, as genetic effects cannot be localized to
271 individual gene variants or transcripts. However, there are global patterns across the loadings that can
272 inform mechanism. For example, heritable variation in cell type composition can be inferred from transcript
273 loadings. We observed above that immune activation in the adipose tissues was a highly enriched process
274 correlating with obesity in the DO population. For example, in humans, it has been extensively observed that
275 macrophage infiltration in adipose tissue is a marker of obesity and metabolic disease [REF]. To determine
276 whether the immune activation reflected a heritable change in cell composition in adipose tissue in DO mice,
277 we compared loadings of cell-type specific genes in adipose tissue (Methods). Consistent with human results,
278 the mean loading of macrophage-specific genes was significantly greater than 0 (Fig. 8A), indicating that
279 obese mice were genetically predisposed to have high levels of macrophage infiltration in adipose tissue in
280 response to the high-fat, high-sugar diet. Loading for marker genes for other cell types were not statistically
281 different from zero, indicating that changes in the abundance of those cell types is not a mediator of metabolic
282 index.

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

290 Notably, the loadings for pancreatic beta cell-type specific loadings was not significantly different from zero.
291 We stress that this is not necessarily reflective of the function of the beta cells in the obese mice, but rather
292 suggests that any variation in the number of beta cells in these mice was unrelated to obesity and insulin
293 resistance, the major contributors to metabolic index. This is further consistent with the islet composition
294 traits having small loadings in the phenome score (Fig. 4).

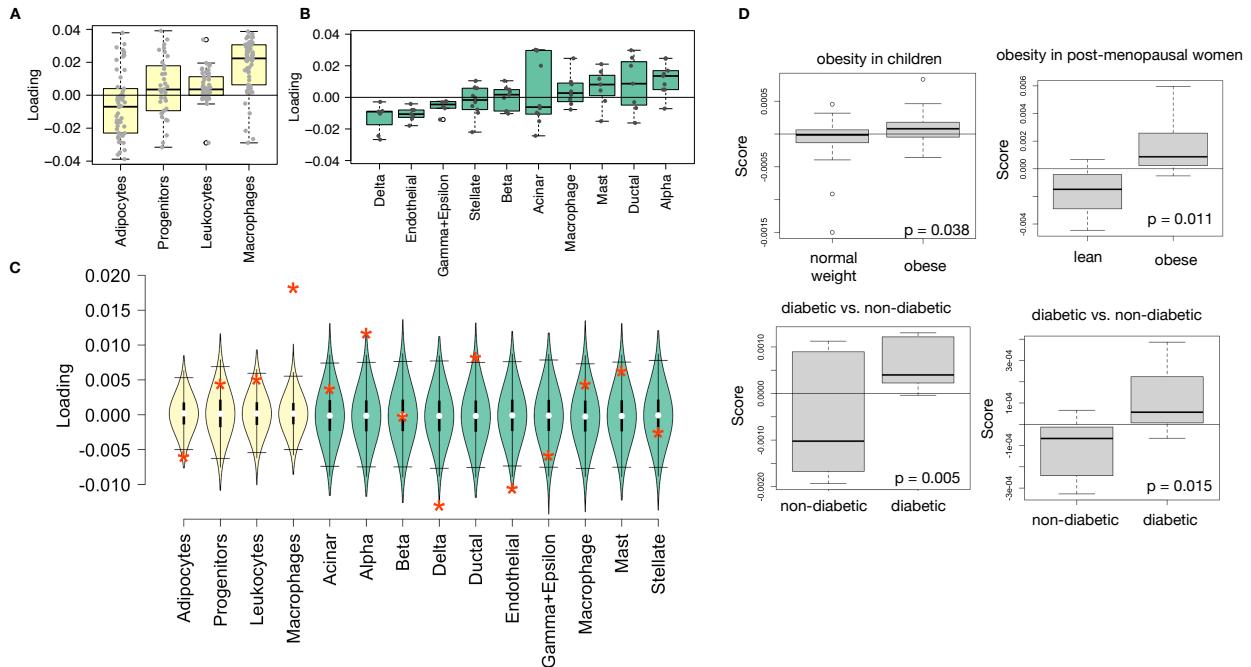


Figure 8: HDMA results translate to humans. **A.** Distribution of loadings for cell-type-specific transcripts in adipose tissue. **B.** Distribution of loadings for cell-type-specific transcripts in pancreatic islets (green). **C.** Null distributions for the mean loading of randomly selected transcripts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

295 Heritable transcriptomic signatures translated to human disease

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

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

307 **Existing therapies are predicted to target mediator gene signatures**

308 Another potential application of the transcript loading landscape is in ranking potential drug candidates
309 for the treatment of metabolic disease. Although high-loading transcripts may be good candidates for
310 understanding specific biology related to obesity, the transcriptome overall is highly interconnected and
311 redundant, and focusing on individual transcripts for treatment may be less effective than using broader
312 transcriptomic signatures that capture the emergent biology [cite or remove]. The ConnectivityMap (CMAP)
313 database³⁸ developed by the Broad Institute allows querying thousands of compounds that reverse or enhance
314 the extreme ends of transcriptomic signatures in multiple different cell types. By identifying drugs that
315 reverse pathogenic transcriptomic signatures, we can potentially identify compounds that have favorable
316 effects on gene expression.

317 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
318 get more tissue-specific results, we also looked at top results in cell types that most closely resembled our
319 tissues. We looked at results in adipocytes (ASC) as well as pancreatic tumor cells (YAPC) regardless of *p*
320 value (Supplemental Figure XXX and XXX).

321 Looking across all cell types, the notable top hits from the adipose tissue loadings included mTOR inhibitors
322 and glucocorticoid agonists (Supplemental Figure XXX). It is thought that metformin, which is commonly
323 used to improve glycemic control, acts, at least in part, by inhibiting mTOR signaling^{39;40}. However,
324 long-term use of other mTOR inhibitors, such as rapamycin, are known to cause insulin resistance and
325 β -cell toxicity^{40–42}. Glucocorticoids are used to reduce inflammation, which was a prominent signature in
326 the adipose tissues, but these drugs also promote hyperglycemia and diabetes^{43;44}. Acute treatment with
327 glucocorticoids has further been shown to reduce thermogenesis in rodent adipocytes^{45–47}, but increase
328 thermogenesis in human adipocytes^{48;49}. Thus, the pathways identified by CMAP across all cell types were
329 highly related to the transcript loading profiles, but the relationship was not a simple reversal.

330 The top hit for the adipose composite transcript in CMAP adipocytes was a PARP inhibitor (Supplemental
331 Figure XXXB). PARPs play a role in lipid metabolism and are involved in the development of obesity and
332 diabetes⁵⁰. PARP1 inhibition increases mitochondrial biogenesis⁵¹. Inhibition of PARP1 activity can further
333 prevent necrosis in favor of the less inflammatory apoptosis⁵², thereby potentially reducing inflammation in
334 stressed adipocytes. Other notable hits among the top 20 were BTK inhibitors, which have been observed
335 to suppress inflammation and improve insulin resistance⁵³ as well as to reduce insulin antibodies in type I
336 diabetes⁵⁴. IKK inhibitors have been shown to improve glucose control in type II diabetes^{55;56}.

338 Among the top most significant hits for the transcript loadings from pancreatic islets (Fig. XXX), was
339 suppression of T cell receptor signaling, which is known to be involved in Type 1 diabetes⁵⁷, as well as
340 TNFR1, which has been associated with mortality in diabetes patients⁵⁸. Suppression of NOD1/2 signaling
341 was also among the top hits. NOD1 and 2 sense ER stress^{59;60}, which is associated with β -cell death in type
342 1 and type 2 diabetes⁶¹. This cell death process is dependent on NOD1/2 signaling⁵⁹, although the specifics
343 have not yet been worked out.

344 We also looked specifically at hits in pancreatic tumor cells (YAPC) regardless of significance level to get a
345 transcriptional response more specific to the pancreas. Hits in this list included widely used diabetes drugs,
346 such as sulfonylureas, PPAR receptor agonists, and insulin sensitizers. Rosiglitazone is a PPAR- γ agonist
347 and was one of the most prescribed drugs for type 2 diabetes before its use was reduced due to cardiac
348 side-effects⁶². Sulfonylureas are another commonly prescribed drug class for type 2 diabetes, but also have
349 notable side effects including hypoglycemia and accelerated β -cell death⁶³.

350 Discussion

351 Here we used a novel high-dimensional mediation analysis (HDMA) to investigate the relative contributions of
352 local and distal gene regulation to heritable trait variation in genetically diverse mouse models of diet-induced
353 obesity and metabolic disease. We identified tissue-specific composite transcripts that are predicted to
354 mediate the effect of genetic background on metabolic traits. Transcripts contributing most strongly to these
355 composite transcripts were distally, but not locally heritable, and composite transcripts were able to predict
356 obesity in a large, independent mouse population with divergent population structure, whereas models using
357 local eQTL only could not. Moreover, the composite transcript from mouse adipose tissue translated to
358 predict obesity and diabetes status in human cohorts with measured adipose gene expression. Taken together,
359 these results support the hypothesis that gene expression mediating the effect of genetic background on
360 metabolic phenotypes is primarily distally regulated, and that the heritable endophenotypes defined by gene
361 expression signatures translate from mice to humans. We speculate that the central importance of distal
362 heritability found in this study is likely to be a generic finding for complex common diseases and could have
363 significant consequences for the development of therapies for these diseases.

364 Genetics is indispensable for the dissection of disease mechanisms because it is one of the only data modalities
365 that supports causal inferences about molecules and disease outcomes [REF]. It has frequently been assumed
366 that gene regulation in *cis* is the primary driver of genetically associated trait variation, but attempts to use
367 local gene regulation to explain phenotypic variation have had limited success^{16;17}. In recent years, evidence
368 has mounted that distal gene regulation may be an important mediator of trait heritability^{19;18;64}. It has

369 been observed that transcripts with high local heritability explain less expression-mediated disease heritability
370 than those with low local heritability¹⁹. Consistent with this observation, genes located near GWAS hits
371 tend to be complexly regulated¹⁸. They also tend to be enriched with functional annotations, in contrast
372 to genes with simple local regulation, which tend to be depleted of functional annotations suggesting they
373 are less likely to be directly involved in disease traits¹⁸. These observations are consistent with principles
374 of robustness in complex systems in which simple regulation of important elements leads to fragility of the
375 system^{65–67}. Our results are consistent, instead, with a more complex picture where genes whose expression
376 can drive trait variation are buffered from local genetic variation but are extensively influenced indirectly by
377 genetic variation in the regulatory networks converging on those genes.

378 Recently, the omnigenic model of complex traits has been proposed, which posits that complex traits are
379 massively polygenic and that their heritability is spread out across the genome⁶⁸. In the omnigenic model,
380 genes are classified either as “core genes,” which directly impinge on the trait, or “peripheral genes,” which
381 are not directly trait-related, but influence core genes through the complex gene regulatory network. HDMA
382 explicitly models a central proposal of the omnigenic model which posits that once the expression of the
383 core genes (i.e. trait-mediating genes) is accounted for, there should be no residual correlation between the
384 genome and the phenotype. Here, when the composite transcript was taken into account there was no residual
385 correlation between the composite genome and composite phenotype (Fig. 3A).

386 Thus, the transcript loadings can be interpreted as indicating higher “core-ness” of a transcript. Unlike in the
387 omnigenic model, we did not observe a clear demarcation between the core and peripheral genes in loading
388 magnitude, but we do not necessarily expect a clear separation given the complexity of gene regulation and
389 the genotype-phenotype map⁶⁹.

390 An extension of the omnigenic model proposed that most heritability of complex traits is driven by weak
391 distal eQTLs that are potentially below the detection threshold in studies with feasible sample sizes⁶⁴. This
392 is consistent with what we observed here. The transcripts with the largest loadings were strongly distally
393 regulated and only weakly locally regulated, suggesting that distal gene regulation plays a primary role in
394 driving heritable trait variation. We saw further that the patterns of distal heritability were not localized to
395 detectable distal eQTL, but rather were complex and spread across the genome, even for transcripts whose
396 expression was strongly regulated by distal factors. For example, *Nucb2*, had a high loading in islets and was
397 also strongly distally regulated (66% distal heritability) (Fig. 5). This gene is expressed in pancreatic β cells
398 and is involved in insulin and glucagon release^{70–72}. Although its transcription was highly heritable in islets,
399 that regulation was distributed across the genome, with no clear distal eQTL (Supp. Fig. 6). Thus, although
400 distal regulation of some genes may be strong, this regulation is likely to be highly complex and not easily

401 localized.

402 We stress that HDMA is a method for causal hypothesis generation. As with any causal inference approach,
403 the output of HDMA can only be said to be consistent with causal mediation but does not prove it. Proving
404 causality requires experimentation with direct control over the mediating variable [REF]. The issue of
405 experimentation, however, is subtle. The dimension-reduction in HDMA is distinguished by the fact that
406 the putative causal intermediates can be emergent states defined by the expression of thousands of genes.
407 This is a strength, because the mediating variable can be a higher-order process such as “macrophage
408 activation and infiltration”, but, in contrast to univariate hypotheses at the level of individual transcripts, the
409 relevant validation experiment may be technologically infeasible, unknowable *a priori*, or both. Nevertheless,
410 downstream analyses of the composite transcripts strongly supports a causal interpretation. Indeed, the
411 composite transcripts identified by HDMA are richly interpretable in both tissue- and gene-specific manners.
412 The transcripts with the strongest loadings were enriched in biological functions previously known to be
413 involved in the pathogenesis of metabolic disease, such as inflammation in adipose tissue. That these processes
414 were identified in this analysis suggests additionally that they have a heritable component, and that some
415 individuals are genetically susceptible to greater adipose inflammation on a high-fat, high-sugar diet.

416 Individual high-loading transcripts also demonstrated biologically interpretable, tissue-specific patterns. We
417 highlighted *Pparg*, which is known to be protective in adipose tissue³² where it was negatively loaded, and
418 harmful in the liver^{33–37}, where it was positively loaded. Such granular patterns may be useful in generating
419 hypotheses for further testing, and prioritizing genes as therapeutic targets. The tissue-specific nature of
420 the loadings also may provide clues to tissue-specific effects, or side effects, of targeting particular genes
421 system-wide.

422 In addition to identifying individual transcripts of interest, the composite transcripts can be used as weighted
423 vectors in multiple types of analysis, such as drug prioritization using gene set enrichment analysis (GSEA)
424 and the CMAP database. In particular, the CMAP analysis identified drugs which have been demonstrated
425 to reverse insulin resistance and other aspects of metabolic disease. This finding supports the causal role of
426 these full gene signatures in pathogenesis of metabolic disease and thus their utility in prioritizing drugs and
427 gene targets as therapeutics.

428 Another useful application of the composite transcripts is to pair them with cell-type specific genes to generate
429 causal hypotheses about changes in cell composition in individual tissues. Combining the multi-tissue,
430 transcriptome-wide weighted vectors with public databases and data sets thus provides a path for generating a
431 wide range of testable hypotheses. Moreover, each data set presented here was derived from human tissues or

432 cell lines, thus demonstrating the translatability of these results. That the mouse-derived adipose composite
433 transcript was able to classify human adipose gene expression in terms of obesity and diabetes status further
434 supports the direct translatablility of these findings, the utility of HDMA, and the continued importance of
435 mouse models of human disease in which it is possible to obtain complete transcriptomes in mutliple tissues
436 across large numbers of individuals.

437 Altogether, our results have shown that both tissue specificity and distal gene regulation are critically
438 important to understanding the genetic architecture of complex traits. We identified important genes and
439 gene signatures that were heritable, plausibly causal of disease, and translatable to other mouse populations
440 and to humans. Finally, we have shown that by directly acknowledging the complexity of both gene regulation
441 and the genotype-to-phenotype map, we can gain a new perspective on disease pathogenesis and develop
442 actionable hypotheses about pathogenic mechanisms and potential treatments.

443 **Data Availability**

444 Here we tell people where to find the data

445 **Acknowledgements**

446 Here we thank people

447 **Supplemental Figures**

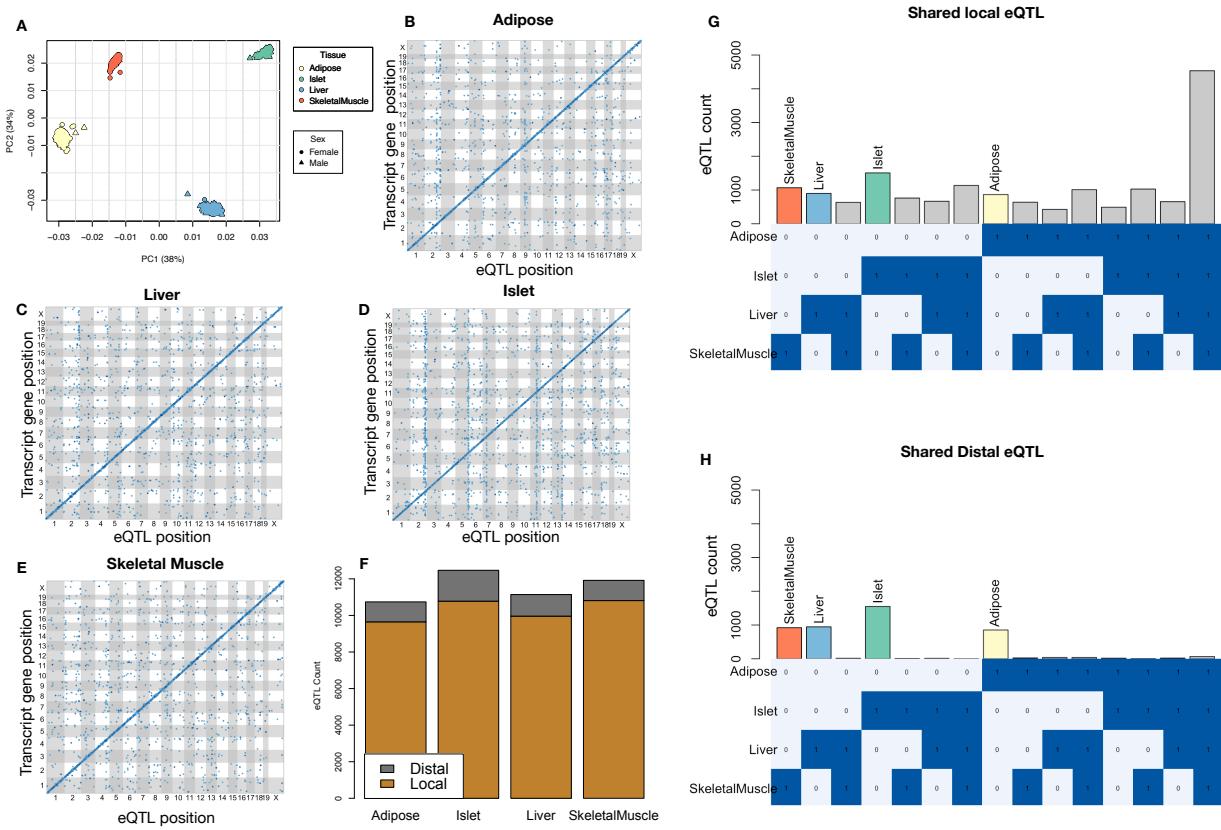


Figure S1: Overview of eQTL analysis in DO mice. **A.** RNA seq samples from the four different tissues clustered by tissue. **B.-E.** eQTL maps are shown for each tissue. The *x*-axis shows the position of the mapped eQTL, and the *y*-axis shows the physical position of the gene encoding each mapped 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

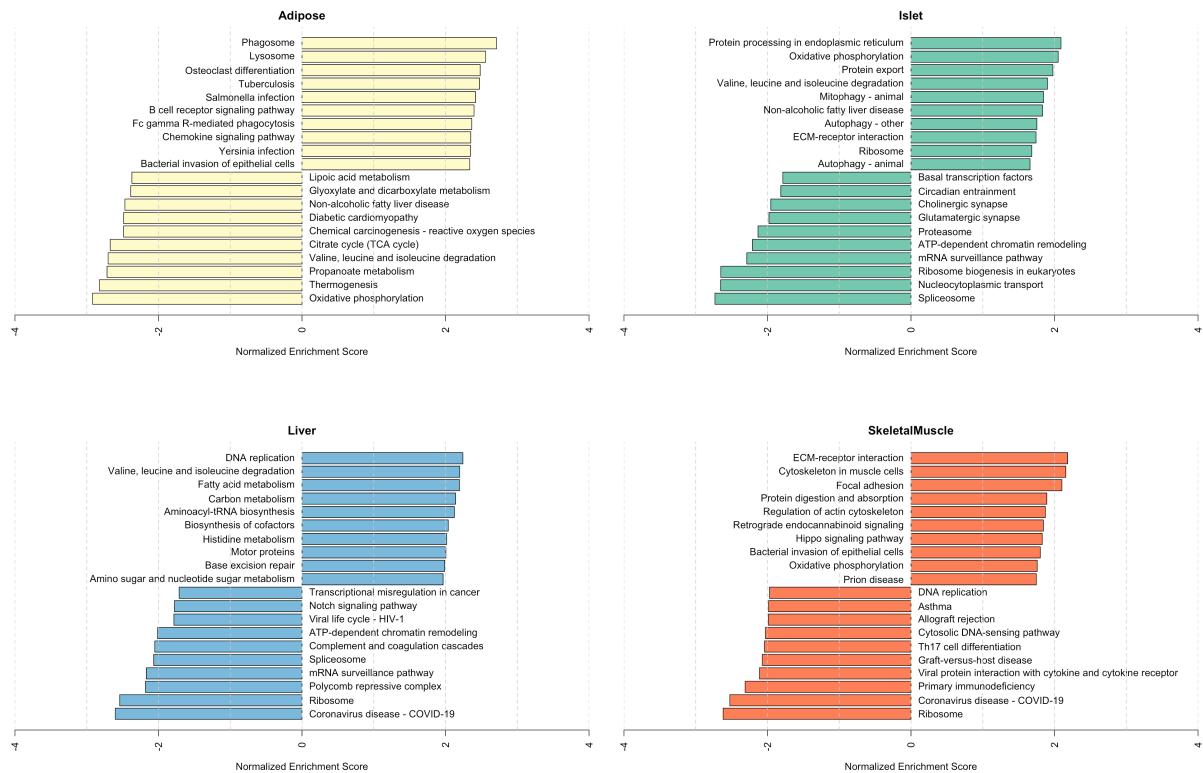


Figure S2: Bar plots showing normalized enrichment scores (NES) for KEGG pathways as determined by fast gene score enrichment analysis (fgsea). Only the top 10 positive and top 10 negative scores are shown. Colors indicate tissue. The name beside each bar shows the name of each enriched KEGG pathway.

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Top GO term enrichments by GSEA

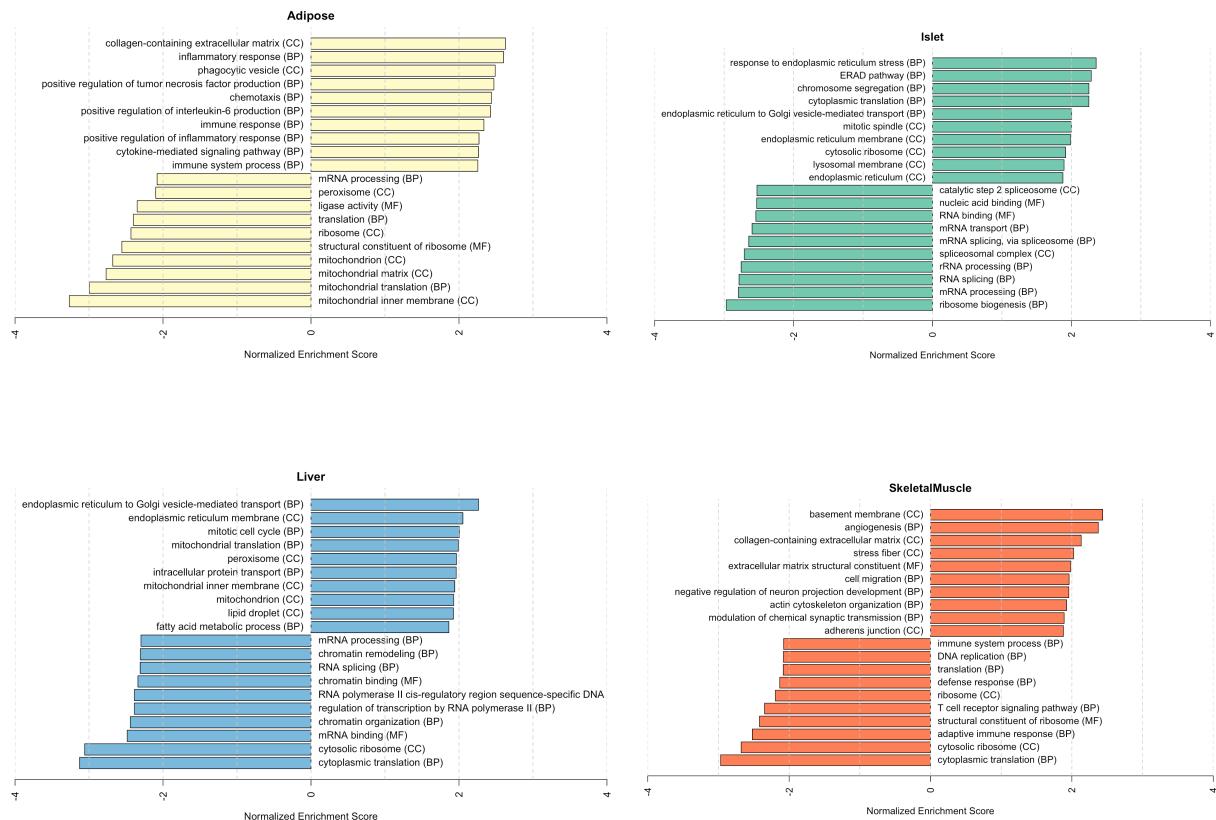


Figure S3: Bar plots showing normalized enrichment scores (NES) for GO terms as determined by fast gene score enrichment analysis (fgsea). Only the top 10 positive and top 10 negative scores are shown. Colors indicate tissue. The name beside each bar shows the name of each enriched GO term. The letters 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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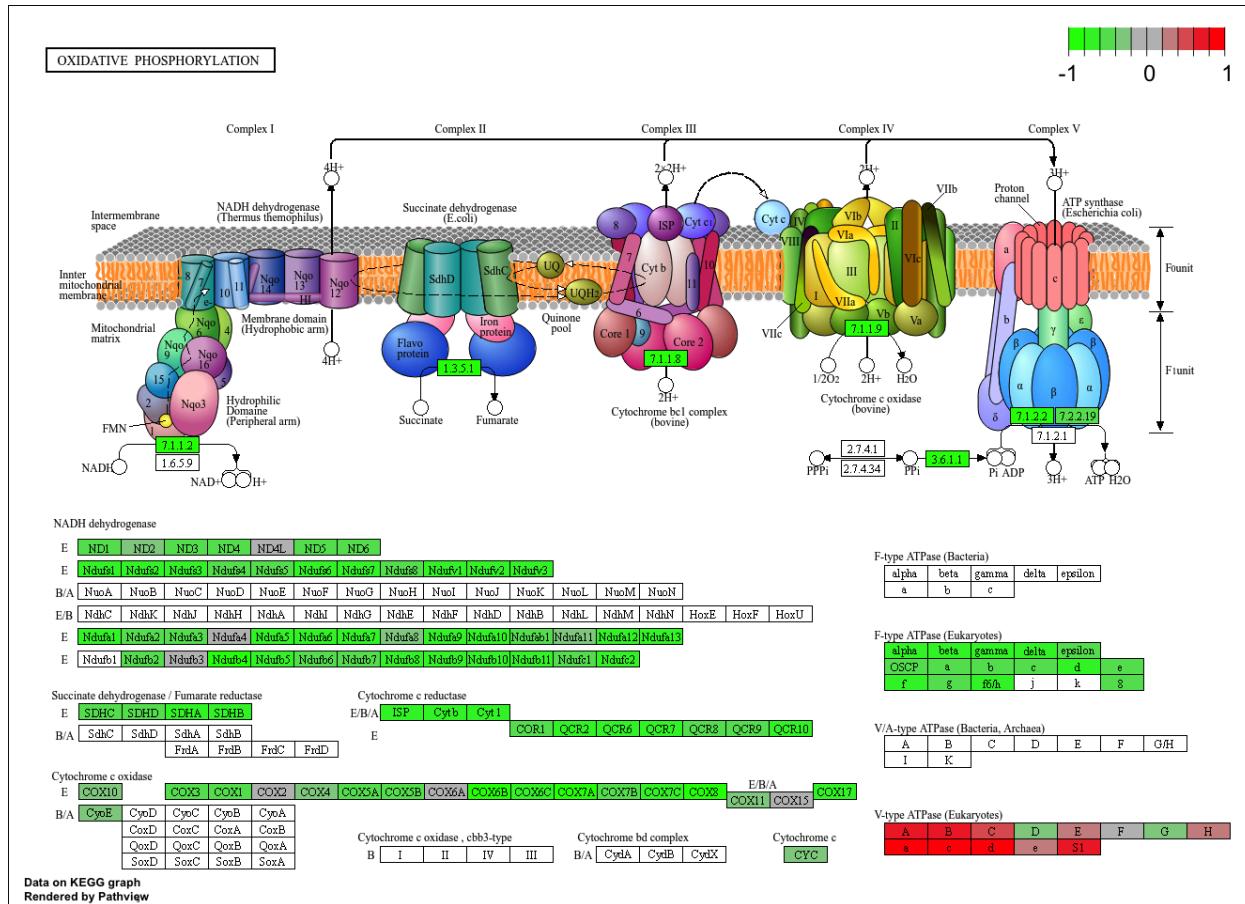


Figure S4: The KEGG pathway for oxidative phosphorylation in mice. Each element is colored based on its HDMA loading from adipose tissue normalized to run from -1 to 1. Genes highlighted in green had negative loadings, and those highlighted in red had positive loadings. Almost the entire pathway was strongly negatively loaded indicating that increased expression of genes involved in oxidative phosphorylation was associated with reduced metabolic index.

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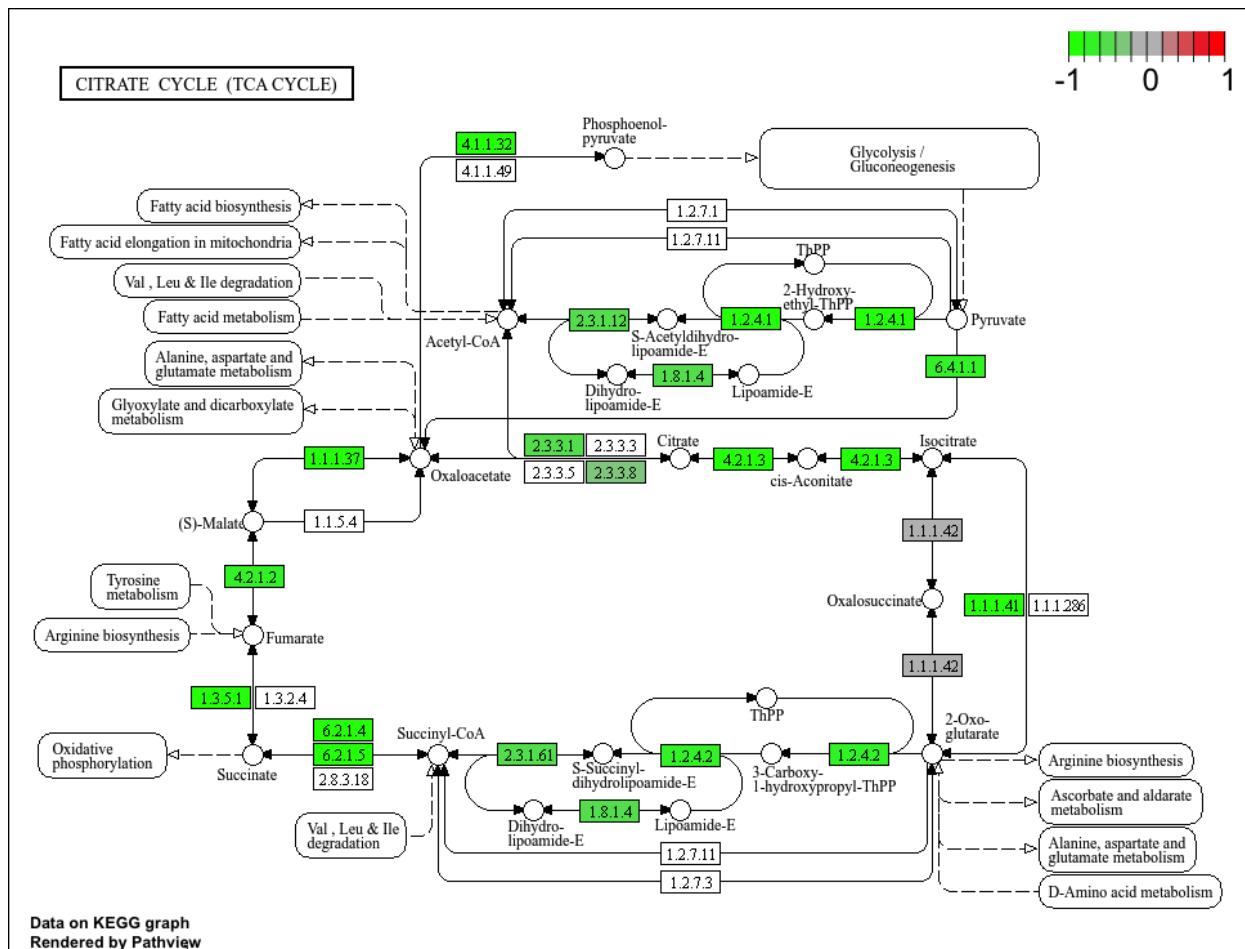


Figure S5: The KEGG pathway for the TCA (citric acid) cycle in mice. Each element is colored based on its HDMA loading from adipose tissue normalized to run from -1 to 1. Genes highlighted in green had negative loadings, and those highlighted in red had positive loadings. Many genes in the cycle were strongly negatively loaded indicating that increased expression of genes involved in branched-chain amino acid degradation was associated with reduced metabolic index.

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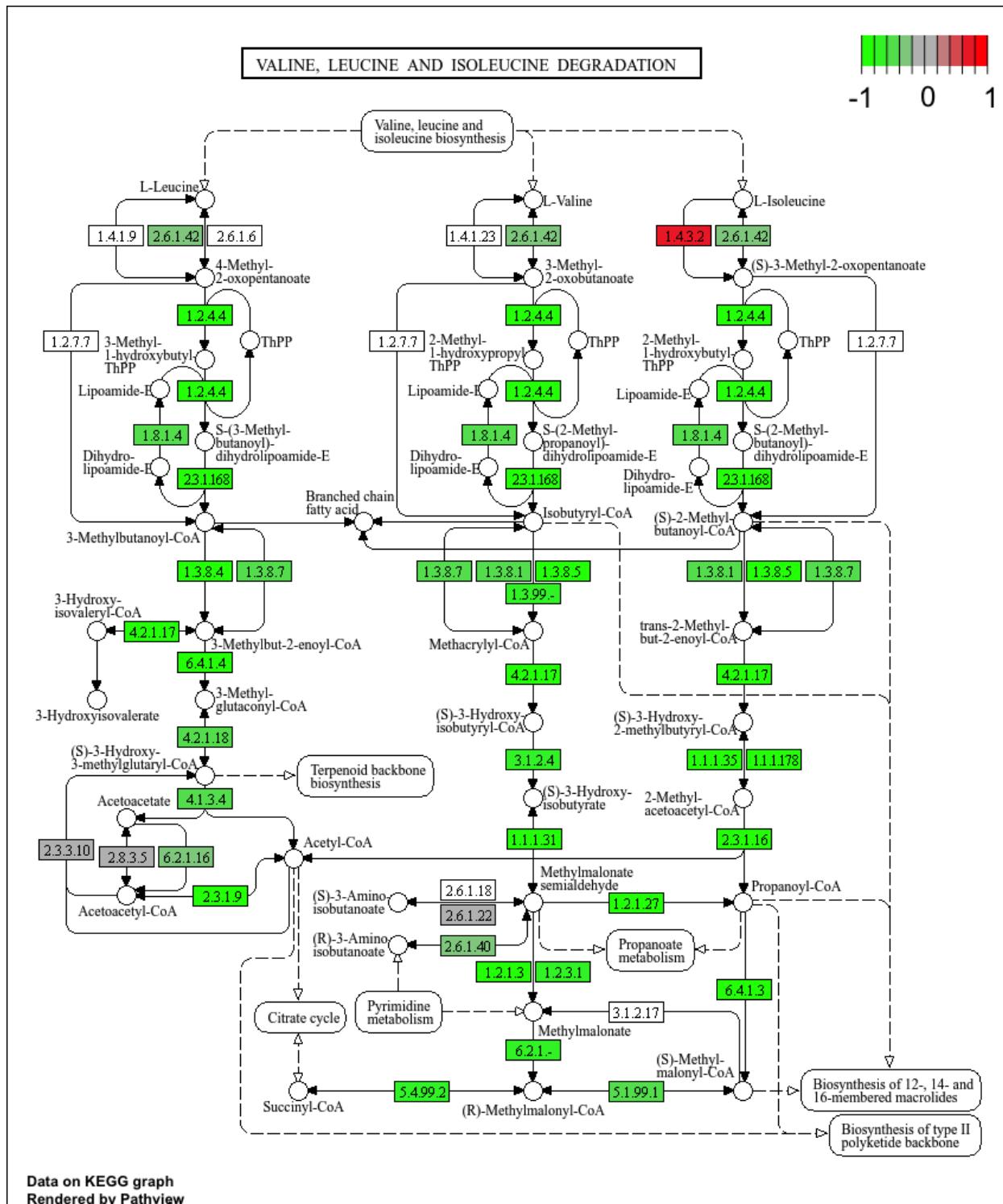


Figure S6: The KEGG pathway for branched-chain amino acid degradation in mice. Each element is colored based on its HDMA loading from adipose tissue normalized to run from -1 to 1. Genes highlighted in green had negative loadings, and those highlighted in red had positive loadings. Almost the entire pathway was strongly negatively loaded indicating that increased expression of genes involved in branched-chain amino acid degradation was associated with reduced metabolic index.

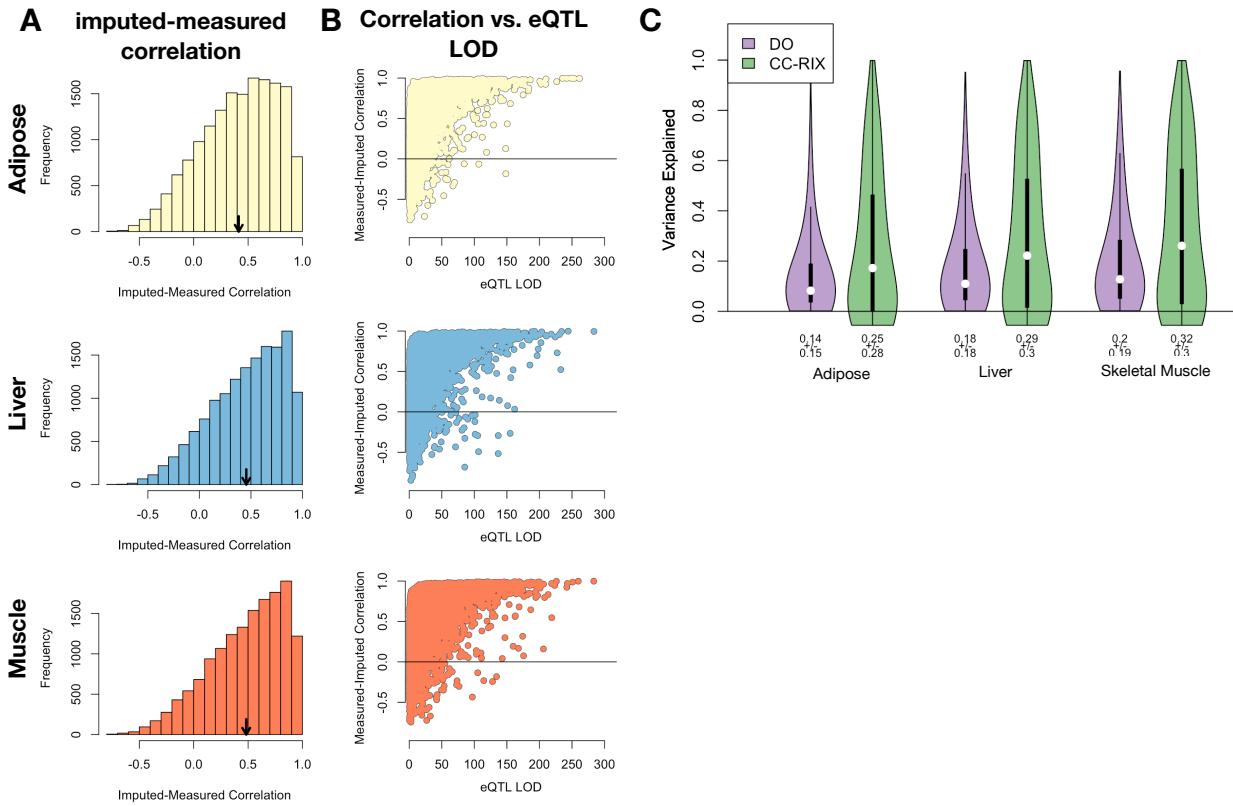


Figure S7: Validation of transcript imputation in the CC-RIX. **A.** Distributions of correlations between imputed and measured transcripts in the CC-RIX. The mean of each distribution is shown by the red line. All distributions were skewed toward positive correlations and had positive means near a Pearson 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.

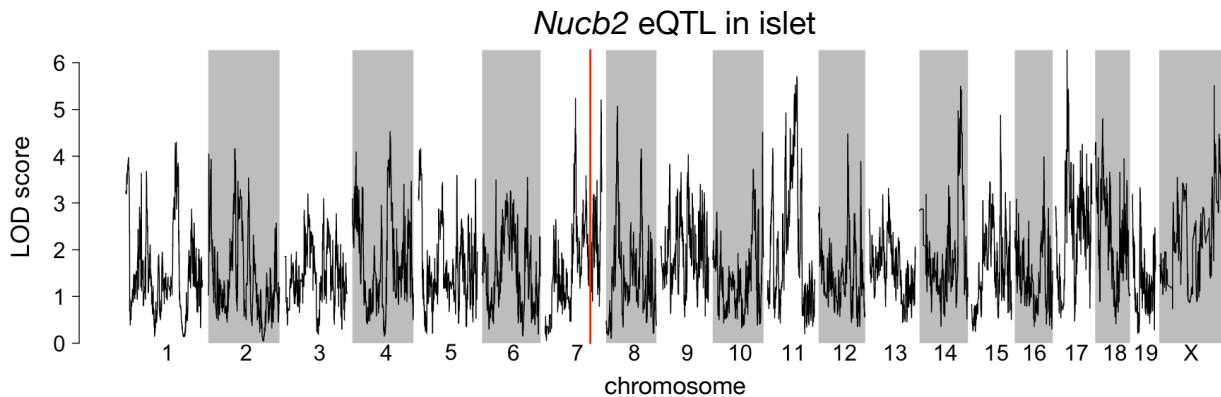


Figure S8: Regulation of *Nucb2* expression in islet. *Nucb2* is encoded on mouse chromosome 7 at 116.5 Mb (red line). In islets the heritability of *Nucb2* expression levels is 69% heritable. This LOD score trace shows that there is no local eQTL at that position, nor any strong distal eQTL anywhere else in the genome.