Clone	STS	Chr	Endsequence data				BAC end-pair Mouse Genome Browser May 2004		STS Mouse Genome Browser May 2004	
			CHR	KB_start	KB_end	Size	CHR	MB	CHR	MB
RP23-148B16	MT1649;D16Mit100	1, 2							16	11.8
RP23-39A3	AA960657	1,2	1	173626	173853	228			1	173.9
			1	173626	173878	252				
RP23-67O16	AA960358	1,7,9	1	171347	171509	162	1	171.3	9	80.2
			1	55235	55470	235				
RP23-5C1	331855; AF035207	1,9	9	19550	19767	217			9	19.6
			9	19550	19809	259			9	70.2
RP23-17N2	686456; AI987944	2,7	2	176813	177003	190	2	176.8	7	28.8
RP23-305K11	682317; AI894140	2,Y					2	160.7	2	160.8
RP23-41G19	X84013	4,18					18	12.8	18	12.9
RP23-110E20	AI035725	5,7,9,12,14,17					9	20.8	9	21.0
RP23-120M19	968707; AW552125	5,9,12,14	12	50200	50267	68	12	50.2	12	50.2
			12	50200	50267	68				
			12	50200	50267	67				
RP23-222O20	781606; AV259865	5,9,12,17	12	18828	18839	11			Chr_random	
			12	18247	18364	117				
			12	19230	19379	149				
			12	18121	18138	17				
			12	18562	18645	82				
RP23-193H8	962934; AW546347	5,14	5	92811	92910	99			13	24.1
			5	92588	92811	223				
			5	92555	92811	256				
RP23-163B8	AU024152	6,7							Chr_random	
RP23-6I17	436332	7	7	131206	131401	196	7	131.2	7	131.4
RP23-113M24	M22602	14,17	17	12502	12692	190	17	12.5	17	7.0
			17	12502	12682	181			17	12.5
RP23-117M12	AI098586	15, 17	17	29033	29227	193	17	29.0	17	29.2
RP23-263M19	AA958834;332872	2,3,4,5,6,7,8,9, 10,11,12,13,14, 15,16,17,18,19,X							16	37.4
RP23-263M19	AA958834;332872	5,11,17							16	37.4
RP23-206D2	MT2432;D8Mit184	12,15,16,18,19							8	101.2
RP23-206D2	MT2432;D8Mit184	4,13,19							8	101.2

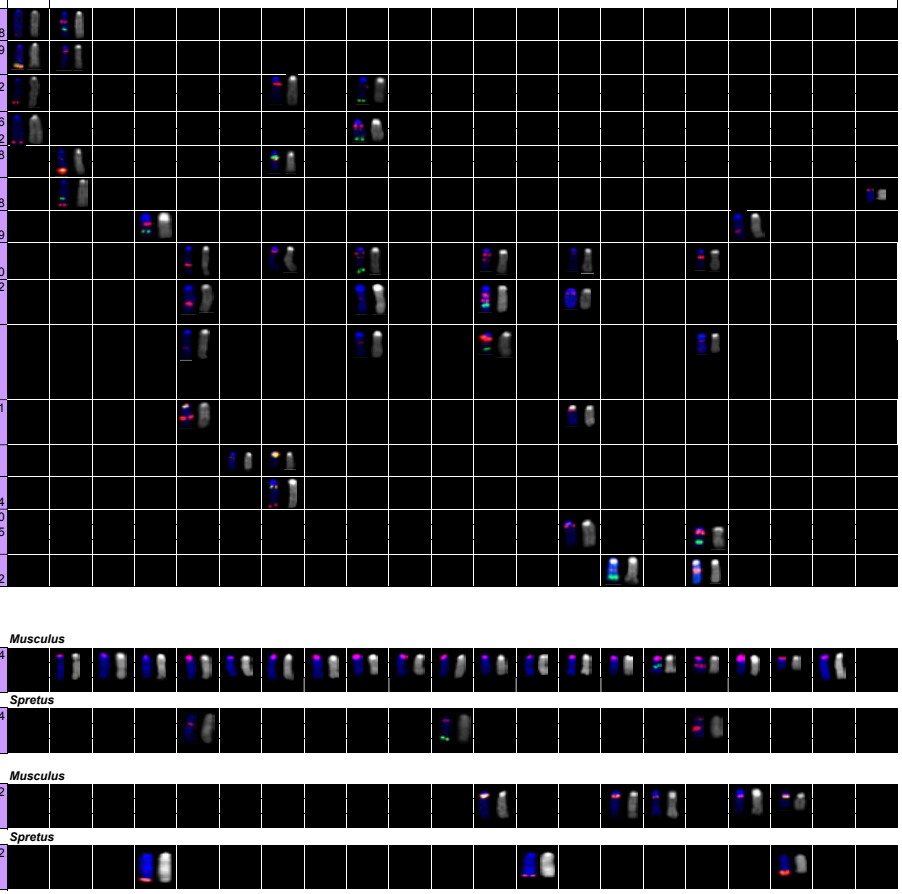

Fig. C FISH mapping results for 17 BACs mapping to more than one place in the genome when hybridized to C57BL/6J metaphase chromosomes. For each BAC we show STS content, chromosomes according to FISH and end-sequence data (n = 9), BAC end-pair (n = 8) and STS mapping data (n = 17) according to the UCSC Genome Browser (May 2004 freeze) followed by a FISH picture of all chromosomes showing hybridization signal. We labeled the polymorphic BACs with Cy3, and in most instances we included an FITC labeled reference BAC with known chromosome location to confirm the identity of the hybridized chromosome. Note the unequal distribution of signals across the genome as well as the bias in distribution of signals towards the centromere. For two BACs, RP23-263M19 and RP23-206D2, we show FISH pictures of both M. musculus and M. spretus chromosomes after hybridization with these BACs.