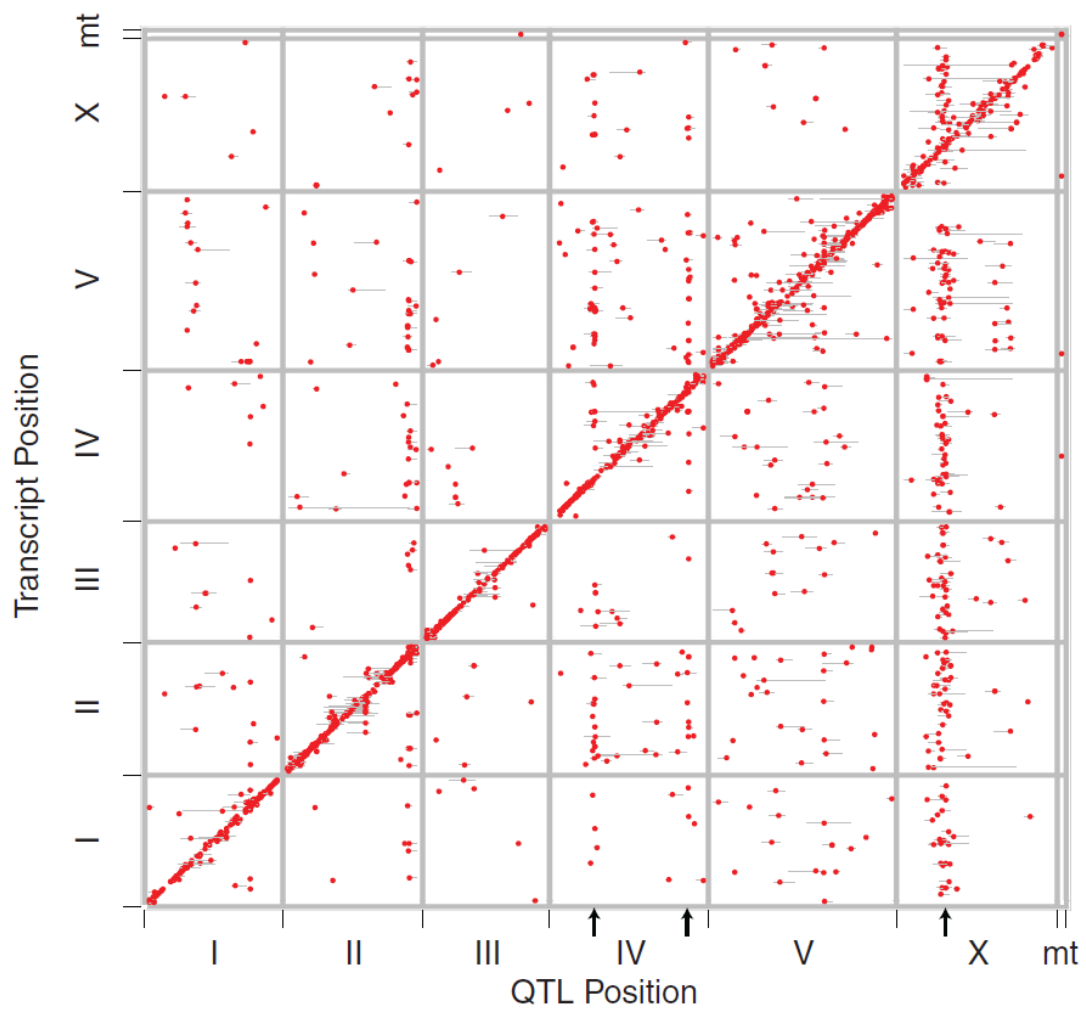


## High Definition eQTL Tables and Figures

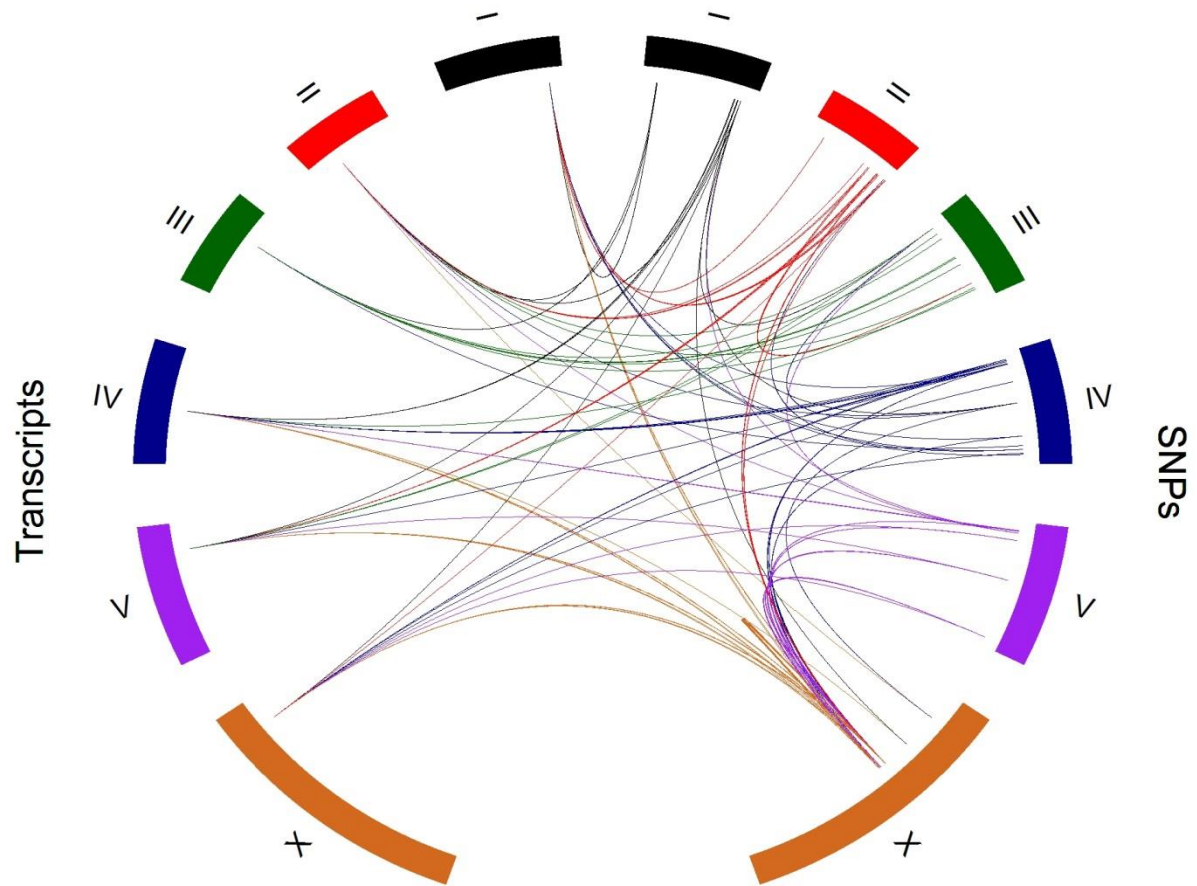
### Figure Legends

**Figure 1** The distribution of eQTLs for each transcript abundance phenotype in *C. elegans*, located at the genomic positions of the transcripts. Those eQTLs on the diagonal are cis-eQTLs, whereas those off the diagonal are trans-eQTLs. Adapted from Rockman et al. (2010).

**Figure 2** Circos plot illustrating the pattern of how a particular gene transcript is regulated by eQTLs on different chromosomes in *C. elegans*.



**Figure 1**



**Figure 2**

Table 1 Results of simulation 1 with  $\sigma = 1$  for the random error with independent predictors.

$\sigma = 1$	Main Effects				Interactions Effects				Model			
Method	Cov	Cor0	Inc0	Exact	Cov	Cor0	Inc0	Exact	Size	MSE	$Adj - R^2$	Time
<b>Single Marker</b>	0	1	0.25	0	NA	NA	NA	NA	3	23.63	0.216	0.824
<b>FS</b>	0.85	0.953	0.0625	0.85	NA	NA	NA	NA	27	10.23	0.660	3.47
<b>FS2</b>	1	0.996	0	1	0.95	0.981	0	0	27	0.302	0.989	72.31
<b>iFORM</b>	0.9	0.999	0.05	0.9	0.9	1	0	0.9	7.55	2.93	0.894	4.08
<b>Oracle</b>	1	1	0	1	1	1	0	1	8	1.023	0.965	NA

Outcomes include the convergence Probability (Cov)  $\sum_{m=1}^M I(\mathcal{T} \subset \hat{\mathcal{T}})/M$ , percentage of correct zeros identified (Cor0)  $\sum_{m=1}^M \sum_{j=1}^p I(\hat{\beta}_j = 0, \beta_j = 0)/[M(p - p_0)]$ , percentage of incorrect zeros identified (Inc0)  $\sum_{m=1}^M \sum_{j=1}^p I(\hat{\beta}_j = 0, \beta_j \neq 0)/[M(p_0)]$ , the exact selection probability (Exact)  $\sum_{m=1}^M I(\mathcal{T} = \hat{\mathcal{T}})/M$ , average model size, Mean Square Error for the model (MSE), the adjusted R-square of the model, and the computational time in seconds.

Table 2 Results of simulation 2 with  $\sigma = 2$  for the random error with independent predictors.

$\sigma = 2$	Main Effects				Interactions Effects				Model			
Method	Cov	Cor0	Inc0	Exact	Cov	Cor0	Inc0	Exact	Size	MSE	$Adj - R^2$	Time
<b>Single Marker</b>	0.02	0.999	0.529	0.029	NA	NA	NA	NA	1.97	27.02	0.178	0.69
<b>FS</b>	0.8	0.953	0.05	0.8	NA	NA	NA	NA	27	11.49	0.651	3.22
<b>FS2</b>	1	0.996	0	1	0.98	0.98	0	0	27	1.17	0.964	68.2
<b>iFORM</b>	0.97	0.998	0.007	0.97	0.95	1	0	0.93	8.7	4.41	0.865	3.84
<b>Oracle</b>	1	1	0	1	1	1	0	1	8	3.92	0.880	NA

Outcomes include the convergence Probability (Cov)  $\sum_{m=1}^M I(\mathcal{T} \subset \hat{\mathcal{T}})/M$ , percentage of correct zeros identified (Cor0)  $\sum_{m=1}^M \sum_{j=1}^p I(\hat{\beta}_j = 0, \beta_j = 0)/[M(p - p_0)]$ , percentage of incorrect zeros identified (Inc0)  $\sum_{m=1}^M \sum_{j=1}^p I(\hat{\beta}_j = 0, \beta_j \neq 0)/[M(p_0)]$ , the exact selection probability (Exact)  $\sum_{m=1}^M I(\mathcal{T} = \hat{\mathcal{T}})/M$ , average model size, Mean Square Error for the model (MSE), the adjusted R-square of the model, and the computational time in seconds.

Table 3 Results of simulation 3 with  $\sigma = 3$  for the random error with independent predictors.

$\sigma = 3$	Main Effects				Interactions Effects				Model			
Method	Cov	Cor0	Inc0	Exact	Cov	Cor0	Inc0	Exact	Size	MSE	Adj - $R^2$	Time
<b>Single Marker</b>	0	0.999	0.612	0	NA	NA	NA	NA	1.65	33.90	0.138	0.69
<b>FS</b>	0.82	0.953	0.043	0.827	NA	NA	NA	NA	27	14.44	0.633	3.22
<b>FS2</b>	1	0.997	0	1	0.98	0.97	0	0	27	2.69	0.931	68.2
<b>iFORM</b>	0.89	0.995	0.060	0.896	0.96	1	0	0.94	7.93	11.10	0.713	3.83
<b>Oracle</b>	1	1	0	1	1	1	0	1	8	8.98	0.771	NA

Outcomes include the convergence Probability (Cov)  $\sum_{m=1}^M I(\mathcal{T} \subset \hat{\mathcal{T}})/M$ , percentage of correct zeros identified (Cor0)  $\sum_{m=1}^M \sum_{j=1}^p I(\hat{\beta}_j = 0, \beta_j = 0)/[M(p - p_0)]$ , percentage of incorrect zeros identified (Inc0)  $\sum_{m=1}^M \sum_{j=1}^p I(\hat{\beta}_j = 0, \beta_j \neq 0)/[M(p_0)]$ , the exact selection probability (Exact)  $\sum_{m=1}^M I(\mathcal{T} = \hat{\mathcal{T}})/M$ , average model size, Mean Square Error for the model (MSE), the adjusted R-square of the model, and the computational time in seconds.

Table 4 Estimated main and epistatic effects of eQTLs by iFORM on gene transcript A\_12\_P103290 on chromosome I , in a comparison with the result by traditional single marker analysis.

eQTL	iFORM				Single Marker Analysis		
	Effect	SE	<i>p</i> -value	Herit-ability(%)	Effect	SE	<i>p</i> -value
X1_2068168 (cis-eQTL)	-0.197	0.035	0.000	0.060	-0.210	0.074	0.005
X2_13516256	-0.069	0.039	0.080	0.007	-0.138	0.075	0.068
X2_13813025	-0.023	0.052	0.665	0.001	-0.095	0.074	0.201
X2_13694563	0.074	0.062	0.238	0.008	-0.089	0.075	0.242
X2_2482896	0.064	0.027	0.017	0.006	-0.057	0.076	0.453
X_15500580	0.073	0.064	0.253	0.008	0.010	0.076	0.899
X_14636404	-1.768	0.092	0.000	4.794	0.024	0.076	0.751
X4_16403215	0.028	0.040	0.489	0.001	0.087	0.075	0.252
X4_15568674	-1.972	0.134	0.000	5.964	0.094	0.075	0.213
X4_1873297	0.044	0.026	0.086	0.003	0.095	0.071	0.185
X4_15632637	1.960	0.143	0.000	5.892	0.104	0.075	0.169
X4_13532205	0.064	0.028	0.024	0.006	0.111	0.075	0.143
X_15820520	-0.014	0.055	0.796	0.000	0.146	0.075	0.054
X_14542103	1.786	0.087	0.000	4.892	0.162	0.075	0.031
X2_13516256.X4_15632637	-3.799	0.268	0.000	5.534	NA	NA	NA
X2_13516256.X4_15568674	3.753	0.276	0.000	5.401	NA	NA	NA
X_15820520.X_14636404	-3.771	0.172	0.000	5.453	NA	NA	NA
X_15820520.X_14542103	3.691	0.172	0.000	5.224	NA	NA	NA
X_14636404.X4_1873297	-3.534	0.163	0.000	4.789	NA	NA	NA
X_14636404.X4_13532205	-3.567	0.166	0.000	4.879	NA	NA	NA
X_14542103.X4_1873297	3.629	0.164	0.000	5.050	NA	NA	NA
X_14542103.X4_13532205	3.469	0.167	0.000	4.614	NA	NA	NA