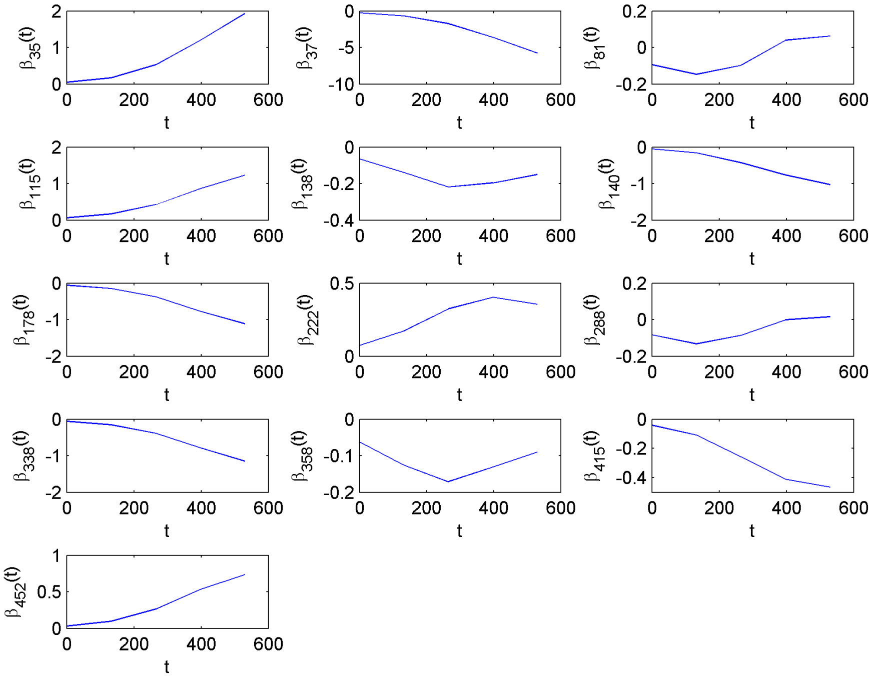


Figure S1 QTLMAS2009 data: estimated trends of genetic effects for the 13 selected markers by using **VBnonfun** which assumed the diagonal residual covariance structure.

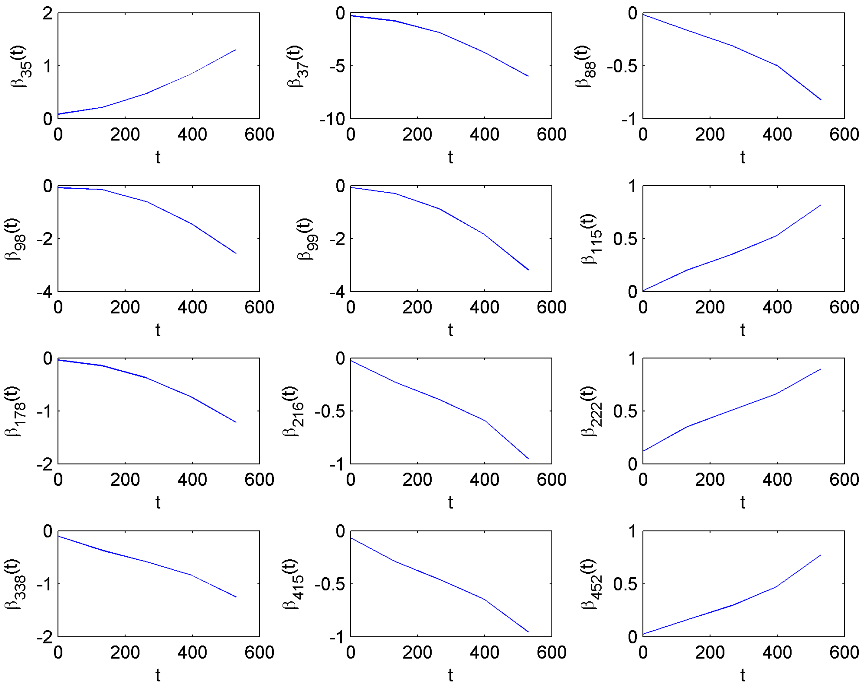


Figure S2 QTLMAS2009 data: estimated trends of genetic effects for the 12 selected markers by using **VBfun** which assumed the AR(1) residual covariance structure in the model.

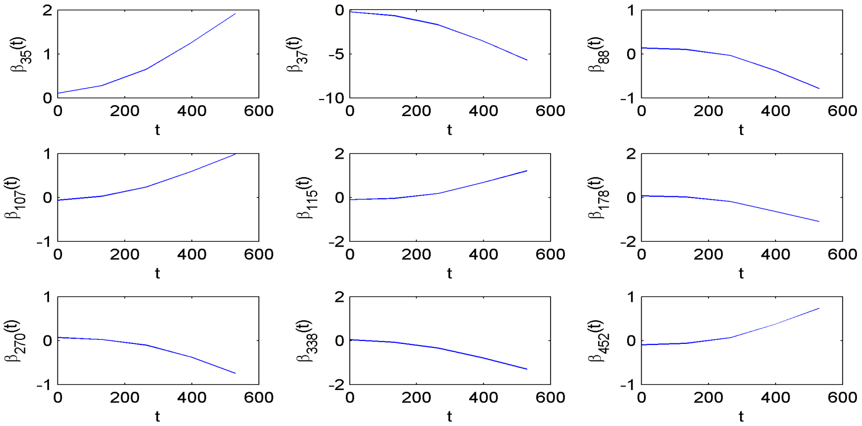
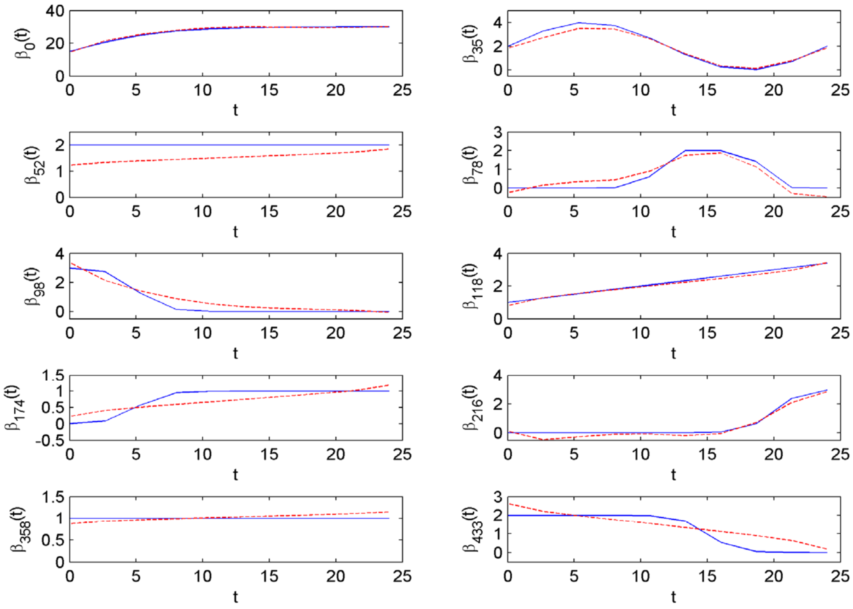
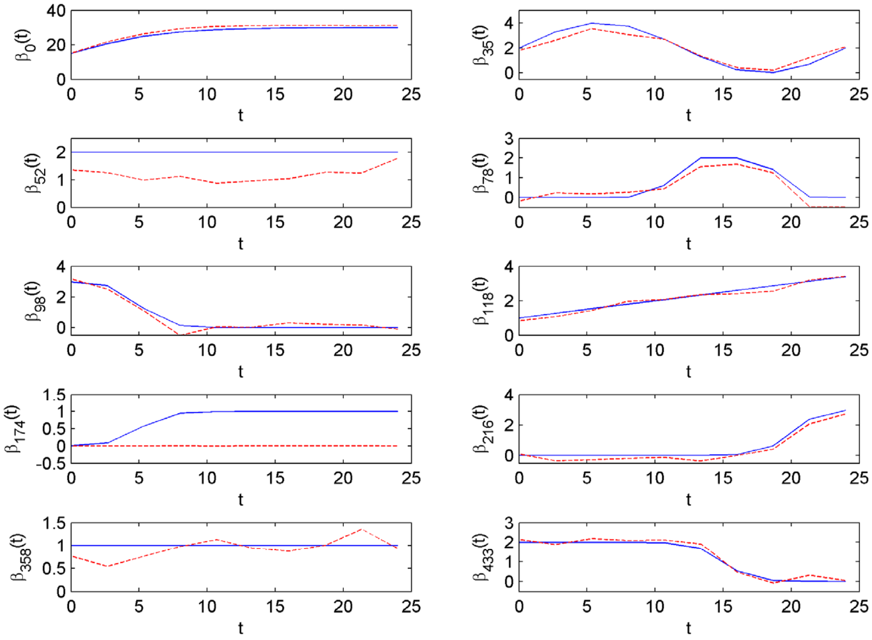


Figure S3 QTLMAS2009 data: estimated trends of genetic effects for the 9 selected markers by using **VBnonfun** which assumed the AR(1) residual covariance structure in the model.

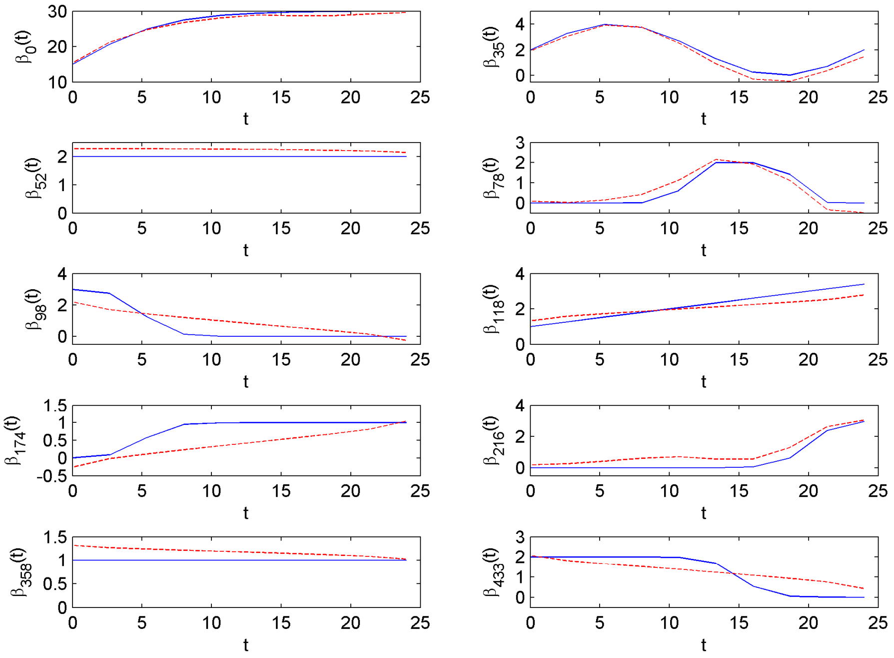


(a) Estimates of **VBfun** which assumed the AR(1) residual covariance structure

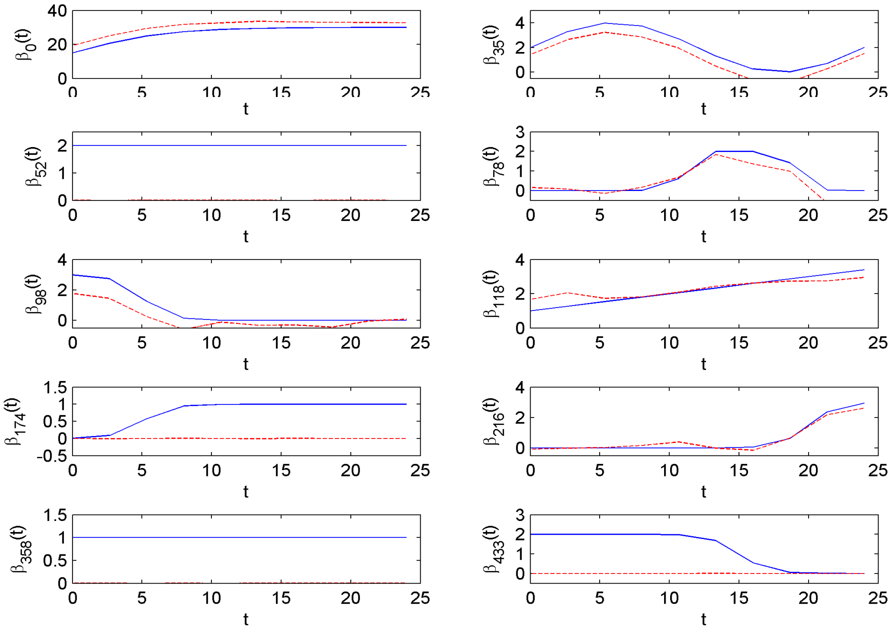


(b) Estimates of **VBnonfun** which assumed the AR(1) residual covariance structure

Figure S4 Simulated data with k = 10, u = 0:5: the estimated trend curves (red dashed lines) against the simulated trend curves (blue solid lines)

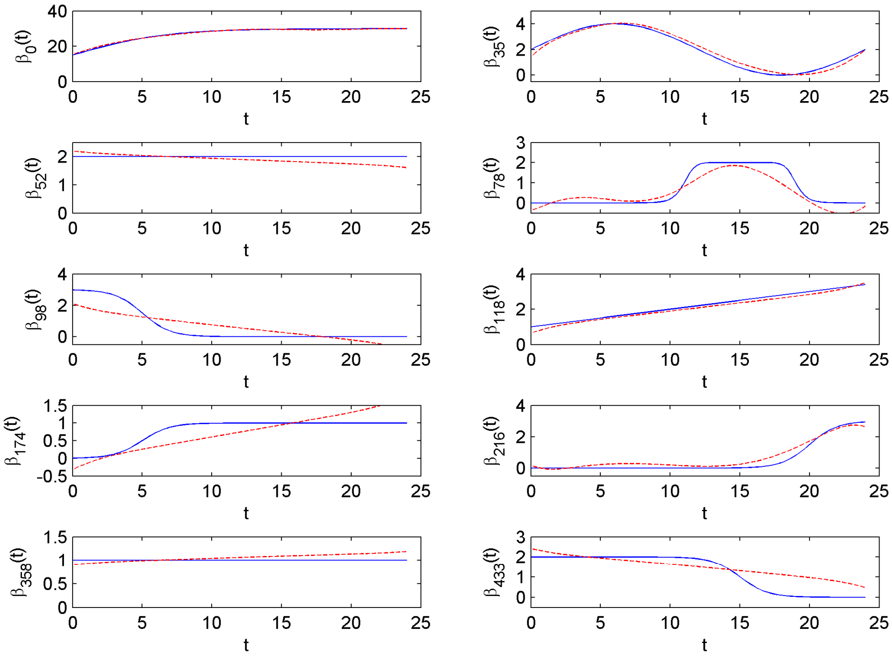


(a) Estimates of **VBfun** which assumed the AR(1) residual covariance structure

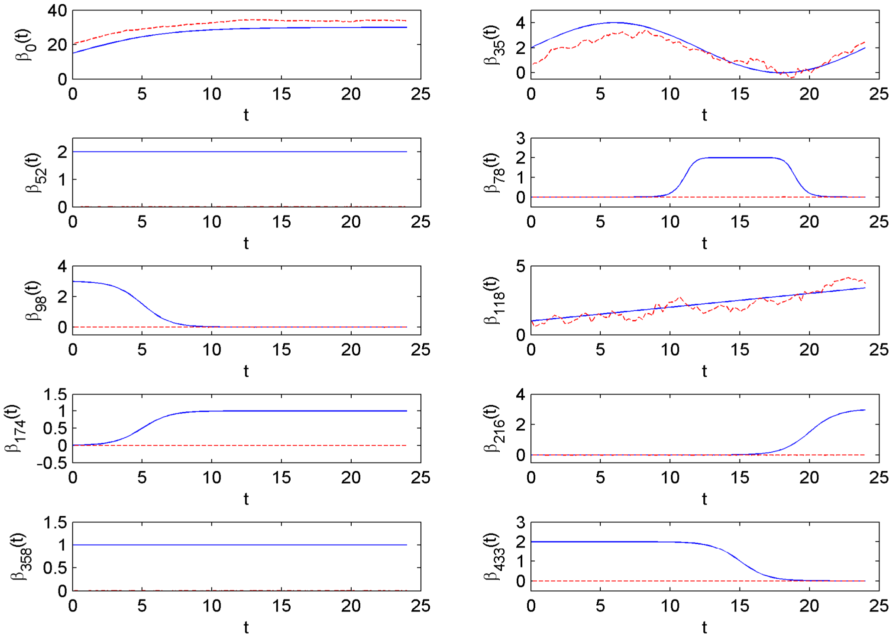


(b) Estimates of **VBnonfun** which assumed the AR(1) residual covariance structure

Figure S5 Simulated data with k = 10, u = 0:8: the estimated trend curves (red dashed lines) against the simulated trend curves (blue solid lines)

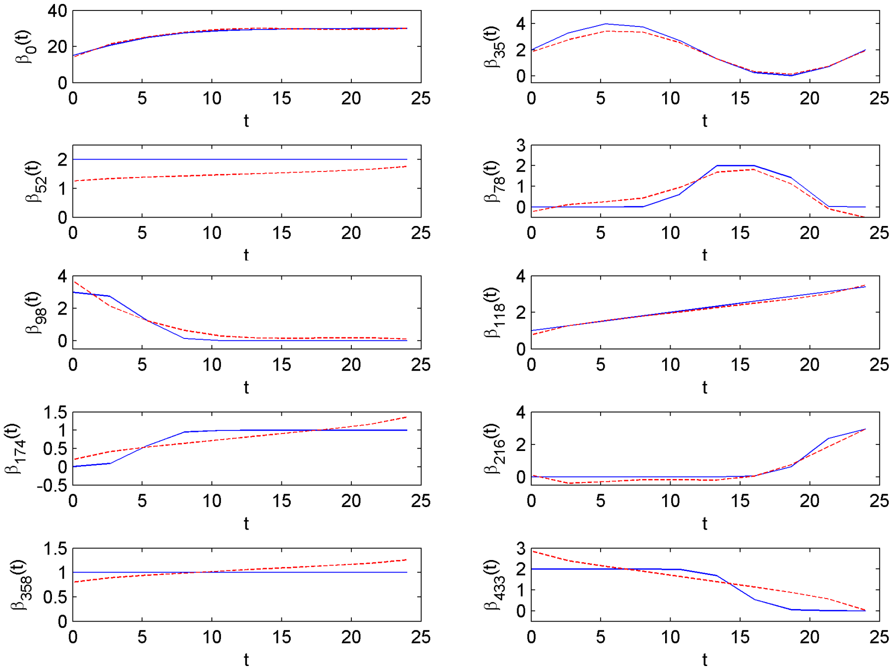


(a) Estimates of **VBfun** which assumed the AR(1) residual covariance structure

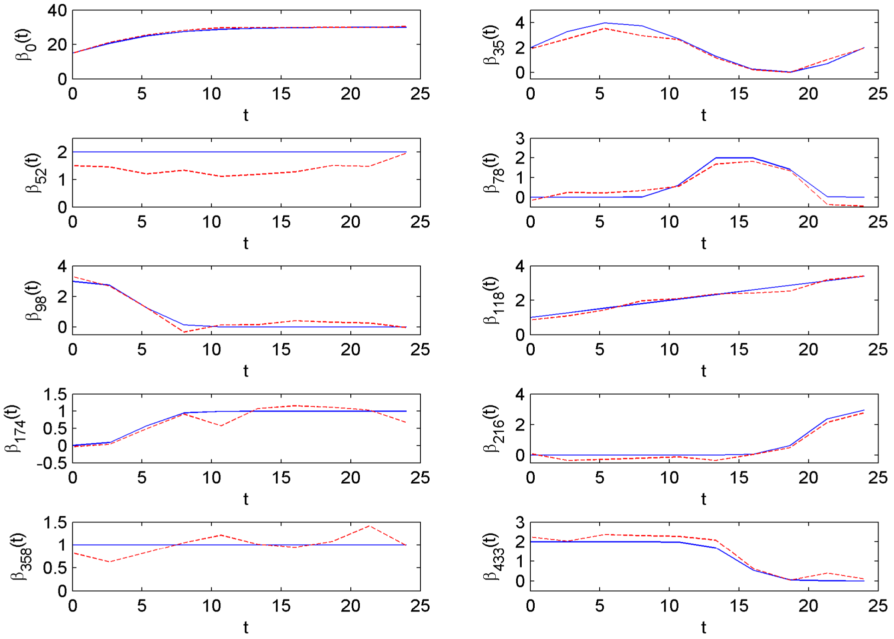


(b) Estimates of **VBnonfun** which assumed the AR(1) residual covariance structure

Figure S6 Simulated data with k = 100, u = 0:8: the estimated trend curves (red dashed lines) against the simulated trend curves (blue solid lines)

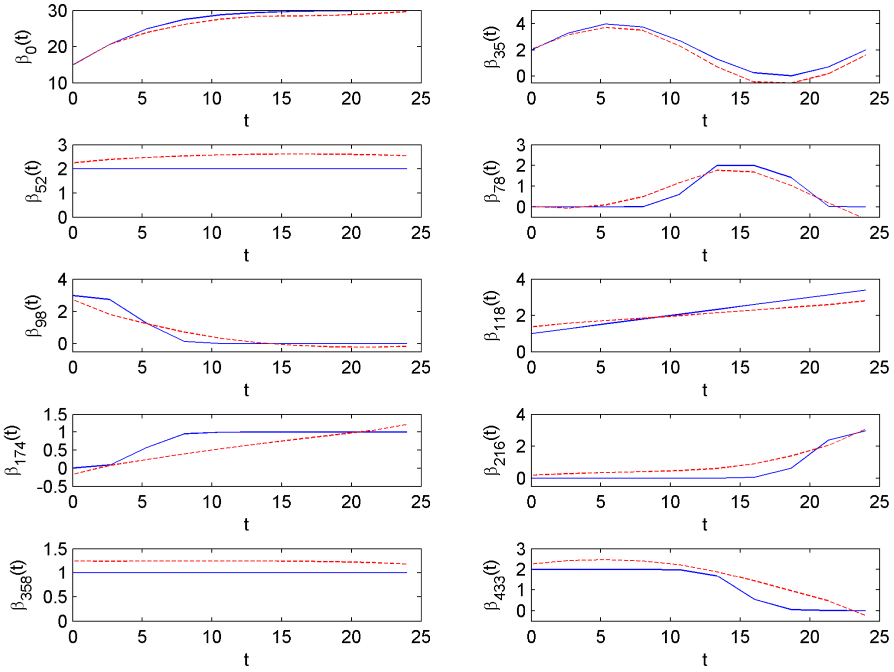


(a) Estimates of **VBfun** which assumed the diagonal residual covariance structure

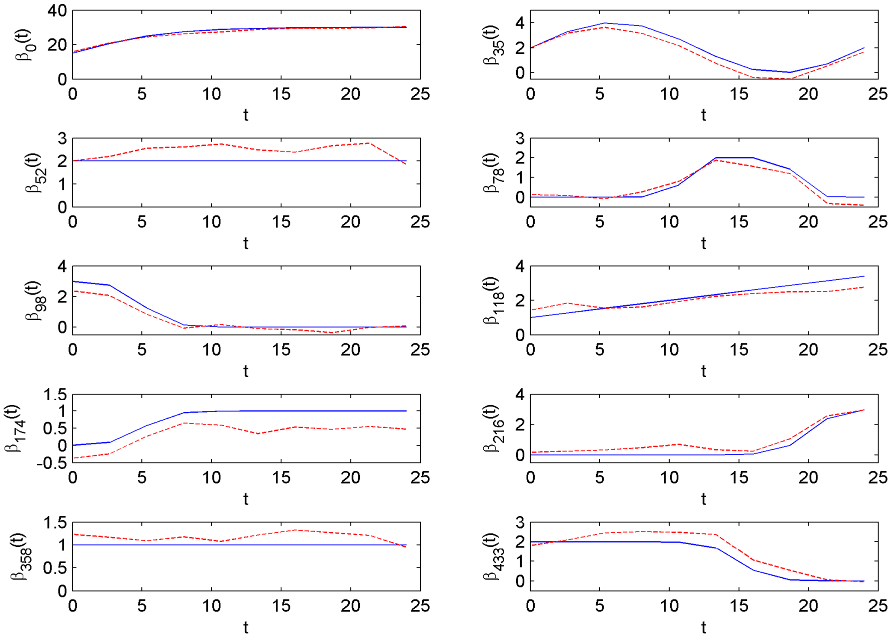


(b) Estimates of **VBnonfun** which assumed the diagonal residual covariance structure

Figure S7 Simulated data with k = 10, u = 0:5: the estimated trend curves (red dashed lines) against the simulated trend curves (blue solid lines)

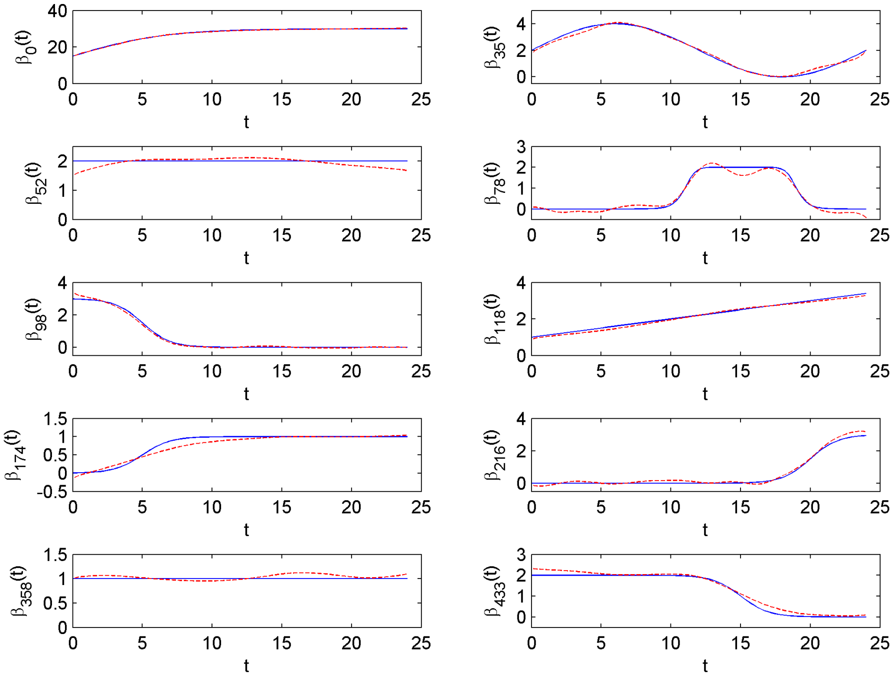


(a) Estimates of **VBfun** which assumed the diagonal residual covariance structure

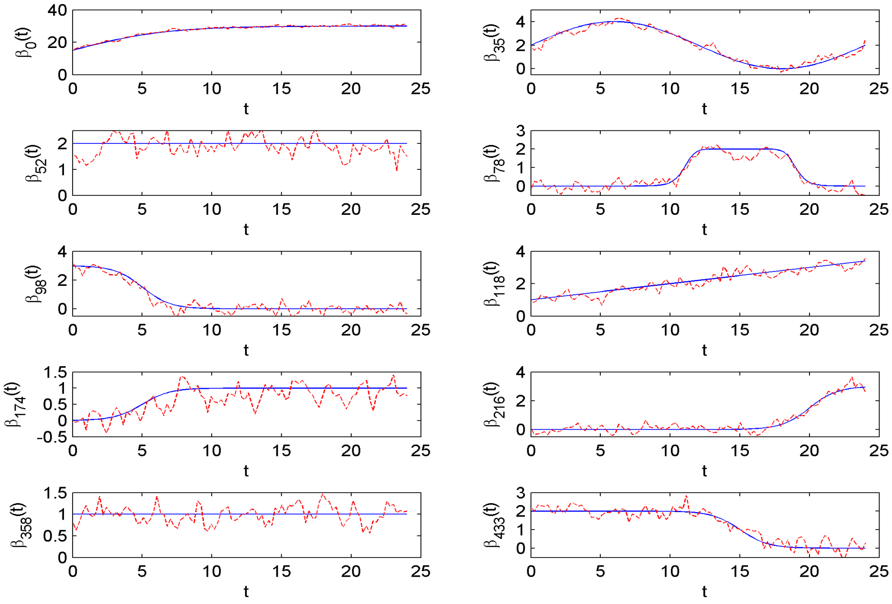


(b) Estimates of **VBnonfun** which assumed the diagonal residual covariance structure

Figure S8 Simulated data with k = 10, u = 0:8: the estimated trend curves (red dashed lines) against the simulated trend curves (blue solid lines)

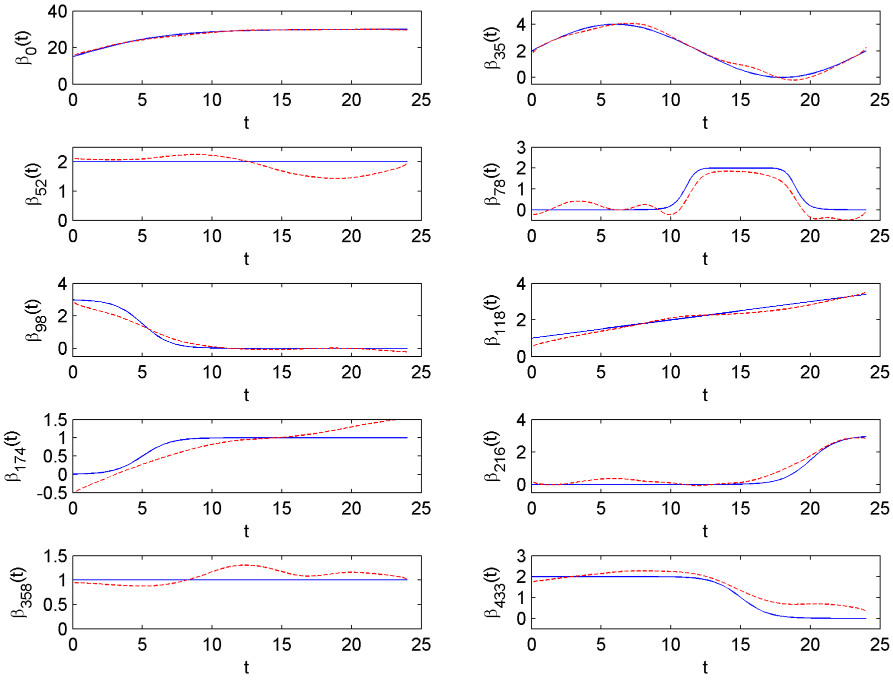


(a) Estimates of **VBfun** which assumed the diagonal residual covariance structure

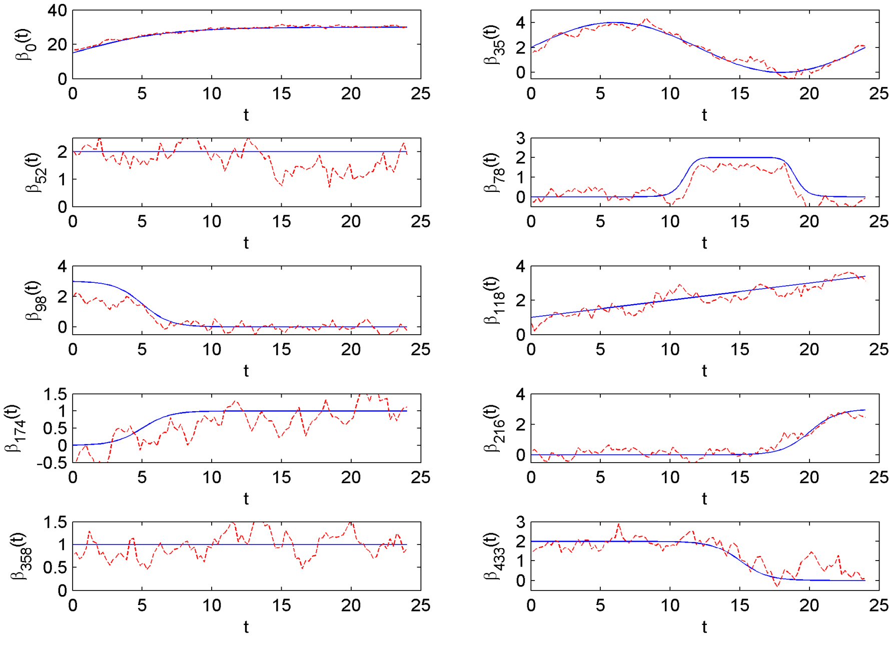


(b) Estimates of **VBnonfun** which assumed the diagonal residual covariance structure

Figure S9 Simulated data with k = 100, u = 0:5: the estimated trend curves (red dashed lines) against the simulated trend curves (blue solid lines)



(a) Estimates of **VBfun** which assumed the diagonal residual covariance structure



(b) Estimates of VBnonfun which assumed the diagonal residual covariance structure

Figure S10 Simulated data with k = 100, u = 0:8: the estimated trend curves (red dashed lines) against the simulated trend curves (blue solid lines)

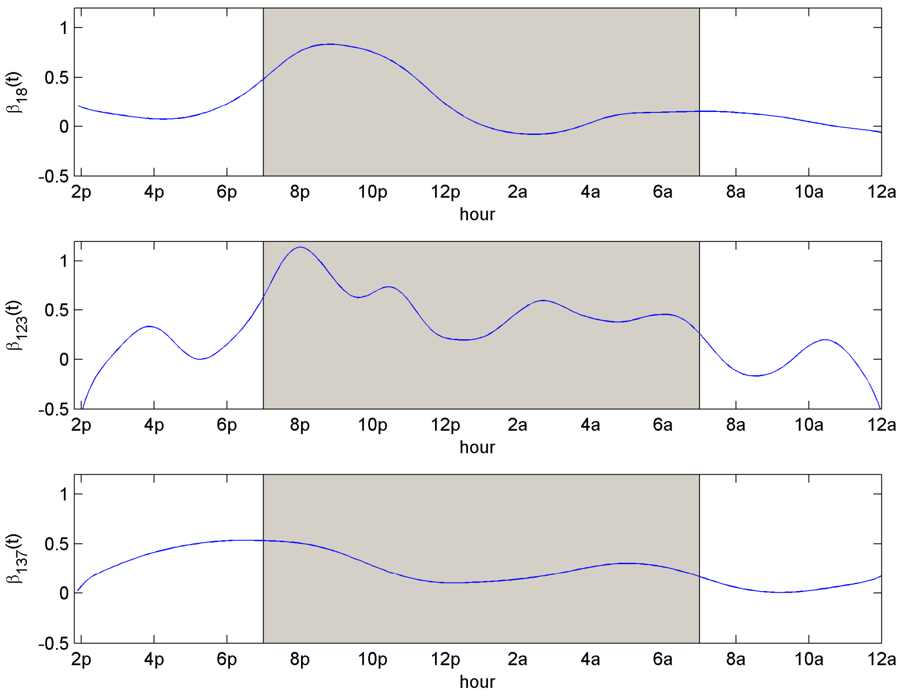


Figure S11 The results of mouse behavioral data analysis by using **VBfun** which assumed the diagonal residual covariance structure: estimated trends of genetic effects (in logit scale) for markers 18, 123, and 137, respectively. The shadow area represents the dark period (7pm-7am).

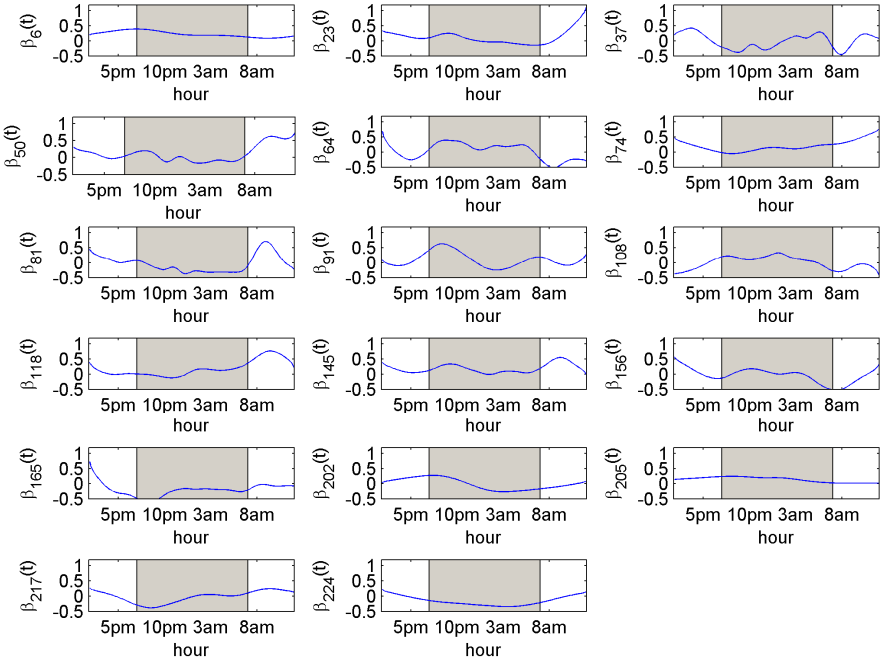


Figure S12 Mouse behavioral data: estimated trends of genetic effects (in logit scale) for markers 6, 23, 37, 50, 64, 74, 81, 91, 108, 118, 145, 156, 165, 202, 205, 217 and 224 by using **VBfun** which assumed the diagonal residual covariance structure. The shadow area represents the dark period (7pm-7am).

File S1

MATLAB codes for implementing VBfun and VBnonfun methods

File S1 is available for download at
http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.113.152736/-/DC1.

Table S1 The results of QTLMAS2009 data analysis, including the selected markers, their locations (in brackets), the corresponding Wald scores, and the closest true simulated QTLs. Regarding to the Wald tests, the critical value corresponding to the significance level 0:05 is 18.31 for the estimates of VBfun (chi-square distribution with 10 degrees of freedom), and 11.07 for the estimates of VBnonfun (with 5 df), respectively (assuming the AR(1) residual covariance structure in the model). The symbols *, † and ‡ indicate the simulated QTLs effects on ϕ_1, ϕ_2, ϕ_3 of the simulated logistic growth curves (traits), respectively.

VBfun		**VBnonfun**		
Marker	Wald score	Marker	Wald score	Closest simulated QTL
35 (0.4029)	163.63	35 (0.4029)	335.64	(0.4525) 36-37*
37 (0.4447)	5844.14	37 (0.4447)	5019.23	(0.4525) 36-37*
88 (0.9952)	82.39	88 (0.9952)	112.35	(0.8765) 77-78‡
98 (1.0359)	1150.48	none	none	(1.0455) 98-99*
99(1.0516)	1914.20	107(1.1536)	130.01	(1.0455) 98-99*
115(1.2566)	63.13	115(1.2566)	177.15	(1.3302) 118-119†
178 (1.9011)	178.99	178 (1.9011)	168.59	(1.8864) 174-175*
216 (1.9011)	102.91	none	none	(2.2622) 216-217*
222 (2.3108)	68.81	none	none	(2.2622) 216-217‡
none	none	270 (2.8203)	73.85	(2.8984) 276-277*
338(3.7168)	154.04	338(3.7168)	202.16	(3.6979) 336-337*
415(4.6311)	95.59	none	none	(4.5971) 411-412†
452 (4.9494)	57.88	452(4.9494)	74.86	(4.7719) 432-433*

Table S2 The mean squared error comparing the estimated trend functions to the simulated ones. F and N represent **VBfun** and **VBnonfun** (assuming the diagonal residual covariance structure in the model), respectively (assuming the diagonal residual covariance structure in the model), and h^2 is the averaged heritability over time.

	k=10 *u*=0.5 h^2=0.2265		*k*=10 *u*=0.8 h^2=0.0922		*k*=100 *u*=0.5 h^2=0.2347		*k*=100 *u*=0.8 h^2=0.1259	
	F	N	F	N	F	N	F	N
0	0.1765	0.2481	0.9436	0.5591	0.0199	0.4005	0.1113	0.6785
35	0.0896	0.1279	0.1863	0.1882	0.0188	0.0811	0.0341	0.1163
52	0.2814	0.4121	0.2839	0.2703	0.0245	0.1376	0.0918	0.2739
78	0.0840	0.0748	0.1214	0.0667	0.0256	0.0693	0.1312	0.2146
98	0.0997	0.0710	0.1480	0.1233	0.0073	0.0931	0.0584	0.2867
118	0.0067	0.0245	0.1209	0.1550	0.0071	0.0719	0.0273	0.1222
174	0.0327	0.0341	0.0877	0.2032	0.0087	0.0941	0.0732	0.1650
216	0.0658	0.0478	0.2431	0.1284	0.0157	0.0608	0.0574	0.1031
358	0.0221	0.0432	0.0556	0.0403	0.0036	0.0403	0.0230	0.0717
453	0.1556	0.0706	0.2629	0.0403	0.0225	0.0864	0.1547	0.2198

Table S3 The number of times each QTL has been correctly selected over 50 replications, together with the average number of wrongly selected markers (false positives). F and N represent **VBfun** and **VBnonfun**, respectively (assuming the diagonal residual covariance structure in the model).

	n=200 *k*=10		*n*=200 *k*=100		*n*=500 *k*=10		*n*=500 *k*=100	
QTL	F	N	F	N	F	N	F	N
35	50	50	50	50	50	50	50	50
52	17	0	50	0	46	0	50	0
78	10	1	50	0	45	34	50	33
98	6	0	45	0	38	0	50	0
118	50	50	50	50	50	50	50	50
174	1	0	11	0	14	0	49	0
216	35	3	49	1	44	46	50	41
358	23	13	50	0	47	25	50	30
433	9	0	0	43	34	0	50	0
ave. fal. pos.	1.34	0.38	1.68	0	0.90	0.90	0.24	0.40

Table S4 The results of mouse behavioral data analysis by using VBfun which assumed the AR(1) residual covariance structure, including the selected markers, their chromosomes, locations, and the corresponding Wald scores. Regarding to the Wald tests, the critical value corresponding to the significance level 0:05 is 67.50 for the estimates (chi-square distribution with 50 degrees of freedom).

Marker	Chromosome	Location (cM)	Wald Score
6 (gnf01_085_746)	1	43.48	292.83
18 (rs3689947)	1	96.11	795.93
23 (rs13476507)	2	30.83	173.80
37 (rs13477019)	3	9.16	277.01
50 (rs3657112)	3	75.42	206.72
64 (rs3688968)	4	54.61	353.39
74 (rs3726547)	5	50.68	278.76
81 (rs13478621)	6	4.38	441.15
91 (rs6387265)	6	77.70	426.03
108 (rs6216320)	7	69.01	280.63
118 (gnf08_109_993)	8	53.04	360.41
123 (rs6207781)	9	20.74	1242.01
137 (rs13480657)	10	39.72	379.31
145 (rs3023251)	11	13.71	241.39
156 (rs13481230)	11	75.02	256.88
165 (rs13481509)	12	26.44	194.32
202 (rs6326790)	15	45.98	346.22
205 (rs4180773)	16	29.53	175.19
217 (rs4231494)	17	19.56	183.36
224 (rs6358426)	18	10.10	375.13