

Table S2: Estimated 5% genome-wide significance thresholds for the maximum LOD score across partitions in the case of four taxa, based on 10,000 simulation replicates. We assumed an autosomal genome modeled after the mouse, with genetic markers at a 10 cM spacing.

total sample size	All partitions		Tree partitions	
	all crosses	minimal crosses	all crosses	minimal crosses
300	4.56	4.48	4.43	4.33
450	4.51	4.47	4.36	4.33
600	4.49	4.44	4.32	4.29