Table 3. Markers used for mapping key deletion endpoints

Mutation	Deletion endpoint	Marker			
		Proximal endpoint		Distal endpoint	
l4Rn1	**11Pu (prox) (lethal)**	jmjdc2c-ex18 (R)	jmjdc2c-ex22 (L)		
	8Pub (prox) (nonlethal)			8Pub74.9 (R)	8Pub75.1 (L)
l4Rn2	**11R30M (dist) (nonlethal)**	286H15 (L)	D4Rck140 (R)		
	9R75VH (dist) (lethal)			Nfibex4lge (L)	Nfib5' (R)
l4Rn3	**46UTHc (dist) (nonlethal)**	Frem1iii-ex4 (L)	DEPC2-823 (R)		
	8Pub (dist) (lethal)			Novel2 (Bnc2) (L)	D4Jkn1 (R)

Mutation	Deletion endpoint	Marker			
		Proximal endpoint		Distal endpoint	
baf	**9R75VH (prox) (prox-baf)**	8Pub75.1 (R)	8Pub75.4 (L)		
	46UTHc (prox) (prox-nonbaf)			r77.3 (R)	129L11 (L)
	173G (dist) (distal-baf)			395J04-10k (L)	s79.48 (R)
	ITHO-IV (dist) (distal-nonbaf)	395J04-SP6 (L)	395J04-10k (R)		

Closest deletion endpoints that define the mutant phenotype in column 1 are listed in column 2; mutations mapping proximal to *Tyrp1* are defined by proximal (prox) endpoints and those mapping distal by distal (dist) endpoints. The key markers that position the endpoints are in columns 3-6, the endpoint being between the marker retained and the marker lost. Retained (R) and lost (L) at the point of marker based on polymorphism between C3H/101 (deletion chromosome) and the *M. Spretus* background.