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# Network-Based Multiple Locus Linkage Analysis of Expression Traits

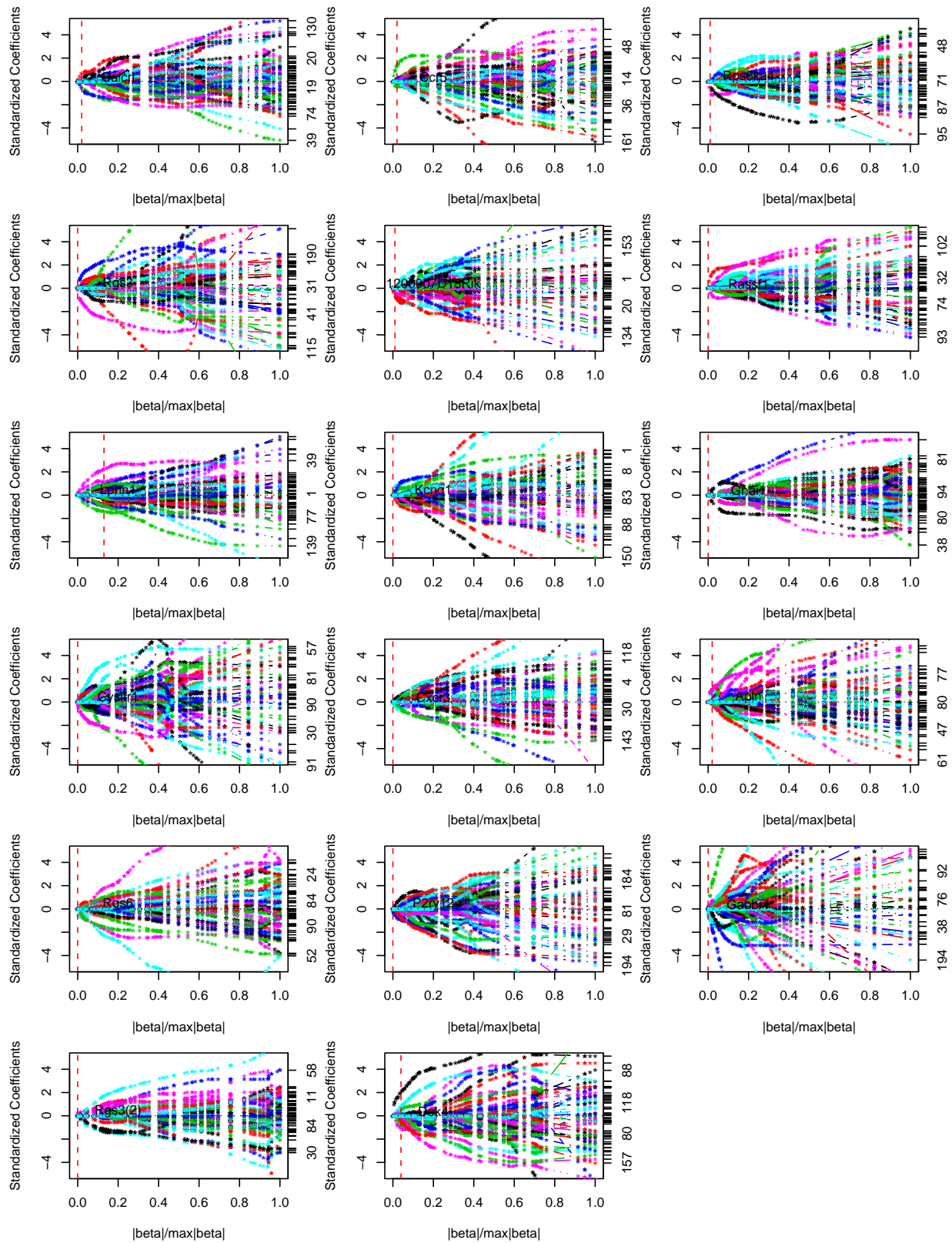
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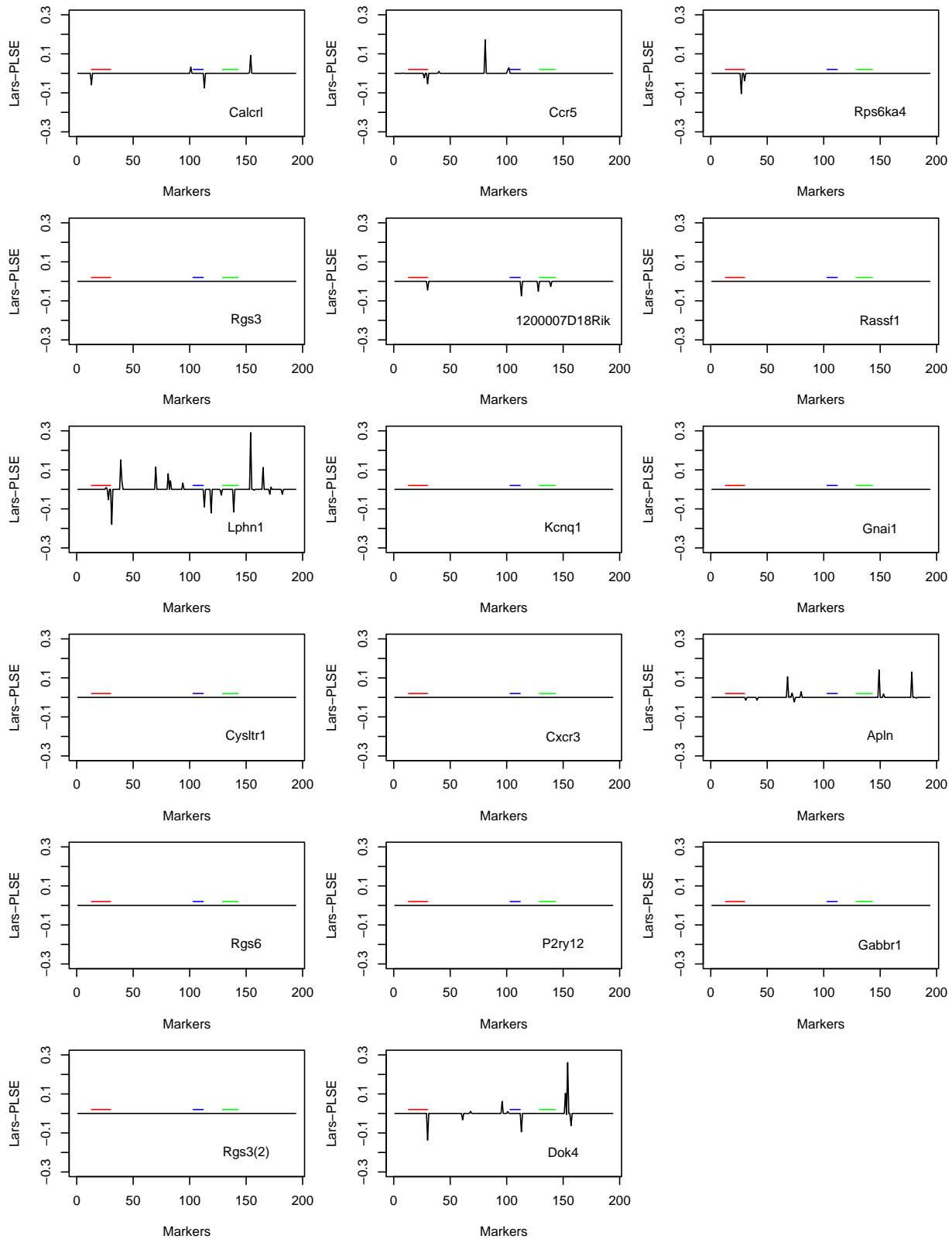
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## SUPPLEMENTARY MATERIALS

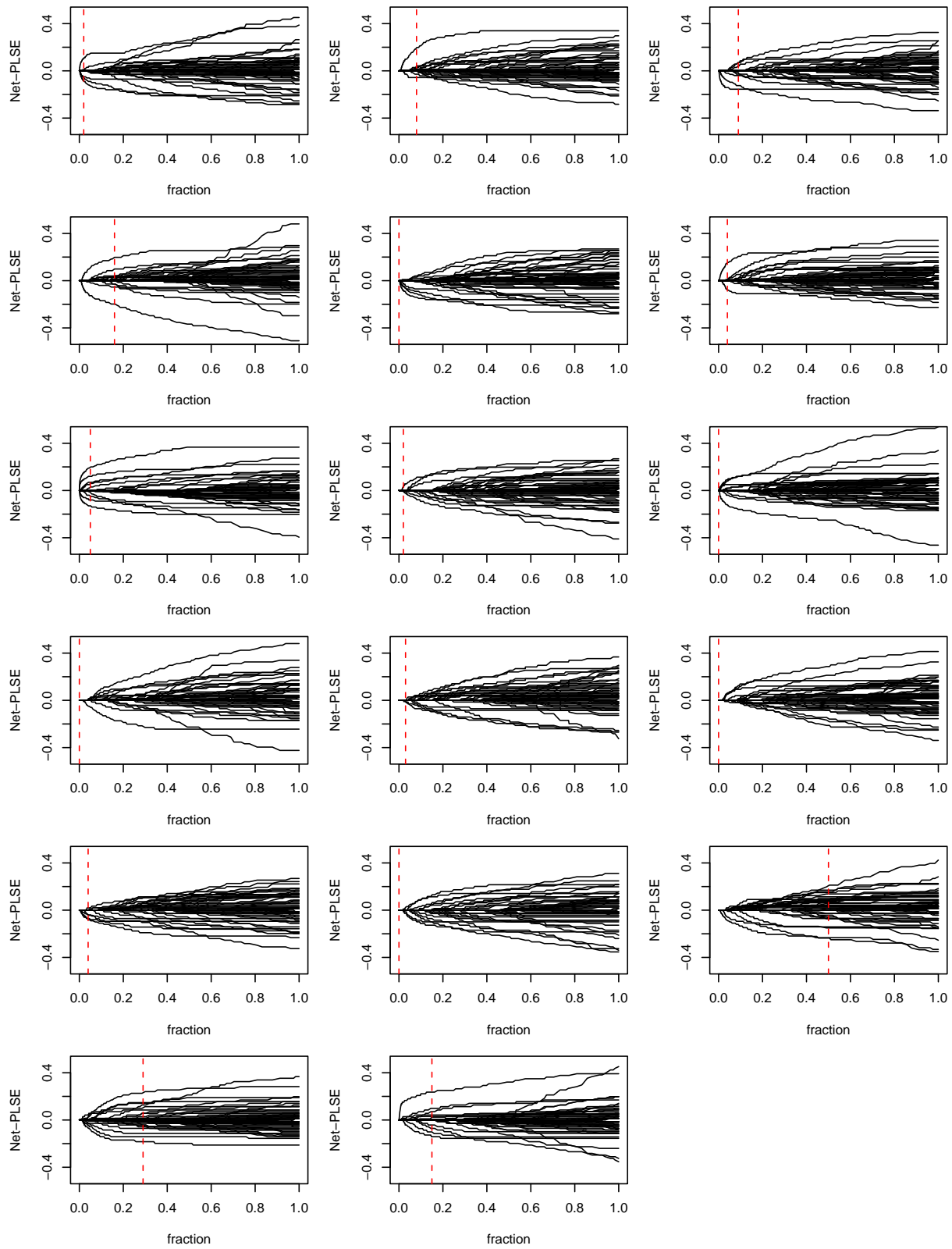
Five Supplementary figures for the analysis of the example mouse data are attached.



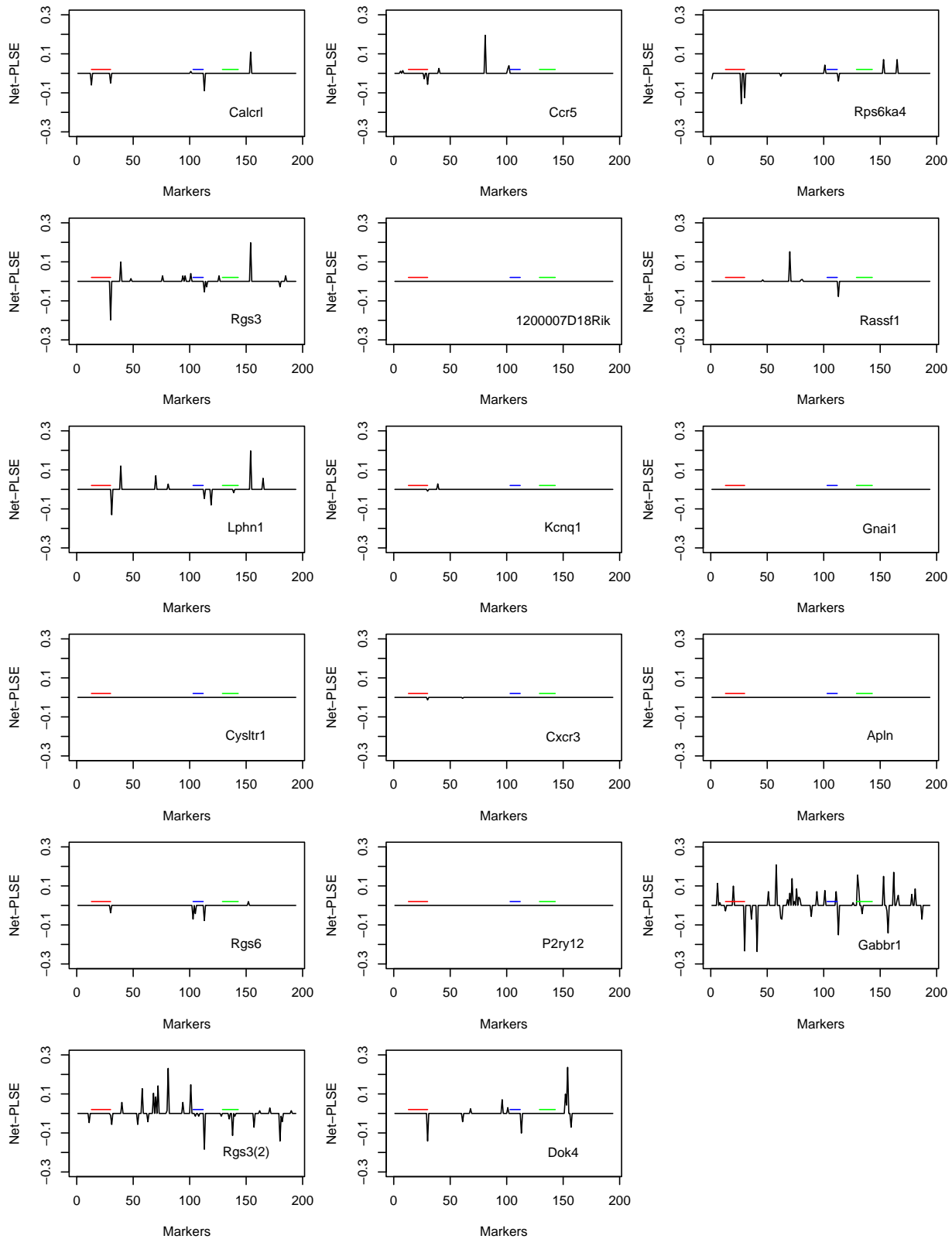
**Fig. 1.** Solution paths by the Lars: each panel corresponds to a gene, as labeled in Fig 2; inside each panel, each curve corresponds to an estimated (non-zero) coefficient as a function of tuning parameter  $s$ , and each vertical line gives the chosen tuning parameter  $\hat{s}_g$  by CV.



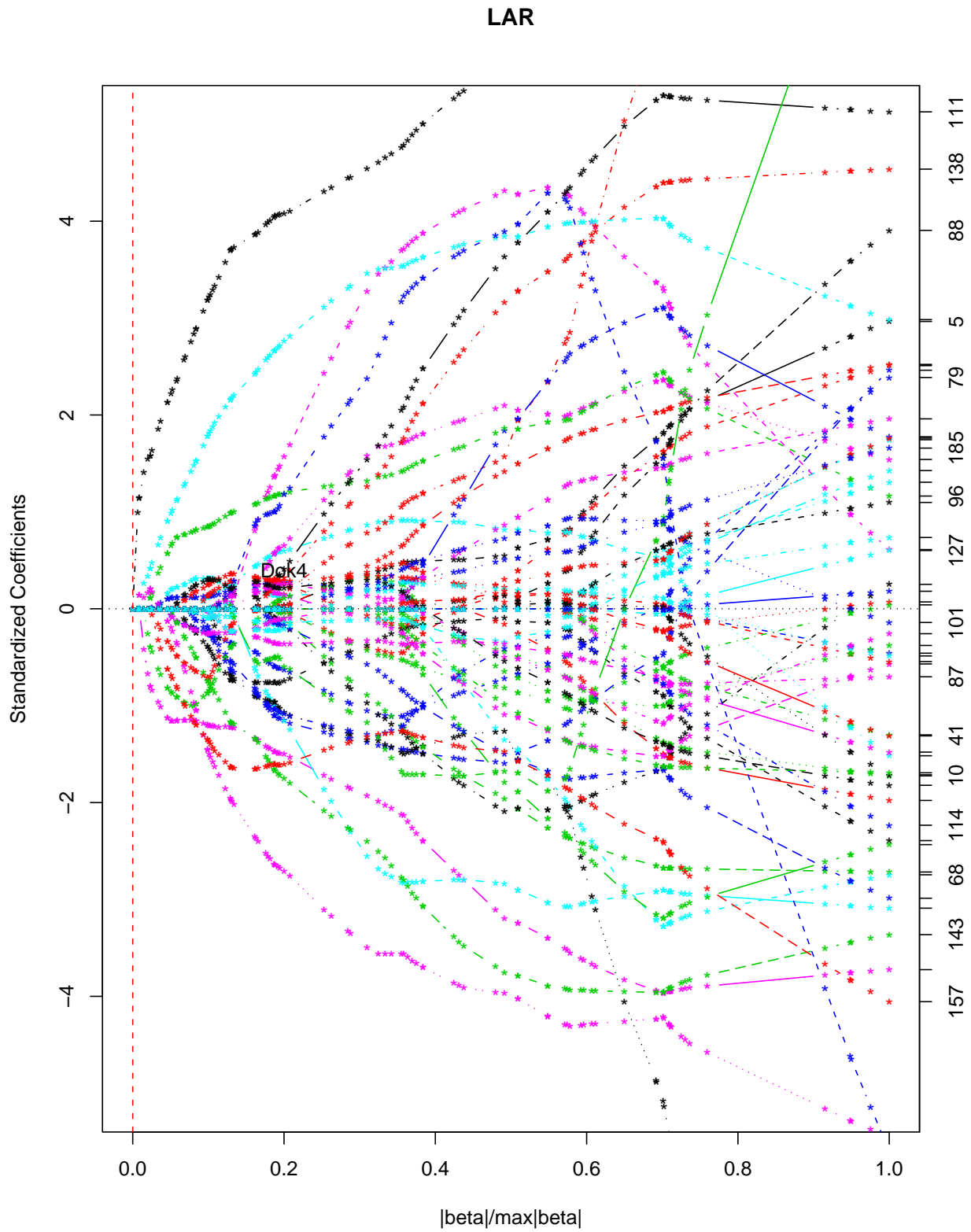
**Fig. 2.** Estimates by the Lars: a non-zero estimate suggests a possible linkage between the expression trait and the corresponding marker; the three short horizontal lines in each panel indicates the markers on chromosomes 2, 10 and 13 respectively.



**Fig. 3.** Solution paths by the Net: each panel corresponds to a gene, as labeled in Fig 4; inside each panel, each curve corresponds to an estimated (non-zero) coefficient as a function of tuning parameter  $s$ , and each vertical line gives the chosen tuning parameter  $\hat{s}_g$  by CV.



**Fig. 4.** Estimates by the Net: a non-zero estimate suggests a possible linkage between the expression trait and the corresponding marker; the three short horizontal lines in each panel indicates the markers on chromosomes 2, 10 and 13 respectively.



**Fig. 5.** Solution paths by the network-averaging (Ave) method: each curve corresponds to an estimated (non-zero) coefficient as a function of tuning parameter  $s$ , and the vertical line gives the chosen tuning parameter  $\hat{s}$  by CV.