

Additional file 5. QTLs for speed

QTL	Marker	Marker	Cent. Dist	CI	SP	LPR	%	<i>a</i> / <i>SD</i>	<i>d</i> / <i>SD</i>
		Dist (cM)	(cM)	(cM)	Interval				
SPD2.1	rs13476352	6	17	11 to 29	SP2	2.61	4.09	-0.08	-0.47**
					SP6	3.57†	5.56	-0.19*	-0.49**
SPD2.2	rs3664044	0	107	90 to 107	SP4	2.49	3.94	-0.25**	0.25*
SPD5.1	rs13478157	10	28	13 to 57	SP1	2.27	3.53	0.28**	0.00
					SP2	3.19	4.92	0.33**	0.15
SPD5.2	mCV22996021	8	57	3 to 73	SP3	3.67†	5.65	0.32**	0.23
					SP6	3.15	4.89	0.30**	0.22
					SP7	2.97	4.61	0.27**	0.26*
SPD8.1	rs3023193	0	47	36 to 84	SP1	2.24	3.46	0.21**	-0.20*
					SP2	2.97	4.56	0.22**	-0.26
					SP3	2.68	4.12	0.22**	-0.23*
					SP4	2.47	3.88	0.15	-0.38**
					SP5	3.70†	5.74	0.24	-0.44**
					SP6	2.37	3.65	0.13	-0.32**
SPD8.2	rs3703161	0	84	73 to 84	SP4	3.50†	5.43	-0.20	0.47**
					SP5	2.16	3.44	-0.38*	0.25
SPD9.1	rs13480073	6	7	1 to 17	SP1	4.23†	6.50	0.30**	0.29*
					SP2	3.75†	5.78	0.25**	0.37**
					SP3	6.85†	10.31	0.39**	0.35**
					SP4	4.89†	7.47	0.36**	0.24
					SP5	4.46†	6.83	0.33**	0.24
					SP6	5.47†	8.31	0.38**	0.22
					SP7	6.53†	9.86	0.43**	0.20
SPD10.1	rs3704618	14	28	20 to 44	SP3	3.03	4.64	0.23**	-0.27*

<i>SPD11.1_M</i>	<i>mCV24434350</i>	14	18	8 to 30	SP5	2.58	8.24	0.34*	-0.50**
<i>SPD13.1</i>	<i>rs6329684</i>	8	9	1 to 17	SP5	2.74	4.24	0.31**	0.05
					SP6	4.81†	7.32	0.43**	0.06
					SP7	2.24	3.48	0.27**	0.14
<i>SPD15.1_F</i>	<i>rs13482429</i>	0	4	4 to 60	SP3	2.16	6.86	-0.36**	-0.01
<i>SPD15.2</i>	<i>rs3686133</i>	0	65	55 to 65	SP3	2.03	3.17	0.23**	-0.11
<i>SPD19.1_F</i>	<i>rs3671328</i>	12	17	5 to 25	SP2	2.43	7.64	0.24	0.57**

Shown are the locations, confidence intervals (CI), LPR scores ($\log_{10}\text{Prob}^{-1}$), percentage of the variation explained (%), and standardized additive (a) and dominance genotypic values (d) for QTLs on all chromosomes affecting speed in any of the 7 time intervals (SP1 through SP7). Each QTL is designated SPD followed by its chromosome number and an extension to indicate whether it is the first or second QTL on that chromosome. Subscripts are given for QTLs if they affect only males (*M*) or only females (*F*). Locations are given as map distances from the nearest proximal marker (Marker Dist) and from the centromere (Cent. Dist) and confidence intervals are expressed as distances from the centromere. Single locations and confidence intervals are indicated for multiple traits when tests suggested pleiotropy of common QTLs. All LPR values are significant at the 5% chromosomeswise level or at the genomewise level (†). * = $P < 0.05$; ** = $P < 0.01$.