I. Numerical Simulation

To evaluate the robustness of our testing procedure across a wide variety of genes, we randomly simulated genes from Chromosome 10. We used the following strategies to conduct realistic simulations. First, we estimated the size of genes (mean=100.8Kb; standard deviation=179.7Kb) and the number of typed SNPs within each gene from the Illumina 300K SNP data, and we approximated the distribution of the gene sizes with a gamma distribution. Second, with the approximated gamma distribution, we generated allele-specific genotype data for two parents (500 mothers and 500 fathers) using HAPGEN[Marchini, et al. 2007] by randomly selecting where genes start and end. HPAGEN software was used to generate allele-specific genotypes of HapMap SNPs for a specified range of genomic location and to preserve the linkage disequilibrium structure of the interval. Third, we generated the HapMap SNP data of one offspring from parents' genotypes assuming no recombination, which resulted in 500 families with one father, one mother and one child.

Once the genotype data were generated, a causal SNP, S^* was randomly selected from the HapMap SNPs within the gene. The causal SNP was then used to generate gene expression (G^*) and the marginal probability of having disease using the following two models:

$$G_i^* = S_i^* \alpha_S^* + \epsilon_{Gi},$$

$$\text{logit}\{P(Y_i = 1 | S_i^*, G_i^*)\} = -0.2 + S_i^* \beta_S^* + G_i^* \beta_G^* + G_i S_i^* \beta_C^*. \quad \text{(A1)}$$

where ϵ_G follow a normal distribution with mean 0 and standard deviation 0.2. Note α_S^* indicates the association of a causal SNP and a gene expression, i.e., the eQTL effect, and is non-zero (=0.3) in our simulation. Within each family, disease status (Y) was generated with the marginal probability generated above and an autoregressive correlation with the first degree correlation of 0.25. To mimic the design of MRCA data by accounting for family ascertainment, we selected

100 cases from the children of 500 families and 100 controls from parents who were non-cases. The 100 cases and 100 controls are the final study subjects in our numerical simulation. Throughout the analysis in simulation studies, we only analyzed the typed SNPs on the Illumina 300K SNP array, which may or may not contain causal SNPs that were used to generate gene expression and disease status.

In order to estimate the empirical size of the testing procedures, we simulated 500,000 data sets. In each analysis, we performed 5,000 to 250,000 resampling perturbations depending on the desired accuracy of p-values. For empirical power, we simulated 2,000 data sets and calculated the statistical power as the proportion of nominal p-values less than 0.05. Different parameter configurations that reflect different disease models (SNP-only model, main effect model and full model) were investigated. Analyses assuming exchangeable working correlation with 0.2 pairwise correlation and working independence were performed. We only presented the results assuming a working exchangeable correlation, because two methods performs similarly under the null, and the procedure assuming a working exchangeable correlation has better statistical power under the alternative.

II. Asthma iGWAS Data Analysis

Forming eQTL SNP Set-Gene Expression Pairs

Our testing procedure is built based upon the SNPs that are associated with gene expression, i.e., eQTL SNPs. Specifically, our analyses focused on the SNPs that are associated with the nearby gene within 1Mb on the same chromosome (*cis*-eQTL) with false discovery rate (FDR)[Benjamini and Hochberg 1995; Storey 2002] less than 1%, which has been published using similar datasets[Liang, et al. 2013]. We then grouped these eQTL SNPs with their corresponding gene expression as a SNPs-expression set. We had a total of 11,198 such sets. Note that the 11,198 sets represent 11,198 unique expression probes, not unique genes. A single gene may contain multiple expression probes and SNPs may be associated with multiple gene expression probes. Thus, the 11,198 sets are not independent and may contain similar gene expression value or SNPs.

iGWAS Analysis of Asthma

The gene-centric iGWAS procedures for TE, ME and AE were then applied on the 11,198 SNPs-expression sets to analyze one set at a time, adjusting for age, gender and the first four principal components of the genome-wide SNP data. With 2.9GHz CPU of a laptop, it takes 54.5 minutes to perform iGWAS analyses (TE, AE and ME; 5000 perturbations) on chromosome 10. Genome-wide statistical significance was set as FDR<1%. For the top candidate genes identified from iGWAS, single-locus analyses were performed on a single eQTL SNP with its associated gene expression. Mediation analyses for each single locus were also performed with adjustment of the same covariates described above. We estimated the Mediation Effect and the Alternative Effect on the log odds ratio scale using equations (3) and (4). The variance was approximated using bootstrap[Vanderweele and Vansteelandt 2010]. The proportion of mediation, a measure of the proportion of the genetic effect mediated by the gene expression,

was calculated on the risk difference scale by $OR^{AE}(OR^{ME}-1)/(OR^{AE}OR^{ME}-1)$, where OR^{AE} and OR^{ME} are the Alternative and Mediation Effect odds ratios, respectively[Vanderweele and Vansteelandt 2010]. Of note, the proportion of mediation is interpretable only if the directionality of the AE and ME is consistent, i.e., both hazardous or both protective.

III. Asymptotics of Q statistics

Asymptotic Distribution of Q^{TE}

Define $\boldsymbol{D} = \begin{bmatrix} \boldsymbol{D}_{XX} & \boldsymbol{D}_{XV} \\ \boldsymbol{D}_{VX} & \boldsymbol{D}_{VV} \end{bmatrix} = m^{-1}\boldsymbol{U}^T\boldsymbol{W}\boldsymbol{U}$, and $\boldsymbol{D}^* = m^{-1}\boldsymbol{U}^T\boldsymbol{W}^{\frac{1}{2}}\boldsymbol{R}^*\boldsymbol{W}^{\frac{1}{2}}\boldsymbol{U}$, where $\boldsymbol{U}^T = (\boldsymbol{U}_1, \dots, \boldsymbol{U}_m)$, $\boldsymbol{U}_i^T = \left(\boldsymbol{X}_i^T, \boldsymbol{R}_i^{-1}\boldsymbol{V}_i^T\right)$, $\boldsymbol{V}_i^T = \left(\sqrt{w_1}\boldsymbol{S}_i^T, \sqrt{w_2}\boldsymbol{G}_i^T, \sqrt{w_3}\boldsymbol{C}_i^T\right)$ for Q_{SGC}^{TE}, $\left(\sqrt{w_1}\boldsymbol{S}_i^T, \sqrt{w_2}\boldsymbol{G}_i^T\right)$ for Q_{SG}^{TE}, or $\left(\sqrt{w_1}\boldsymbol{S}_i^T\right)$ for Q_S^{TE}, $\boldsymbol{R}^*$ is the true correlation matrix, $\boldsymbol{W} = diag\{\boldsymbol{W}_i\}$ and $\boldsymbol{W}_i = diag\left\{\frac{\exp\left(\boldsymbol{X}_{ij}^T\widehat{\boldsymbol{\beta}}_{X0}\right)}{\left(1+\exp\left(\boldsymbol{X}_{ij}^T\widehat{\boldsymbol{\beta}}_{X0}\right)\right)^2}\right\}$, $j = 1, \dots, n_i$ (the number of subject in family i), $i = 1, \dots, m$ (the number of families). Furthermore, we let $\boldsymbol{\epsilon}$ denote a Normal $(\boldsymbol{0}, \boldsymbol{D}^*)$ random vector and $\boldsymbol{A} = [-\boldsymbol{D}_{XV}^T\boldsymbol{D}_{XX}^{-1}, \boldsymbol{I}]$ where $\boldsymbol{I}$ is an identity matrix. It can be shown that under the null, the limiting distribution of test statistic Q^{TE} is a mixture of χ^2 distribution:

$$Q^{TE} \xrightarrow{d} \|\boldsymbol{A}\boldsymbol{\epsilon}\|^2. \qquad \text{(A2)}$$

The mixture of χ^2 distribution can be approximated with the inversion of characteristic function[Davies 1980]. Alternatively, we use the asymptotic distribution to develop a perturbation procedure to approximate the distribution by resampling the limiting distribution[Huang, et al. 2014]. Our discussion will focus on the perturbation method because it can be easily adapted to construct an omnibus test that accommodates various candidate models. We use (A2) to develop a perturbation procedure, approximating the respective distribution of Q_S^{TE}, Q_{SG}^{TE} and Q_{SGC}^{TE} under the null using the empirical counterpart of $\boldsymbol{A}$ and $\boldsymbol{\epsilon}$.

Asymptotic Distribution of Q^{ME} and GCV function

It can be shown that for $\lambda = o(\sqrt{m})$, the test statistic as a function of the tuning parameter, $\widehat{\boldsymbol{\beta}}_{X0}$ and $\widehat{\boldsymbol{\beta}}_{S0}$, $Q^{ME}(\lambda, \widehat{\boldsymbol{\beta}}_{X0}, \widehat{\boldsymbol{\beta}}_{S0})$ follows a similar asymptotic distribution as the Total Effect. Denote $\boldsymbol{\epsilon} \sim N(\boldsymbol{0}, \boldsymbol{D}^*)$ and $\boldsymbol{D}^* = m^{-1}\boldsymbol{U}^T\boldsymbol{W}_{ME}^{\frac{1}{2}}\boldsymbol{R}^*\boldsymbol{W}_{ME}^{\frac{1}{2}}\boldsymbol{U}$, the asymptotic distribution of the test statistic is:

$$Q^{ME}(\lambda, \widehat{\boldsymbol{\beta}}_{X0}, \widehat{\boldsymbol{\beta}}_{S0}) \xrightarrow{d} \|\boldsymbol{A}(\lambda)\boldsymbol{\epsilon}\|^2, \quad \text{(A3)}$$

where $\boldsymbol{A}(\lambda) = [-\boldsymbol{D}_{\tilde{X}V}^T \boldsymbol{D}_{\tilde{X}\tilde{X}}^{-1}, \boldsymbol{I}]$, $\boldsymbol{D}(\lambda) = \begin{bmatrix} \boldsymbol{D}_{\tilde{X}\tilde{X}} & \boldsymbol{D}_{\tilde{X}V} \\ \boldsymbol{D}_{V\tilde{X}} & \boldsymbol{D}_{VV} \end{bmatrix} = m^{-1}\boldsymbol{U}^T\boldsymbol{W}_{ME}\boldsymbol{U} + \lambda\boldsymbol{I}_2$, $\boldsymbol{U}^T = (\boldsymbol{U}_1, \dots, \boldsymbol{U}_m)$, $\boldsymbol{U}_i^T = \left(\widetilde{\boldsymbol{X}}_i^T, \boldsymbol{R}_i^{-1}\boldsymbol{V}_i^T\right)$, $\widetilde{\boldsymbol{X}}_i^T = (\boldsymbol{X}_i^T, \boldsymbol{S}_i^T)$, $\boldsymbol{V}_i^T = \left(\sqrt{w_2}\boldsymbol{G}_i^T, \sqrt{w_3}\boldsymbol{C}_i^T\right)$ for Q_{SGC}^{ME} or $\sqrt{w_2}G_i$ for Q_{SG}^{ME}, $\boldsymbol{W}_{ME} = diag\{\boldsymbol{W}_{ME,i}\}$ and $\boldsymbol{W}_{ME,i} = diag\left\{\frac{\exp\left(\boldsymbol{X}_{ij}^T\widehat{\boldsymbol{\beta}}_{X0} + \boldsymbol{S}_{ij}^T\widehat{\boldsymbol{\beta}}_{S0}\right)}{\left(1+\exp\left(\boldsymbol{X}_{ij}^T\widehat{\boldsymbol{\beta}}_{X0} + \boldsymbol{S}_{ij}^T\widehat{\boldsymbol{\beta}}_{S0}\right)\right)^2}\right\}$, and $\boldsymbol{I}_2$ is a $(q+2p+1)\times(q+2p+1)$ block diagonal matrix with the top $q \times q$ block diagonal matrix being 0, the middle $p \times p$ diagonal matrix being an identify matrix, $\boldsymbol{I}_{p\times p}$ and the bottom $(p+1)\times(p+1)$ diagonal matrix being 0 for Q_{SGC}^{ME}, and a $(q+p+1)\times(q+p+1)$ block diagonal matrix for Q_{SG}^{ME}. The tuning parameter λ can be chosen as a minimizer of the GCV function $\frac{(\boldsymbol{Y}-\hat{\boldsymbol{\mu}}_0)^T\boldsymbol{W}_{ME}^{-1}(\boldsymbol{Y}-\hat{\boldsymbol{\mu}}_0)}{m(1-\mathrm{tr}(\boldsymbol{H}))^2}$, where $\boldsymbol{H} = \boldsymbol{W}_{ME}^{-1}\widetilde{\boldsymbol{X}}\left(\widetilde{\boldsymbol{X}}^T\boldsymbol{W}_{ME}\widetilde{\boldsymbol{X}} + \hat{\lambda}\boldsymbol{I}_2\right)^{-1}\widetilde{\boldsymbol{X}}^T$ and $\widetilde{\boldsymbol{X}}^T = (\widetilde{\boldsymbol{X}}_1, \dots, \widetilde{\boldsymbol{X}}_m)$.

IV. Numerical Results for AE, ME and TE

Under the null

Empirical sizes for the proposed tests of AE, ME and TE under the family-based design are presented in Table S1. The iGWAS testing procedures for the AE and ME under the two candidate models: 1) main effect model of SNPs and gene expression (Q_{SG}), and 2) full model allowing for both main effects and SNP-by-expression interactions (Q_{SGC}) protects Type I error and so does the omnibus tests. Type I error is also well protected in tests for the TE under the three model assumptions: 1) SNP-only model (Q_S), 2) main effect model (Q_{SG}), and 3) full model (Q_{SGC}) as well as the omnibus test (Q_{omb}) that does not require assuming which of the three models is the true model. Under the null of no effect of the gene on disease risk, all three tests are valid. Note that the simulation studies were conducted for random genes with various sizes across different regions on Chromosome 10. Therefore, the results for AE, ME and TE are robust under a wide variety of linkage disequilibrium structures and different numbers of typed SNPs within a gene. Also, the proposed tests based on estimating equations are not biased by the family ascertainment. For smaller sizes (5×10^{-4} or 5×10^{-5}), the tests are a little conservative. The conservative test size may be due to the modest sample size in the simulation studies (100 cases and 100 controls) that was used to mimic the motivating example. The iGWAS approach is based on variance component score tests, the size of which has been shown to approach the low nominal level when the sample size becomes large [Wu, et al. 2011].

Under the alternative

The performance of three tests for AE or ME (Q_{SG}, Q_{SGC} and Q_{omb}) under the alternative hypotheses was compared under two different disease models with the family-based design. The numerical results are presented in Figure S1. The first scenario is that both the causal SNP and gene expression have effects on the outcome but there is no SNP-by-gene expresssion

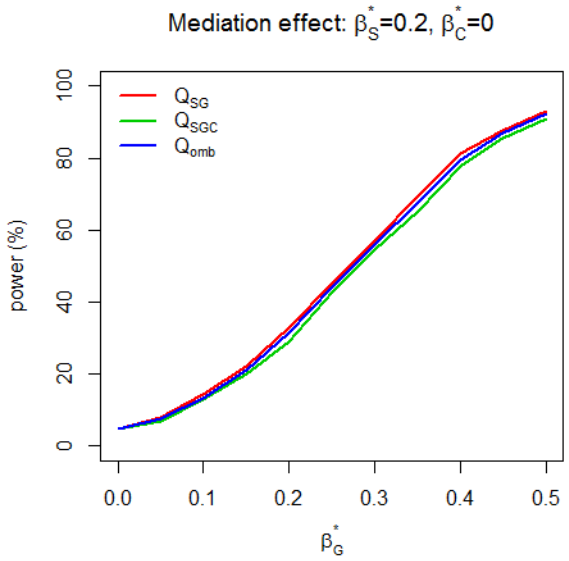
interaction ($\beta_G^* = 0.2, \beta_C^* = 0$ in (A1)). In this setting, the main effect model, Q_{SG} for ME assuming the correct model has the optimal statistical power (Figure S1A). For AE, the full model (Q_{SGC}) has a comparable performance with the main effect model (Q_{SG}) (Figure S1C). The omnibus test (Q_{omb}) can almost reach the optimal power. The second scenario allows for an interaction between gene expression and the causal SNP ($\beta_G^* = 0.2$, $\beta_C^* = 0.3$ in (A1)). The Q_{SGC}'s for ME and AE under the full model perform optimally as it assumes a correct model form (Figures S1B and S1D). The main effect model (Q_{SG}) has a very similar performance to the full model (Q_{SGC}). Although the full model assumes a correct model specification, it also spends extra degrees of freedom to test for the interactive effects. The trade-off between the two may lead to the similar performance in the main effect model and the full model. Again, the omnibus test (Q_{omb}) can almost reach the best power without the need of assuming which is the true model.

The performance of four tests for the TE (Q_S, Q_{SG}, Q_{SGC} and Q_{omb}) was compared under three different disease models under the family-based design, presented in Figure S2. The first scenario is that the causal SNP has an effect on the outcome, but both gene expression and the SNP-by-expression interaction have no effect ($\beta_G^* = \beta_C^* = 0$ in (A1)). When the effect of SNP is modest, the SNP-only model, Q_S outperforms the other models; when the effect of the SNP becomes larger, the main effect model, Q_{SG} performs better (Figure S2A). Because the causal SNP is not necessarily a typed SNP in our simulation, gene expression may better capture the effect of causal SNP than the typed SNPs. This may explain the power gain of the main effect model (Q_{SG}) under strong SNP-only effects. The omnibus test (Q_{omb}) reaches the optimal test regardless of the magnitude of SNP effect. For the second scenario under the main effect model ($\beta_G^* = 0.2, \beta_C^* = 0$ in (A1)), Q_{SG} for TE assuming the correct model has the optimal statistical power (Figure S2B). The SNP-only model, Q_S, in contrast, has a poor performance as it fails to capture the effect of gene expression. The omnibus test (Q_{omb}) can almost reach the optimal power of the main effect model, Q_{SG}. Under the third scenario ($\beta_G^* = 0.2$, $\beta_C^* = 0.3$ in (A1)), Q_{SGC}

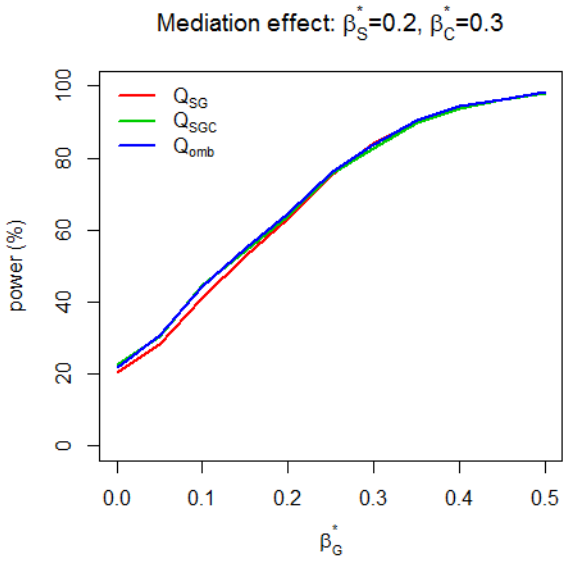
performs optimally as it assumes a correct model form, and the SNP-only model, Q_S loses considerable power (Figure S2C). The main effect model (Q_{SG}) has a very similar performance to the full model (Q_{SGC}) due to the trade-off between correct model specification and extra degrees of freedom for the interactive effects. Again, the omnibus test (Q_{omb}) can almost reach the optimal power.

Figure S1. Power for the tests of Alternative and Mediation Effects from simulation studies under the family-based design. Q_{SG} assumes a model with main effects of SNP and gene expression; Q_{SGC} assumes a model with SNP, gene expression and their interaction; Q_{omb} is the omnibus test for Q_{SG} and Q_{SGC}. A. Power of testing the Mediation Effect under a main effect model ($\beta_S^* = 0.2$ and $\beta_C^* = 0$); B. Power of testing the Mediation Effect under an interaction model ($\beta_S^* = 0.2$ and $\beta_C^* = 0.3$); C. Power of testing the Alternative Effect under a main effect model ($\beta_G^* = 0.2$ and $\beta_C^* = 0$); D. Power of testing the Alternative Effect under an interaction model ($\beta_G^* = 0.2$ and $\beta_C^* = 0.3$).

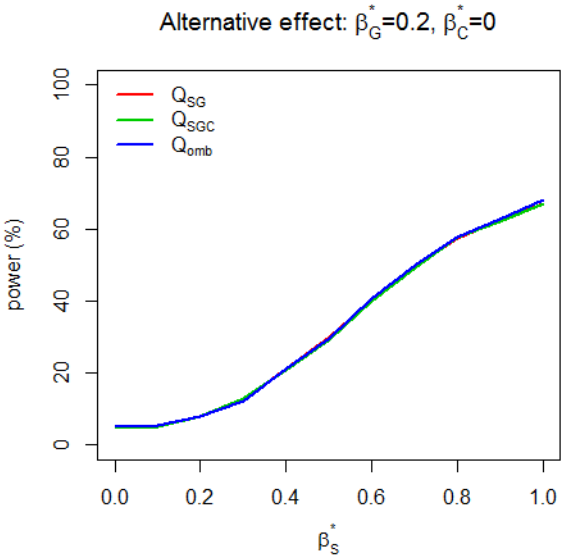
A



B



C


Alternative effect: β_G^*=0.2, β_C^*=0
Q_{SG}
Q_{SGC}
Q_{omb}
power (%)
0
20
40
60
80
100
0.0
0.2
0.4
0.6
0.8
1.0
β_S^*

D

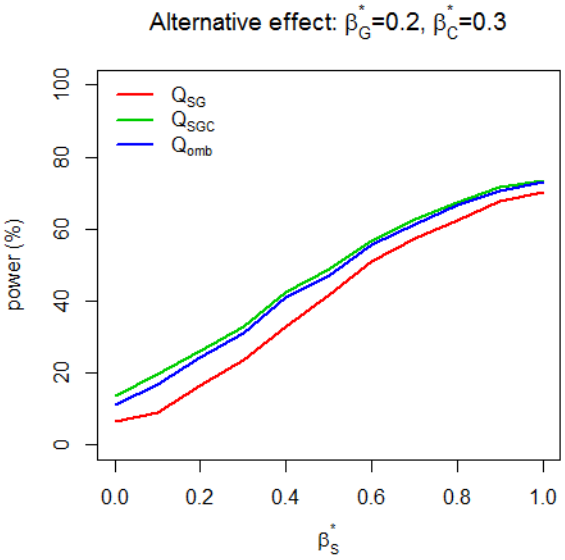
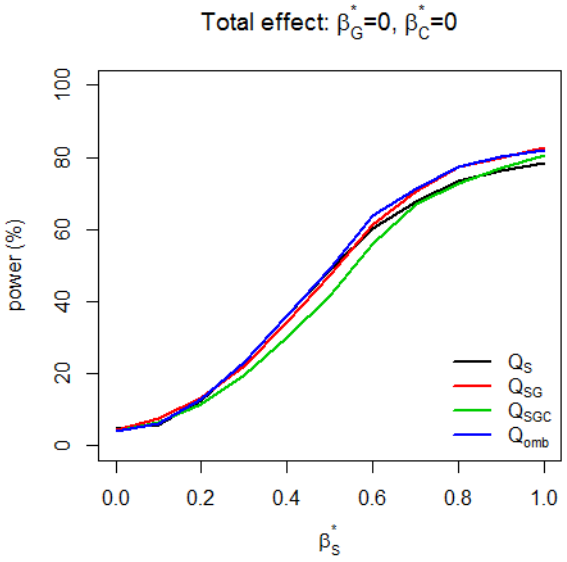
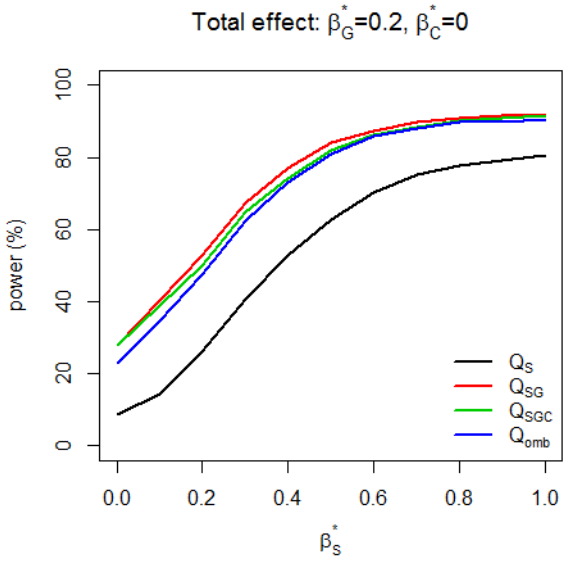

Alternative effect: β_G^*=0.2, β_C^*=0.3
Q_{SG}
Q_{SGC}
Q_{omb}
power (%)
0
20
40
60
80
100
0.0
0.2
0.4
0.6
0.8
1.0
β_S^*

Figure S2. Power for the test of Total Effect from simulation studies under the family-based design. Q_S assumes an SNP-only model; Q_{SG} assumes a model with main effects of SNP and gene expression; Q_{SGC} assumes a model with SNP, gene expression and their interaction; Q_{omb} is the omnibus test for Q_S, Q_{SG} and Q_{SGC}. A. True underlying disease model is an SNP-only model ($\beta_G^* = \beta_C^* = 0$); B. true model is a main effect model ($\beta_G^* = 0.2$ and $\beta_C^* = 0$); C. true model is an interaction model ($\beta_G^* = 0.2$ and $\beta_C^* = 0.3$).

A



B



C

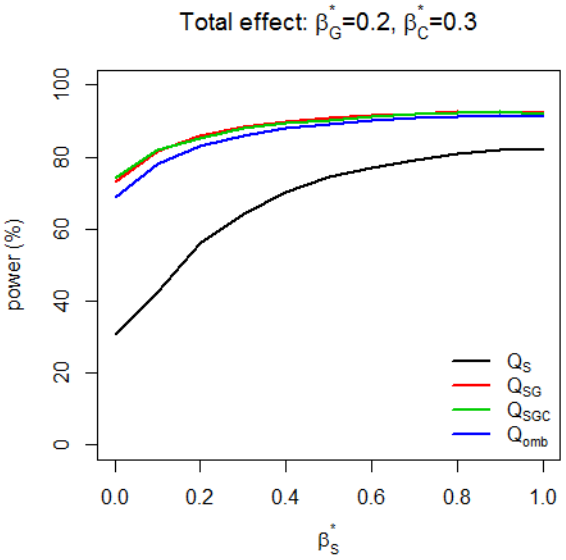
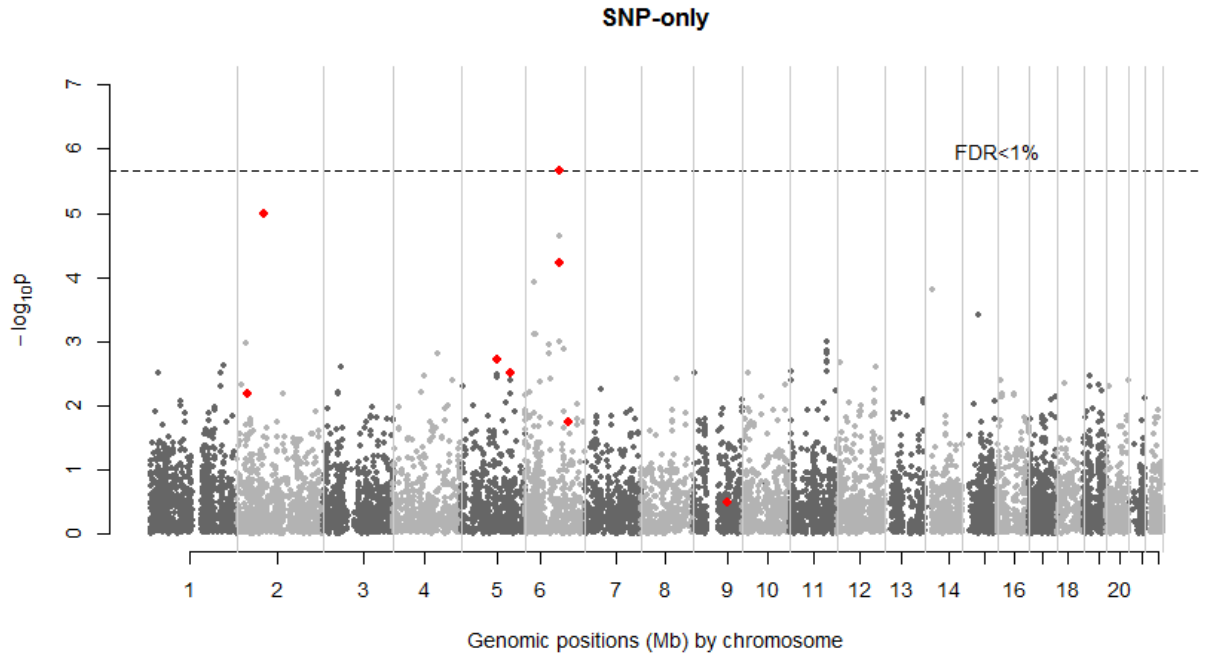

Total effect: β_G^*=0.2, β_C^*=0.3
power (%)
0
20
40
60
80
100
0.0
0.2
0.4
0.6
0.8
1.0
β_S^*
Q_S
Q_{SG}
Q_{SGC}
Q_{omb}

Figure S3. Manhattan plots of genome-wide scan for total effects with gene-centric iGWAS approach. A. SNP-only analyses (Q_S); B. analyses with both SNPs and gene expression (Q_{SG}); C. analyses with SNPs, gene expression and their cross-product interactions (Q_{SGC}). Red dots indicate the eight transcripts found from the omnibus test with FDR<1%.

A



B


SNP and gene expression
FDR<1%
$-\log_{10}p$
0 1 2 3 4 5 6 7
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 18 20
Genomic positions (Mb) by chromosome

C

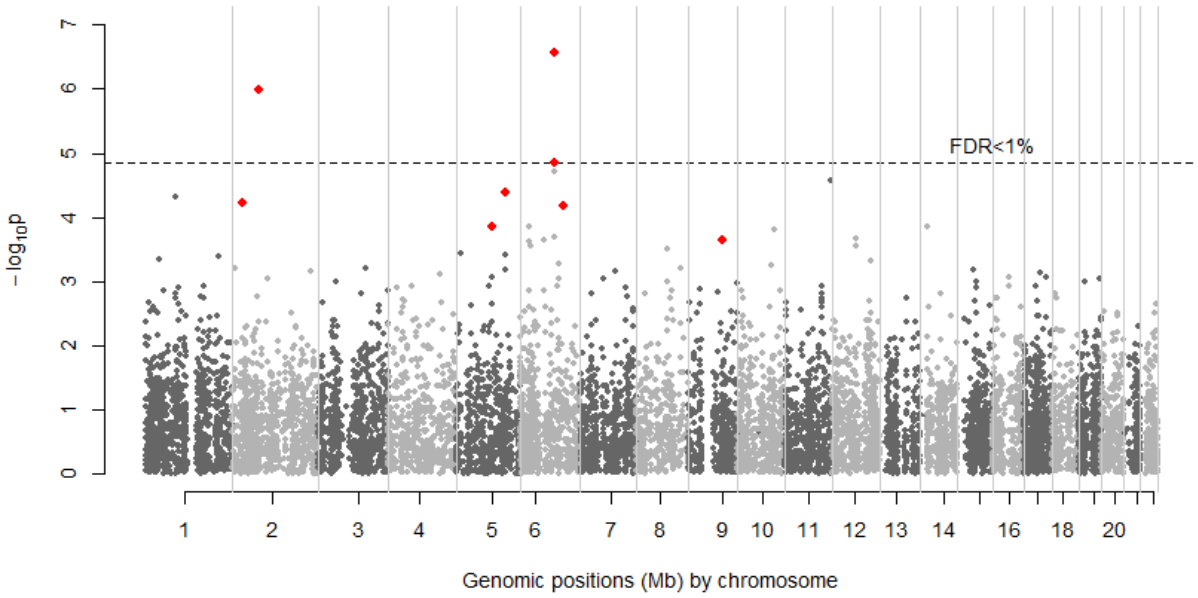
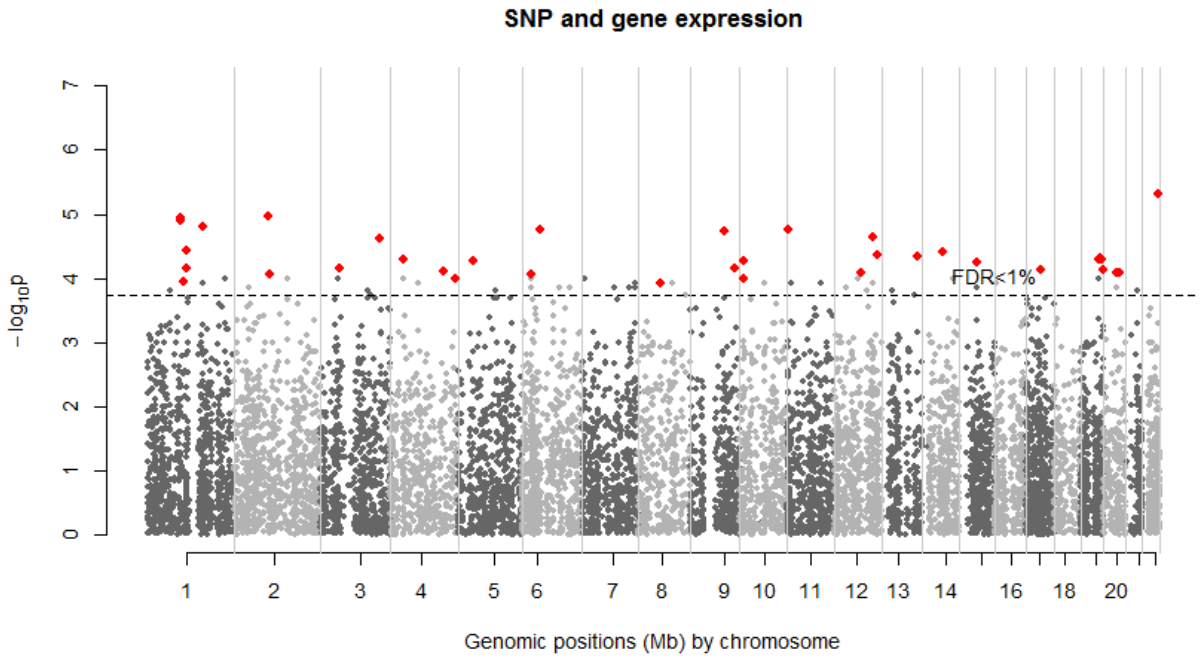

SNP, gene expression and interaction
FDR<1%
$-\log_{10}p$
0 1 2 3 4 5 6 7
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 18 20
Genomic positions (Mb) by chromosome

Figure S4. Manhattan plots of genome-wide scan for mediation effects with gene-centric iGWAS approach. A. analyses with both SNPs and gene expression main effects (Q_{SG}^{ME}); B. analyses with SNPs, gene expression and their cross-product interactions (Q_{SGC}^{ME}). Red dots indicate the transcripts found from the omnibus test with FDR<1%.

A


SNP and gene expression
FDR<1%
$-\log_{10}p$
0 1 2 3 4 5 6 7
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 18 20
Genomic positions (Mb) by chromosome

B

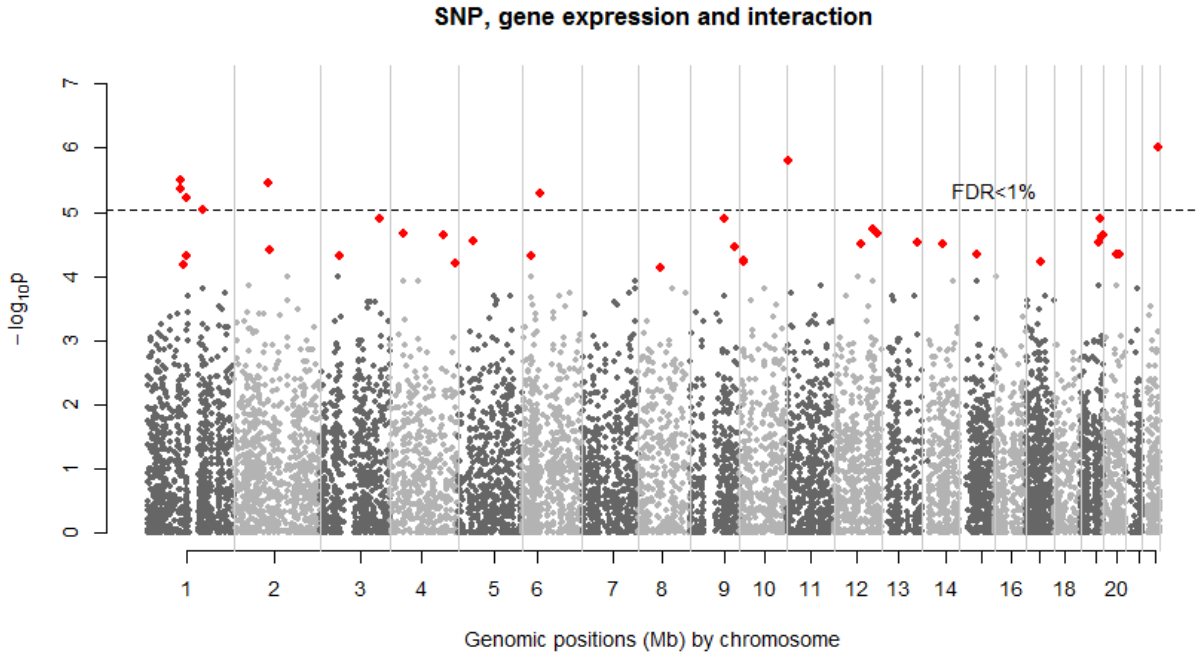
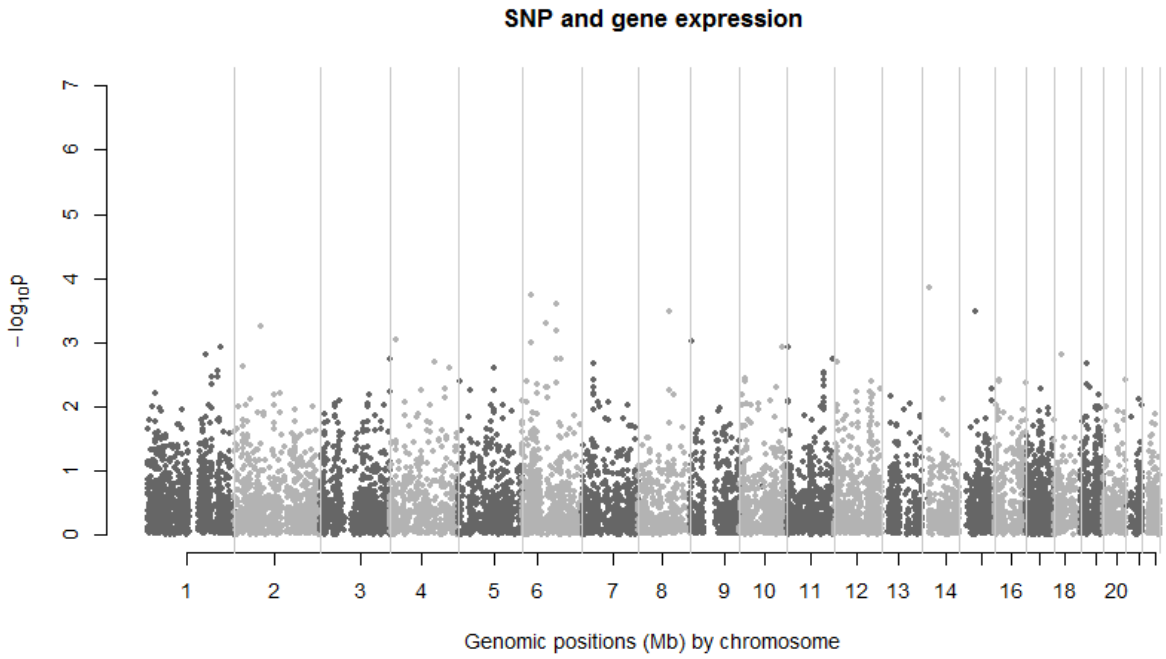

SNP, gene expression and interaction
FDR<1%
$-\log_{10}p$
0 1 2 3 4 5 6 7
1 2 3 4 5 6 7 8 9 10 11 12 13 14 16 18 20
Genomic positions (Mb) by chromosome

Figure S5. Manhattan plots of genome-wide scan for alternative effects with gene-centric iGWAS approach. A. analyses with both SNPs and gene expression main effects (Q_{SG}^{AE}); B. analyses with SNPs, gene expression and their cross-product interactions (Q_{SGC}^{AE}).

A


SNP and gene expression
$-\log_{10}p$
0
1
2
3
4
5
6
7
1
2
3
4
5
6
7
8
9
10
11
12
13
14
16
18
20
Genomic positions (Mb) by chromosome

B

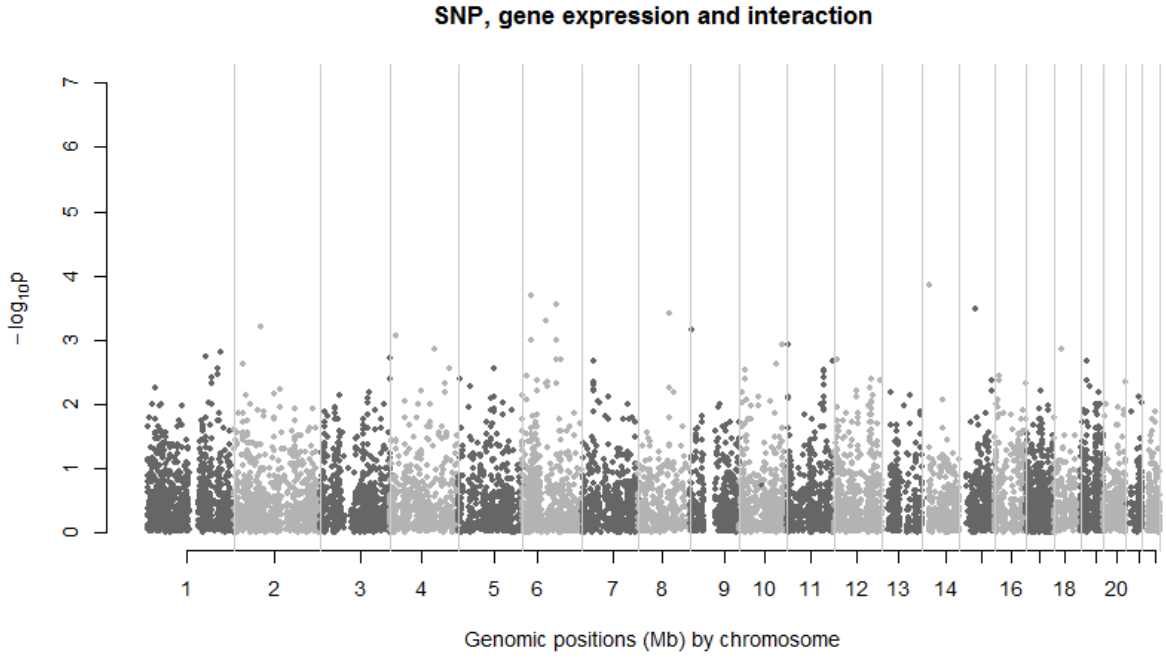

SNP, gene expression and interaction
$-\log_{10}p$
0
1
2
3
4
5
6
7
1
2
3
4
5
6
7
8
9
10
11
12
13
14
16
18
20
Genomic positions (Mb) by chromosome

Figure S6. Plots of p-values from different tests in single-locus analyses for *LYCAT*. Lower panel represents the pairwise linkage disequilibrium structure for the SNPs within each gene, measured as r^2 ranging from 0 (white) to 1 (black). TE: total effect; AE: alternative effect; ME: mediation effect; Q_S: tests assuming a SNP-only model; Q_{SG}: tests assuming a model with main effects of SNPs and gene expression; Q_{SG}: tests assuming a model with effects of SNPs, gene expression and their interactions; Q_{omb}: omnibus tests.

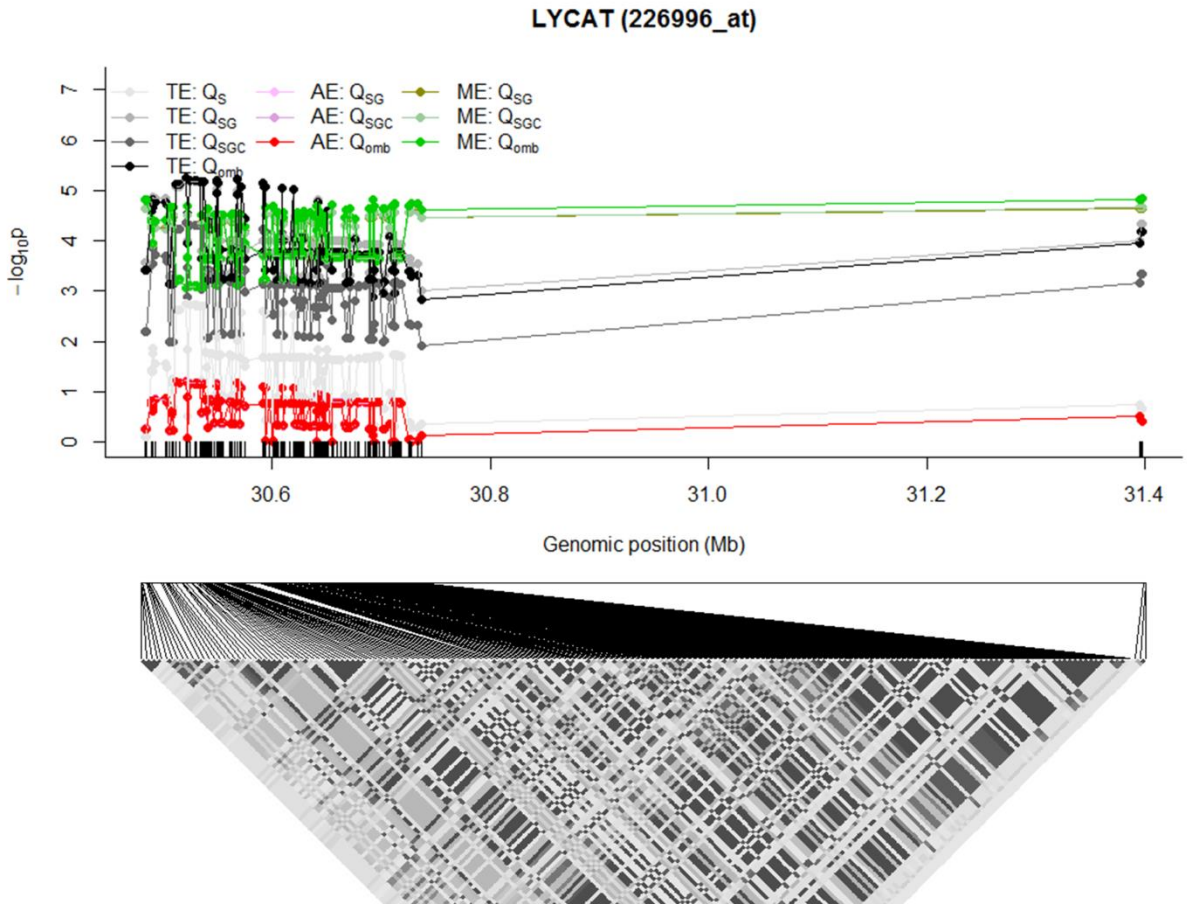


Figure S7. Plots of p-values from different tests in single-locus analyses for *ST8SIA4*. Abbreviations and notations are the same as those in Figure S1.

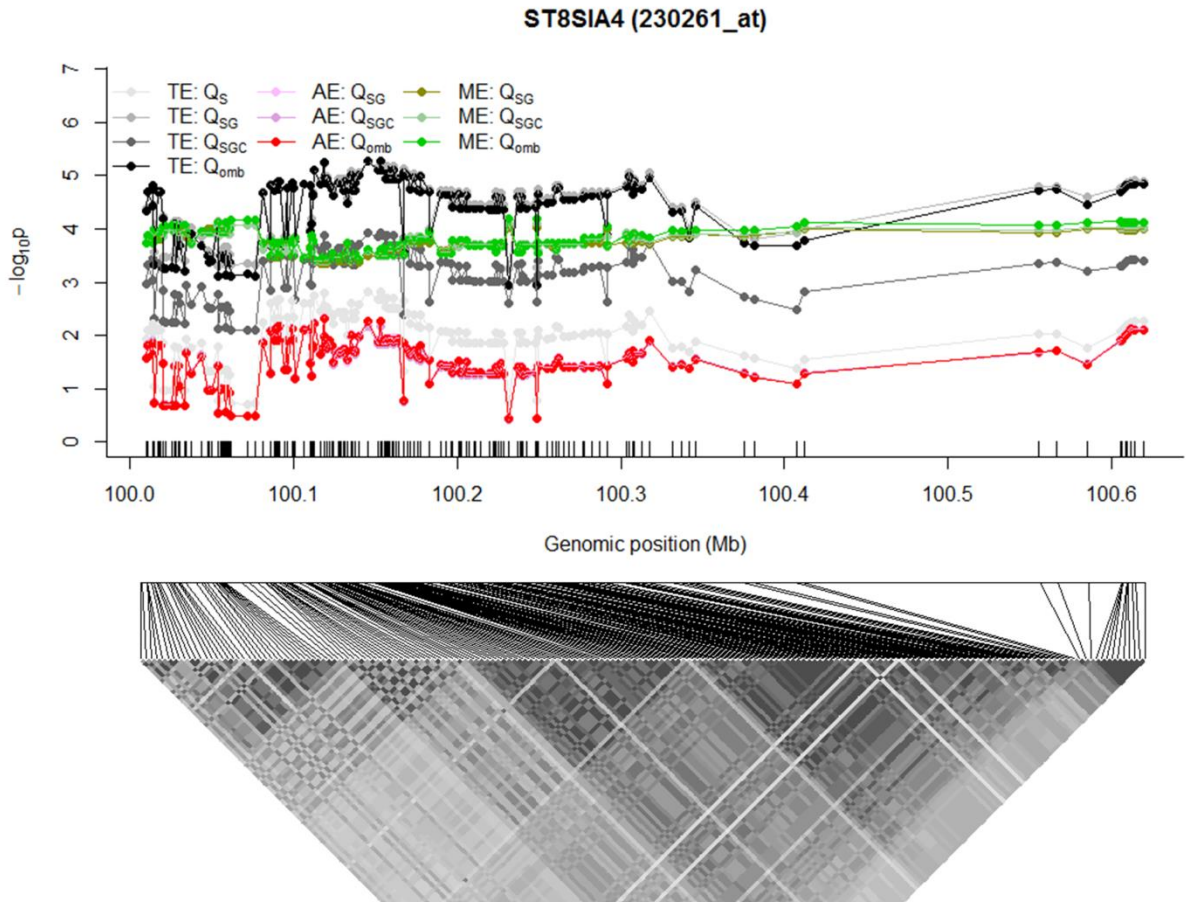


Figure S8. Plots of p-values from different tests in single-locus analyses for *NDFIP1*. Abbreviations and notations are the same as those in Figure S1.

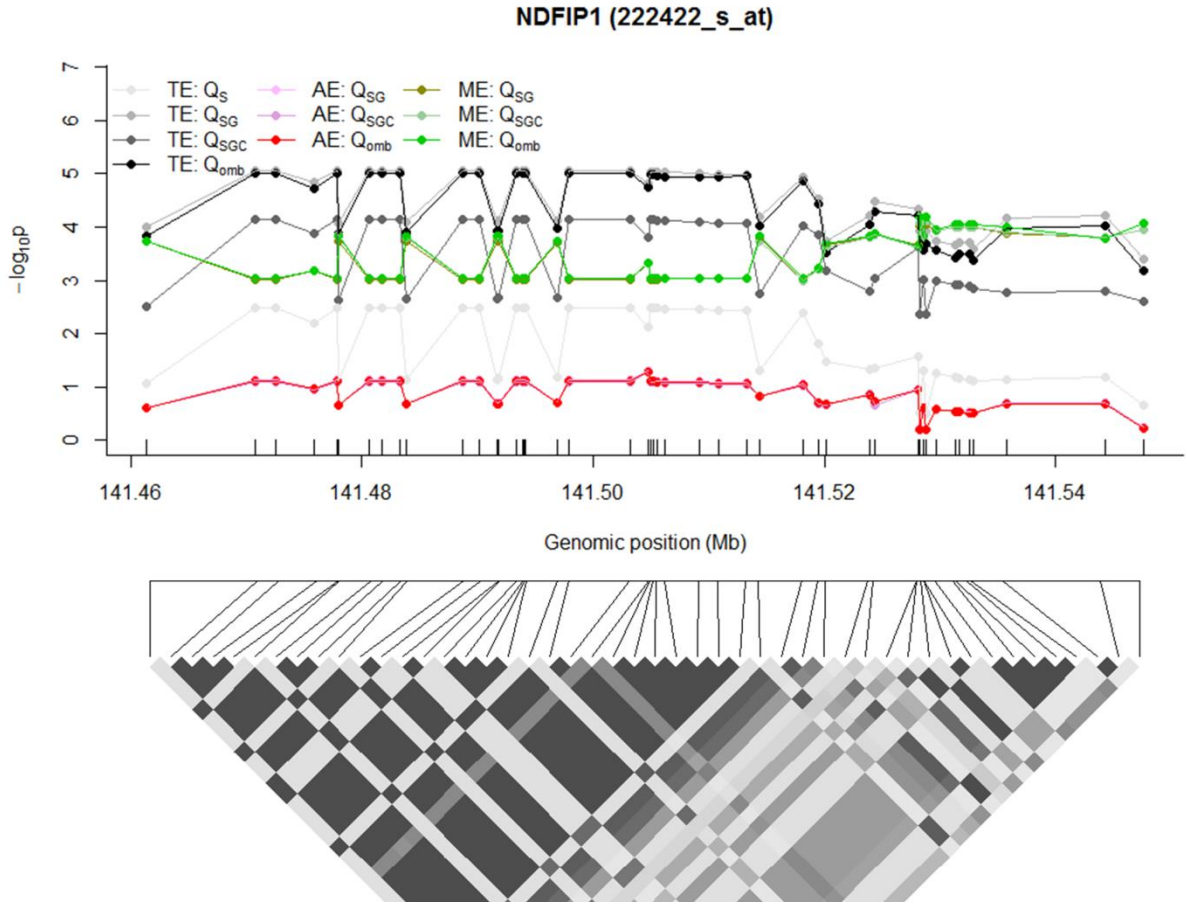


Figure S9. Plots of p-values from different tests in single-locus analyses for *MANEA* (1554193_s_at). Abbreviations and notations are the same as those in Figure S1.

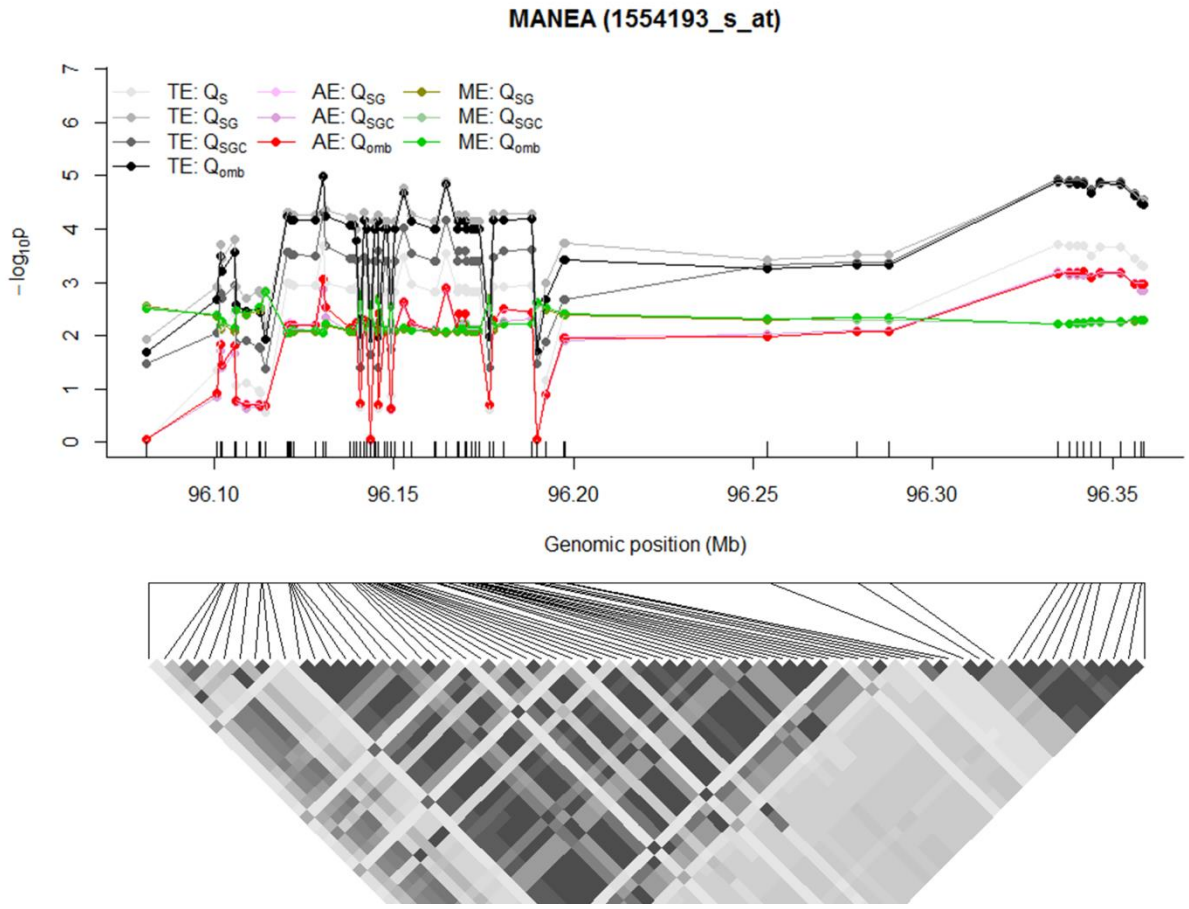


Figure S10. Plots of p-values from different tests in single-locus analyses for 229319_at. Abbreviations and notations are the same as those in Figure S1.

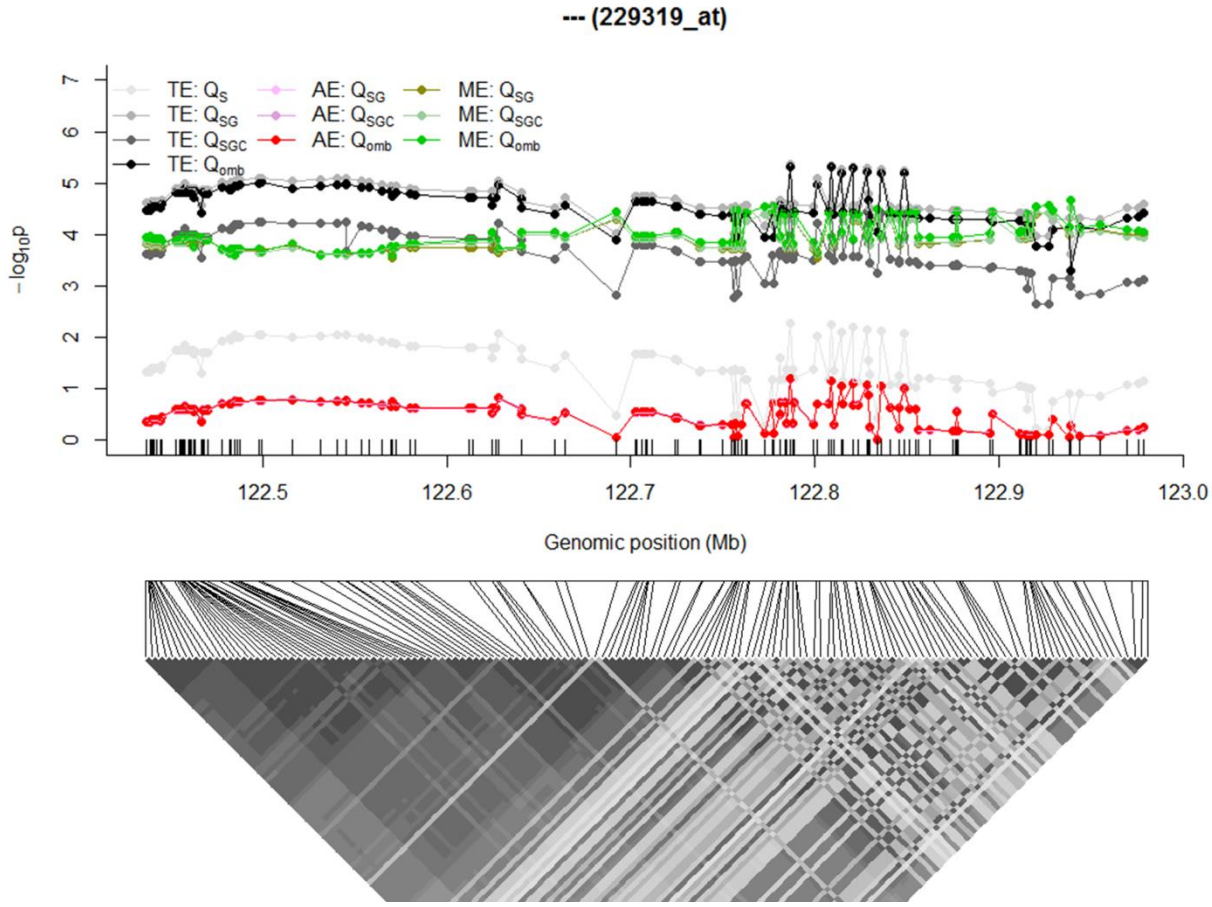


Figure S11. Plots of p-values from different tests in single-locus analyses for *PTCH1*. Abbreviations and notations are the same as those in Figure S1.

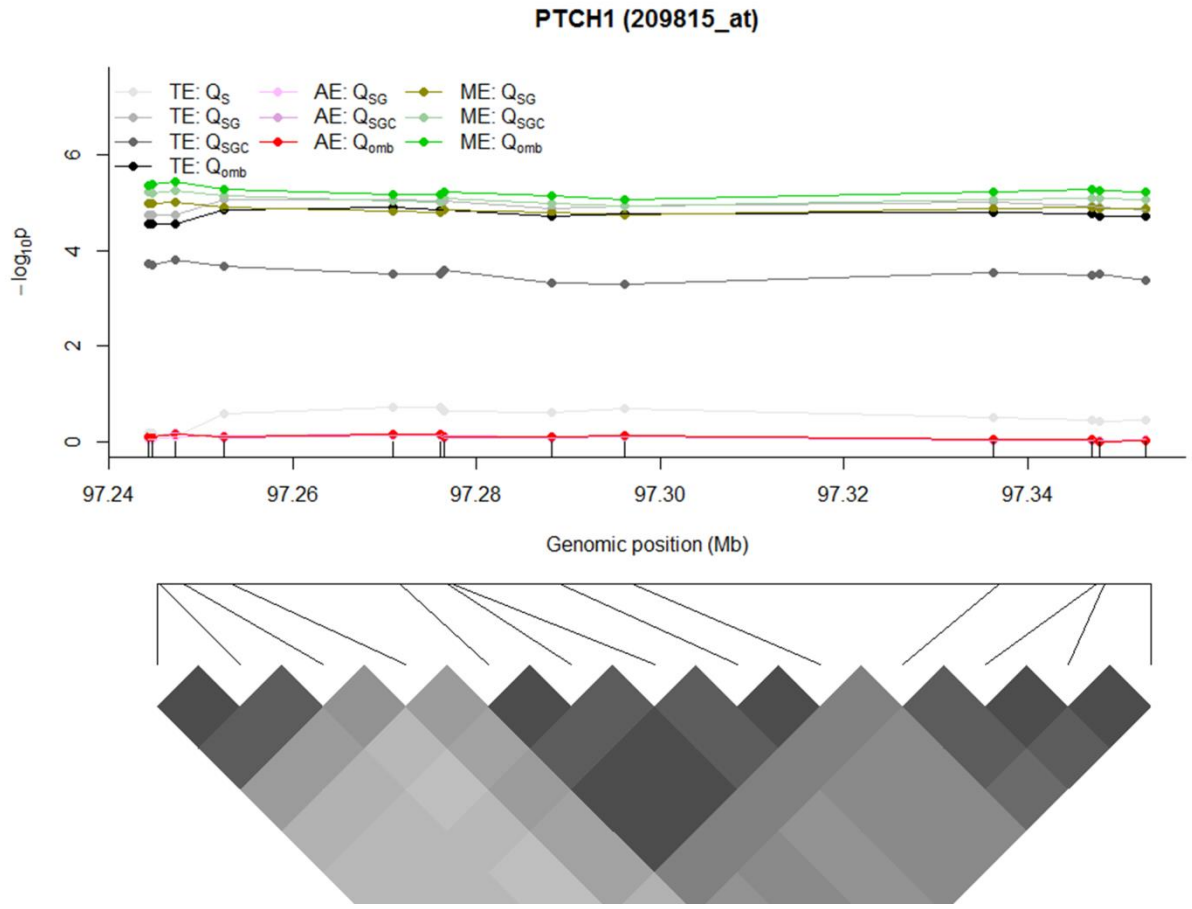


Table S1. Empirical size of iGWAS testing procedure using simulation studies under the family-based design. Q_S: test with only SNP-set, the SNP-only model; Q_{SG}: test with both SNP set and gene expression (without interaction), the main effect model; Q_{SGC}: test with SNP set, gene expression and their cross-product interactions, the full model; Q_{omb}: omnibus test for Q_S, Q_{SG} and Q_{SGC}.

Size	Q_{omb}	Q_S	Q_{SG}	Q_{SGC}
Alternative Effect				
5%	4.45%	-	4.63%	4.35%
0.5%	0.366%	-	0.364%	0.306%
0.05%	0.0246%	-	0.0293%	0.0199%
0.005%	0.00152%	-	0.00084%	0.00135%
Mediation Effect				
5%	4.21%	-	4.34%	4.09%
0.5%	0.361%	-	0.340%	0.299%
0.05%	0.0241%	-	0.0254%	0.0214%
0.005%	0.00118%	-	0.00135%	0.00084%
Total Effect				
5%	4.64%	4.55%	4.75%	4.68%
0.5%	0.362%	0.340%	0.397%	0.384%
0.05%	0.0276%	0.0256%	0.0310%	0.0283%
0.005%	0.00404%	0.00354%	0.00185%	0.00152%

Table S2. P-values of total effect, mediation effect and alternative effect for the 36 genes with most significant mediation effect (FDR <1%) using the asthma data. Symbols and notations are the same as Table 1 in main text.

Probe	Gene	Ch	No. of eQTL	Alternative effect			Mediation effect			Total effect			
				Q_{omb}	Q_{SG}	Q_{SGC}	Q_{omb}	Q_{SG}	Q_{SGC}	Q_{omb}	Q_S	Q_{SG}	Q_{SGC}
218421_at	*CERK*	22	31	0.50	0.50	0.50	4.5E-7	4.9E-6	1.0E-6	3.8E-5	0.77	2.8E-5	0.0023
1553943_at	*NS3BP*	11	21	0.69	0.68	0.68	9.1E-7	1.8E-5	1.6E-6	3.9E-4	0.61	2.8E-4	0.0059
200028_s_at	*STARD7*	2	30	0.56	0.56	0.56	2.0E-6	1.1E-5	3.6E-6	3.9E-4	0.92	2.4E-4	0.0043
213689_x_at	*FAM69A*	1	23	0.53	0.52	0.52	2.1E-6	1.1E-5	3.2E-6	4.4E-5	0.30	2.7E-5	0.0013
210638_s_at	*FBXO9*	6	13	0.43	0.42	0.43	3.3E-6	1.8E-5	5.1E-6	4.1E-4	0.52	2.4E-4	0.0050
216044_x_at	*FAM69A*	1	18	0.44	0.43	0.43	3.4E-6	1.3E-5	4.4E-6	2.1E-4	0.24	1.2E-4	0.0023
203416_at	*CD53*	1	30	0.46	0.46	0.46	3.4E-6	3.6E-5	6.1E-6	0.0013	0.38	9.0E-4	0.011
235168_at	*PIGM*	1	8	0.72	0.71	0.72	8.1E-6	1.5E-5	9.2E-6	3.7E-4	0.91	2.2E-4	0.0041
204950_at	*CARD8*	19	67	0.011	0.011	0.010	8.7E-6	4.9E-5	1.3E-5	0.0025	0.16	0.0016	0.018
1552790_a_at	*TLOC1*	3	55	0.65	0.64	0.66	9.2E-6	2.5E-5	1.2E-5	2.5E-4	0.74	1.8E-4	0.0048
209815_at	*PTCH1*	9	13	0.92	0.91	0.93	1.2E-5	1.8E-5	1.3E-5	1.6E-5	0.32	8.5E-6	2.3E-4
225558_at	*GIT2*	12	51	0.94	0.94	0.94	1.3E-5	2.3E-5	1.9E-5	4.9E-4	0.70	2.6E-4	0.0032
228099_at	*ZNF550*	19	21	0.70	0.71	0.69	1.6E-5	7.3E-5	2.3E-5	4.7E-4	0.24	2.8E-4	0.0041
214109_at	*LRBA*	4	151	0.75	0.74	0.76	1.7E-5	7.9E-5	2.3E-5	6.7E-4	0.18	4.8E-4	0.0021

219035_s_at	*RNF34*	12	8	0.93	0.92	0.93	1.7E-5	4.4E-5	2.2E-5	0.0012	0.94	7.6E-4	0.010
227565_at	---	4	4	0.15	0.17	0.14	1.8E-5	5.0E-5	2.2E-5	0.0023	0.38	0.0014	0.0032
227045_at	*ZNF614*	19	50	0.11	0.11	0.11	1.9E-5	5.0E-5	2.4E-5	1.9E-4	0.16	1.4E-4	9.2E-4
235291_s_at	*FLJ32255*	5	46	0.057	0.055	0.060	2.1E-5	5.4E-5	2.9E-5	7.7E-4	0.15	5.0E-4	0.0068
225666_at	*TMTC4*	13	97	0.40	0.40	0.40	2.2E-5	4.5E-5	3.0E-5	0.0061	0.99	0.0040	0.024
225429_at	*PPP6C*	9	272	0.59	0.61	0.58	2.2E-5	7.0E-5	3.4E-5	0.0015	0.50	0.0010	0.0054
214085_x_at	*GLIPR1*	12	148	0.059	0.056	0.063	2.4E-5	8.5E-5	3.2E-5	0.0015	0.36	0.0010	0.0094
229123_at	*ZNF225*	19	22	0.48	0.47	0.48	2.4E-5	5.2E-5	3.0E-5	0.0013	0.99	0.0010	0.012
241017_at	*TBC1D8*	2	28	0.58	0.57	0.61	2.9E-5	8.7E-5	3.9E-5	2.5E-4	0.13	1.8E-4	9.0E-4
206099_at	*PRKCH*	14	2	0.60	0.59	0.65	3.1E-5	3.9E-5	3.2E-5	2.5E-4	0.65	1.4E-4	0.0016
213491_x_at	*RPN2*	20	15	0.62	0.64	0.62	3.2E-5	8.2E-5	4.5E-5	0.0011	0.78	0.0010	0.015
224818_at	*SORT1*	1	79	0.038	0.039	0.036	3.2E-5	6.9E-5	5.0E-5	0.0031	0.29	0.0022	0.0080
215693_x_at	*DDX27*	20	20	0.16	0.16	0.16	3.3E-5	8.1E-5	4.7E-5	8.1E-4	0.40	5.0E-4	0.0064
225327_at	*KIAA1370*	15	85	0.59	0.61	0.58	3.4E-5	5.6E-5	4.7E-5	1.6E-4	0.70	1.0E-4	0.0021
208180_s_at	*HIST1H4H*	6	29	0.081	0.083	0.077	3.8E-5	8.9E-5	4.8E-5	0.0025	0.32	0.0014	0.0063
202395_at	*NSF*	17	638	0.72	0.71	0.71	4.0E-5	7.2E-5	6.1E-5	7.9E-4	0.65	4.0E-4	0.0035
227178_at	*CUGBP2*	10	25	0.12	0.13	0.12	4.1E-5	1.0E-4	5.8E-5	0.0012	0.20	8.2E-4	0.010
235531_at	---	3	5	0.57	0.56	0.58	4.3E-5	6.9E-5	4.7E-5	5.7E-4	0.86	3.0E-4	0.0051
202763_at	*CASP3*	4	105	0.19	0.19	0.19	4.5E-5	1.0E-4	6.3E-5	5.3E-4	0.064	3.6E-4	0.0033
208732_at	*RAB2A*	8	152	0.40	0.39	0.42	5.3E-5	1.2E-4	7.6E-5	0.0019	0.48	0.0010	0.0094

238164_at	*USP6NL*	10	2	0.46	0.45	0.48	5.3E-5	5.2E-5	6.1E-5	4.1E-4	0.69	2.2E-4	0.0044
204642_at	*EDG1*	1	19	0.56	0.55	0.57	5.4E-5	1.1E-4	6.8E-5	2.1E-4	0.30	1.2E-4	0.0030

Table S3. P-values of total effect, mediation effect and alternative effect for the top 10 genes with most significant alternative effect (FDR ≤67%) using the asthma data. Symbols and notations are the same as Table 1 in main text.

Probe	Gene	Ch	No. of eQTL	Alternative effect			Mediation effect			Total effect			
				Q_{omb}	Q_{SG}	Q_{SGC}	Q_{omb}	Q_{SG}	Q_{SGC}	Q_{omb}	Q_{S}	Q_{SG}	Q_{SGC}
225074_at	*RAB2B*	14	16	1.5E-4	1.4E-4	1.4E-4	0.33	0.28	0.41	2.3E-4	1.6E-4	2.8E-4	1.4E-4
213875_x_at	*C6orf62*	6	3	1.9E-4	1.8E-4	2.0E-4	0.34	0.27	0.51	1.5E-4	1.2E-4	1.0E-4	1.4E-4
219003_s_at	*MANEA*	6	159	2.9E-4	2.6E-4	2.8E-4	0.0079	0.0076	0.0082	4.8E-7	2.1E-6	2.9E-7	2.8E-7
209932_s_at	*DUT*	15	2	3.5E-4	3.4E-4	3.4E-4	0.38	0.31	0.47	5.3E-4	3.8E-4	4.2E-4	6.6E-4
1555241_at	*C8orf59*	8	203	3.9E-4	3.4E-4	3.8E-4	0.0011	0.0012	0.0012	0.0015	0.012	0.0068	0.001
218191_s_at	*LMBRD1*	6	89	5.1E-4	5.2E-4	5.2E-4	0.0055	0.0054	0.0054	1.2E-4	0.0011	9.6E-5	2.3E-4
225523_at	*MRPL53*	2	175	5.7E-4	5.8E-4	6.2E-4	0.055	0.053	0.060	1.9E-6	1.0E-5	5.2E-6	1.0E-6
1555227_a_at	*MANEA*	6	79	7.5E-4	6.8E-4	0.001	0.088	0.082	0.085	3.8E-5	2.3E-5	3.3E-5	2.0E-5
204836_at	*GLDC*	9	33	8.3E-4	9.6E-4	7.2E-4	0.011	0.010	0.011	0.0037	0.0032	0.0084	0.0022
208809_s_at	*C6orf62*	6	19	9.0E-4	0.001	0.001	0.050	0.043	0.075	3.5E-4	7.8E-4	2.6E-4	2.4E-4

Table S4. Single-locus analyses for eQTL SNPs of *MANEA* (219003_s_at). (Ch: chromosome; ME: mediation effect; AE: alternative effect; CI: confidence interval).

SNP	Ch	Location (Mb)	ME	95% CI		P-value	AE	95% CI		P-value	Proportion Of Mediation
rs2613562	6	95.995	1.04	1.01	1.08	0.01	1.59	1.08	2.24	0.014	0.098
rs6938032	6	95.996	1.05	1.02	1.09	0.003	1.57	1.1	2.1	0.007	0.118
rs9322578	6	95.998	1.05	1.02	1.08	0.002	1.54	1.09	2.05	0.008	0.119
rs9399724	6	95.999	1.05	1.02	1.08	0.002	1.53	1.09	2.04	0.008	0.119
rs2613565	6	96.001	1.04	1.01	1.08	0.009	1.53	1.05	2.14	0.018	0.105
rs2380224	6	96.002	1.14	1.01	1.35	0.08	1.85	0.85	2.84	0.058	0.237
rs2716074	6	96.014	1.14	1.01	1.35	0.081	1.84	0.85	2.82	0.058	0.236
rs2613547	6	96.017	1.14	1.01	1.35	0.081	1.84	0.86	2.81	0.058	0.236
rs2716070	6	96.019	1.14	1.01	1.35	0.081	1.84	0.86	2.81	0.058	0.235
rs2716069	6	96.02	1.14	1.01	1.35	0.081	1.84	0.86	2.81	0.058	0.235
rs2613551	6	96.021	1.14	1.01	1.35	0.081	1.84	0.86	2.81	0.058	0.236
rs7776189	6	96.023	1.05	1.02	1.08	0.003	1.54	1.09	2.06	0.007	0.119
rs2613553	6	96.023	1.14	1.01	1.35	0.081	1.84	0.86	2.81	0.058	0.235
rs9322786	6	96.024	1.05	1.02	1.08	0.003	1.54	1.09	2.06	0.007	0.119
rs10498994	6	96.038	0.93	0.86	0.98	0.042	0.85	0.47	1.17	0.499	0.281
rs877096	6	96.044	1.14	1.01	1.35	0.081	1.84	0.86	2.82	0.058	0.236
rs9486300	6	96.045	1.05	1.02	1.08	0.003	1.55	1.09	2.06	0.007	0.119
rs2613528	6	96.046	1.14	1.01	1.35	0.081	1.84	0.86	2.82	0.058	0.236
rs10046249	6	96.049	1.05	1.02	1.08	0.003	1.55	1.09	2.06	0.007	0.119
rs9386595	6	96.052	0.97	0.94	0.99	0.014	0.76	0.45	1.06	0.222	0.1
rs2386670	6	96.053	1.05	1.02	1.08	0.003	1.55	1.09	2.06	0.007	0.119
rs6939947	6	96.058	1.05	1.02	1.08	0.003	1.55	1.09	2.06	0.007	0.119
rs7449934	6	96.059	0.95	0.9	0.99	0.024	0.79	0.48	1.09	0.277	0.16
rs9400133	6	96.059	1.05	1.02	1.08	0.003	1.55	1.09	2.06	0.007	0.119
rs7757160	6	96.061	1.05	1.02	1.08	0.003	1.55	1.09	2.06	0.007	0.119
rs6939353	6	96.065	1.05	1.02	1.09	0.003	1.55	1.09	2.06	0.007	0.119
rs4535556	6	96.068	1.05	1.02	1.09	0.003	1.55	1.09	2.06	0.007	0.119
rs9386748	6	96.07	1.05	1.02	1.09	0.006	1.47	1.03	2.13	0.031	0.134
rs2380220	6	96.074	1.1	1	1.25	0.072	1.83	0.93	2.93	0.045	0.186
rs2890372	6	96.075	1.04	1.02	1.07	0.003	1.58	1.12	2.11	0.004	0.091
rs4270788	6	96.076	1.1	1	1.23	0.075	1.84	0.92	2.95	0.041	0.175
rs729278	6	96.076	1.04	1.02	1.06	0.003	1.58	1.13	2.12	0.004	0.089
rs6931299	6	96.077	1.09	1	1.22	0.078	1.84	0.94	2.94	0.04	0.168
rs6923253	6	96.077	1.08	1	1.2	0.085	1.83	0.95	2.96	0.039	0.153
rs9374107	6	96.078	1.03	1.01	1.06	0.003	1.58	1.13	2.12	0.004	0.083
rs9400318	6	96.079	1.08	0.99	1.18	0.092	1.83	0.95	2.97	0.039	0.142
rs13196543	6	96.081	0.97	0.93	0.99	0.069	0.8	0.02	1.84	0.884	0.106
rs2380222	6	96.082	1.06	0.99	1.14	0.109	1.81	0.94	2.93	0.043	0.118

rs9386880	6	96.083	1.03	1.01	1.05	0.003	1.58	1.13	2.14	0.004	0.076
rs6568636	6	96.085	1	1	1.01	0.015	1.61	1.11	2.25	0.009	0.008
rs9374178	6	96.087	1.07	1.01	1.16	0.061	1.57	0.89	2.33	0.065	0.167
rs9374179	6	96.087	0.96	0.91	0.99	0.03	0.76	0.43	1.06	0.228	0.121
rs9400397	6	96.087	1.07	1.01	1.16	0.059	1.57	0.89	2.32	0.063	0.167
rs9384792	6	96.095	1.03	1.02	1.06	0.002	1.49	1.06	2.01	0.016	0.095
rs4448101	6	96.095	1.02	1.01	1.05	0.011	1.5	1.02	2.09	0.029	0.067
rs4546494	6	96.097	1.06	0.99	1.13	0.123	1.73	0.85	2.88	0.077	0.117
rs7754906	6	96.099	1.07	1.01	1.16	0.056	1.37	0.8	2	0.202	0.21
rs9481199	6	96.101	0.99	0.98	1	0.085	1.2	0.76	1.73	0.431	-0.052
rs9320386	6	96.102	1.06	0.99	1.14	0.133	1.76	0.86	2.92	0.069	0.116
rs7744714	6	96.102	1.04	1.02	1.08	0.004	1.34	0.95	1.87	0.093	0.14
rs4435952	6	96.102	1.05	1.02	1.08	0.004	1.31	0.91	1.86	0.147	0.164
rs7750757	6	96.104	1.07	0.99	1.16	0.114	1.94	0.99	3.29	0.028	0.121
rs7766765	6	96.104	1.07	1	1.15	0.087	1.36	0.76	2.03	0.215	0.197
rs9400526	6	96.105	1.07	1	1.15	0.088	1.36	0.76	2.03	0.213	0.196
rs11153357	6	96.105	0.96	0.92	0.98	0.012	0.75	0.42	1.06	0.225	0.112
rs9374321	6	96.106	1.04	1.02	1.08	0.006	1.34	0.91	1.88	0.117	0.141
rs9487909	6	96.106	0.98	0.95	1.02	0.366	1.38	0.75	2.11	0.267	-0.067
rs4560656	6	96.106	1.05	1.02	1.09	0.005	1.44	1.03	2.03	0.038	0.139
rs9400554	6	96.107	1.05	1.02	1.09	0.005	1.44	1.03	2.03	0.038	0.139
rs7748857	6	96.109	1.07	0.99	1.17	0.13	2.01	1.03	3.35	0.024	0.119
rs7749364	6	96.109	0.99	0.99	1	0.093	1.13	0.71	1.65	0.582	-0.059
rs9487975	6	96.11	1.01	1	1.02	0.009	1.26	0.84	1.75	0.207	0.052
rs9488059	6	96.113	0.98	0.95	1.02	0.372	1.36	0.73	2.03	0.299	-0.072
rs9488061	6	96.113	0.98	0.94	1.02	0.376	1.34	0.72	2.02	0.317	-0.076
rs10735717	6	96.114	1.09	1.01	1.21	0.064	1.68	0.94	2.53	0.033	0.18
rs10782175	6	96.114	1.09	1.03	1.17	0.008	1.86	1.26	2.69	0.001	0.164
rs7748108	6	96.115	1.09	1.01	1.2	0.051	1.82	1.1	2.7	0.008	0.166
rs4308568	6	96.116	1.1	1.01	1.24	0.078	2.18	1.14	3.51	0.005	0.155
rs9398365	6	96.12	1.05	1.02	1.09	0.006	1.43	0.99	2.03	0.05	0.14
rs9372382	6	96.121	1.05	1.02	1.09	0.006	1.43	0.99	2.03	0.05	0.14
rs9398367	6	96.121	1.05	1.02	1.09	0.006	1.43	0.99	2.03	0.051	0.139
rs6932267	6	96.121	1.05	1.02	1.09	0.006	1.43	0.99	2.02	0.053	0.139
rs9488308	6	96.122	1.05	1.02	1.09	0.006	1.43	0.99	2.01	0.053	0.138
rs9320497	6	96.128	1.05	1.02	1.09	0.006	1.42	0.99	2.01	0.054	0.138
rs6937479	6	96.13	1.05	1.02	1.1	0.005	1.56	1.12	2.18	0.01	0.13
rs9374502	6	96.131	1.05	1.02	1.08	0.004	1.49	1.07	2.08	0.023	0.124
rs9384949	6	96.138	1.05	1.02	1.08	0.006	1.42	0.99	1.99	0.057	0.136
rs9387352	6	96.139	1.05	1.02	1.08	0.006	1.41	0.99	1.99	0.057	0.136
rs7758062	6	96.14	1.04	1.01	1.07	0.007	1.41	0.98	2.04	0.067	0.116
rs9374586	6	96.142	1.04	1.01	1.07	0.007	1.42	0.99	2.04	0.065	0.107
rs6940020	6	96.143	1.05	1.02	1.08	0.006	1.41	0.99	1.98	0.06	0.136

rs9400893	6	96.145	1.05	1.02	1.08	0.006	1.41	0.99	1.98	0.06	0.136
rs9372457	6	96.145	1.05	1.02	1.08	0.006	1.41	0.99	1.98	0.06	0.136
rs9488910	6	96.146	1.05	1.02	1.09	0.004	1.47	1.06	2.06	0.026	0.127
rs9320566	6	96.148	1.05	1.02	1.08	0.006	1.41	0.99	1.98	0.06	0.136
rs7773709	6	96.148	1.05	1.02	1.08	0.006	1.41	0.99	1.98	0.06	0.136
rs4498363	6	96.149	1.1	1	1.25	0.075	2.24	1.18	3.62	0.004	0.158
rs7757276	6	96.149	0.98	0.95	1.02	0.37	1.33	0.7	2	0.329	-0.075
rs4466257	6	96.15	1.05	1.02	1.08	0.006	1.41	0.99	1.98	0.06	0.136
rs9387442	6	96.153	1.06	1.02	1.11	0.007	1.7	1.1	2.48	0.01	0.121
rs4486026	6	96.155	1.05	1.02	1.08	0.006	1.45	1.01	2.03	0.038	0.126
rs1133503	6	96.161	1.05	1.02	1.08	0.006	1.41	0.99	1.98	0.06	0.136
rs9387522	6	96.162	1.05	1.02	1.08	0.006	1.41	0.99	1.98	0.06	0.136
rs9387567	6	96.165	1.05	1.02	1.1	0.005	1.54	1.1	2.14	0.011	0.135
rs9387591	6	96.168	1.05	1.02	1.08	0.006	1.41	0.99	1.98	0.06	0.136
rs4339467	6	96.168	1.05	1.02	1.08	0.004	1.47	1.05	2.06	0.026	0.127
rs9387601	6	96.17	1.05	1.02	1.08	0.004	1.47	1.05	2.06	0.026	0.127
rs9387603	6	96.17	1.05	1.02	1.08	0.006	1.41	0.99	1.98	0.06	0.136
rs9387605	6	96.17	1.05	1.02	1.08	0.006	1.41	0.99	1.98	0.06	0.136
rs9489578	6	96.172	1.05	1.02	1.08	0.006	1.41	0.99	1.98	0.06	0.136
rs7774322	6	96.173	1.05	1.02	1.08	0.006	1.41	0.99	1.98	0.06	0.136
rs12333032	6	96.174	1.05	1.02	1.08	0.006	1.41	0.99	1.98	0.06	0.136
rs9481950	6	96.178	1.04	1.01	1.07	0.007	1.42	0.99	2.06	0.065	0.106
rs6926916	6	96.181	1.05	1.02	1.08	0.004	1.48	1.06	2.08	0.025	0.125
rs6937569	6	96.188	1.05	1.02	1.08	0.004	1.49	1.06	2.11	0.024	0.122
rs4413619	6	96.19	0.98	0.93	0.99	0.131	0.78	0	1.5	0.903	0.08
rs4579361	6	96.191	0.94	0.82	0.98	0.184	0.87	0	1.62	0.944	0.277
rs4074107	6	96.192	0.94	0.81	0.98	0.188	0.86	0	1.62	0.945	0.285
rs9490118	6	96.192	0.99	0.96	1.02	0.356	1.44	0.74	2.21	0.228	-0.046
rs9490131	6	96.193	0.97	0.93	0.99	0.02	0.65	0.38	0.93	0.06	0.057
rs7767166	6	96.195	0.96	0.93	0.99	0.017	0.71	0.42	1.01	0.126	0.084
rs12525999	6	96.197	1.02	0.99	1.05	0.212	1.72	0.97	2.56	0.038	0.044
rs12529535	6	96.198	1.02	0.99	1.05	0.211	1.72	0.97	2.56	0.038	0.044
rs9398717	6	96.212	0.97	0.93	0.99	0.018	0.7	0.42	1	0.123	0.076
rs9375221	6	96.213	0.97	0.93	0.99	0.018	0.7	0.42	1	0.122	0.076
rs9401648	6	96.214	0.97	0.93	0.99	0.018	0.7	0.42	0.99	0.122	0.076
rs9320938	6	96.216	1.03	1.01	1.07	0.035	1.62	0.91	2.33	0.04	0.078
rs9482561	6	96.226	0.97	0.93	0.99	0.018	0.71	0.43	0.99	0.121	0.076
rs11154243	6	96.226	0.97	0.93	0.99	0.018	0.71	0.43	0.99	0.121	0.076
rs9375380	6	96.231	0.97	0.93	0.99	0.018	0.71	0.43	0.99	0.121	0.076
rs7740900	6	96.234	0.97	0.93	0.99	0.019	0.7	0.42	0.99	0.12	0.075
rs7764473	6	96.234	0.97	0.93	0.99	0.019	0.7	0.42	0.99	0.119	0.075
rs4535555	6	96.25	0.95	0.9	0.99	0.033	0.7	0.42	0.97	0.112	0.102
rs11758159	6	96.254	0.94	0.87	0.98	0.026	0.68	0.4	0.92	0.077	0.119

rs6913326	6	96.256	0.95	0.9	0.99	0.032	0.7	0.42	0.96	0.102	0.099
rs13215970	6	96.256	0.94	0.9	0.98	0.011	0.62	0.4	0.85	0.02	0.086
rs4382270	6	96.266	0.95	0.9	0.99	0.031	0.69	0.42	0.95	0.093	0.098
rs6933408	6	96.267	0.95	0.9	0.99	0.034	0.69	0.41	0.95	0.093	0.098
rs9388655	6	96.267	0.95	0.9	0.99	0.034	0.69	0.41	0.95	0.093	0.098
rs9482958	6	96.271	0.95	0.9	0.99	0.034	0.69	0.41	0.95	0.092	0.098
rs12662075	6	96.279	0.94	0.88	0.98	0.025	0.67	0.4	0.91	0.065	0.113
rs9388798	6	96.287	0.95	0.9	0.99	0.031	0.69	0.42	0.95	0.092	0.097
rs7765615	6	96.288	0.94	0.88	0.98	0.025	0.67	0.4	0.91	0.065	0.112
rs9321246	6	96.288	0.95	0.9	0.99	0.031	0.69	0.42	0.95	0.091	0.097
rs11757682	6	96.291	0.95	0.9	0.99	0.025	0.64	0.35	0.91	0.071	0.08
rs12213767	6	96.292	0.95	0.9	0.99	0.033	0.68	0.41	0.95	0.089	0.098
rs9388907	6	96.297	0.95	0.89	0.99	0.036	0.67	0.39	0.94	0.084	0.1
rs7743203	6	96.31	1.05	0.99	1.12	0.127	1.73	0.96	2.49	0.028	0.101
rs9389160	6	96.325	0.93	0.85	1	0.088	0.67	0.36	0.95	0.103	0.116
rs9493940	6	96.326	0.93	0.85	1	0.089	0.67	0.36	0.95	0.102	0.116
rs13212315	6	96.333	0.94	0.89	0.97	0.005	0.51	0.32	0.7	0.001	0.061
rs4840033	6	96.335	0.93	0.87	0.97	0.011	0.58	0.37	0.8	0.006	0.087
rs13203167	6	96.336	0.94	0.89	0.97	0.005	0.51	0.33	0.71	0.001	0.062
rs17774669	6	96.338	0.93	0.87	0.97	0.011	0.58	0.37	0.8	0.006	0.088
rs12530302	6	96.34	0.93	0.87	0.97	0.011	0.58	0.37	0.8	0.006	0.088
rs13206934	6	96.342	0.93	0.87	0.97	0.011	0.58	0.38	0.81	0.006	0.089
rs12200752	6	96.344	0.94	0.89	0.98	0.011	0.59	0.39	0.82	0.007	0.079
rs1857482	6	96.346	0.93	0.87	0.97	0.011	0.58	0.38	0.81	0.006	0.09
rs9494535	6	96.347	0.94	0.89	0.98	0.011	0.59	0.39	0.82	0.007	0.08
rs13205985	6	96.352	0.93	0.87	0.97	0.011	0.59	0.39	0.81	0.006	0.091
rs9494669	6	96.353	0.94	0.89	0.98	0.011	0.59	0.39	0.82	0.007	0.081
rs9494677	6	96.353	0.94	0.89	0.98	0.011	0.59	0.39	0.82	0.007	0.081
rs11154931	6	96.356	0.94	0.89	0.97	0.005	0.52	0.33	0.71	0.001	0.065
rs10872473	6	96.356	0.93	0.87	0.97	0.011	0.59	0.38	0.83	0.009	0.094
rs9321610	6	96.356	0.94	0.89	0.98	0.011	0.59	0.38	0.83	0.009	0.082
rs4493748	6	96.358	0.93	0.87	0.97	0.011	0.59	0.37	0.84	0.011	0.095
rs13203882	6	96.359	0.93	0.87	0.97	0.011	0.59	0.37	0.84	0.012	0.095
rs9399238	6	96.366	0.94	0.89	0.98	0.011	0.59	0.37	0.85	0.014	0.083
rs9321670	6	96.368	0.94	0.89	0.98	0.011	0.59	0.37	0.85	0.014	0.083

Table S5. Single-locus analyses for eQTL SNPs of *MRPL53*. (Ch: chromosome; ME: mediation effect; AE: alternative effect; CI: confidence interval).

SNP	Ch	Location (Mb)	ME	95% CI		P-value	AE	95% CI		P-value	Proportion Of Mediation
rs6739466	2	74.27	0.74	0.45	1.09	0.174	0.56	0.03	1.44	0.589	0.245
rs17009735	2	74.283	0.75	0.46	1.08	0.175	0.56	0.03	1.37	0.589	0.245
rs13385639	2	74.285	0.75	0.46	1.08	0.175	0.56	0.03	1.37	0.588	0.245
rs10199560	2	74.297	0.75	0.46	1.07	0.17	0.56	0.03	1.38	0.586	0.246
rs6745054	2	74.304	0.94	0.86	1.01	0.137	1.01	0.37	1.58	0.989	1.1
rs7565640	2	74.307	0.73	0.46	1.02	0.129	0.52	0.03	1.32	0.532	0.225
rs3796109	2	74.314	0.68	0.43	0.96	0.075	0.39	0.02	1.13	0.43	0.17
rs872293	2	74.332	0.6	0.31	0.9	0.072	0.27	0	0.93	0.514	0.127
rs6734233	2	74.338	0.88	0.76	0.96	0.036	0.58	0.24	0.99	0.153	0.138
rs3771724	2	74.339	0.88	0.76	0.96	0.036	0.58	0.24	1	0.145	0.137
rs1006502	2	74.34	0.89	0.77	0.96	0.035	0.58	0.25	0.99	0.135	0.136
rs3755438	2	74.342	0.89	0.78	0.96	0.033	0.57	0.26	0.93	0.101	0.125
rs11897130	2	74.349	0.9	0.79	0.97	0.031	0.58	0.27	0.94	0.095	0.124
rs10169443	2	74.352	0.9	0.8	0.97	0.03	0.58	0.29	0.93	0.091	0.124
rs7593190	2	74.353	0.9	0.8	0.97	0.03	0.59	0.29	0.94	0.09	0.123
rs3771727	2	74.357	0.9	0.8	0.97	0.03	0.59	0.29	0.94	0.089	0.123
rs7560244	2	74.369	0.94	0.85	1.01	0.207	0.92	0.36	1.69	0.862	0.409
rs7575147	2	74.369	0.9	0.79	0.97	0.036	0.64	0.29	1.08	0.214	0.156
rs3771731	2	74.37	0.73	0.43	0.95	0.114	0.27	0.01	0.67	0.265	0.091
rs2191309	2	74.371	0.73	0.44	0.95	0.113	0.29	0.01	0.69	0.272	0.097
rs3771733	2	74.375	0.73	0.44	0.95	0.119	0.28	0.01	0.68	0.27	0.095
rs3771735	2	74.381	0.55	0.11	0.82	0.336	0.19	0	0.79	0.895	0.092
rs3771737	2	74.385	0.56	0.11	0.83	0.339	0.19	0	0.8	0.897	0.092
rs9309483	2	74.385	0.91	0.81	0.97	0.053	0.59	0.18	1	0.275	0.119
rs10182348	2	74.386	0.98	0.94	1	0.171	0.63	0.11	1.13	0.496	0.038
rs9789404	2	74.388	0.98	0.93	1	0.171	0.63	0.12	1.13	0.497	0.039
rs2421844	2	74.394	0.97	0.93	1	0.171	0.63	0.12	1.13	0.497	0.041
rs3771738	2	74.394	0.98	0.93	1	0.175	0.78	0.16	1.37	0.67	0.079
rs10185658	2	74.396	0.91	0.8	0.97	0.058	0.6	0.2	0.99	0.277	0.123
rs11126430	2	74.398	0.91	0.8	0.97	0.059	0.6	0.2	0.99	0.277	0.123
rs7567768	2	74.401	0.97	0.93	1	0.17	0.63	0.11	1.14	0.496	0.045
rs10211612	2	74.402	0.91	0.8	0.97	0.06	0.6	0.2	1	0.277	0.124
rs7571411	2	74.402	0.97	0.93	1	0.171	0.78	0.16	1.37	0.67	0.086
rs3771740	2	74.408	0.97	0.92	1	0.168	0.64	0.12	1.16	0.493	0.049
rs3755440	2	74.414	0.97	0.92	1	0.166	0.78	0.17	1.39	0.668	0.093
rs13387588	2	74.416	0.97	0.92	1	0.166	0.64	0.12	1.16	0.491	0.05
rs3771741	2	74.418	0.97	0.92	1	0.16	0.79	0.18	1.39	0.667	0.099
rs2098128	2	74.419	0.91	0.81	0.97	0.061	0.62	0.22	0.99	0.274	0.127

rs7592599	2	74.419	0.97	0.92	1	0.156	0.79	0.19	1.39	0.665	0.102
rs6546902	2	74.42	0.91	0.81	0.97	0.061	0.62	0.22	0.99	0.274	0.127
rs3821303	2	74.421	0.97	0.92	1	0.156	0.65	0.14	1.16	0.481	0.056
rs12151688	2	74.422	0.6	0.12	0.9	0.623	0.24	0	0.85	0.983	0.11
rs3755441	2	74.423	0.97	0.92	1	0.145	0.8	0.21	1.38	0.66	0.11
rs3755442	2	74.424	0.97	0.92	1	0.151	0.66	0.15	1.17	0.476	0.058
rs3755443	2	74.424	0.97	0.92	1	0.15	0.66	0.15	1.17	0.474	0.059
rs3771742	2	74.424	0.97	0.92	1	0.14	0.8	0.22	1.38	0.657	0.113
rs6714954	2	74.426	0.97	0.92	1	0.14	0.8	0.22	1.38	0.657	0.113
rs6732913	2	74.426	0.97	0.92	1	0.146	0.66	0.15	1.16	0.471	0.06
rs6546903	2	74.427	0.97	0.92	1	0.137	0.8	0.22	1.38	0.657	0.115
rs7581836	2	74.431	0.97	0.92	0.99	0.144	0.67	0.16	1.16	0.468	0.061
rs3771744	2	74.432	0.92	0.82	0.98	0.059	0.64	0.25	0.99	0.266	0.129
rs6546904	2	74.433	0.94	0.83	1.01	0.253	0.73	0.19	1.3	0.559	0.13
rs3771747	2	74.437	0.97	0.92	0.99	0.126	0.8	0.23	1.38	0.642	0.117
rs9309484	2	74.44	0.97	0.91	0.99	0.12	0.65	0.16	1.14	0.425	0.061
rs741788	2	74.443	0.97	0.92	0.99	0.11	0.79	0.23	1.38	0.605	0.114
rs909177	2	74.449	0.97	0.92	0.99	0.101	0.79	0.24	1.38	0.587	0.113
rs740277	2	74.451	0.96	0.9	0.99	0.103	0.78	0.23	1.37	0.587	0.136
rs2075743	2	74.456	1.08	1	1.22	0.171	0.32	0	0.73	0.494	-0.037
rs3213672	2	74.458	1.08	1	1.22	0.171	0.32	0.01	0.73	0.493	-0.036
rs3815241	2	74.458	1.07	1	1.21	0.171	0.32	0.01	0.73	0.49	-0.035
rs3771748	2	74.46	0.94	0.85	0.99	0.103	0.64	0.17	1.15	0.366	0.1
rs6713611	2	74.465	0.94	0.86	0.99	0.098	0.78	0.24	1.35	0.575	0.182
rs6745355	2	74.466	0.94	0.85	0.99	0.102	0.64	0.17	1.14	0.362	0.104
rs6740802	2	74.47	0.92	0.8	0.98	0.115	0.62	0.15	1.08	0.325	0.115
rs7570851	2	74.472	0.92	0.8	0.98	0.107	0.77	0.23	1.36	0.535	0.209
rs12328744	2	74.473	0.92	0.79	0.98	0.115	0.63	0.17	1.09	0.325	0.126
rs12328185	2	74.475	0.91	0.79	0.98	0.104	0.63	0.18	1.09	0.312	0.13
rs17009922	2	74.476	0.91	0.79	0.98	0.104	0.78	0.26	1.36	0.543	0.229
rs6751601	2	74.478	0.91	0.78	0.98	0.116	0.64	0.18	1.09	0.329	0.133
rs9309485	2	74.491	0.87	0.73	0.96	0.055	0.61	0.23	1	0.199	0.168
rs10187051	2	74.493	0.87	0.73	0.96	0.055	0.62	0.24	1	0.201	0.172
rs10187076	2	74.493	0.87	0.73	0.96	0.055	0.62	0.24	1.01	0.202	0.174
rs2240444	2	74.495	0.87	0.73	0.96	0.055	0.62	0.24	1.01	0.204	0.176
rs2268424	2	74.502	0.87	0.73	0.96	0.04	0.73	0.32	1.21	0.349	0.261
rs2268420	2	74.508	0.89	0.7	1.03	0.252	0.71	0.14	1.33	0.632	0.212
rs2268421	2	74.508	0.87	0.72	0.96	0.059	0.61	0.23	1	0.19	0.168
rs2268418	2	74.518	0.87	0.72	0.96	0.051	0.63	0.25	1.01	0.196	0.184
rs11694367	2	74.519	0.86	0.73	0.95	0.037	0.73	0.33	1.21	0.331	0.267
rs11695896	2	74.52	0.86	0.73	0.95	0.037	0.73	0.33	1.2	0.327	0.267
rs7556852	2	74.523	0.9	0.79	0.96	0.028	0.86	0.43	1.3	0.59	0.391
rs7562663	2	74.53	0.87	0.72	0.96	0.055	0.62	0.23	1.02	0.198	0.181

rs6746854	2	74.535	0.87	0.71	0.96	0.065	0.6	0.21	0.99	0.183	0.165
rs2268417	2	74.536	0.87	0.73	0.97	0.063	0.63	0.25	1	0.197	0.176
rs2270016	2	74.54	0.88	0.74	0.97	0.066	0.64	0.28	1	0.197	0.176
rs1063588	2	74.544	0.89	0.77	0.98	0.061	0.71	0.35	1.11	0.267	0.214
rs2284708	2	74.546	0.89	0.76	0.98	0.072	0.66	0.3	1	0.202	0.177
rs1047911	2	74.553	0.89	0.77	0.98	0.061	0.71	0.35	1.11	0.267	0.214
rs6707475	2	74.564	0.89	0.76	0.98	0.072	0.66	0.3	1.01	0.205	0.178
rs17009980	2	74.573	0.89	0.76	0.98	0.061	0.71	0.34	1.11	0.267	0.214
rs2301984	2	74.575	0.89	0.76	0.98	0.071	0.66	0.3	1	0.198	0.176
rs3755445	2	74.576	0.89	0.76	0.98	0.071	0.66	0.3	1	0.194	0.175
rs3755446	2	74.576	0.89	0.75	0.98	0.071	0.65	0.3	1	0.192	0.175
rs10454145	2	74.579	0.88	0.75	0.97	0.059	0.69	0.33	1.11	0.241	0.207
rs17009998	2	74.579	0.89	0.75	0.97	0.06	0.7	0.33	1.11	0.245	0.208
rs11688069	2	74.58	0.88	0.75	0.97	0.059	0.69	0.32	1.1	0.236	0.205
rs11676323	2	74.583	0.88	0.75	0.97	0.059	0.69	0.32	1.1	0.235	0.205
rs2240443	2	74.586	0.87	0.73	0.97	0.053	0.7	0.31	1.16	0.304	0.232
rs3806607	2	74.589	0.88	0.74	0.98	0.075	0.61	0.27	0.97	0.145	0.154
rs997564	2	74.591	0.73	0.31	0.98	0.391	0.13	0	0.54	0.774	0.039
rs3755447	2	74.594	0.88	0.74	0.97	0.067	0.63	0.29	0.98	0.16	0.167
rs3815476	2	74.599	0.94	0.78	1.01	0.367	0.28	0	0.63	0.553	0.022
rs6546909	2	74.6	0.91	0.8	1	0.119	0.53	0.26	0.82	0.038	0.09
rs10779958	2	74.609	0.91	0.8	1	0.115	0.55	0.27	0.87	0.045	0.095
rs2231250	2	74.61	0.91	0.8	1	0.115	0.55	0.27	0.87	0.043	0.094
rs2241028	2	74.612	0.94	0.78	1.01	0.379	0.27	0	0.63	0.577	0.021
rs6707302	2	74.615	0.91	0.79	1	0.117	0.52	0.26	0.8	0.031	0.087
rs715407	2	74.619	0.91	0.8	0.99	0.105	0.56	0.29	0.89	0.046	0.1
rs11126435	2	74.643	0.93	0.8	1.01	0.253	0.34	0.12	0.55	0.035	0.035
rs2021725	2	74.656	0.93	0.8	1.01	0.233	0.34	0.12	0.55	0.032	0.035
rs752070	2	74.678	0.93	0.8	1.01	0.215	0.33	0.11	0.54	0.028	0.035
rs363691	2	74.695	0.93	0.77	1.01	0.294	0.32	0.09	0.53	0.052	0.033
rs363697	2	74.701	0.95	0.79	1.01	0.436	0.24	0	0.59	0.698	0.016
rs205651	2	74.71	0.97	0.93	0.99	0.037	0.77	0.52	1.1	0.172	0.095
rs6739708	2	74.719	0.92	0.79	1.01	0.21	0.31	0.11	0.5	0.024	0.033
rs7603085	2	74.722	0.93	0.81	1	0.192	0.35	0.13	0.56	0.028	0.038
rs6546917	2	74.727	0.92	0.8	1	0.163	0.33	0.13	0.52	0.013	0.037
rs6718184	2	74.727	0.93	0.8	1	0.186	0.35	0.13	0.56	0.025	0.038
rs363607	2	74.75	0.92	0.8	1	0.158	0.31	0.13	0.5	0.008	0.035
rs10200121	2	74.753	0.92	0.81	1	0.125	0.34	0.14	0.53	0.006	0.039
rs3025991	2	74.753	0.92	0.81	1	0.121	0.34	0.14	0.53	0.005	0.039
rs205648	2	74.754	0.92	0.81	1	0.118	0.34	0.15	0.54	0.004	0.039
rs2075214	2	74.755	0.93	0.84	0.99	0.09	0.37	0.17	0.57	0.006	0.041
rs363608	2	74.755	0.92	0.82	0.99	0.107	0.34	0.15	0.54	0.004	0.041
rs363609	2	74.756	0.92	0.82	1	0.111	0.35	0.16	0.54	0.004	0.04

rs13387355	2	74.757	0.92	0.82	1	0.112	0.35	0.16	0.55	0.004	0.04
rs363610	2	74.759	0.92	0.82	1	0.122	0.35	0.16	0.55	0.004	0.04
rs363611	2	74.76	0.93	0.82	1	0.131	0.36	0.16	0.57	0.005	0.04
rs3771749	2	74.761	0.93	0.82	1	0.131	0.36	0.16	0.57	0.005	0.04
rs3025994	2	74.762	0.93	0.82	1	0.131	0.36	0.16	0.57	0.005	0.04
rs6716578	2	74.763	0.93	0.82	1	0.131	0.36	0.16	0.57	0.005	0.04
rs363612	2	74.765	0.93	0.82	1	0.131	0.36	0.16	0.57	0.005	0.04
rs10183097	2	74.768	0.93	0.82	1	0.134	0.36	0.16	0.56	0.005	0.039
rs363614	2	74.769	0.93	0.82	1	0.135	0.35	0.16	0.56	0.005	0.039
rs363647	2	74.769	0.93	0.82	1	0.134	0.36	0.16	0.56	0.005	0.039
rs2022187	2	74.77	0.93	0.82	1	0.136	0.35	0.16	0.56	0.005	0.039
rs363615	2	74.771	0.93	0.82	1	0.136	0.35	0.16	0.56	0.005	0.039
rs363617	2	74.772	0.93	0.82	1	0.135	0.35	0.16	0.56	0.005	0.039
rs363618	2	74.773	0.93	0.82	1	0.135	0.35	0.16	0.56	0.005	0.039
rs11691947	2	74.774	0.93	0.82	1	0.138	0.35	0.16	0.56	0.005	0.039
rs6734139	2	74.778	0.93	0.82	1	0.14	0.35	0.16	0.56	0.005	0.039
rs363619	2	74.779	0.93	0.82	1	0.14	0.35	0.16	0.56	0.005	0.039
rs7355739	2	74.78	0.93	0.82	1	0.143	0.35	0.16	0.56	0.005	0.039
rs2041835	2	74.781	0.93	0.82	1	0.145	0.35	0.16	0.56	0.005	0.038
rs11126439	2	74.782	0.93	0.82	1	0.146	0.35	0.16	0.56	0.005	0.038
rs363620	2	74.782	0.93	0.82	1	0.147	0.35	0.16	0.56	0.005	0.038
rs363621	2	74.782	0.93	0.82	1	0.149	0.35	0.16	0.56	0.005	0.038
rs11126440	2	74.783	0.93	0.82	1	0.155	0.35	0.16	0.55	0.005	0.038
rs363622	2	74.783	0.93	0.82	1	0.152	0.35	0.16	0.56	0.005	0.038
rs363668	2	74.783	0.93	0.82	1	0.152	0.35	0.16	0.56	0.005	0.038
rs363670	2	74.783	0.93	0.82	1	0.156	0.35	0.16	0.55	0.005	0.038
rs3026000	2	74.784	0.93	0.82	1	0.157	0.35	0.16	0.55	0.005	0.037
rs363624	2	74.784	0.93	0.82	1	0.158	0.35	0.15	0.55	0.005	0.037
rs363625	2	74.784	0.93	0.82	1	0.159	0.35	0.16	0.55	0.005	0.037
rs363626	2	74.785	0.93	0.82	1.01	0.16	0.34	0.16	0.55	0.005	0.037
rs363627	2	74.785	0.93	0.82	1.01	0.161	0.34	0.16	0.55	0.005	0.037
rs363628	2	74.785	0.93	0.82	1.01	0.162	0.34	0.16	0.55	0.005	0.037
rs363629	2	74.787	0.93	0.82	1.01	0.164	0.34	0.16	0.55	0.005	0.037
rs363630	2	74.787	0.93	0.82	1.01	0.164	0.34	0.16	0.55	0.005	0.037
rs363673	2	74.787	0.93	0.82	1.01	0.164	0.35	0.16	0.55	0.005	0.037
rs9636445	2	74.787	0.93	0.82	1.01	0.163	0.34	0.16	0.55	0.005	0.037
rs9636446	2	74.787	0.93	0.82	1.01	0.163	0.34	0.16	0.55	0.005	0.037
rs12615011	2	74.788	0.93	0.82	1.01	0.164	0.35	0.16	0.55	0.005	0.037
rs12621560	2	74.788	0.93	0.82	1.01	0.164	0.35	0.16	0.55	0.005	0.037
rs205645	2	74.792	0.96	0.92	0.99	0.053	0.49	0.23	0.74	0.024	0.035
rs1137	2	74.793	0.96	0.92	0.99	0.054	0.49	0.23	0.73	0.023	0.035
rs150138	2	74.793	0.96	0.92	0.99	0.054	0.49	0.23	0.73	0.023	0.035
rs205643	2	74.796	0.96	0.92	0.99	0.055	0.49	0.22	0.73	0.024	0.034

rs205638	2	74.804	0.96	0.92	0.99	0.057	0.49	0.22	0.74	0.025	0.033
rs205636	2	74.805	0.96	0.92	0.99	0.056	0.49	0.21	0.74	0.028	0.033
rs205637	2	74.805	0.96	0.92	0.99	0.056	0.49	0.21	0.74	0.028	0.034
rs12621015	2	74.807	0.9	0.74	1	0.172	0.34	0.05	0.64	0.193	0.05
rs205634	2	74.809	0.97	0.93	0.99	0.064	0.48	0.21	0.74	0.031	0.028
rs205631	2	74.812	0.95	0.88	1	0.122	0.43	0.18	0.69	0.015	0.035
rs6710960	2	74.814	0.89	0.75	0.99	0.103	0.37	0.03	0.78	0.269	0.06
rs10185931	2	74.815	0.9	0.74	1.01	0.196	0.41	0.03	0.82	0.544	0.068

Table S6. Single-locus analyses for eQTL SNPs of *LYCAT*. (Ch: chromosome; ME: mediation effect; AE: alternative effect; CI: confidence interval).

SNP	Ch	Location (Mb)	ME	95% CI		P-value	AE	95% CI		P-value	Proportion Of Mediation
rs829613	2	30.484	0.84	0.71	0.91	0.004	1.13	0.7	2.17	0.671	3.42
rs829614	2	30.484	0.84	0.71	0.91	0.004	1.13	0.7	2.17	0.671	3.42
rs829610	2	30.485	0.84	0.71	0.91	0.004	1.13	0.71	2.15	0.672	3.38
rs829611	2	30.485	0.84	0.71	0.91	0.004	1.13	0.71	2.15	0.671	3.4
rs829612	2	30.485	0.84	0.71	0.91	0.004	1.13	0.7	2.16	0.671	3.4
rs829603	2	30.489	0.94	0.88	0.96	0.007	0.75	0.49	1.21	0.197	0.156
rs2076932	2	30.49	0.86	0.77	0.92	0.001	0.77	0.47	1.18	0.258	0.316
rs829601	2	30.49	0.93	0.87	0.96	0.008	0.77	0.52	1.24	0.236	0.187
rs12990925	2	30.491	0.82	0.71	0.89	0.001	0.74	0.4	1.25	0.286	0.346
rs711240	2	30.491	0.94	0.87	0.96	0.007	0.78	0.53	1.23	0.242	0.189
rs829596	2	30.493	0.94	0.88	0.97	0.007	0.76	0.51	1.18	0.188	0.163
rs711237	2	30.503	0.94	0.88	0.97	0.007	0.77	0.52	1.19	0.201	0.164
rs864910	2	30.504	0.94	0.88	0.97	0.008	0.77	0.52	1.21	0.22	0.171
rs829697	2	30.506	1.11	0.95	1.5	0.381	0.82	0.29	1.54	0.657	-0.981
rs12714306	2	30.508	0.94	0.87	0.97	0.011	0.79	0.52	1.29	0.279	0.191
rs6727836	2	30.508	0.95	0.9	0.97	0.005	0.81	0.54	1.24	0.308	0.185
rs829692	2	30.51	1.1	0.95	1.5	0.383	0.83	0.29	1.55	0.658	-0.973
rs829693	2	30.511	0.77	0.6	0.87	0.008	0.73	0.47	1.18	0.19	0.386
rs829689	2	30.515	0.77	0.6	0.88	0.01	0.73	0.47	1.2	0.193	0.388
rs1723175	2	30.521	0.77	0.59	0.89	0.016	0.72	0.47	1.16	0.164	0.375
rs13017224	2	30.522	0.86	0.74	0.94	0.011	0.94	0.51	1.34	0.814	0.682
rs13413678	2	30.522	0.7	0.42	0.87	0.063	0.77	0.47	2.03	0.514	0.504
rs1662955	2	30.524	0.77	0.6	0.9	0.018	0.73	0.48	1.17	0.168	0.378
rs1723156	2	30.529	0.77	0.6	0.9	0.018	0.73	0.48	1.17	0.168	0.378
rs1612616	2	30.53	0.77	0.6	0.9	0.018	0.73	0.48	1.17	0.168	0.378
rs1614348	2	30.53	0.77	0.6	0.9	0.018	0.73	0.48	1.17	0.168	0.378
rs829584	2	30.531	0.77	0.6	0.9	0.018	0.73	0.48	1.17	0.169	0.378
rs829576	2	30.534	0.77	0.6	0.9	0.018	0.73	0.48	1.17	0.169	0.378
rs17394450	2	30.535	0.94	0.9	0.96	0	0.72	0.3	1.16	0.351	0.141
rs829573	2	30.536	0.77	0.6	0.9	0.018	0.73	0.48	1.17	0.17	0.378
rs829571	2	30.537	0.77	0.6	0.9	0.018	0.73	0.48	1.17	0.17	0.378
rs10198587	2	30.539	0.7	0.43	0.87	0.067	0.78	0.47	2.05	0.526	0.506
rs12469849	2	30.539	0.7	0.43	0.87	0.067	0.78	0.47	2.05	0.526	0.507
rs10199517	2	30.54	0.92	0.87	0.95	0	0.69	0.34	1.12	0.194	0.149
rs829568	2	30.541	1.09	0.94	1.44	0.412	0.83	0.29	1.56	0.659	-0.748
rs10169001	2	30.542	0.7	0.43	0.87	0.067	0.78	0.47	2.05	0.528	0.506
rs10208299	2	30.542	0.7	0.43	0.87	0.067	0.78	0.47	2.05	0.529	0.506
rs10208587	2	30.542	0.7	0.43	0.87	0.067	0.78	0.47	2.06	0.529	0.506

rs11901989	2	30.542	0.7	0.43	0.87	0.067	0.78	0.47	2.05	0.527	0.506
rs13430515	2	30.543	0.71	0.43	0.87	0.068	0.78	0.47	2.06	0.53	0.506
rs13430622	2	30.543	0.71	0.43	0.87	0.068	0.78	0.47	2.06	0.531	0.506
rs1997036	2	30.543	0.7	0.43	0.87	0.068	0.78	0.47	2.06	0.529	0.506
rs1997037	2	30.543	0.7	0.43	0.87	0.068	0.78	0.47	2.06	0.53	0.506
rs13424441	2	30.545	0.71	0.43	0.87	0.068	0.78	0.47	2.06	0.531	0.506
rs829566	2	30.546	1.11	0.96	1.48	0.351	0.89	0.35	1.73	0.769	-5.22
rs1357850	2	30.549	0.87	0.79	0.92	0.001	0.72	0.45	1.14	0.159	0.249
rs829562	2	30.549	0.77	0.6	0.9	0.018	0.73	0.48	1.18	0.175	0.379
rs1357849	2	30.55	0.91	0.85	0.94	0	0.67	0.33	1.09	0.17	0.163
rs2692041	2	30.55	0.77	0.6	0.9	0.017	0.73	0.47	1.18	0.171	0.377
rs829645	2	30.55	0.77	0.6	0.9	0.018	0.73	0.48	1.18	0.176	0.379
rs13393150	2	30.552	0.71	0.44	0.88	0.069	0.78	0.47	2.06	0.536	0.505
rs4952129	2	30.552	0.71	0.44	0.88	0.069	0.78	0.47	2.06	0.535	0.505
rs4952130	2	30.552	0.71	0.44	0.88	0.069	0.78	0.47	2.06	0.535	0.505
rs829643	2	30.552	1.11	0.96	1.48	0.354	0.88	0.35	1.72	0.761	-3.97
rs829640	2	30.554	1.11	0.96	1.48	0.355	0.88	0.35	1.72	0.758	-3.65
rs711241	2	30.555	1.11	0.96	1.48	0.355	0.88	0.35	1.72	0.758	-3.6
rs2363294	2	30.561	0.71	0.44	0.88	0.069	0.78	0.47	2.06	0.538	0.504
rs829683	2	30.562	1.1	0.96	1.47	0.356	0.88	0.35	1.72	0.755	-3.32
rs4952132	2	30.563	0.72	0.45	0.88	0.069	0.78	0.47	2.06	0.539	0.503
rs829676	2	30.564	1.1	0.96	1.47	0.358	0.88	0.36	1.71	0.749	-2.87
rs829674	2	30.565	1.1	0.96	1.47	0.358	0.88	0.36	1.71	0.748	-2.8
rs10180482	2	30.568	0.88	0.8	0.93	0.001	0.73	0.46	1.13	0.164	0.243
rs1723167	2	30.568	0.78	0.61	0.9	0.019	0.72	0.47	1.15	0.159	0.362
rs11899182	2	30.57	0.72	0.46	0.88	0.068	0.79	0.48	2.05	0.543	0.504
rs829652	2	30.57	1.1	0.96	1.47	0.359	0.87	0.36	1.7	0.738	-2.38
rs829650	2	30.572	0.78	0.61	0.9	0.018	0.74	0.48	1.18	0.191	0.386
rs12476805	2	30.575	0.72	0.43	0.9	0.086	0.78	0.46	2.27	0.57	0.506
rs1880540	2	30.575	0.93	0.88	0.95	0	0.7	0.36	1.09	0.194	0.145
rs17009601	2	30.591	0.72	0.46	0.88	0.068	0.79	0.48	2.06	0.546	0.506
rs829636	2	30.591	0.79	0.62	0.91	0.02	0.73	0.47	1.19	0.177	0.36
rs12467831	2	30.592	0.72	0.46	0.88	0.068	0.79	0.48	2.06	0.546	0.506
rs1252639	2	30.593	0.78	0.61	0.9	0.018	0.74	0.49	1.19	0.195	0.389
rs1252643	2	30.593	0.78	0.61	0.9	0.018	0.74	0.49	1.19	0.195	0.389
rs17038632	2	30.594	0.88	0.8	0.94	0.003	0.92	0.45	1.34	0.797	0.584
rs10170012	2	30.597	0.72	0.46	0.88	0.068	0.79	0.48	2.07	0.546	0.506
rs13034406	2	30.601	0.88	0.8	0.94	0.003	0.93	0.47	1.35	0.827	0.623
rs17322869	2	30.601	0.88	0.8	0.94	0.003	0.92	0.45	1.34	0.797	0.583
rs766880	2	30.602	0.72	0.46	0.88	0.068	0.79	0.48	2.07	0.546	0.506
rs1982286	2	30.603	0.72	0.46	0.88	0.068	0.79	0.48	2.07	0.546	0.506
rs2363311	2	30.603	0.72	0.46	0.88	0.068	0.79	0.48	2.07	0.546	0.506
rs10176138	2	30.604	0.72	0.46	0.88	0.068	0.79	0.48	2.07	0.546	0.506

rs1252627	2	30.604	1.1	0.96	1.47	0.359	0.87	0.36	1.68	0.73	-2.14
rs2028668	2	30.605	0.72	0.46	0.88	0.068	0.79	0.48	2.07	0.546	0.506
rs4952141	2	30.605	0.72	0.46	0.88	0.068	0.79	0.48	2.07	0.546	0.506
rs829621	2	30.605	1.1	0.96	1.47	0.354	0.87	0.36	1.68	0.735	-2.43
rs10206668	2	30.606	0.72	0.46	0.88	0.068	0.79	0.48	2.07	0.546	0.506
rs13432085	2	30.608	0.72	0.46	0.88	0.068	0.79	0.48	2.07	0.546	0.506
rs829623	2	30.609	0.78	0.61	0.9	0.017	0.74	0.49	1.2	0.199	0.394
rs829624	2	30.61	1.11	0.96	1.47	0.344	0.88	0.36	1.7	0.747	-3.25
rs829625	2	30.61	1.11	0.96	1.47	0.343	0.88	0.36	1.7	0.748	-3.3
rs829626	2	30.61	0.96	0.92	0.98	0.013	0.85	0.57	1.3	0.438	0.184
rs829628	2	30.61	0.96	0.92	0.98	0.013	0.85	0.57	1.3	0.438	0.184
rs2167970	2	30.611	0.72	0.46	0.88	0.068	0.79	0.48	2.07	0.546	0.506
rs1404607	2	30.616	0.72	0.46	0.88	0.068	0.79	0.48	2.07	0.546	0.505
rs13413980	2	30.62	0.72	0.46	0.88	0.068	0.79	0.48	2.07	0.546	0.505
rs7562645	2	30.62	0.78	0.61	0.9	0.016	0.75	0.49	1.2	0.203	0.397
rs10495776	2	30.621	0.95	0.89	0.98	0.028	0.83	0.56	1.35	0.403	0.203
rs13417949	2	30.621	0.72	0.46	0.88	0.068	0.79	0.48	2.07	0.546	0.505
rs11692096	2	30.623	1.11	0.96	1.48	0.328	0.89	0.36	1.7	0.766	-6.48
rs6712951	2	30.624	0.96	0.92	0.98	0.013	0.84	0.57	1.29	0.405	0.172
rs10205934	2	30.626	0.96	0.92	0.98	0.013	0.85	0.57	1.3	0.44	0.184
rs12477267	2	30.626	0.72	0.46	0.88	0.068	0.79	0.48	2.07	0.547	0.507
rs13388156	2	30.627	0.72	0.46	0.88	0.067	0.79	0.48	2.08	0.55	0.508
rs13414468	2	30.627	0.72	0.46	0.88	0.067	0.79	0.48	2.09	0.55	0.509
rs4951993	2	30.628	0.72	0.45	0.88	0.066	0.79	0.48	2.1	0.552	0.51
rs10197664	2	30.629	0.96	0.92	0.98	0.013	0.84	0.57	1.29	0.41	0.172
rs4144806	2	30.629	0.72	0.45	0.88	0.066	0.79	0.48	2.11	0.553	0.511
rs17395007	2	30.63	1.12	0.97	1.48	0.311	0.9	0.36	1.69	0.785	-312
rs11901266	2	30.635	1.12	0.97	1.48	0.302	0.9	0.36	1.68	0.797	12.5
rs4951994	2	30.635	0.72	0.45	0.88	0.064	0.79	0.48	2.16	0.559	0.516
rs4952149	2	30.635	0.72	0.45	0.88	0.064	0.79	0.48	2.16	0.558	0.515
rs12621663	2	30.638	0.96	0.92	0.98	0.014	0.86	0.57	1.3	0.449	0.184
rs9789517	2	30.639	0.96	0.92	0.98	0.014	0.86	0.57	1.3	0.45	0.184
rs10201020	2	30.641	0.68	0.36	0.88	0.105	0.83	0.43	5.53	0.774	0.6
rs10495777	2	30.641	0.89	0.81	0.94	0.003	0.93	0.46	1.35	0.816	0.598
rs9309681	2	30.641	0.72	0.45	0.88	0.062	0.79	0.48	2.19	0.563	0.52
rs1869431	2	30.642	0.92	0.87	0.95	0	0.64	0.33	1.03	0.129	0.129
rs12474202	2	30.643	0.71	0.43	0.89	0.067	0.73	0.4	2.65	0.525	0.445
rs17395091	2	30.643	1.12	0.97	1.48	0.29	0.91	0.36	1.68	0.811	5.77
rs4952150	2	30.643	0.71	0.43	0.89	0.068	0.73	0.4	2.65	0.523	0.444
rs7602714	2	30.643	0.96	0.92	0.98	0.014	0.86	0.57	1.31	0.456	0.185
rs12475104	2	30.644	0.71	0.43	0.89	0.067	0.73	0.4	2.65	0.526	0.446
rs11676852	2	30.646	0.96	0.92	0.98	0.014	0.85	0.57	1.29	0.426	0.174
rs1464817	2	30.646	0.98	0.96	0.99	0.007	0.77	0.49	1.16	0.226	0.071

rs13392757	2	30.647	0.77	0.56	0.89	0.033	0.84	0.53	1.88	0.586	0.551
rs11127276	2	30.648	0.96	0.92	0.98	0.014	0.86	0.58	1.31	0.461	0.186
rs17009805	2	30.649	0.71	0.44	0.87	0.059	0.8	0.48	2.34	0.577	0.53
rs2363073	2	30.65	0.96	0.92	0.98	0.014	0.86	0.58	1.31	0.463	0.186
rs4952151	2	30.65	0.71	0.46	0.87	0.043	0.8	0.49	2.09	0.554	0.534
rs17009808	2	30.651	0.71	0.44	0.87	0.058	0.8	0.48	2.38	0.581	0.532
rs4952152	2	30.651	0.71	0.44	0.87	0.059	0.8	0.48	2.37	0.58	0.532
rs11127277	2	30.652	0.71	0.44	0.87	0.058	0.8	0.48	2.39	0.582	0.533
rs12993664	2	30.654	0.89	0.82	0.94	0.002	0.95	0.48	1.36	0.861	0.661
rs7355326	2	30.655	0.71	0.44	0.87	0.057	0.8	0.48	2.48	0.591	0.54
rs7355456	2	30.656	0.71	0.44	0.87	0.057	0.8	0.48	2.49	0.592	0.54
rs2363851	2	30.659	0.71	0.44	0.87	0.057	0.8	0.48	2.49	0.592	0.541
rs4952154	2	30.663	0.7	0.44	0.87	0.057	0.8	0.48	2.49	0.592	0.54
rs2593432	2	30.667	0.95	0.88	0.98	0.031	0.84	0.57	1.37	0.426	0.207
rs2253299	2	30.668	1.13	0.97	1.49	0.251	0.93	0.38	1.66	0.861	2.17
rs10204301	2	30.672	0.7	0.43	0.87	0.057	0.8	0.48	2.47	0.589	0.54
rs13412012	2	30.672	0.7	0.43	0.87	0.058	0.8	0.48	2.46	0.589	0.539
rs2593473	2	30.672	1.13	0.97	1.49	0.246	0.94	0.38	1.66	0.867	2.03
rs2593438	2	30.676	0.95	0.88	0.97	0.031	0.84	0.57	1.36	0.423	0.212
rs13427862	2	30.678	0.7	0.43	0.87	0.058	0.8	0.48	2.44	0.586	0.538
rs10514772	2	30.679	0.7	0.43	0.87	0.058	0.8	0.48	2.44	0.586	0.538
rs1074066	2	30.68	0.7	0.43	0.87	0.058	0.8	0.48	2.43	0.585	0.538
rs4952161	2	30.685	0.7	0.43	0.87	0.059	0.8	0.48	2.43	0.584	0.538
rs4952162	2	30.685	0.7	0.43	0.87	0.059	0.8	0.48	2.42	0.583	0.537
rs1869425	2	30.688	0.7	0.43	0.87	0.059	0.79	0.48	2.4	0.582	0.537
rs2166669	2	30.688	0.7	0.43	0.87	0.059	0.79	0.48	2.4	0.582	0.537
rs11895131	2	30.689	1.14	0.98	1.5	0.233	0.95	0.38	1.66	0.886	1.71
rs7597579	2	30.689	0.7	0.43	0.87	0.06	0.79	0.48	2.37	0.58	0.536
rs11127281	2	30.69	1.14	0.98	1.49	0.232	0.95	0.38	1.66	0.887	1.7
rs4951998	2	30.69	0.7	0.43	0.87	0.06	0.79	0.48	2.35	0.578	0.536
rs1869422	2	30.692	1.14	0.98	1.49	0.228	0.95	0.38	1.66	0.892	1.63
rs4952000	2	30.692	0.7	0.43	0.87	0.06	0.79	0.48	2.34	0.577	0.535
rs4952163	2	30.692	0.7	0.43	0.87	0.06	0.79	0.48	2.33	0.577	0.535
rs6718730	2	30.692	0.89	0.8	0.94	0.003	1.04	0.62	1.52	0.871	1.52
rs958580	2	30.693	0.89	0.81	0.94	0.003	0.96	0.54	1.38	0.869	0.711
rs12469630	2	30.694	0.7	0.42	0.87	0.061	0.79	0.48	2.29	0.575	0.534
rs12469745	2	30.694	0.7	0.42	0.87	0.061	0.79	0.48	2.27	0.573	0.534
rs13419435	2	30.695	0.7	0.42	0.87	0.061	0.79	0.48	2.27	0.572	0.534
rs13383939	2	30.696	0.7	0.42	0.87	0.061	0.79	0.48	2.28	0.572	0.534
rs2084301	2	30.698	0.7	0.42	0.87	0.061	0.79	0.48	2.28	0.571	0.533
rs2100112	2	30.698	0.7	0.42	0.87	0.061	0.79	0.48	2.28	0.57	0.533
rs2100113	2	30.698	0.7	0.42	0.87	0.061	0.79	0.48	2.28	0.571	0.533
rs2593445	2	30.702	1.14	0.98	1.5	0.216	0.96	0.39	1.64	0.908	1.46

rs2609920	2	30.703	1.14	0.98	1.5	0.214	0.96	0.39	1.64	0.911	1.44
rs736256	2	30.708	0.94	0.86	0.97	0.029	0.83	0.56	1.36	0.402	0.234
rs12052260	2	30.71	0.89	0.81	0.94	0.003	0.96	0.54	1.38	0.881	0.73
rs10469986	2	30.711	0.69	0.42	0.87	0.062	0.79	0.48	2.16	0.558	0.531
rs12052683	2	30.711	0.89	0.81	0.94	0.003	0.96	0.53	1.38	0.883	0.734
rs11127282	2	30.712	0.89	0.81	0.94	0.003	0.95	0.5	1.39	0.864	0.685
rs12613783	2	30.712	0.89	0.81	0.94	0.003	0.96	0.53	1.38	0.887	0.741
rs10469987	2	30.713	0.69	0.42	0.87	0.062	0.79	0.48	2.14	0.558	0.532
rs4952003	2	30.714	0.69	0.42	0.87	0.062	0.79	0.48	2.14	0.559	0.533
rs13405340	2	30.715	0.69	0.42	0.87	0.062	0.79	0.48	2.12	0.56	0.535
rs4952004	2	30.715	0.69	0.42	0.87	0.062	0.79	0.48	2.13	0.56	0.533
rs12466818	2	30.716	0.69	0.42	0.87	0.062	0.79	0.48	2.12	0.561	0.535
rs13408621	2	30.716	0.69	0.42	0.87	0.062	0.79	0.48	2.12	0.56	0.535
rs10200589	2	30.717	0.69	0.42	0.87	0.063	0.79	0.48	2.13	0.564	0.537
rs12467646	2	30.717	0.69	0.42	0.87	0.062	0.79	0.48	2.12	0.561	0.535
rs12471868	2	30.717	0.69	0.42	0.87	0.062	0.79	0.48	2.12	0.561	0.535
rs6723023	2	30.718	0.69	0.41	0.87	0.064	0.79	0.48	2.15	0.566	0.538
rs3816593	2	30.719	0.69	0.41	0.86	0.065	0.79	0.47	2.2	0.572	0.541
rs6548026	2	30.726	0.9	0.82	0.95	0.003	0.94	0.55	1.35	0.794	0.617
rs7583600	2	30.726	0.9	0.82	0.95	0.003	0.94	0.55	1.35	0.796	0.62
rs8179733	2	30.727	0.91	0.84	0.95	0.002	0.94	0.5	1.32	0.796	0.578
rs2602777	2	30.733	0.91	0.85	0.96	0.003	0.94	0.52	1.32	0.784	0.559
rs2602775	2	30.737	0.71	0.45	0.9	0.043	1.24	0.74	3.71	0.602	3
rs1864281	2	31.395	0.89	0.76	0.98	0.059	0.89	0.51	1.28	0.632	0.487
rs10153659	2	31.397	0.87	0.68	1.01	0.173	0.88	0.27	1.3	0.783	0.483
rs13397598	2	31.397	0.87	0.67	1	0.173	0.88	0.25	1.32	0.791	0.488

Table S7. Single-locus analyses for eQTL SNPs of *ST8SIA4*. (Ch: chromosome; ME: mediation effect; AE: alternative effect; CI: confidence interval).

SNP	Ch	Location (Mb)	ME	95% CI		P-value	AE	95% CI		P-value	Proportion Of Mediation
rs10059478	5	100.01	1.02	1.01	1.04	0.004	1.52	1.01	2.26	0.033	0.063
rs7736625	5	100.011	1.05	1.02	1.08	0.002	1.49	1.04	2.16	0.032	0.123
rs6861241	5	100.014	1.02	1.01	1.04	0.005	1.54	1.03	2.27	0.027	0.062
rs6866306	5	100.014	1.05	1.03	1.09	0.002	1.24	0.89	1.8	0.247	0.21
rs6880868	5	100.014	1.05	1.02	1.08	0.002	1.5	1.06	2.18	0.026	0.121
rs7718146	5	100.017	1.05	1.03	1.08	0.002	1.52	1.05	2.19	0.026	0.122
rs6879808	5	100.018	1.05	1.03	1.08	0.002	1.52	1.05	2.19	0.026	0.122
rs6888825	5	100.018	1.05	1.03	1.08	0.002	1.52	1.05	2.18	0.026	0.122
rs13188041	5	100.02	1.06	1.03	1.11	0.002	1.26	0.87	1.83	0.219	0.231
rs905829	5	100.02	1.03	1.01	1.06	0.006	1.59	1.06	2.41	0.026	0.077
rs10900756	5	100.022	1.06	1.03	1.11	0.002	1.25	0.86	1.82	0.222	0.232
rs7738040	5	100.026	1.06	1.03	1.11	0.002	1.25	0.86	1.82	0.226	0.232
rs10053332	5	100.027	1.03	1.01	1.06	0.006	1.57	1.05	2.38	0.032	0.077
rs1445173	5	100.028	1.06	1.03	1.11	0.002	1.25	0.86	1.82	0.227	0.233
rs6595366	5	100.03	1.05	1.03	1.09	0.002	1.36	0.97	1.94	0.085	0.166
rs6896126	5	100.03	1.03	1.01	1.06	0.006	1.57	1.04	2.38	0.033	0.078
rs12514914	5	100.033	1.06	1.03	1.11	0.002	1.25	0.86	1.81	0.235	0.235
rs12519913	5	100.033	1.06	1.03	1.11	0.002	1.25	0.86	1.81	0.234	0.235
rs6595367	5	100.034	1.05	1.03	1.1	0.001	1.52	1.04	2.16	0.025	0.137
rs4703110	5	100.037	1.11	0.99	1.31	0.131	1.8	0.74	3.04	0.106	0.202
rs7702043	5	100.044	1.05	1.03	1.1	0.001	1.51	1.03	2.15	0.03	0.139
rs6595380	5	100.047	1.05	1.03	1.09	0.002	1.33	0.95	1.89	0.109	0.172
rs2590411	5	100.048	1.05	1.03	1.09	0.002	1.33	0.94	1.89	0.111	0.173
rs2590413	5	100.05	1.05	1.03	1.09	0.002	1.33	0.94	1.89	0.112	0.173
rs10515269	5	100.054	1.06	1.03	1.11	0.001	1.19	0.82	1.71	0.356	0.276
rs2725112	5	100.054	1.03	1.01	1.06	0.006	1.55	1.03	2.33	0.035	0.078
rs2590421	5	100.055	1.05	1.03	1.09	0.002	1.34	0.95	1.9	0.105	0.17
rs2590422	5	100.056	1.05	1.03	1.09	0.002	1.33	0.95	1.89	0.111	0.173
rs2590424	5	100.057	1.05	1.03	1.09	0.002	1.33	0.94	1.88	0.113	0.173
rs2725110	5	100.058	1.05	1.03	1.09	0.002	1.32	0.94	1.87	0.121	0.177
rs12517897	5	100.059	1.06	1.03	1.11	0.001	1.18	0.82	1.72	0.363	0.28
rs2725106	5	100.06	1.05	1.03	1.09	0.002	1.3	0.92	1.86	0.144	0.173
rs2725107	5	100.06	1.05	1.03	1.09	0.002	1.31	0.93	1.86	0.125	0.179
rs2725105	5	100.061	1.05	1.03	1.09	0.002	1.3	0.92	1.86	0.144	0.173
rs6867428	5	100.061	1.06	1.03	1.1	0.001	1.17	0.81	1.69	0.406	0.282
rs7732166	5	100.071	1.06	1.03	1.1	0.001	1.17	0.81	1.69	0.407	0.282
rs6890822	5	100.076	1.06	1.03	1.1	0.001	1.17	0.81	1.69	0.407	0.282
rs11241664	5	100.081	1.12	1.06	1.22	0.001	1.53	1	2.2	0.035	0.264

rs13173503	5	100.086	1.12	1.06	1.21	0.002	1.35	0.93	1.87	0.104	0.313
rs2590433	5	100.086	1.07	1.01	1.16	0.039	1.77	1.05	2.71	0.019	0.146
rs12515114	5	100.088	1.13	1.06	1.23	0.001	1.55	1.02	2.22	0.029	0.265
rs13163793	5	100.088	1.13	1.06	1.23	0.001	1.55	1.02	2.22	0.029	0.265
rs6875815	5	100.089	1.07	1.01	1.16	0.04	1.77	1.05	2.72	0.019	0.143
rs2590432	5	100.09	1.07	1.01	1.16	0.041	1.77	1.05	2.72	0.018	0.142
rs13158383	5	100.091	1.07	1.01	1.15	0.042	1.78	1.06	2.72	0.018	0.139
rs13162330	5	100.091	1.13	1.06	1.23	0.001	1.55	1.02	2.23	0.028	0.265
rs9986302	5	100.091	1.07	1.01	1.15	0.042	1.78	1.06	2.72	0.018	0.139
rs11241671	5	100.094	1.12	1.06	1.22	0.002	1.36	0.93	1.88	0.096	0.313
rs10751461	5	100.096	1.13	1.06	1.23	0.001	1.55	1.01	2.23	0.029	0.267
rs2120913	5	100.096	1.12	1.06	1.22	0.002	1.36	0.93	1.88	0.097	0.315
rs279090	5	100.099	1.07	1.01	1.15	0.042	1.76	1.03	2.71	0.02	0.14
rs279091	5	100.099	1.07	1.01	1.15	0.042	1.76	1.03	2.71	0.02	0.141
rs157178	5	100.1	1.13	1.07	1.23	0.001	1.54	1.01	2.23	0.03	0.268
rs279095	5	100.101	1.11	1.05	1.2	0.002	1.33	0.91	1.9	0.133	0.311
rs279112	5	100.106	1.07	1.01	1.15	0.043	1.74	1.02	2.69	0.023	0.142
rs279108	5	100.11	1.12	1.06	1.21	0.002	1.37	0.95	1.91	0.084	0.301
rs279109	5	100.11	1.07	1.01	1.15	0.043	1.74	1.01	2.68	0.024	0.143
rs157180	5	100.111	1.13	1.06	1.22	0.001	1.52	1	2.16	0.034	0.268
rs279106	5	100.111	1.13	1.06	1.22	0.001	1.5	0.99	2.13	0.039	0.274
rs279107	5	100.111	1.12	1.06	1.21	0.001	1.27	0.81	1.81	0.246	0.357
rs279105	5	100.113	1.07	1.02	1.15	0.035	1.68	1.03	2.56	0.02	0.144
rs277861	5	100.116	1.07	1.02	1.15	0.029	1.47	0.95	2.2	0.064	0.178
rs2725127	5	100.118	1.08	1.02	1.16	0.024	1.64	1.02	2.45	0.018	0.161
rs157041	5	100.119	1.07	1.02	1.14	0.024	1.48	0.97	2.18	0.048	0.175
rs277863	5	100.119	1.07	1.02	1.15	0.031	1.58	0.99	2.33	0.034	0.158
rs277864	5	100.12	1.07	1.02	1.14	0.023	1.47	0.97	2.16	0.049	0.177
rs277868	5	100.122	1.07	1.02	1.15	0.029	1.56	0.98	2.3	0.037	0.163
rs278493	5	100.123	1.07	1.02	1.15	0.026	1.53	0.97	2.27	0.042	0.169
rs278494	5	100.125	1.06	1.02	1.14	0.028	1.42	0.92	2.08	0.083	0.18
rs278495	5	100.127	1.07	1.02	1.14	0.017	1.44	0.98	2.09	0.052	0.189
rs278496	5	100.128	1.07	1.02	1.14	0.017	1.44	0.98	2.09	0.052	0.189
rs278497	5	100.128	1.07	1.02	1.14	0.017	1.44	0.98	2.09	0.051	0.188
rs2548262	5	100.129	1.07	1.02	1.14	0.017	1.44	0.98	2.09	0.051	0.188
rs278500	5	100.13	1.07	1.02	1.15	0.024	1.51	0.97	2.24	0.046	0.173
rs157181	5	100.131	1.07	1.02	1.15	0.024	1.51	0.97	2.24	0.046	0.173
rs278502	5	100.131	1.07	1.02	1.14	0.017	1.44	0.98	2.09	0.051	0.188
rs32441	5	100.133	1.12	1.06	1.22	0.001	1.31	0.89	1.81	0.14	0.334
rs157043	5	100.135	1.08	1.03	1.16	0.017	1.54	1.01	2.23	0.027	0.179
rs157042	5	100.136	1.07	1.02	1.15	0.025	1.51	0.96	2.24	0.047	0.173
rs276459	5	100.136	1.07	1.02	1.15	0.025	1.51	0.96	2.23	0.048	0.173
rs276458	5	100.137	1.07	1.02	1.15	0.025	1.51	0.96	2.23	0.048	0.173

rs149895	5	100.138	1.07	1.02	1.14	0.017	1.44	0.98	2.09	0.051	0.188
rs277871	5	100.14	1.08	1.03	1.16	0.017	1.54	1.01	2.22	0.028	0.18
rs277872	5	100.14	1.08	1.03	1.16	0.017	1.54	1.01	2.22	0.028	0.18
rs6883673	5	100.145	1.05	1.01	1.11	0.03	1.59	1.06	2.32	0.018	0.123
rs6864315	5	100.152	1.05	1.01	1.1	0.028	1.5	1.02	2.15	0.03	0.125
rs7710701	5	100.153	1.05	1.01	1.11	0.03	1.59	1.06	2.32	0.018	0.124
rs10060686	5	100.154	1.05	1.01	1.1	0.028	1.5	1.02	2.15	0.03	0.125
rs2548261	5	100.155	1.05	1.01	1.1	0.028	1.5	1.02	2.15	0.03	0.125
rs4703115	5	100.156	1.05	1.01	1.1	0.042	1.55	1.01	2.36	0.035	0.116
rs10059953	5	100.157	1.05	1.01	1.1	0.028	1.5	1.02	2.15	0.03	0.125
rs4703116	5	100.157	1.05	1.01	1.1	0.028	1.5	1.02	2.15	0.03	0.125
rs13354552	5	100.158	1.05	1.01	1.1	0.042	1.55	1.01	2.36	0.036	0.116
rs17778837	5	100.159	1.05	1.01	1.1	0.042	1.55	1.01	2.35	0.036	0.116
rs13358607	5	100.16	1.05	1.01	1.1	0.042	1.55	1.01	2.35	0.037	0.117
rs11745097	5	100.161	1.05	1.01	1.1	0.042	1.55	1.01	2.35	0.037	0.117
rs3846626	5	100.161	1.05	1.01	1.1	0.028	1.5	1.02	2.15	0.03	0.125
rs4703117	5	100.162	1.05	1.01	1.1	0.043	1.55	1.01	2.35	0.037	0.117
rs4703118	5	100.164	1.05	1.01	1.1	0.043	1.54	1.01	2.34	0.038	0.117
rs6886392	5	100.164	1.05	1.01	1.1	0.043	1.54	1.01	2.35	0.038	0.117
rs17722835	5	100.167	1.08	0.98	1.27	0.233	1.36	0.59	2.58	0.405	0.242
rs2548274	5	100.167	1.05	1.01	1.1	0.028	1.49	1.02	2.15	0.032	0.126
rs2544920	5	100.169	1.05	1.02	1.1	0.009	1.48	1.03	2.09	0.027	0.133
rs13857	5	100.171	1.05	1.02	1.1	0.013	1.5	1.01	2.18	0.033	0.126
rs11584	5	100.173	1.05	1.02	1.1	0.009	1.47	1.03	2.08	0.028	0.134
rs3776155	5	100.176	1.05	1.02	1.1	0.012	1.49	1	2.16	0.035	0.128
rs10057237	5	100.177	1.05	1.02	1.1	0.012	1.49	1	2.16	0.035	0.128
rs3909452	5	100.178	1.05	1.02	1.11	0.009	1.53	1.04	2.15	0.02	0.137
rs12332642	5	100.183	1.06	1.03	1.12	0.004	1.41	0.94	2.08	0.087	0.176
rs3843478	5	100.183	1.05	1.02	1.1	0.012	1.49	1	2.15	0.036	0.129
rs2544913	5	100.19	1.07	1.03	1.14	0.005	1.39	0.99	1.96	0.059	0.208
rs2548278	5	100.193	1.07	1.03	1.14	0.005	1.39	0.99	1.95	0.059	0.209
rs2548276	5	100.196	1.07	1.03	1.14	0.005	1.39	0.99	1.96	0.06	0.209
rs1559059	5	100.197	1.07	1.03	1.14	0.006	1.42	0.98	2.01	0.061	0.197
rs2548263	5	100.201	1.08	1.04	1.15	0.004	1.45	0.99	2.04	0.039	0.204
rs10078934	5	100.202	1.07	1.03	1.14	0.006	1.42	0.98	2.02	0.059	0.196
rs4703126	5	100.202	1.07	1.03	1.14	0.006	1.42	0.98	2.02	0.059	0.196
rs2548279	5	100.205	1.08	1.04	1.15	0.004	1.45	0.99	2.05	0.039	0.203
rs3756350	5	100.206	1.07	1.03	1.14	0.006	1.43	0.98	2.02	0.059	0.196
rs3822366	5	100.207	1.07	1.03	1.14	0.006	1.43	0.98	2.02	0.058	0.196
rs726971	5	100.21	1.07	1.03	1.14	0.006	1.43	0.98	2.02	0.058	0.196
rs11738152	5	100.211	1.07	1.03	1.14	0.006	1.43	0.98	2.02	0.058	0.195
rs13358325	5	100.211	1.07	1.03	1.14	0.006	1.43	0.98	2.02	0.058	0.195
rs4703127	5	100.214	1.07	1.03	1.14	0.006	1.43	0.98	2.02	0.058	0.195

rs11742480	5	100.219	1.07	1.03	1.14	0.006	1.43	0.98	2.02	0.057	0.195
rs11742504	5	100.219	1.07	1.03	1.14	0.006	1.43	0.99	2.02	0.057	0.195
rs3776167	5	100.222	1.07	1.03	1.14	0.006	1.43	0.99	2.02	0.056	0.195
rs3846627	5	100.222	1.07	1.03	1.14	0.006	1.43	0.99	2.02	0.056	0.195
rs7737721	5	100.223	1.07	1.03	1.14	0.005	1.4	0.99	1.99	0.058	0.206
rs966257	5	100.225	1.07	1.03	1.14	0.006	1.43	0.99	2.02	0.056	0.195
rs3776168	5	100.227	1.08	1.04	1.15	0.005	1.45	1	2.05	0.038	0.203
rs2059845	5	100.229	1.07	1.03	1.14	0.006	1.43	0.99	2.02	0.056	0.195
rs11746550	5	100.232	1.05	0.83	1.42	0.737	1.38	0.12	4.36	0.736	0.143
rs7703643	5	100.237	1.07	1.03	1.14	0.005	1.4	0.98	1.99	0.058	0.206
rs10043056	5	100.239	1.07	1.03	1.14	0.006	1.43	0.98	2.02	0.056	0.195
rs3776170	5	100.239	1.07	1.03	1.14	0.005	1.4	0.98	1.98	0.058	0.207
rs3776171	5	100.24	1.07	1.03	1.13	0.007	1.38	0.96	1.97	0.084	0.198
rs13355889	5	100.243	1.07	1.03	1.14	0.006	1.43	0.98	2.02	0.057	0.195
rs11241752	5	100.248	1.07	1.03	1.14	0.006	1.43	0.99	2.03	0.055	0.196
rs11241755	5	100.249	1.08	1.04	1.16	0.005	1.47	0.98	2.07	0.041	0.206
rs11739418	5	100.249	1.05	0.82	1.47	0.727	1.4	0.12	4.48	0.724	0.149
rs1423380	5	100.249	1.08	1.03	1.15	0.005	1.41	0.99	1.99	0.052	0.21
rs2400313	5	100.255	1.08	1.03	1.15	0.006	1.46	1	2.07	0.044	0.201
rs17725452	5	100.258	1.08	1.03	1.15	0.005	1.46	1	2.07	0.042	0.202
rs3776176	5	100.26	1.08	1.04	1.16	0.004	1.44	0.99	1.99	0.044	0.215
rs1423384	5	100.262	1.09	1.04	1.17	0.004	1.5	1.02	2.07	0.026	0.214
rs3756352	5	100.265	1.08	1.04	1.16	0.005	1.47	1	2.08	0.038	0.205
rs3756355	5	100.268	1.08	1.04	1.16	0.005	1.48	1	2.08	0.038	0.206
rs1833862	5	100.271	1.08	1.04	1.16	0.005	1.48	1	2.08	0.037	0.206
rs17782250	5	100.277	1.08	1.04	1.15	0.005	1.43	0.99	2.04	0.054	0.212
rs4703131	5	100.277	1.08	1.04	1.16	0.005	1.48	1	2.08	0.036	0.207
rs10214216	5	100.278	1.08	1.04	1.15	0.005	1.43	0.99	2.03	0.052	0.213
rs4702993	5	100.282	1.08	1.04	1.15	0.005	1.43	0.99	2.03	0.051	0.214
rs10059470	5	100.287	1.08	1.04	1.16	0.005	1.44	0.99	2.03	0.05	0.214
rs11742323	5	100.292	1.06	1.03	1.11	0.001	1.4	0.95	1.96	0.073	0.171
rs11748772	5	100.292	1.09	1.04	1.17	0.004	1.49	1.01	2.07	0.032	0.218
rs10515303	5	100.303	1.07	1.03	1.13	0.008	1.53	1.04	2.14	0.022	0.16
rs17726244	5	100.305	1.07	1.03	1.13	0.007	1.51	1.05	2.14	0.023	0.166
rs13354021	5	100.307	1.06	1.03	1.11	0.003	1.45	1.02	2.05	0.034	0.161
rs10035529	5	100.308	1.06	1.03	1.1	0.003	1.47	1.03	2.1	0.026	0.148
rs17726346	5	100.308	1.06	1.02	1.12	0.009	1.56	1.06	2.19	0.017	0.146
rs6893927	5	100.308	1.06	1.03	1.12	0.003	1.49	1.04	2.11	0.02	0.166
rs4703134	5	100.313	1.05	1.03	1.1	0.003	1.48	1.04	2.12	0.023	0.141
rs2161280	5	100.318	1.06	1.03	1.11	0.003	1.53	1.07	2.17	0.013	0.149
rs17782915	5	100.332	1.09	1.04	1.16	0.002	1.51	0.99	2.11	0.029	0.21
rs2216614	5	100.337	1.09	1.04	1.16	0.002	1.52	1	2.13	0.026	0.21
rs3995468	5	100.342	1.09	1.04	1.16	0.002	1.49	0.98	2.1	0.032	0.215

rs1895467	5	100.346	1.09	1.05	1.16	0.001	1.45	1.01	2	0.032	0.218
rs1345829	5	100.376	1.09	1.04	1.16	0.002	1.45	0.96	2.03	0.046	0.222
rs2052564	5	100.382	1.09	1.04	1.16	0.002	1.43	0.94	2	0.056	0.225
rs502652	5	100.407	1.08	1.04	1.15	0.002	1.43	0.92	2.02	0.073	0.218
rs511870	5	100.412	1.07	1.04	1.12	0.001	1.36	0.96	1.86	0.064	0.203
rs11739385	5	100.556	1.04	1.02	1.06	0.002	1.55	1.09	2.18	0.011	0.092
rs1355595	5	100.567	1.04	1.02	1.07	0.002	1.55	1.08	2.19	0.012	0.093
rs17796189	5	100.586	1.06	1.03	1.1	0.001	1.45	1.01	1.95	0.033	0.153
rs12153330	5	100.606	1.04	1.02	1.06	0.002	1.63	1.07	2.32	0.012	0.083
rs12187983	5	100.606	1.03	1.02	1.06	0.002	1.63	1.07	2.31	0.012	0.083
rs1512252	5	100.606	1.04	1.02	1.06	0.002	1.63	1.07	2.33	0.012	0.083
rs1512254	5	100.606	1.04	1.02	1.06	0.002	1.63	1.07	2.32	0.012	0.083
rs1912993	5	100.609	1.04	1.02	1.07	0.002	1.66	1.08	2.39	0.011	0.086
rs3957707	5	100.609	1.04	1.02	1.07	0.002	1.66	1.08	2.39	0.011	0.086
rs11741574	5	100.61	1.04	1.02	1.07	0.002	1.67	1.08	2.4	0.01	0.087
rs11241953	5	100.612	1.04	1.02	1.07	0.002	1.69	1.08	2.45	0.01	0.089
rs12189225	5	100.614	1.04	1.02	1.08	0.002	1.71	1.09	2.5	0.01	0.091
rs1459573	5	100.62	1.05	1.02	1.09	0.002	1.79	1.11	2.66	0.01	0.096

Table S8. Single-locus analyses for eQTL SNPs of *NDFIP1*. (Ch: chromosome; ME: mediation effect; AE: alternative effect; CI: confidence interval).

SNP	Ch	Location (Mb)	ME	95% CI		P-value	AE	95% CI		P-value	Proportion Of Mediation
rs4912802	5	141.461	1.13	0.97	1.31	0.109	1.33	0.64	2.19	0.366	0.345
rs4912622	5	141.471	1.23	1.11	1.41	0.001	1.24	0.83	1.85	0.278	0.545
rs7705042	5	141.473	1.23	1.11	1.41	0.001	1.24	0.83	1.85	0.278	0.545
rs10875596	5	141.476	1.25	1.11	1.45	0.001	1.24	0.82	1.9	0.31	0.561
rs12109804	5	141.478	1.13	0.97	1.3	0.096	1.34	0.66	2.18	0.339	0.336
rs9324866	5	141.478	1.23	1.11	1.41	0.001	1.24	0.83	1.85	0.278	0.545
rs11749731	5	141.481	1.23	1.11	1.41	0.001	1.24	0.83	1.85	0.278	0.545
rs1835966	5	141.482	1.23	1.11	1.41	0.001	1.24	0.83	1.85	0.278	0.545
rs2338822	5	141.483	1.23	1.11	1.41	0.001	1.24	0.83	1.85	0.278	0.545
rs10463349	5	141.484	1.12	0.97	1.29	0.1	1.34	0.66	2.18	0.342	0.332
rs11739961	5	141.489	1.23	1.11	1.41	0.001	1.24	0.83	1.85	0.278	0.545
rs6860138	5	141.49	1.23	1.11	1.41	0.001	1.24	0.83	1.85	0.278	0.545
rs10515512	5	141.492	1.12	0.97	1.29	0.104	1.33	0.66	2.18	0.344	0.329
rs2338820	5	141.492	1.12	0.97	1.29	0.103	1.33	0.66	2.18	0.343	0.329
rs6863411	5	141.493	1.23	1.11	1.41	0.001	1.24	0.83	1.85	0.278	0.545
rs2043280	5	141.494	1.23	1.11	1.41	0.001	1.24	0.83	1.85	0.278	0.545
rs7709361	5	141.494	1.23	1.11	1.41	0.001	1.24	0.83	1.85	0.278	0.545
rs7723666	5	141.494	1.23	1.11	1.41	0.001	1.24	0.83	1.85	0.278	0.545
rs7725157	5	141.497	1.12	0.97	1.29	0.108	1.33	0.66	2.16	0.347	0.326
rs3765011	5	141.498	1.23	1.11	1.41	0.001	1.24	0.83	1.85	0.278	0.545
rs1062158	5	141.503	1.23	1.11	1.41	0.001	1.24	0.83	1.85	0.278	0.545
rs10068466	5	141.505	1.13	1.06	1.23	0.001	1.38	0.92	2.17	0.129	0.326
rs249641	5	141.505	1.23	1.11	1.41	0.001	1.25	0.83	1.87	0.278	0.544
rs249642	5	141.505	1.23	1.11	1.41	0.001	1.24	0.83	1.86	0.279	0.544
rs249643	5	141.505	1.23	1.11	1.41	0.001	1.24	0.83	1.86	0.278	0.544
rs181826	5	141.506	1.24	1.11	1.42	0.001	1.25	0.83	1.88	0.278	0.543
rs166079	5	141.509	1.24	1.11	1.42	0.001	1.25	0.82	1.88	0.278	0.542
rs249638	5	141.511	1.24	1.11	1.42	0.001	1.25	0.83	1.89	0.277	0.541
rs449454	5	141.513	1.24	1.11	1.42	0.001	1.25	0.83	1.89	0.277	0.54
rs10463350	5	141.514	1.13	0.97	1.32	0.099	1.43	0.67	2.33	0.263	0.31
rs249681	5	141.518	1.23	1.11	1.41	0.001	1.26	0.83	1.89	0.27	0.534
rs2338819	5	141.52	0.85	0.77	0.93	0.001	0.78	0.44	1.13	0.283	0.335
rs249677	5	141.52	0.81	0.71	0.89	0	0.76	0.47	1.1	0.21	0.378
rs2915866	5	141.524	0.99	0.97	1	0.036	1.16	0.76	1.65	0.459	-0.105
rs4100171	5	141.524	1.14	0.98	1.33	0.094	1.45	0.71	2.34	0.235	0.31
rs2288820	5	141.528	1.04	0.99	1.1	0.097	1.02	0.55	1.56	0.93	0.65
rs2288822	5	141.528	0.89	0.82	0.95	0.001	0.73	0.43	1.07	0.164	0.234
rs10074925	5	141.529	0.86	0.78	0.94	0.002	0.79	0.46	1.17	0.325	0.344

rs6892764	5	141.529	1.04	0.99	1.1	0.098	1.02	0.54	1.56	0.938	0.672
rs6892781	5	141.529	1.04	0.99	1.1	0.099	1.02	0.54	1.56	0.94	0.68
rs17649451	5	141.53	0.86	0.78	0.94	0.001	0.8	0.47	1.18	0.348	0.357
rs3764	5	141.531	0.86	0.78	0.94	0.001	0.82	0.49	1.21	0.392	0.383
rs11742584	5	141.532	0.87	0.78	0.94	0.001	0.82	0.49	1.22	0.403	0.387
rs3899510	5	141.532	0.86	0.78	0.94	0.001	0.82	0.49	1.21	0.396	0.385
rs11745706	5	141.533	0.87	0.79	0.94	0.001	0.83	0.49	1.22	0.414	0.389
rs9324871	5	141.536	1.12	0.97	1.29	0.119	1.32	0.67	2.22	0.353	0.328
rs13153236	5	141.544	1.11	0.96	1.3	0.17	1.31	0.65	2.22	0.39	0.323
rs17098224	5	141.548	0.89	0.81	0.95	0.002	0.87	0.48	1.33	0.606	0.44

Table S9. Single-locus analyses for eQTL SNPs of *MANEA* (1554193_s_at). (Ch: chromosome; ME: mediation effect; AE: alternative effect; CI: confidence interval).

SNP	Ch	Location (Mb)	ME	95% CI		P-value	AE	95% CI		P-value	Proportion of Mediation
rs13196543	6	96.081	0.92	0.79	1.02	0.225	0.99	0.19	1.96	0.987	0.881
rs9481199	6	96.101	1	1	1	0.165	1.2	0.73	1.76	0.438	-0.008
rs4435952	6	96.102	1.01	1	1.03	0.009	1.34	0.92	1.91	0.114	0.054
rs7744714	6	96.102	1	1	1	0.008	1.37	0.95	1.89	0.079	0
rs9374321	6	96.106	1.01	1	1.01	0.017	1.38	0.92	1.93	0.089	0.019
rs9487909	6	96.106	1	0.97	1.02	0.72	1.33	0.63	2.04	0.364	-0.02
rs7749364	6	96.109	1	0.99	1	0.191	1.14	0.69	1.69	0.587	-0.024
rs9488059	6	96.113	1	0.96	1.02	0.741	1.3	0.61	1.98	0.405	-0.023
rs9488061	6	96.113	1	0.96	1.02	0.75	1.29	0.6	1.96	0.427	-0.024
rs13203302	6	96.114	0.92	0.74	1.06	0.369	1.51	0.24	2.96	0.596	-0.31
rs9398365	6	96.12	1.01	1	1.03	0.018	1.47	1.03	2.07	0.031	0.044
rs6932267	6	96.121	1.01	1	1.03	0.018	1.47	1.03	2.06	0.033	0.043
rs9372382	6	96.121	1.01	1	1.03	0.018	1.47	1.03	2.07	0.031	0.044
rs9398367	6	96.121	1.01	1	1.03	0.018	1.47	1.03	2.07	0.032	0.044
rs9488308	6	96.122	1.01	1	1.03	0.018	1.47	1.03	2.05	0.034	0.042
rs9320497	6	96.128	1.01	1	1.03	0.018	1.47	1.03	2.05	0.034	0.042
rs6937479	6	96.13	1	1	1.01	0.008	1.59	1.14	2.17	0.006	0.012
rs9374502	6	96.131	1.01	1	1.02	0.006	1.49	1.08	2.08	0.018	0.028
rs9384949	6	96.138	1.01	1	1.02	0.018	1.46	1.02	2.04	0.037	0.039
rs9387352	6	96.139	1.01	1	1.02	0.018	1.45	1.02	2.03	0.037	0.039
rs7758062	6	96.14	1	1	1.01	0.028	1.45	1.01	2.04	0.042	0.008
rs13205436	6	96.141	0.96	0.87	1.01	0.267	1.46	0.08	2.82	0.706	-0.149
rs9374586	6	96.142	1	1	1	0.029	1.45	1	2.05	0.042	0
rs6940020	6	96.143	1.01	1	1.02	0.017	1.45	1	2.02	0.039	0.039
rs12525680	6	96.144	1	1	1	0.091	0.9	0.54	1.29	0.627	0.013
rs9372457	6	96.145	1.01	1	1.02	0.017	1.45	1	2.02	0.039	0.039
rs9400893	6	96.145	1.01	1	1.02	0.017	1.45	1	2.02	0.039	0.039
rs13192906	6	96.146	0.96	0.87	1.01	0.274	1.44	0.08	2.79	0.722	-0.154
rs9488910	6	96.146	1.01	1	1.02	0.006	1.48	1.07	2.05	0.021	0.033
rs7773709	6	96.148	1.01	1	1.02	0.017	1.45	1	2.02	0.039	0.039
rs9320566	6	96.148	1.01	1	1.02	0.017	1.45	1	2.02	0.039	0.039
rs7757276	6	96.149	0.99	0.96	1.03	0.758	1.28	0.61	1.96	0.437	-0.026
rs4466257	6	96.15	1.01	1	1.02	0.017	1.45	1	2.02	0.039	0.039
rs9387442	6	96.153	1.02	1	1.03	0.024	1.72	1.12	2.5	0.009	0.035
rs4486026	6	96.155	1.01	1	1.02	0.017	1.48	1.03	2.07	0.027	0.038
rs1133503	6	96.161	1.01	1	1.02	0.017	1.45	1	2.02	0.039	0.039
rs9387522	6	96.162	1.01	1	1.02	0.017	1.45	1	2.02	0.039	0.039
rs9387567	6	96.165	1.01	1	1.01	0.008	1.57	1.12	2.14	0.007	0.019

rs4339467	6	96.168	1.01	1	1.02	0.006	1.47	1.07	2.04	0.021	0.033
rs9387591	6	96.168	1.01	1	1.02	0.017	1.45	1	2.02	0.039	0.039
rs9387601	6	96.17	1.01	1	1.02	0.006	1.47	1.07	2.04	0.021	0.033
rs9387603	6	96.17	1.01	1	1.02	0.017	1.45	1	2.02	0.039	0.039
rs9387605	6	96.17	1.01	1	1.02	0.017	1.45	1	2.02	0.039	0.039
rs9489578	6	96.172	1.01	1	1.02	0.017	1.45	1	2.02	0.039	0.039
rs7774322	6	96.173	1.01	1	1.02	0.017	1.45	1	2.02	0.039	0.039
rs12333032	6	96.174	1.01	1	1.02	0.017	1.45	1	2.02	0.039	0.039
rs13209376	6	96.177	0.96	0.87	1.01	0.277	1.43	0.08	2.79	0.727	-0.156
rs9481950	6	96.178	1	1	1	0.029	1.45	1	2.06	0.041	0.002
rs6926916	6	96.181	1.01	1	1.02	0.006	1.48	1.07	2.07	0.02	0.034
rs6937569	6	96.188	1.01	1	1.02	0.006	1.49	1.07	2.08	0.02	0.034
rs4413619	6	96.19	0.97	0.94	0.99	0.074	0.8	0.04	1.46	0.816	0.096
rs9490118	6	96.192	1	0.96	1.02	0.749	1.38	0.65	2.14	0.316	-0.018
rs12525999	6	96.197	1	0.99	1.01	0.834	1.61	0.86	2.39	0.086	-0.002
rs12529535	6	96.198	1	0.99	1.01	0.834	1.62	0.86	2.39	0.086	-0.002
rs11758159	6	96.254	0.96	0.92	0.99	0.042	0.67	0.41	0.89	0.055	0.077
rs12662075	6	96.279	0.96	0.92	0.99	0.041	0.66	0.4	0.88	0.047	0.07
rs7765615	6	96.288	0.96	0.92	0.99	0.041	0.66	0.4	0.88	0.047	0.069
rs4840033	6	96.335	0.95	0.91	0.99	0.021	0.57	0.36	0.78	0.004	0.058
rs17774669	6	96.338	0.95	0.91	0.99	0.022	0.57	0.36	0.78	0.004	0.058
rs12530302	6	96.34	0.95	0.91	0.99	0.021	0.57	0.37	0.78	0.004	0.059
rs13206934	6	96.342	0.95	0.91	0.99	0.022	0.57	0.37	0.79	0.004	0.059
rs12200752	6	96.344	0.95	0.9	0.99	0.028	0.59	0.38	0.81	0.006	0.068
rs1857482	6	96.346	0.95	0.91	0.99	0.021	0.57	0.37	0.79	0.004	0.06
rs13205985	6	96.352	0.95	0.91	0.99	0.021	0.58	0.37	0.79	0.004	0.061
rs10872473	6	96.356	0.95	0.91	0.99	0.021	0.58	0.37	0.8	0.006	0.062
rs4493748	6	96.358	0.95	0.91	0.99	0.021	0.58	0.36	0.8	0.008	0.063
rs13203882	6	96.359	0.95	0.91	0.99	0.021	0.58	0.36	0.81	0.008	0.063

Table S10. Single-locus analyses for eQTL SNPs of 229319 _at. (Ch: chromosome; ME: mediation effect; AE: alternative effect; CI: confidence interval).

SNP	Ch	Location (Mb)	ME	95% CI		P-value	AE	95% CI		P-value	Proportion of Mediation
rs2679650	6	122.437	0.67	0.48	0.84	0.006	1.12	0.65	2.56	0.752	1.5
rs2816096	6	122.439	0.68	0.49	0.84	0.005	1.12	0.66	2.5	0.75	1.5
rs2816095	6	122.439	0.68	0.49	0.84	0.005	1.12	0.66	2.49	0.749	1.5
rs2315812	6	122.439	0.68	0.48	0.84	0.006	1.1	0.66	2.5	0.787	1.41
rs2684247	6	122.44	0.68	0.48	0.84	0.006	1.1	0.66	2.5	0.787	1.41
rs7738997	6	122.44	0.68	0.49	0.84	0.006	1.1	0.66	2.5	0.786	1.41
rs2816094	6	122.441	0.68	0.49	0.84	0.006	1.1	0.66	2.5	0.784	1.41
rs2816092	6	122.442	0.68	0.49	0.84	0.006	1.1	0.66	2.5	0.782	1.42
rs2679708	6	122.442	0.68	0.49	0.84	0.006	1.1	0.66	2.5	0.783	1.42
rs2816088	6	122.445	0.68	0.49	0.84	0.006	1.12	0.66	2.55	0.762	1.47
rs2684235	6	122.445	0.67	0.48	0.84	0.007	1.1	0.64	2.56	0.806	1.36
rs2684241	6	122.453	0.7	0.5	0.86	0.009	0.98	0.6	2.09	0.951	0.935
rs2198863	6	122.454	0.7	0.5	0.86	0.009	0.98	0.6	2.09	0.95	0.934
rs2684244	6	122.456	0.7	0.5	0.86	0.009	0.98	0.6	2.09	0.951	0.936
rs2606604	6	122.456	0.7	0.51	0.86	0.008	0.98	0.6	2.08	0.953	0.938
rs1521223	6	122.457	0.7	0.51	0.86	0.008	0.98	0.6	2.09	0.955	0.941
rs2606611	6	122.457	0.7	0.51	0.86	0.008	0.98	0.61	2.09	0.956	0.942
rs1402537	6	122.458	0.7	0.51	0.86	0.009	0.96	0.59	2.08	0.897	0.872
rs2606622	6	122.459	0.7	0.51	0.86	0.008	0.98	0.61	2.09	0.958	0.945
rs2606626	6	122.46	0.7	0.51	0.86	0.008	0.98	0.61	2.09	0.959	0.945
rs2816085	6	122.46	0.7	0.51	0.86	0.008	0.98	0.61	2.09	0.961	0.948
rs1379094	6	122.461	0.7	0.51	0.86	0.008	0.98	0.61	2.08	0.962	0.949
rs2606630	6	122.462	0.7	0.51	0.86	0.008	0.98	0.61	2.08	0.962	0.949
rs2679703	6	122.462	0.7	0.51	0.86	0.008	0.99	0.61	2.08	0.963	0.952
rs2606631	6	122.462	0.71	0.52	0.87	0.008	0.95	0.58	1.97	0.879	0.857
rs2606632	6	122.463	0.7	0.52	0.85	0.006	1.01	0.63	2.14	0.969	1.04
rs2606634	6	122.463	0.71	0.51	0.86	0.008	0.99	0.62	2.07	0.969	0.959
rs2606642	6	122.467	0.69	0.48	0.86	0.011	1.05	0.64	2.44	0.887	1.19
rs2606643	6	122.467	0.71	0.52	0.86	0.008	0.98	0.62	2.05	0.96	0.947
rs2606644	6	122.468	0.71	0.52	0.86	0.008	0.98	0.62	2.05	0.959	0.946
rs720205	6	122.47	0.71	0.53	0.86	0.007	0.99	0.63	2.04	0.963	0.951
rs1379095	6	122.47	0.71	0.53	0.86	0.007	0.98	0.62	2.03	0.958	0.945
rs2816165	6	122.478	0.71	0.51	0.87	0.012	0.93	0.58	2	0.829	0.793
rs2606647	6	122.482	0.71	0.52	0.88	0.012	0.89	0.54	1.92	0.733	0.708
rs2606648	6	122.482	0.71	0.52	0.88	0.012	0.89	0.54	1.93	0.733	0.708
rs2045352	6	122.483	0.71	0.51	0.87	0.012	0.93	0.58	2.01	0.827	0.792
rs1379098	6	122.485	0.7	0.51	0.87	0.01	0.91	0.54	2.01	0.763	0.739
rs2816159	6	122.485	0.71	0.51	0.87	0.012	0.93	0.57	2.02	0.823	0.789

rs2606650	6	122.486	0.71	0.51	0.87	0.012	0.93	0.57	2.02	0.823	0.788
rs2816157	6	122.487	0.71	0.51	0.87	0.012	0.93	0.57	2.03	0.822	0.788
rs2816156	6	122.487	0.71	0.5	0.87	0.012	0.93	0.57	2.03	0.822	0.788
rs1456706	6	122.498	0.7	0.5	0.86	0.013	0.92	0.57	2.02	0.818	0.785
rs2606651	6	122.499	0.7	0.5	0.86	0.013	0.92	0.57	2.03	0.818	0.784
rs2606656	6	122.516	0.69	0.48	0.85	0.009	0.95	0.57	2.11	0.872	0.846
rs2606624	6	122.532	0.69	0.47	0.85	0.013	0.95	0.57	2.14	0.874	0.844
rs2816142	6	122.54	0.69	0.47	0.85	0.012	0.94	0.57	2.13	0.871	0.841
rs2816139	6	122.545	0.69	0.47	0.85	0.012	0.94	0.57	2.12	0.871	0.841
rs2606617	6	122.545	1.48	1.18	2.23	0.014	1.35	0.69	2	0.334	0.649
rs2606609	6	122.553	0.69	0.47	0.85	0.012	0.96	0.57	2.14	0.896	0.869
rs2606608	6	122.558	0.69	0.47	0.85	0.012	0.96	0.58	2.14	0.905	0.879
rs2816078	6	122.565	0.69	0.47	0.85	0.011	0.97	0.59	2.15	0.931	0.91
rs2606598	6	122.569	0.69	0.47	0.85	0.011	0.98	0.59	2.17	0.945	0.927
rs2816146	6	122.57	0.57	0.35	0.75	0.004	1.15	0.61	3.14	0.747	1.42
rs2045354	6	122.572	0.69	0.47	0.85	0.011	0.98	0.59	2.18	0.955	0.939
rs9490411	6	122.58	0.69	0.48	0.85	0.01	0.99	0.59	2.2	0.983	0.976
rs9320856	6	122.583	0.69	0.48	0.85	0.01	0.99	0.59	2.2	0.983	0.977
rs928011	6	122.612	0.69	0.48	0.85	0.01	0.99	0.6	2.2	0.986	0.981
rs9632500	6	122.614	0.69	0.49	0.85	0.01	0.99	0.6	2.2	0.987	0.981
rs696650	6	122.624	0.69	0.49	0.85	0.01	1	0.6	2.19	0.987	0.983
rs170422	6	122.624	0.68	0.48	0.84	0.008	1.06	0.64	2.37	0.879	1.2
rs225071	6	122.627	0.69	0.49	0.85	0.009	1	0.6	2.19	0.988	0.984
rs225074	6	122.628	0.69	0.47	0.84	0.009	0.95	0.56	2.14	0.888	0.859
rs225087	6	122.641	0.69	0.48	0.84	0.008	1.02	0.62	2.26	0.961	1.06
rs225088	6	122.641	0.68	0.48	0.84	0.007	1.06	0.65	2.42	0.86	1.23
rs225080	6	122.659	0.7	0.48	0.87	0.018	1.04	0.64	2.62	0.927	1.13
rs7752093	6	122.664	0.69	0.48	0.85	0.009	1.02	0.62	2.31	0.955	1.07
rs9401508	6	122.692	0.81	0.7	0.91	0.002	1.03	0.64	1.79	0.91	1.18
rs7771090	6	122.703	0.69	0.49	0.85	0.01	1	0.61	2.26	0.992	1.01
rs17729938	6	122.703	0.69	0.49	0.85	0.01	1	0.61	2.26	0.993	1.01
rs7767993	6	122.706	0.69	0.49	0.85	0.01	1	0.61	2.26	0.993	1.01
rs1339532	6	122.708	0.69	0.49	0.85	0.01	1	0.61	2.26	0.993	1.01
rs12201010	6	122.709	0.69	0.49	0.85	0.01	1	0.61	2.26	0.993	1.01
rs17662514	6	122.709	0.69	0.49	0.85	0.01	1	0.61	2.26	0.993	1.01
rs1339533	6	122.712	0.69	0.49	0.85	0.01	1.01	0.61	2.27	0.985	1.02
rs9490430	6	122.724	0.68	0.46	0.86	0.017	1	0.58	2.47	0.998	0.997
rs11154070	6	122.726	0.68	0.47	0.85	0.011	1.05	0.63	2.43	0.892	1.18
rs11154072	6	122.737	0.68	0.47	0.84	0.01	1.1	0.65	2.57	0.793	1.4
rs12189881	6	122.738	0.68	0.47	0.85	0.01	1.1	0.65	2.56	0.795	1.39
rs11154077	6	122.75	0.68	0.47	0.85	0.01	1.1	0.64	2.55	0.803	1.38
rs11154078	6	122.75	0.68	0.47	0.85	0.01	1.1	0.64	2.55	0.804	1.37
rs510471	6	122.755	0.68	0.47	0.85	0.01	1.09	0.63	2.5	0.813	1.35

rs472070	6	122.756	0.82	0.71	0.91	0.002	0.98	0.61	1.65	0.947	0.915
rs477425	6	122.756	0.68	0.47	0.85	0.01	1.09	0.63	2.49	0.817	1.34
rs571706	6	122.757	0.69	0.48	0.85	0.012	1.06	0.61	2.52	0.882	1.21
rs549215	6	122.758	0.83	0.72	0.92	0.002	0.98	0.6	1.6	0.94	0.899
rs563084	6	122.76	0.68	0.47	0.85	0.009	1.09	0.63	2.48	0.819	1.33
rs6926219	6	122.763	0.89	0.83	0.95	0.001	0.8	0.54	1.15	0.233	0.294
rs1741820	6	122.763	0.89	0.83	0.95	0.001	0.8	0.54	1.15	0.234	0.295
rs17199931	6	122.773	0.81	0.66	0.92	0.011	1.09	0.42	1.76	0.804	1.75
rs549302	6	122.777	0.89	0.83	0.95	0.001	0.8	0.54	1.15	0.231	0.293
rs3799545	6	122.777	0.81	0.66	0.92	0.011	1.09	0.43	1.76	0.802	1.76
rs502071	6	122.781	0.68	0.46	0.85	0.013	0.99	0.57	2.29	0.968	0.956
rs564611	6	122.781	0.89	0.83	0.95	0.001	0.8	0.54	1.14	0.226	0.291
rs578868	6	122.784	0.89	0.83	0.95	0.001	0.79	0.54	1.13	0.224	0.29
rs492250	6	122.785	0.68	0.47	0.85	0.009	1.08	0.63	2.42	0.837	1.28
rs556439	6	122.787	0.82	0.71	0.91	0.003	0.77	0.52	1.25	0.245	0.371
rs9320872	6	122.788	0.68	0.47	0.85	0.009	1.08	0.63	2.42	0.84	1.28
rs576247	6	122.789	0.89	0.83	0.95	0.001	0.79	0.53	1.14	0.221	0.289
rs502252	6	122.799	0.68	0.47	0.85	0.009	1.07	0.63	2.43	0.841	1.28
rs577838	6	122.801	0.7	0.5	0.86	0.007	0.92	0.55	1.82	0.805	0.786
rs487098	6	122.808	0.9	0.83	0.95	0.001	0.79	0.53	1.14	0.223	0.287
rs12524	6	122.808	0.9	0.83	0.95	0.001	0.79	0.53	1.14	0.223	0.287
rs520046	6	122.809	0.82	0.71	0.91	0.003	0.77	0.52	1.25	0.245	0.369
rs577744	6	122.811	0.68	0.47	0.85	0.01	1.07	0.63	2.41	0.841	1.28
rs510283	6	122.814	0.84	0.73	0.92	0.002	0.76	0.51	1.18	0.189	0.334
rs1267948	6	122.815	0.9	0.83	0.95	0.001	0.79	0.54	1.14	0.225	0.286
rs573709	6	122.821	0.83	0.71	0.92	0.003	0.77	0.51	1.25	0.244	0.368
rs474440	6	122.821	0.9	0.83	0.95	0.001	0.79	0.54	1.14	0.226	0.285
rs4945703	6	122.823	0.9	0.83	0.95	0.001	0.79	0.54	1.14	0.226	0.285
rs520867	6	122.828	0.83	0.71	0.92	0.003	0.77	0.51	1.25	0.246	0.367
rs693669	6	122.829	0.83	0.71	0.92	0.003	0.77	0.51	1.25	0.246	0.367
rs13437168	6	122.829	0.89	0.82	0.95	0.001	0.72	0.46	1.08	0.122	0.221
rs562616	6	122.83	0.68	0.48	0.85	0.011	1.07	0.62	2.4	0.845	1.27
rs17201852	6	122.834	0.82	0.67	0.93	0.014	1.05	0.43	1.66	0.894	1.31
rs471620	6	122.836	0.83	0.71	0.92	0.003	0.77	0.51	1.25	0.247	0.367
rs509596	6	122.841	0.9	0.84	0.95	0.001	0.8	0.54	1.15	0.231	0.281
rs560717	6	122.846	0.68	0.48	0.86	0.011	1.07	0.63	2.39	0.845	1.27
rs561470	6	122.846	0.9	0.84	0.95	0.001	0.8	0.54	1.15	0.233	0.28
rs538457	6	122.848	0.83	0.71	0.92	0.003	0.77	0.51	1.25	0.249	0.366
rs7767237	6	122.851	0.9	0.84	0.95	0.001	0.8	0.54	1.15	0.235	0.279
rs7767114	6	122.851	0.9	0.84	0.95	0.001	0.8	0.54	1.15	0.235	0.279
rs11751662	6	122.855	0.9	0.84	0.95	0.001	0.8	0.54	1.15	0.236	0.278
rs155458	6	122.856	0.69	0.48	0.86	0.011	1.07	0.63	2.37	0.845	1.27
rs155461	6	122.862	0.69	0.48	0.86	0.011	1.07	0.63	2.37	0.845	1.27

rs155467	6	122.875	0.69	0.49	0.86	0.011	1.07	0.63	2.35	0.845	1.27
rs197691	6	122.876	0.69	0.49	0.86	0.011	1.07	0.63	2.35	0.845	1.27
rs129830	6	122.877	0.9	0.85	0.95	0.001	0.8	0.54	1.15	0.243	0.277
rs197692	6	122.878	0.69	0.49	0.86	0.011	1.07	0.63	2.35	0.845	1.27
rs197676	6	122.895	0.69	0.49	0.87	0.011	1.08	0.63	2.35	0.827	1.31
rs197678	6	122.897	0.91	0.85	0.95	0.001	0.8	0.54	1.15	0.254	0.274
rs197679	6	122.911	0.7	0.5	0.87	0.012	1.07	0.63	2.24	0.843	1.28
rs197680	6	122.912	0.7	0.5	0.87	0.012	1.07	0.64	2.23	0.842	1.28
rs197681	6	122.915	0.7	0.5	0.87	0.012	1.07	0.64	2.23	0.841	1.28
rs197682	6	122.915	0.7	0.5	0.87	0.012	1.07	0.64	2.23	0.837	1.29
rs197683	6	122.915	0.84	0.72	0.92	0.003	0.92	0.54	1.52	0.741	0.644
rs197684	6	122.917	0.7	0.5	0.87	0.011	1.08	0.65	2.25	0.81	1.35
rs197685	6	122.917	0.7	0.5	0.87	0.011	1.09	0.65	2.25	0.806	1.36
rs197686	6	122.92	0.84	0.73	0.92	0.002	1.01	0.61	1.66	0.968	1.07
rs197687	6	122.921	0.84	0.73	0.92	0.002	1.01	0.61	1.67	0.963	1.08
rs9388097	6	122.927	0.84	0.73	0.92	0.002	1.01	0.61	1.67	0.958	1.09
rs9375150	6	122.929	0.92	0.86	0.96	0.001	0.82	0.54	1.19	0.305	0.276
rs11154087	6	122.938	0.7	0.51	0.87	0.009	1.11	0.66	2.31	0.744	1.52
rs11968579	6	122.939	2.02	0.56	16.7	0.424	0.77	0	2.01	0.889	1.41
rs12212981	6	122.944	1.43	1.15	1.96	0.009	1.05	0.56	1.5	0.865	0.907
rs1430816	6	122.955	1.63	1.28	2.41	0.002	1.03	0.47	1.53	0.935	0.962
rs9482260	6	122.97	1.63	1.27	2.47	0.003	1.11	0.53	1.64	0.718	0.863
rs9490495	6	122.976	1.62	1.27	2.47	0.003	1.12	0.54	1.66	0.697	0.854
rs9490497	6	122.979	1.6	1.25	2.39	0.004	1.14	0.6	1.7	0.63	0.826

Table S11. Single-locus analyses for eQTL SNPs of *PTCH1*. (Ch: chromosome; ME: mediation effect; AE: alternative effect; CI: confidence interval).

SNP	Ch	Location (Mb)	ME	95% CI		P-value	AE	95% CI		P-value	Proportion of Mediation
rs16909856	9	97.244	1.01	1.01	1.01	<0.001	0.91	0.41	1.78	0.79	-0.103
rs16909859	9	97.245	1.02	1.01	1.02	<0.001	0.91	0.41	1.77	0.787	-0.171
rs16909865	9	97.247	1	0.99	1	<0.001	0.86	0.38	1.73	0.699	0.022
rs2282043	9	97.252	1.03	1.01	1.04	<0.001	1.08	0.51	2.23	0.827	0.259
rs16909898	9	97.271	1.07	1.04	1.12	<0.001	1.1	0.55	2.2	0.779	0.447
rs16909902	9	97.276	1.08	1.04	1.13	<0.001	1.09	0.55	2.14	0.787	0.484
rs3824488	9	97.276	1.06	1.03	1.1	<0.001	1.07	0.53	2.13	0.848	0.481
rs2282041	9	97.288	1.11	1.06	1.19	<0.001	1.04	0.56	1.96	0.91	0.769
rs10512249	9	97.296	1.12	1.06	1.2	<0.001	1.05	0.59	1.9	0.873	0.729
rs10512247	9	97.336	1.09	1.05	1.15	<0.001	1	0.53	1.78	0.989	1.05
rs16909975	9	97.347	1.08	1.04	1.13	<0.001	0.99	0.53	1.8	0.985	1.08
rs16909978	9	97.348	1.09	1.04	1.14	<0.001	0.97	0.49	1.78	0.914	1.74
rs16909981	9	97.353	1.1	1.05	1.15	<0.001	0.98	0.52	1.76	0.957	1.22

Table S12. Single-locus analyses for eQTL SNPs of the probe 223259_at at *ORMDL3*. (Ch: chromosome; ME: mediation effect; AE: alternative effect; CI: confidence interval).

SNP	Ch	Location (Mb)	ME	95% CI		p-value	AE	95% CI		p-value	Proportion of Mediation
rs1007654	17	35.365	1.05	0.992	1.12	0.152	0.737	0.483	1.06	0.129	-0.158
rs1007655	17	35.365	1.05	0.991	1.13	0.155	0.738	0.481	1.07	0.134	-0.162
rs1008723	17	35.320	1.2	1.03	1.45	0.0448	0.536	0.316	0.795	0.00876	-0.296
rs10445306	17	34.845	1.06	0.973	1.17	0.208	0.805	0.521	1.14	0.272	-0.335
rs10445308	17	35.192	1.15	1.03	1.32	0.0319	0.472	0.277	0.714	0.00172	-0.154
rs10491128	17	34.806	1.06	0.973	1.17	0.195	0.8	0.512	1.14	0.259	-0.338
rs10491129	17	34.715	1.07	0.977	1.18	0.181	0.772	0.494	1.1	0.183	-0.286
rs1053651	17	35.076	1.06	0.965	1.18	0.227	0.797	0.513	1.16	0.278	-0.323
rs1054609	17	35.287	1.15	1.01	1.35	0.0621	0.532	0.319	0.791	0.00739	-0.2
rs1058808	17	35.138	1.05	0.944	1.15	0.353	0.644	0.373	0.98	0.079	-0.0926
rs11078893	17	34.650	1.08	0.974	1.21	0.172	0.747	0.454	1.07	0.163	-0.293
rs11078894	17	34.650	1	0.991	1.02	0.699	0.614	0.298	0.975	0.106	-0.00408
rs11078895	17	34.655	1	0.99	1.02	0.654	0.63	0.319	0.986	0.103	-0.00574
rs11078897	17	34.669	1.07	0.977	1.18	0.18	0.75	0.481	1.05	0.133	-0.246
rs11078898	17	34.790	1.06	0.974	1.17	0.193	0.798	0.511	1.13	0.253	-0.335
rs11078901	17	34.879	1.06	0.972	1.17	0.205	0.805	0.519	1.14	0.274	-0.346
rs11078902	17	34.885	1.08	0.97	1.23	0.166	0.804	0.492	1.18	0.302	-0.532
rs11078903	17	34.885	1.08	0.971	1.23	0.166	0.804	0.492	1.18	0.302	-0.534
rs11078907	17	34.916	1.07	0.974	1.18	0.193	0.803	0.515	1.15	0.27	-0.369
rs11078912	17	34.925	1.07	0.977	1.19	0.178	0.802	0.516	1.15	0.264	-0.397
rs11078913	17	34.925	1.07	0.977	1.19	0.174	0.803	0.516	1.15	0.265	-0.409
rs11078915	17	34.969	1.07	0.975	1.2	0.169	0.806	0.527	1.19	0.291	-0.451
rs11078919	17	35.089	1.06	0.945	1.18	0.304	0.725	0.443	1.07	0.162	-0.185
rs11078925	17	35.279	1.15	1.01	1.35	0.0585	0.521	0.307	0.785	0.00651	-0.192
rs11078927	17	35.318	1.14	1.01	1.34	0.0759	0.578	0.343	0.852	0.0199	-0.233
rs11078930	17	35.395	0.998	0.995	1	0.119	0.814	0.538	1.19	0.324	0.00836
rs11557466	17	35.278	1.15	1.01	1.35	0.0584	0.521	0.306	0.785	0.00646	-0.191
rs11654018	17	34.957	1.08	0.975	1.2	0.167	0.804	0.522	1.16	0.276	-0.446
rs11654954	17	35.000	1.01	0.977	1.04	0.554	0.75	0.427	1.18	0.263	-0.0287
rs11655972	17	34.661	1	0.989	1.02	0.626	0.643	0.337	0.992	0.104	-0.00705
rs11657058	17	34.953	1.01	0.977	1.04	0.643	0.696	0.376	1.09	0.201	-0.0158
rs11657153	17	34.953	1.01	0.977	1.04	0.642	0.695	0.372	1.1	0.201	-0.016
rs11658678	17	34.934	1.07	0.977	1.19	0.173	0.803	0.516	1.15	0.265	-0.413
rs11869286	17	35.067	1.05	0.961	1.14	0.28	0.891	0.596	1.29	0.548	-0.644
rs11870631	17	34.899	1.06	0.973	1.18	0.198	0.804	0.515	1.15	0.272	-0.36
rs11870965	17	35.284	1.15	1.01	1.35	0.0618	0.531	0.318	0.79	0.0073	-0.2
rs12150079	17	35.279	1.22	1.05	1.51	0.0358	0.545	0.346	0.847	0.00824	-0.367
rs12150298	17	35.088	1.06	0.945	1.18	0.305	0.729	0.447	1.08	0.166	-0.187

rs12232497	17	35.294	1.15	1.01	1.35	0.0626	0.534	0.321	0.793	0.00757	-0.202
rs12449852	17	34.886	1.01	0.977	1.04	0.695	0.666	0.315	1.09	0.196	-0.0113
rs12450559	17	34.948	1.07	0.978	1.19	0.168	0.804	0.524	1.15	0.261	-0.431
rs12452880	17	34.845	1.06	0.973	1.17	0.205	0.804	0.52	1.14	0.269	-0.336
rs12453198	17	34.995	1.01	0.976	1.04	0.562	0.744	0.422	1.18	0.255	-0.0276
rs12453682	17	35.024	1.05	0.98	1.13	0.224	0.848	0.57	1.23	0.4	-0.355
rs12600751	17	34.807	1.06	0.973	1.17	0.196	0.801	0.513	1.14	0.26	-0.338
rs12603332	17	35.336	1.14	1.01	1.33	0.0677	0.548	0.337	0.801	0.00882	-0.202
rs12936231	17	35.283	1.2	1.03	1.45	0.0433	0.492	0.295	0.735	0.00244	-0.239
rs12936996	17	34.919	1.07	0.975	1.18	0.189	0.803	0.515	1.15	0.269	-0.376
rs12937013	17	34.919	1	0.984	1.03	0.667	0.704	0.375	1.08	0.208	-0.0114
rs12938099	17	34.866	1	0.987	1.02	0.686	0.713	0.389	1.1	0.21	-0.00874
rs12947506	17	34.961	1.01	0.977	1.04	0.636	0.696	0.378	1.11	0.202	-0.0171
rs12950186	17	34.647	1	0.991	1.02	0.726	0.606	0.282	0.968	0.108	-0.00321
rs12950743	17	35.303	1.2	1.02	1.45	0.0448	0.5	0.303	0.745	0.00274	-0.246
rs13695	17	35.799	0.976	0.849	1.12	0.731	1.06	0.683	1.84	0.806	-0.696
rs1476278	17	35.090	1.06	0.945	1.18	0.304	0.724	0.442	1.07	0.162	-0.184
rs1565922	17	35.085	1.05	0.952	1.17	0.302	0.758	0.479	1.1	0.199	-0.205
rs1565923	17	35.112	1.04	0.949	1.14	0.366	0.67	0.386	1.02	0.103	-0.0942
rs1619021	17	34.993	1.07	0.973	1.18	0.186	0.817	0.539	1.21	0.329	-0.418
rs17609240	17	35.364	1.06	0.993	1.15	0.136	0.7	0.458	1.02	0.0848	-0.155
rs1810132	17	35.120	1.04	0.948	1.14	0.367	0.661	0.376	1.01	0.0983	-0.0912
rs1874226	17	34.983	1.01	0.976	1.05	0.59	0.721	0.397	1.15	0.228	-0.0235
rs1874228	17	35.029	1.07	0.972	1.19	0.179	0.894	0.579	1.33	0.598	-1.37
rs1877030	17	34.994	1.01	0.976	1.04	0.568	0.738	0.415	1.18	0.248	-0.0266
rs1877031	17	35.068	1.05	0.961	1.14	0.281	0.89	0.594	1.28	0.543	-0.628
rs2018026	17	34.913	1.07	0.974	1.18	0.195	0.804	0.516	1.15	0.271	-0.364
rs2061342	17	34.659	1.07	0.977	1.18	0.18	0.742	0.479	1.04	0.115	-0.23
rs2168785	17	34.661	1.07	0.977	1.18	0.18	0.744	0.479	1.04	0.119	-0.234
rs2271308	17	35.071	1.06	0.965	1.18	0.228	0.802	0.518	1.16	0.288	-0.331
rs2271309	17	35.039	1.02	0.962	1.07	0.528	0.82	0.5	1.28	0.417	-0.0782
rs2290400	17	35.320	1.19	1.03	1.43	0.0485	0.537	0.315	0.793	0.00832	-0.28
rs2302073	17	34.711	1	0.988	1.03	0.607	0.674	0.354	1.04	0.154	-0.00987
rs2303316	17	34.958	1.08	0.975	1.2	0.167	0.804	0.522	1.17	0.277	-0.447
rs2305479	17	35.316	1.19	1.02	1.44	0.0533	0.528	0.309	0.78	0.00734	-0.263
rs2305480	17	35.316	1.14	1.01	1.33	0.0769	0.574	0.341	0.852	0.0179	-0.225
rs2313171	17	35.087	1.06	0.945	1.18	0.306	0.731	0.45	1.08	0.168	-0.188
rs2313640	17	35.365	1.05	0.992	1.12	0.154	0.743	0.487	1.07	0.141	-0.163
rs2338755	17	34.673	1.07	0.977	1.18	0.179	0.751	0.482	1.06	0.135	-0.247
rs2338799	17	34.767	1.01	0.988	1.03	0.591	0.7	0.372	1.08	0.2	-0.0128
rs2338800	17	34.752	1.06	0.977	1.18	0.182	0.786	0.507	1.11	0.218	-0.312
rs2517954	17	35.097	1.04	0.95	1.14	0.351	0.687	0.409	1.04	0.118	-0.107
rs2517955	17	35.097	1.05	0.95	1.16	0.308	0.663	0.397	1	0.0906	-0.118

rs2517956	17	35.097	1.04	0.95	1.14	0.352	0.685	0.408	1.04	0.117	-0.107
rs2517957	17	35.092	1.06	0.945	1.18	0.303	0.721	0.438	1.07	0.159	-0.182
rs2517958	17	35.092	1.06	0.945	1.18	0.303	0.719	0.435	1.07	0.157	-0.181
rs2872507	17	35.294	1.15	1.01	1.35	0.0628	0.534	0.322	0.794	0.00763	-0.203
rs2879258	17	34.653	1	0.991	1.02	0.691	0.617	0.305	0.977	0.105	-0.00436
rs2934952	17	35.086	1.05	0.952	1.17	0.302	0.754	0.474	1.09	0.195	-0.202
rs2934953	17	35.086	1.05	0.952	1.17	0.302	0.755	0.475	1.09	0.196	-0.203
rs2941504	17	35.084	1.05	0.952	1.17	0.302	0.758	0.479	1.1	0.199	-0.205
rs2941505	17	35.086	1.06	0.946	1.18	0.307	0.739	0.458	1.08	0.176	-0.193
rs2941506	17	35.087	1.06	0.946	1.18	0.307	0.737	0.455	1.08	0.174	-0.192
rs2952151	17	35.082	1.05	0.953	1.17	0.3	0.767	0.484	1.12	0.219	-0.22
rs2952155	17	35.115	1.01	0.954	1.05	0.723	0.711	0.388	1.14	0.196	-0.0206
rs2952156	17	35.130	1.04	0.948	1.14	0.367	0.66	0.375	1.01	0.0976	-0.0907
rs3744348	17	34.671	1.07	0.977	1.18	0.179	0.751	0.481	1.06	0.134	-0.247
rs3744349	17	34.668	1	0.989	1.02	0.622	0.649	0.337	0.999	0.114	-0.00754
rs3816470	17	35.239	1.2	1.03	1.44	0.038	0.471	0.282	0.703	0.00154	-0.212
rs3894194	17	35.376	1.06	0.974	1.17	0.201	0.671	0.43	0.94	0.0405	-0.142
rs3902025	17	35.373	1.05	0.987	1.13	0.154	0.639	0.414	0.9	0.0236	-0.0966
rs3964723	17	34.658	1.07	0.975	1.18	0.179	0.742	0.475	1.04	0.122	-0.239
rs4065985	17	35.355	1.09	1.01	1.21	0.0457	0.504	0.3	0.749	0.00288	-0.104
rs4239222	17	34.950	1.07	0.977	1.2	0.167	0.804	0.523	1.16	0.266	-0.437
rs4378650	17	35.334	1.14	1.01	1.32	0.0692	0.55	0.336	0.812	0.00977	-0.198
rs4390625	17	34.874	1.06	0.971	1.17	0.211	0.806	0.521	1.14	0.275	-0.337
rs4488484	17	34.971	1.01	0.975	1.04	0.615	0.705	0.382	1.13	0.21	-0.0201
rs4533315	17	34.865	1.02	0.976	1.09	0.364	0.996	0.696	1.41	0.984	1.17
rs4794820	17	35.343	1.1	0.996	1.24	0.103	0.616	0.374	0.916	0.0365	-0.184
rs4795355	17	34.681	1.07	0.977	1.18	0.18	0.753	0.483	1.06	0.14	-0.252
rs4795357	17	34.823	1.06	0.973	1.17	0.203	0.803	0.519	1.14	0.266	-0.336
rs4795358	17	34.827	1	0.987	1.02	0.644	0.713	0.388	1.1	0.212	-0.0109
rs4795369	17	34.863	1.05	0.975	1.15	0.218	0.758	0.494	1.09	0.16	-0.205
rs4795384	17	34.970	1.07	0.974	1.2	0.171	0.807	0.53	1.18	0.299	-0.449
rs4795385	17	34.987	1.01	0.968	1.05	0.623	0.731	0.421	1.17	0.218	-0.0273
rs4795397	17	35.277	1.15	1.01	1.35	0.0583	0.521	0.306	0.785	0.00643	-0.191
rs4795400	17	35.321	1.15	1.01	1.35	0.0724	0.581	0.341	0.867	0.0226	-0.257
rs4795402	17	35.339	0.979	0.852	1.09	0.741	1.23	0.726	1.85	0.378	-0.125
rs4795405	17	35.342	1.1	1	1.25	0.086	0.602	0.37	0.896	0.0252	-0.185
rs4795408	17	35.361	1.08	0.973	1.2	0.169	0.647	0.416	0.897	0.0261	-0.163
rs584377	17	34.714	1	0.988	1.03	0.605	0.676	0.355	1.04	0.158	-0.0101
rs588193	17	34.694	1.07	0.976	1.18	0.18	0.759	0.487	1.07	0.152	-0.261
rs590051	17	34.700	1	0.988	1.03	0.611	0.668	0.349	1.03	0.145	-0.0093
rs600010	17	34.687	1.07	0.976	1.18	0.18	0.755	0.484	1.06	0.143	-0.254
rs602688	17	34.693	1.07	0.976	1.18	0.179	0.757	0.487	1.07	0.149	-0.26
rs620686	17	34.707	1.07	0.977	1.18	0.18	0.766	0.491	1.08	0.169	-0.275

rs632202	17	34.707	1.07	0.977	1.18	0.18	0.767	0.492	1.08	0.171	-0.276
rs649180	17	34.718	1	0.988	1.03	0.602	0.681	0.358	1.05	0.166	-0.0106
rs6503503	17	34.768	1.06	0.976	1.17	0.185	0.792	0.509	1.13	0.236	-0.325
rs6503504	17	34.768	1.01	0.987	1.03	0.595	0.703	0.375	1.09	0.204	-0.0128
rs6503507	17	34.779	1.06	0.974	1.17	0.19	0.796	0.51	1.13	0.248	-0.332
rs6503513	17	34.815	1	0.982	1.02	0.739	0.724	0.403	1.11	0.206	-0.00919
rs6503521	17	34.969	1.01	0.976	1.04	0.626	0.7	0.377	1.11	0.205	-0.0187
rs6503525	17	35.349	1.08	0.974	1.21	0.158	0.632	0.399	0.881	0.0209	-0.159
rs6503526	17	35.368	1.07	0.972	1.2	0.173	0.644	0.416	0.896	0.0232	-0.155
rs6503527	17	35.368	1.05	0.991	1.12	0.159	0.762	0.504	1.11	0.183	-0.179
rs667239	17	34.696	1	0.988	1.03	0.611	0.666	0.348	1.03	0.142	-0.00915
rs676882	17	34.687	1	0.987	1.03	0.657	0.664	0.315	1.06	0.182	-0.00837
rs7207600	17	35.345	1.06	0.992	1.14	0.144	0.718	0.458	1.05	0.112	-0.164
rs7208487	17	34.797	1.01	0.987	1.03	0.607	0.712	0.388	1.1	0.215	-0.0132
rs7212938	17	35.376	1.05	0.977	1.14	0.217	0.655	0.42	0.943	0.0373	-0.109
rs7214151	17	34.761	1.02	0.978	1.07	0.37	1.03	0.739	1.47	0.862	0.409
rs7216086	17	34.963	1.08	0.975	1.2	0.169	0.805	0.522	1.18	0.286	-0.45
rs7216389	17	35.323	1.21	1.03	1.47	0.041	0.538	0.315	0.796	0.0095	-0.317
rs7218321	17	35.368	1.05	0.992	1.12	0.157	0.751	0.494	1.09	0.159	-0.17
rs7218742	17	35.368	1.05	0.992	1.12	0.155	0.746	0.49	1.08	0.148	-0.166
rs7219080	17	35.368	1.05	0.992	1.12	0.157	0.752	0.495	1.09	0.162	-0.171
rs7219923	17	35.328	1.21	1.03	1.47	0.0416	0.54	0.314	0.802	0.01	-0.32
rs7220650	17	34.741	1.07	0.977	1.18	0.182	0.781	0.503	1.11	0.207	-0.304
rs7221875	17	34.797	1.06	0.974	1.17	0.192	0.799	0.511	1.14	0.256	-0.337
rs7223438	17	34.775	1.06	0.974	1.17	0.188	0.795	0.51	1.13	0.244	-0.33
rs7224129	17	35.329	1.21	1.02	1.47	0.042	0.541	0.314	0.809	0.0104	-0.321
rs7225096	17	34.918	1.07	0.974	1.18	0.191	0.803	0.515	1.15	0.27	-0.372
rs7359623	17	35.303	1.2	1.03	1.46	0.042	0.488	0.295	0.725	0.00192	-0.239
rs7501488	17	34.830	1.06	0.973	1.17	0.204	0.803	0.52	1.14	0.268	-0.336
rs7503069	17	34.951	1.07	0.976	1.2	0.167	0.804	0.521	1.16	0.272	-0.444
rs7503195	17	34.976	1.03	0.971	1.11	0.338	0.913	0.622	1.34	0.635	-0.505
rs7503377	17	34.962	1.01	0.976	1.04	0.636	0.696	0.378	1.11	0.202	-0.0171
rs7503705	17	34.923	1.07	0.976	1.19	0.179	0.802	0.515	1.15	0.264	-0.395
rs752314	17	34.664	1.07	0.977	1.18	0.18	0.748	0.481	1.05	0.128	-0.241
rs755500	17	34.663	1.07	0.977	1.18	0.18	0.746	0.48	1.05	0.125	-0.238
rs801418	17	34.712	1	0.988	1.03	0.606	0.675	0.354	1.04	0.156	-0.00996
rs801426	17	34.695	1.07	0.977	1.18	0.18	0.761	0.488	1.07	0.157	-0.266
rs8065126	17	35.353	1.05	0.992	1.13	0.148	0.725	0.472	1.05	0.117	-0.159
rs8065963	17	34.935	1.07	0.978	1.19	0.172	0.803	0.516	1.15	0.262	-0.414
rs8066704	17	34.731	1.07	0.977	1.18	0.181	0.777	0.498	1.1	0.195	-0.295
rs8067378	17	35.305	1.2	1.02	1.45	0.0453	0.502	0.304	0.748	0.00286	-0.248
rs8069074	17	34.939	1.01	0.981	1.04	0.65	0.699	0.368	1.08	0.203	-0.014
rs8069176	17	35.311	1.14	1.01	1.35	0.069	0.554	0.327	0.822	0.0128	-0.219

rs8069451	17	34.758	1.07	0.977	1.18	0.181	0.792	0.509	1.13	0.239	-0.336
rs8070695	17	34.732	1.07	0.977	1.18	0.181	0.778	0.499	1.11	0.198	-0.297
rs8073907	17	34.678	1	0.989	1.02	0.62	0.654	0.339	1	0.121	-0.00789
rs8076131	17	35.334	1.13	1.01	1.3	0.0794	0.597	0.356	0.902	0.028	-0.231
rs8076462	17	34.654	1.07	0.974	1.2	0.176	0.744	0.468	1.05	0.141	-0.262
rs8076474	17	35.365	1.05	0.991	1.13	0.153	0.734	0.477	1.06	0.127	-0.159
rs8076494	17	34.770	1.06	0.976	1.17	0.186	0.793	0.51	1.13	0.239	-0.326
rs8076546	17	34.809	1.06	0.973	1.17	0.197	0.801	0.514	1.14	0.262	-0.338
rs8078228	17	35.089	1.06	0.945	1.18	0.304	0.726	0.443	1.07	0.163	-0.185
rs8079416	17	35.346	1.08	0.975	1.21	0.159	0.636	0.4	0.884	0.0214	-0.16
rs8182252	17	34.981	1.01	0.975	1.04	0.602	0.734	0.43	1.14	0.229	-0.0244
rs869402	17	35.322	1.21	1.03	1.47	0.0414	0.538	0.315	0.795	0.00937	-0.314
rs879606	17	35.035	1.02	0.967	1.07	0.468	0.855	0.497	1.33	0.547	-0.119
rs881844	17	35.064	1.05	0.961	1.14	0.28	0.892	0.597	1.3	0.552	-0.657
rs903501	17	35.093	1.05	0.938	1.18	0.363	0.708	0.417	1.06	0.161	-0.147
rs903502	17	35.083	1.06	0.946	1.17	0.31	0.752	0.466	1.1	0.195	-0.204
rs903507	17	34.980	1.01	0.975	1.05	0.595	0.718	0.393	1.15	0.224	-0.0228
rs907089	17	35.087	1.06	0.946	1.18	0.306	0.733	0.451	1.08	0.17	-0.189
rs907091	17	35.175	1.21	1.06	1.43	0.0191	0.424	0.255	0.637	0.000337	-0.18
rs907092	17	35.176	1.15	1.03	1.33	0.0268	0.462	0.273	0.698	0.00124	-0.149
rs907094	17	35.044	1.02	0.962	1.07	0.529	0.821	0.5	1.28	0.419	-0.0783
rs9303274	17	35.090	1.06	0.945	1.18	0.303	0.723	0.439	1.07	0.16	-0.183
rs9303277	17	35.230	1.19	1.03	1.42	0.038	0.475	0.282	0.704	0.00135	-0.203
rs9303280	17	35.328	1.19	1.03	1.45	0.0446	0.522	0.307	0.78	0.00697	-0.268
rs9303281	17	35.328	1.21	1.03	1.47	0.0412	0.539	0.315	0.799	0.00973	-0.318
rs931992	17	35.075	1.05	0.961	1.14	0.279	0.879	0.575	1.27	0.51	-0.57
rs9635726	17	35.274	1.01	0.884	1.1	0.832	0.674	0.313	1.15	0.239	-0.0242
rs9646419	17	34.851	1	0.987	1.02	0.682	0.715	0.39	1.1	0.212	-0.00872
rs9892055	17	34.764	1.06	0.977	1.17	0.183	0.79	0.508	1.12	0.23	-0.32
rs9894586	17	34.759	1.06	0.977	1.18	0.183	0.789	0.508	1.12	0.226	-0.318
rs9895948	17	35.362	1.05	0.991	1.13	0.152	0.731	0.476	1.06	0.124	-0.159
rs9901146	17	35.297	1.2	1.02	1.45	0.0443	0.497	0.301	0.742	0.00265	-0.244
rs9904334	17	34.722	1.07	0.977	1.18	0.181	0.776	0.497	1.1	0.193	-0.293
rs9904919	17	34.810	1.06	0.973	1.17	0.199	0.801	0.516	1.14	0.262	-0.337
rs9906612	17	34.801	1.01	0.987	1.03	0.607	0.712	0.388	1.1	0.215	-0.0132
rs9907088	17	35.289	1.15	1.01	1.35	0.0623	0.533	0.32	0.792	0.00748	-0.201
rs9908131	17	34.774	1.01	0.987	1.03	0.598	0.705	0.378	1.09	0.207	-0.0129
rs9909593	17	35.224	1.14	1.02	1.32	0.0487	0.505	0.302	0.753	0.00367	-0.164
rs9915323	17	35.024	1.06	0.97	1.17	0.202	0.819	0.542	1.21	0.336	-0.38
rs9916302	17	34.753	1.06	0.977	1.18	0.182	0.787	0.507	1.11	0.221	-0.314
rs9944411	17	34.737	1.07	0.977	1.18	0.181	0.78	0.502	1.11	0.204	-0.302
rs9972882	17	35.061	1.06	0.969	1.18	0.205	0.82	0.515	1.17	0.343	-0.408

Table S13. Single-locus analyses for eQTL SNPs of the probe 235136_at at *ORMDL3*. (Ch: chromosome; ME: mediation effect; AE: alternative effect; CI: confidence interval).

SNP	Ch	Location (Mb)	ME	95% CI		p-value	AE	95% CI		p-value	Proportion of Mediation
rs1007654	17	35.365	1.02	0.934	1.15	0.692	0.776	0.513	1.09	0.19	-0.0825
rs1007655	17	35.365	1.02	0.933	1.16	0.683	0.775	0.512	1.09	0.192	-0.0868
rs1008723	17	35.320	1.05	0.917	1.24	0.493	0.637	0.4	0.884	0.0236	-0.104
rs10445308	17	35.192	1.07	0.91	1.27	0.458	0.596	0.382	0.868	0.0143	-0.107
rs1053651	17	35.076	1.01	0.935	1.12	0.783	0.803	0.48	1.12	0.327	-0.0573
rs1054609	17	35.287	1.05	0.902	1.25	0.539	0.654	0.426	0.935	0.0346	-0.109
rs1058808	17	35.138	1.02	0.91	1.15	0.756	0.716	0.424	1.07	0.149	-0.0504
rs11078919	17	35.089	1.01	0.919	1.12	0.839	0.777	0.487	1.11	0.245	-0.0379
rs11078925	17	35.279	1.05	0.902	1.26	0.523	0.645	0.418	0.926	0.0305	-0.111
rs11078927	17	35.318	1.03	0.905	1.22	0.645	0.694	0.449	1.01	0.0717	-0.0846
rs11557466	17	35.278	1.05	0.902	1.26	0.522	0.645	0.418	0.926	0.0303	-0.111
rs11869286	17	35.067	1.01	0.947	1.09	0.776	0.887	0.588	1.24	0.534	-0.0862
rs11870965	17	35.284	1.05	0.902	1.25	0.537	0.654	0.426	0.935	0.0342	-0.109
rs12150079	17	35.279	1.08	0.952	1.27	0.297	0.69	0.448	1.01	0.0771	-0.215
rs12150298	17	35.088	1.01	0.92	1.12	0.843	0.781	0.492	1.12	0.249	-0.0371
rs12232497	17	35.294	1.05	0.902	1.25	0.541	0.656	0.428	0.938	0.0353	-0.109
rs12603332	17	35.336	1.04	0.924	1.2	0.545	0.641	0.416	0.889	0.024	-0.0797
rs12936231	17	35.283	1.07	0.913	1.27	0.447	0.6	0.384	0.847	0.00885	-0.11
rs12950743	17	35.303	1.06	0.913	1.27	0.454	0.607	0.392	0.849	0.00981	-0.11
rs1476278	17	35.090	1.01	0.919	1.12	0.838	0.777	0.486	1.11	0.244	-0.0381
rs1565923	17	35.112	1.01	0.91	1.13	0.874	0.727	0.421	1.07	0.168	-0.025
rs1619021	17	34.993	1.01	0.941	1.11	0.778	0.802	0.473	1.12	0.314	-0.0537
rs17609240	17	35.364	1.03	0.934	1.16	0.611	0.739	0.484	1.06	0.125	-0.0899
rs1810132	17	35.120	1.01	0.909	1.14	0.868	0.72	0.415	1.06	0.161	-0.0257
rs1877031	17	35.068	1.01	0.948	1.09	0.777	0.887	0.589	1.24	0.532	-0.0852
rs2271308	17	35.071	1.01	0.935	1.12	0.793	0.808	0.488	1.13	0.333	-0.0553
rs2271309	17	35.039	1.05	0.92	1.31	0.579	0.845	0.261	1.3	0.672	-0.377
rs2290400	17	35.320	1.05	0.918	1.24	0.499	0.637	0.403	0.875	0.0214	-0.101
rs2305479	17	35.316	1.05	0.919	1.22	0.532	0.63	0.402	0.866	0.0189	-0.0855
rs2305480	17	35.316	1.03	0.906	1.2	0.67	0.688	0.446	0.985	0.065	-0.0724
rs2313171	17	35.087	1.01	0.92	1.12	0.846	0.783	0.495	1.12	0.253	-0.0365
rs2313640	17	35.365	1.02	0.933	1.16	0.689	0.779	0.514	1.1	0.2	-0.0873
rs2517954	17	35.097	1.01	0.912	1.13	0.883	0.739	0.435	1.08	0.188	-0.0234
rs2517955	17	35.097	1.02	0.914	1.14	0.778	0.725	0.438	1.08	0.161	-0.0446
rs2517956	17	35.097	1.01	0.911	1.13	0.883	0.737	0.435	1.08	0.187	-0.0234
rs2517957	17	35.092	1.01	0.918	1.12	0.834	0.774	0.481	1.11	0.24	-0.0388
rs2517958	17	35.092	1.01	0.918	1.13	0.832	0.772	0.481	1.11	0.237	-0.0392
rs2872507	17	35.294	1.05	0.902	1.25	0.542	0.656	0.429	0.939	0.0356	-0.109

rs2941505	17	35.086	1.01	0.922	1.12	0.854	0.789	0.501	1.13	0.263	-0.035
rs2941506	17	35.087	1.01	0.921	1.12	0.851	0.787	0.499	1.13	0.26	-0.0355
rs2952151	17	35.082	1	0.923	1.11	0.956	0.8	0.493	1.13	0.292	-0.0106
rs2952155	17	35.115	1.05	0.892	1.28	0.639	0.765	0.349	1.19	0.385	-0.175
rs2952156	17	35.130	1.01	0.908	1.14	0.868	0.719	0.414	1.06	0.159	-0.0258
rs3816470	17	35.239	1.07	0.916	1.29	0.418	0.577	0.368	0.812	0.00549	-0.109
rs3894194	17	35.376	1.02	0.925	1.13	0.739	0.687	0.45	0.952	0.0435	-0.0401
rs3902025	17	35.373	1.03	0.92	1.17	0.613	0.698	0.465	0.98	0.0645	-0.081
rs4065985	17	35.355	1.04	0.924	1.22	0.54	0.606	0.384	0.899	0.0215	-0.0725
rs4378650	17	35.334	1.04	0.921	1.2	0.558	0.649	0.421	0.906	0.0292	-0.0811
rs4794820	17	35.343	1.03	0.906	1.2	0.684	0.729	0.485	1.08	0.127	-0.0863
rs4795397	17	35.277	1.06	0.902	1.26	0.522	0.644	0.418	0.926	0.0302	-0.111
rs4795400	17	35.321	1.04	0.9	1.23	0.629	0.705	0.456	1.02	0.0863	-0.0996
rs4795405	17	35.342	1.03	0.912	1.19	0.664	0.706	0.467	1.02	0.0865	-0.077
rs4795408	17	35.361	1.02	0.919	1.16	0.691	0.666	0.436	0.929	0.031	-0.0519
rs6503525	17	35.349	1.03	0.922	1.17	0.666	0.657	0.431	0.918	0.0258	-0.0547
rs6503526	17	35.368	1.02	0.921	1.15	0.711	0.655	0.434	0.917	0.0257	-0.0432
rs6503527	17	35.368	1.02	0.93	1.17	0.679	0.792	0.52	1.13	0.237	-0.105
rs7207600	17	35.345	1.02	0.921	1.17	0.708	0.769	0.504	1.11	0.187	-0.0836
rs7212938	17	35.376	1.02	0.918	1.15	0.747	0.632	0.406	0.91	0.0243	-0.0333
rs7216389	17	35.323	1.05	0.916	1.24	0.496	0.645	0.41	0.903	0.0281	-0.109
rs7218321	17	35.368	1.02	0.931	1.16	0.684	0.784	0.515	1.11	0.216	-0.0948
rs7218742	17	35.368	1.02	0.932	1.16	0.687	0.781	0.515	1.11	0.207	-0.0903
rs7219080	17	35.368	1.02	0.931	1.16	0.684	0.785	0.515	1.12	0.219	-0.096
rs7219923	17	35.328	1.05	0.915	1.24	0.495	0.646	0.41	0.904	0.029	-0.11
rs7224129	17	35.329	1.05	0.914	1.24	0.495	0.647	0.409	0.906	0.0298	-0.112
rs7359623	17	35.303	1.07	0.914	1.27	0.433	0.591	0.386	0.835	0.00776	-0.11
rs7503195	17	34.976	1	0.944	1.06	0.946	0.973	0.679	1.39	0.884	-0.0823
rs8065126	17	35.353	1.02	0.927	1.16	0.703	0.77	0.508	1.09	0.185	-0.0824
rs8067378	17	35.305	1.06	0.913	1.27	0.457	0.609	0.396	0.851	0.0102	-0.11
rs8069176	17	35.311	1.04	0.904	1.22	0.618	0.675	0.435	0.974	0.0523	-0.0867
rs8076131	17	35.334	1.03	0.896	1.22	0.661	0.723	0.47	1.06	0.118	-0.0973
rs8076474	17	35.365	1.02	0.932	1.16	0.688	0.773	0.51	1.09	0.187	-0.0844
rs8078228	17	35.089	1.01	0.919	1.12	0.84	0.778	0.488	1.11	0.245	-0.0378
rs8079416	17	35.346	1.03	0.92	1.17	0.669	0.66	0.432	0.923	0.0264	-0.0545
rs8182252	17	34.981	1.05	0.914	1.35	0.582	0.745	0.174	1.19	0.548	-0.188
rs869402	17	35.322	1.05	0.916	1.24	0.494	0.643	0.41	0.898	0.0272	-0.108
rs881844	17	35.064	1.01	0.947	1.09	0.776	0.887	0.589	1.24	0.536	-0.0871
rs903501	17	35.093	1.01	0.916	1.13	0.853	0.767	0.462	1.13	0.256	-0.0344
rs903502	17	35.083	1.01	0.923	1.11	0.873	0.799	0.508	1.14	0.284	-0.0314
rs907089	17	35.087	1.01	0.921	1.12	0.847	0.784	0.496	1.12	0.254	-0.0364
rs907091	17	35.175	1.08	0.922	1.31	0.358	0.532	0.331	0.77	0.00263	-0.105
rs907092	17	35.176	1.07	0.908	1.28	0.447	0.588	0.38	0.856	0.0122	-0.106

rs907094	17	35.044	1.05	0.92	1.31	0.579	0.846	0.26	1.3	0.673	-0.378
rs9303274	17	35.090	1.01	0.918	1.12	0.836	0.775	0.483	1.11	0.241	-0.0384
rs9303277	17	35.230	1.07	0.918	1.28	0.419	0.577	0.371	0.812	0.00507	-0.105
rs9303280	17	35.328	1.05	0.919	1.24	0.478	0.609	0.387	0.858	0.014	-0.0934
rs9303281	17	35.328	1.05	0.915	1.24	0.496	0.646	0.41	0.903	0.0285	-0.11
rs931992	17	35.075	1.01	0.945	1.09	0.782	0.881	0.579	1.23	0.515	-0.0809
rs9635726	17	35.274	1.03	0.826	1.35	0.786	0.777	0.351	1.24	0.437	-0.135
rs9895948	17	35.362	1.02	0.931	1.16	0.692	0.772	0.509	1.09	0.186	-0.0839
rs9901146	17	35.297	1.06	0.913	1.27	0.452	0.605	0.389	0.847	0.00952	-0.11
rs9907088	17	35.289	1.05	0.902	1.25	0.54	0.655	0.427	0.937	0.035	-0.109
rs9909593	17	35.224	1.06	0.911	1.26	0.488	0.622	0.399	0.894	0.0194	-0.108
rs9915323	17	35.024	1.02	0.942	1.11	0.724	0.81	0.488	1.14	0.335	-0.0743

Table S14. Single-locus analyses for eQTL SNPs of the probe 240701_at at *ORMDL3*. (Ch: chromosome; ME: mediation effect; AE: alternative effect; CI: confidence interval).

SNP	Ch	Location (Mb)	ME	95% CI		p-value	AE	95% CI		p-value	Proportion of Mediation
rs1008723	17	35.320	0.931	0.843	1.03	0.158	0.655	0.427	0.954	0.037	0.116
rs10445308	17	35.192	0.934	0.853	1.03	0.161	0.638	0.42	0.937	0.0277	0.104
rs1054609	17	35.287	0.93	0.849	1.02	0.13	0.701	0.472	1.03	0.074	0.141
rs11078925	17	35.279	0.93	0.847	1.02	0.135	0.692	0.463	1.01	0.0656	0.136
rs11078927	17	35.318	0.941	0.868	1.02	0.15	0.689	0.452	1	0.0643	0.116
rs11557466	17	35.278	0.93	0.847	1.02	0.135	0.691	0.462	1.01	0.0654	0.136
rs11870965	17	35.284	0.93	0.848	1.02	0.13	0.7	0.471	1.02	0.0736	0.141
rs12150079	17	35.279	0.951	0.866	1.06	0.317	0.733	0.448	1.12	0.179	0.118
rs12232497	17	35.294	0.93	0.849	1.02	0.129	0.702	0.474	1.03	0.0751	0.142
rs12603332	17	35.336	0.953	0.892	1.03	0.171	0.65	0.438	0.952	0.0273	0.0798
rs12936231	17	35.283	0.924	0.832	1.03	0.154	0.668	0.452	0.993	0.0426	0.133
rs12950743	17	35.303	0.924	0.833	1.03	0.151	0.675	0.456	1	0.0468	0.136
rs2290400	17	35.320	0.933	0.847	1.03	0.16	0.656	0.426	0.957	0.0352	0.114
rs2305479	17	35.316	0.932	0.842	1.03	0.173	0.654	0.421	0.976	0.0361	0.114
rs2305480	17	35.316	0.94	0.864	1.02	0.157	0.691	0.455	1.01	0.0669	0.119
rs2872507	17	35.294	0.93	0.849	1.02	0.129	0.703	0.474	1.03	0.0755	0.142
rs3816470	17	35.239	0.925	0.83	1.03	0.17	0.643	0.427	0.96	0.0274	0.119
rs4378650	17	35.334	0.951	0.888	1.03	0.165	0.661	0.449	0.962	0.0338	0.0879
rs4795397	17	35.277	0.93	0.847	1.02	0.136	0.691	0.462	1.01	0.0652	0.136
rs4795400	17	35.321	0.936	0.861	1.02	0.132	0.7	0.456	1.01	0.0791	0.13
rs7216389	17	35.323	0.928	0.839	1.03	0.15	0.662	0.442	0.96	0.042	0.123
rs7219923	17	35.328	0.928	0.838	1.03	0.148	0.664	0.443	0.963	0.0438	0.125
rs7224129	17	35.329	0.928	0.838	1.03	0.147	0.666	0.444	0.969	0.0453	0.126
rs7359623	17	35.303	0.923	0.826	1.04	0.174	0.666	0.445	1.01	0.0464	0.133
rs8067378	17	35.305	0.924	0.833	1.03	0.15	0.677	0.458	1	0.0484	0.137
rs8069176	17	35.311	0.935	0.855	1.02	0.147	0.693	0.456	1.02	0.0694	0.127
rs8076131	17	35.334	0.94	0.87	1.02	0.122	0.73	0.479	1.07	0.119	0.14
rs869402	17	35.322	0.929	0.839	1.03	0.151	0.66	0.439	0.954	0.041	0.122
rs907091	17	35.175	0.932	0.84	1.04	0.207	0.586	0.38	0.875	0.00916	0.0873
rs907092	17	35.176	0.936	0.856	1.03	0.167	0.624	0.411	0.914	0.0208	0.0963
rs9303277	17	35.230	0.927	0.833	1.03	0.173	0.641	0.427	0.943	0.0255	0.116
rs9303280	17	35.328	0.943	0.869	1.03	0.17	0.623	0.4	0.909	0.0203	0.0862
rs9303281	17	35.328	0.928	0.839	1.03	0.149	0.663	0.443	0.961	0.0428	0.124
rs9901146	17	35.297	0.924	0.833	1.03	0.151	0.673	0.455	0.998	0.0455	0.135
rs9907088	17	35.289	0.93	0.849	1.02	0.129	0.702	0.473	1.03	0.0747	0.141
rs9909593	17	35.224	0.932	0.849	1.03	0.146	0.67	0.447	0.982	0.0453	0.122

Table S15. Single-locus analyses for eQTL SNPs of the probe 209395_at at *CHI3L1*. (Ch: chromosome; ME: mediation effect; AE: alternative effect; CI: confidence interval).

SNP	Ch	Location (Mb)	ME	95% CI		p-value	AE	95% CI		p-value	Proportion of Mediation
rs10399931	1	201.423	1.24	1.08	1.58	0.0394	0.933	0.284	1.3	0.881	1.44
rs10920579	1	201.426	1.14	1.04	1.45	0.151	0.787	0.162	1.08	0.698	-1.06
rs1538372	1	201.421	0.829	0.71	0.909	0.00332	1.26	0.825	2.56	0.415	-4.52
rs2153101	1	201.435	1.13	1.04	1.43	0.155	0.785	0.179	1.09	0.671	-0.885
rs2486064	1	201.435	0.947	0.896	0.978	0.0173	0.913	0.531	1.42	0.713	0.356
rs2494277	1	201.435	1.13	1.04	1.43	0.155	0.784	0.177	1.09	0.673	-0.882
rs4950882	1	201.431	1.13	1.04	1.43	0.152	0.782	0.162	1.08	0.686	-0.898
rs4950928	1	201.423	1.26	1.08	1.68	0.0616	0.679	0.0977	1	0.613	-1.17
rs4950929	1	201.427	1.14	1.04	1.44	0.151	0.785	0.161	1.08	0.694	-0.999
rs7518666	1	201.430	1.13	1.04	1.44	0.152	0.783	0.161	1.08	0.69	-0.943
rs7541061	1	201.430	1.13	1.04	1.44	0.152	0.784	0.161	1.08	0.69	-0.947
rs7556099	1	201.433	1.14	1.04	1.49	0.181	0.764	0.143	1.08	0.7	-0.835
rs946262	1	201.425	1.14	1.04	1.45	0.151	0.788	0.162	1.08	0.7	-1.08
rs946263	1	201.432	1.13	1.04	1.42	0.153	0.781	0.162	1.08	0.683	-0.863

Table S16. Single-locus analyses for eQTL SNPs of the probe 209396_s_at at *CHI3L1*. (Ch: chromosome; ME: mediation effect; AE: alternative effect; CI: confidence interval).

SNP	Ch	Location (Mb)	ME	95% CI		p-value	AE	95% CI		p-value	Proportion of Mediation
rs10399931	1	201.423	1.08	0.985	1.25	0.174	1.01	0.581	1.39	0.96	0.876
rs10920579	1	201.426	1.06	0.991	1.21	0.246	0.805	0.406	1.11	0.418	-0.342
rs1538372	1	201.421	0.908	0.83	0.968	0.0161	1.06	0.689	1.71	0.796	2.7
rs2153101	1	201.435	1.06	0.989	1.2	0.258	0.795	0.398	1.11	0.399	-0.294
rs2486064	1	201.435	0.964	0.929	0.991	0.0254	0.928	0.58	1.36	0.727	0.32
rs2494277	1	201.435	1.06	0.989	1.2	0.257	0.795	0.398	1.1	0.398	-0.296
rs4950882	1	201.431	1.06	0.992	1.2	0.246	0.8	0.402	1.11	0.405	-0.313
rs4950928	1	201.423	1.1	0.99	1.31	0.184	0.773	0.372	1.09	0.367	-0.495
rs4950929	1	201.427	1.06	0.991	1.2	0.246	0.803	0.405	1.11	0.413	-0.332
rs7518666	1	201.430	1.06	0.992	1.2	0.246	0.801	0.404	1.11	0.408	-0.321
rs7541061	1	201.430	1.06	0.992	1.2	0.246	0.801	0.404	1.11	0.409	-0.322
rs7556099	1	201.433	1.05	0.983	1.2	0.311	0.774	0.368	1.1	0.378	-0.23
rs946262	1	201.425	1.06	0.99	1.21	0.245	0.805	0.407	1.11	0.42	-0.347
rs946263	1	201.432	1.06	0.992	1.2	0.246	0.799	0.404	1.11	0.402	-0.306

Table S17. Single-locus analyses for eQTL SNPs of the probe 226333_at at *IL6R*. (Ch: chromosome; ME: mediation effect; AE: alternative effect; CI: confidence interval).

SNP	Ch	Location (Mb)	ME	95% CI		p-value	AE	95% CI		p-value	Proportion of Mediation
rs10908423	1	152.911	1	1	1.01	0.00674	1.01	0.579	1.43	0.979	0.346
rs10908835	1	152.623	1.02	1	1.05	0.0433	0.945	0.582	1.36	0.785	-0.602
rs11265604	1	152.619	0.989	0.98	0.996	0.00825	0.912	0.595	1.33	0.652	0.1
rs11265608	1	152.631	1.02	0.83	1.39	0.873	0.542	0.116	0.967	0.288	-0.0256
rs11808153	1	152.505	1.02	0.904	1.16	0.806	0.648	0.218	1.14	0.325	-0.0296
rs11809740	1	152.586	1.02	0.992	1.08	0.248	0.855	0.48	1.25	0.519	-0.171
rs11811448	1	152.531	0.999	0.886	1.16	0.991	0.638	0.19	1.22	0.354	0.00134
rs1194610	1	152.563	1.13	1.02	1.26	0.0259	0.957	0.612	1.44	0.841	1.53
rs12121085	1	152.622	0.995	0.992	0.998	0.00686	0.888	0.572	1.31	0.582	0.0346
rs1212352	1	152.506	0.973	0.951	0.99	0.00773	0.751	0.527	1.04	0.0939	0.0767
rs12127600	1	152.623	1.02	1	1.05	0.0431	0.944	0.581	1.36	0.781	-0.62
rs1685633	1	152.558	1.08	0.859	1.5	0.607	0.694	0.206	1.19	0.443	-0.219
rs1760796	1	152.574	1.03	0.99	1.08	0.253	0.869	0.488	1.27	0.565	-0.202
rs2274988	1	152.583	1.03	0.991	1.08	0.247	0.856	0.486	1.26	0.524	-0.177
rs2297606	1	152.588	1.05	1	1.12	0.0901	0.987	0.61	1.39	0.95	1.37
rs2297607	1	152.588	1.02	0.976	1.09	0.444	0.826	0.417	1.25	0.503	-0.115
rs2481065	1	152.579	1.08	0.863	1.5	0.587	0.688	0.195	1.15	0.431	-0.222
rs2988721	1	152.575	1.03	0.99	1.08	0.251	0.869	0.488	1.27	0.563	-0.202
rs4075015	1	152.656	0.988	0.978	0.996	0.00676	0.86	0.523	1.35	0.52	0.0682
rs4103781	1	152.547	0.991	0.984	0.998	0.0109	1.06	0.715	1.47	0.756	-0.183
rs4845617	1	152.645	1.05	1.01	1.09	0.0249	1.04	0.631	1.53	0.87	0.578
rs6427560	1	152.554	1.03	0.991	1.1	0.225	0.903	0.505	1.35	0.686	-0.428
rs6427627	1	152.626	1.02	1	1.05	0.0434	0.945	0.583	1.36	0.785	-0.601
rs7521837	1	152.519	1.01	0.996	1.02	0.305	0.605	0.318	0.921	0.068	-0.00788
rs9330261	1	152.902	1.01	1	1.01	0.0121	1.18	0.811	1.62	0.349	0.0372
rs9426832	1	152.899	1	1	1.01	0.0111	1.18	0.819	1.61	0.339	0.0248
rs9427117	1	152.899	1.01	1	1.01	0.012	1.18	0.815	1.63	0.334	0.0354
rs9427118	1	152.904	1.04	0.993	1.12	0.16	1.22	0.746	1.91	0.396	0.197
rs952146	1	152.636	1.02	1	1.05	0.042	0.951	0.586	1.37	0.809	-0.756

Table S18. Single-locus analyses for eQTL SNPs of the probe 205945_at at *IL6R*. (Ch: chromosome; ME: mediation effect; AE: alternative effect; CI: confidence interval).

SNP	Ch	Location (Mb)	ME	95% CI		p-value	AE	95% CI		p-value	Proportion of Mediation
rs10908831	1	152.595	1.01	0.984	1.04	0.405	1.09	0.748	1.49	0.637	0.129
rs10908835	1	152.623	1	0.999	1	0.97	0.994	0.62	1.41	0.974	0.00337
rs11265604	1	152.619	0.992	0.973	1.01	0.458	0.929	0.559	1.34	0.738	0.092
rs11265608	1	152.631	0.993	0.728	1.29	0.961	0.787	0.176	1.23	0.772	0.0263
rs11808153	1	152.505	0.954	0.831	1.08	0.458	0.743	0.255	1.3	0.484	0.118
rs11809740	1	152.586	0.998	0.961	1.04	0.915	0.948	0.535	1.34	0.821	0.037
rs11811448	1	152.531	0.937	0.814	1.06	0.332	0.756	0.214	1.46	0.559	0.163
rs1194610	1	152.563	1.04	0.951	1.13	0.356	1.05	0.692	1.53	0.804	0.462
rs12121085	1	152.622	0.993	0.978	1.01	0.384	0.904	0.526	1.32	0.669	0.0626
rs12127600	1	152.623	1	1	1	0.965	0.994	0.621	1.41	0.976	0.000156
rs1685633	1	152.558	1.04	0.767	1.4	0.78	0.979	0.328	1.49	0.965	1.92
rs1760796	1	152.574	0.998	0.959	1.04	0.904	0.967	0.539	1.36	0.886	0.0664
rs2274988	1	152.583	0.998	0.96	1.04	0.922	0.951	0.533	1.34	0.83	0.0365
rs2297607	1	152.588	0.994	0.944	1.05	0.815	0.982	0.505	1.41	0.945	0.246
rs2481065	1	152.579	1.05	0.779	1.4	0.756	0.954	0.311	1.42	0.924	38.9
rs2988721	1	152.575	0.998	0.959	1.04	0.908	0.966	0.539	1.36	0.883	0.0623
rs4075015	1	152.656	0.991	0.971	1.01	0.379	0.883	0.493	1.34	0.617	0.0627
rs4845617	1	152.645	1	0.993	1.01	0.853	1.05	0.645	1.5	0.81	0.0127
rs6427560	1	152.554	1	0.948	1.06	0.99	1.01	0.585	1.44	0.975	0.0444
rs6427627	1	152.626	1	0.999	1	0.97	0.994	0.62	1.41	0.974	0.00342
rs7521837	1	152.519	0.999	0.995	1	0.344	0.606	0.299	0.871	0.0773	0.00229
rs952146	1	152.636	1	0.999	1	0.963	0.999	0.624	1.42	0.996	0.0211

Table S19. Single-locus analyses for eQTL SNPs of the probe 206618_at at *IL18R1*. (Ch: chromosome; ME: mediation effect; AE: alternative effect; CI: confidence interval).

SNP	Ch	Location (Mb)	ME	95% CI		p-value	AE	95% CI		p-value	Proportion of Mediation
rs10170583	2	102.341	0.986	0.911	1.08	0.748	1.09	0.712	1.59	0.666	-0.191
rs10176664	2	102.343	0.987	0.913	1.08	0.762	1.07	0.694	1.54	0.728	-0.227
rs10192157	2	102.335	0.989	0.914	1.08	0.783	1.05	0.682	1.51	0.804	-0.307
rs10200952	2	102.394	0.994	0.935	1.07	0.865	1.22	0.817	1.72	0.292	-0.033
rs10203558	2	102.394	0.994	0.935	1.07	0.865	1.22	0.817	1.72	0.292	-0.0331
rs10206291	2	102.405	0.994	0.935	1.07	0.866	1.22	0.817	1.72	0.285	-0.0324
rs10208196	2	102.363	0.994	0.935	1.07	0.867	1.22	0.815	1.73	0.282	-0.0322
rs10208293	2	102.333	1.03	0.936	1.13	0.552	0.912	0.543	1.36	0.688	-0.412
rs10439410	2	102.357	0.994	0.935	1.07	0.866	1.22	0.814	1.72	0.28	-0.0323
rs11123934	2	102.482	0.998	0.963	1.05	0.939	1.09	0.635	1.54	0.682	-0.0194
rs13021177	2	102.423	0.994	0.935	1.07	0.866	1.22	0.816	1.72	0.282	-0.0322
rs13424006	2	102.334	0.989	0.914	1.08	0.788	1.04	0.677	1.5	0.838	-0.384
rs1362348	2	102.351	0.987	0.913	1.08	0.759	1.08	0.699	1.57	0.703	-0.207
rs1420094	2	102.382	0.994	0.935	1.07	0.865	1.21	0.814	1.72	0.303	-0.0336
rs1420097	2	102.376	0.994	0.935	1.07	0.866	1.21	0.815	1.72	0.3	-0.0333
rs1420100	2	102.403	0.994	0.935	1.07	0.866	1.22	0.817	1.72	0.286	-0.0325
rs1420105	2	102.402	0.994	0.935	1.07	0.865	1.22	0.817	1.72	0.288	-0.0327
rs1523198	2	102.465	0.995	0.958	1.04	0.817	1.12	0.703	1.56	0.552	-0.0483
rs1592458	2	102.398	0.994	0.935	1.07	0.865	1.22	0.817	1.72	0.29	-0.0329
rs17027173	2	102.423	0.991	0.931	1.07	0.794	1.06	0.669	1.78	0.816	-0.192
rs1861245	2	102.333	0.989	0.914	1.08	0.788	1.04	0.676	1.5	0.841	-0.392
rs1974675	2	102.353	0.988	0.913	1.08	0.774	1.08	0.709	1.6	0.7	-0.186
rs2041739	2	102.361	0.994	0.935	1.07	0.867	1.22	0.815	1.73	0.282	-0.0322
rs2058659	2	102.421	0.994	0.935	1.07	0.866	1.22	0.816	1.72	0.282	-0.0322
rs2075188	2	102.487	0.999	0.966	1.04	0.95	1.07	0.619	1.51	0.743	-0.0176
rs2075189	2	102.485	0.999	0.966	1.04	0.948	1.08	0.62	1.52	0.732	-0.0179
rs2110662	2	102.387	0.994	0.935	1.07	0.865	1.22	0.816	1.72	0.297	-0.0333
rs2287033	2	102.378	0.994	0.935	1.07	0.865	1.21	0.814	1.72	0.303	-0.0336
rs2293224	2	102.402	0.994	0.935	1.07	0.865	1.22	0.817	1.72	0.287	-0.0326
rs2310300	2	102.416	0.994	0.935	1.07	0.866	1.22	0.816	1.72	0.283	-0.0321
rs3213732	2	102.365	0.994	0.935	1.07	0.867	1.22	0.815	1.73	0.285	-0.0323
rs3732124	2	102.384	0.994	0.935	1.07	0.865	1.21	0.815	1.72	0.301	-0.0336
rs3755265	2	102.419	0.994	0.935	1.07	0.866	1.22	0.816	1.72	0.282	-0.0321
rs3755266	2	102.409	0.994	0.935	1.07	0.866	1.22	0.816	1.72	0.283	-0.0321
rs3755276	2	102.345	0.987	0.913	1.08	0.762	1.07	0.694	1.55	0.724	-0.223
rs3771154	2	102.406	0.994	0.935	1.07	0.866	1.22	0.817	1.72	0.285	-0.0324
rs3771155	2	102.404	0.994	0.935	1.07	0.866	1.22	0.817	1.72	0.285	-0.0324
rs3771166	2	102.353	0.988	0.913	1.08	0.775	1.08	0.705	1.59	0.717	-0.198

rs4479442	2	102.421	0.994	0.935	1.07	0.866	1.22	0.816	1.72	0.282	-0.0321
rs4851004	2	102.376	0.994	0.935	1.07	0.865	1.21	0.814	1.72	0.303	-0.0336
rs4851571	2	102.385	0.994	0.935	1.07	0.865	1.21	0.816	1.72	0.299	-0.0334
rs4851572	2	102.385	0.994	0.935	1.07	0.865	1.21	0.816	1.72	0.298	-0.0334
rs4988955	2	102.334	0.989	0.914	1.08	0.786	1.05	0.679	1.51	0.823	-0.346
rs4988956	2	102.334	0.989	0.914	1.08	0.785	1.05	0.68	1.51	0.818	-0.335
rs4988957	2	102.335	0.989	0.914	1.08	0.785	1.05	0.68	1.51	0.815	-0.328
rs4988958	2	102.335	0.989	0.914	1.08	0.784	1.05	0.681	1.51	0.81	-0.318
rs6543135	2	102.429	0.981	0.896	1.08	0.685	1.08	0.688	1.77	0.74	-0.323
rs6543150	2	102.480	0.998	0.961	1.05	0.935	1.1	0.635	1.54	0.654	-0.0203
rs6706002	2	102.373	0.994	0.935	1.07	0.867	1.22	0.815	1.73	0.293	-0.0328
rs6710034	2	102.390	0.994	0.935	1.07	0.865	1.22	0.816	1.72	0.296	-0.0332
rs6710528	2	102.383	0.994	0.935	1.07	0.865	1.21	0.815	1.72	0.302	-0.0336
rs6741235	2	102.484	0.999	0.965	1.04	0.945	1.08	0.623	1.53	0.718	-0.0184
rs6743516	2	102.403	0.994	0.935	1.07	0.866	1.22	0.817	1.72	0.286	-0.0325
rs6749014	2	102.373	0.994	0.935	1.07	0.867	1.22	0.815	1.73	0.295	-0.033
rs6749114	2	102.334	0.989	0.914	1.08	0.787	1.04	0.678	1.51	0.83	-0.362
rs6751967	2	102.334	0.989	0.914	1.08	0.788	1.04	0.677	1.5	0.837	-0.38
rs6758936	2	102.358	0.994	0.935	1.07	0.867	1.22	0.814	1.73	0.281	-0.0323
rs6759479	2	102.406	0.994	0.935	1.07	0.866	1.22	0.816	1.72	0.284	-0.0323
rs6760621	2	102.366	0.994	0.935	1.07	0.867	1.22	0.815	1.73	0.288	-0.0325
rs7558013	2	102.359	0.983	0.911	1.07	0.68	1.02	0.643	1.64	0.922	-2.67
rs7559566	2	102.394	0.994	0.935	1.07	0.865	1.22	0.817	1.72	0.292	-0.033
rs7559845	2	102.413	0.994	0.935	1.07	0.866	1.22	0.816	1.72	0.283	-0.0321
rs7573566	2	102.482	0.998	0.962	1.05	0.938	1.1	0.637	1.54	0.673	-0.0197
rs7594402	2	102.388	0.994	0.935	1.07	0.865	1.22	0.816	1.72	0.296	-0.0333
rs7603730	2	102.341	0.988	0.913	1.08	0.771	1.06	0.694	1.52	0.77	-0.267
rs885088	2	102.405	0.994	0.935	1.07	0.866	1.22	0.817	1.72	0.285	-0.0324

Table S20. Single-locus analyses for eQTL SNPs of the probe 209349_at at *RAD50*. (Ch: chromosome; ME: mediation effect; AE: alternative effect; CI: confidence interval).

SNP	Ch	Location (Mb)	ME	95% CI		p-value	AE	95% CI		p-value	Proportion of Mediation
rs11738703	5	131.884	1.02	0.892	1.18	0.799	1.17	0.727	1.74	0.483	0.109
rs11739623	5	131.892	1.02	0.891	1.16	0.821	1.14	0.708	1.68	0.57	0.113
rs11741255	5	131.839	0.993	0.927	1.07	0.853	1.01	0.627	1.45	0.955	-1.25
rs11745207	5	131.884	1.02	0.89	1.18	0.807	1.16	0.722	1.73	0.513	0.11
rs17622656	5	131.849	0.997	0.938	1.06	0.929	0.997	0.633	1.4	0.987	0.46
rs17691077	5	132.071	1.51	0.666	4.02	0.365	3.28	0.561	12.6	0.109	0.422
rs17772583	5	131.981	0.991	0.806	1.22	0.932	0.89	0.548	1.49	0.652	0.0653
rs2057687	5	131.915	1	0.94	1.08	0.9	1.04	0.636	1.57	0.852	0.0939
rs2069812	5	131.908	1.02	0.873	1.18	0.841	0.881	0.554	1.42	0.601	-0.129
rs2237060	5	131.999	1.02	0.941	1.12	0.672	1.16	0.752	1.69	0.476	0.121
rs4705959	5	131.894	1.01	0.889	1.16	0.863	1.18	0.737	1.77	0.469	0.0717
rs743562	5	131.900	0.992	0.933	1.05	0.798	1.23	0.822	1.77	0.296	-0.044

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