

Supplemental Table 3. PCR content maps of human chromosome 21 cross-species markers to dog BACs. The maps are organized based on the 340-kb segments of chromosome 21 sequence retrieved from GenBank (Hattori et al. 2000). Marker and clone names are separated into columns and rows, respectively. Dog BACs were scored for the presence or absence of specific cross-species markers by PCR analysis, where “+” = present and “–” = absent.

Table 3A	Map of Segments 69 – 76
Table 3B	Map of Segments 77 – 88

Supplemental Table 3A. PCR Content Map of Dog BACs for Segments 69 – 76.

	69.02B	69.01NT	70.02B	71.04NT	71.02B	71.03NT	72.03NT	72.04NT	74.02NT	75.01NT	76.03B	76.02B
201B13	+	+	-									
72P6	-	+	-									
332B12	-	+	-									
367J21	-	+	-									
73L8	-	+	-	-	-							
242G14	-	-	+	-	-							
416B13	-	-	+	-	-							
303B1		-	+	+	-	-						
35C7		-	+	+	-	-						
71O19		-	-	+	-	-						
173I12			-	-	+	-	-	-	-			
240E8			-	-	+	+	+	-	-			
130A21			-	-	-	+	+	-	-			
249A3			-	-	-	+	+	-	-			
45H11			-	-	-	+	+	-	-			
177N3					-	-	+	-	-			
256P12						-	+	-	-	-	-	
136G4						-	-	+	+	-	-	
147B10							-	-	+	-	-	
390J24							-	-	+	-	-	

[illegible]

Supplemental Table 3B. PCR Content Map of Dog BACs for Segments 77- 88.

	77.01NT	79.01NT	79.02NT	80.01NT	81.01B	82.01B	84.02NT	85.01B	88.01B
175J2	+	-	-						
419D14	+	-	-						
87I1	+	-	-						
194E19	+	+	-	-					
189J22		-	+	-	-				
313M5		-	+	-	-				
180F20		-	+	+	-	-			
277E8		-	+	+	-	-			
19K16		-	-	+	-				
228B16			-	+					
207J20			-	-	+	-			
262E23			-	-	+	-	-		
341F3			-	-	+	-	-		
57B12			-	-	+	-	-		
133J1				-	-	+	-		
415K21				-	-	+	-		
48J13				-	-	+	-		
202N1					-	-	+	-	
267J19					-	-	+	-	
320O6					-	-	+	-	

Segment		Size (bp)	# Tiled bps	Total bps hybridized	NIE							IE						
					# of elements	# of bps	% of hyb'd bps	LENGTH (bp)				# of elements	# of bps	% of hyb'd bps	LENGTH (bp)			
								Mean	S.D.	Min.	Max.				Mean	S.D.	Min.	Max.
1	AL163201	281,116	142,077	0	0							0						
2	AL163202	340,000	174,817	0	0							0						
3	AL163203	340,000	204,745	0	0							0						
4	AL163204	340,000	219,072	0	0							0						
5	AP001660	340,000	220,772	7,807	1	130	1.7	130.0	0.0	130	130	0						
6	AL163206	340,000	234,922	234,922	43	4,170	1.8	97.0	95.3	30	470	14	1,620	0.7	115.7	97.8	30	350
7	AL163207	340,000	222,005	222,005	39	3,610	1.6	92.6	86.5	30	390	20	2,620	1.2	131.0	144.6	30	530
8	AL163208	340,000	271,689	271,689	109	10,250	3.8	94.0	107.2	30	650	0						
9	AL163209	340,000	229,815	133,822	52	5,160	3.9	99.2	122.2	30	530	0						
10	AL163210	340,000	241,560	241,560	31	1,890	0.8	61.0	104.7	30	530	28	2,460	1.0	87.9	63.3	30	230
11	AP001666	340,000	258,400	258,400	58	4,440	1.7	76.6	97.6	30	490	4	1,460	0.6	365.0	253.2	90	590
12	AP001667	340,000	246,233	182,969	52	4,380	2.4	84.2	129.8	30	690	5	1,330	0.7	266.0	288.2	30	610
13	AL163213	340,000	223,173	0	0							0						
14	AP001669	340,000	164,449	0	0							0						
15	AP001670	340,000	200,705	174,773	26	1,420	0.8	54.6	71.8	30	390	16	1,760	1.0	110.0	157.5	30	650
16	AP001671	340,000	209,109	209,109	18	800	0.4	44.4	36.2	30	150	3	290	0.1	96.7	50.3	50	150
17	AP001672	340,000	245,160	245,142	54	3,560	1.5	65.9	89.5	30	530	14	1,000	0.4	71.4	73.4	30	290
18	AL163218	340,000	237,873	225,999	31	2,230	1.0	71.9	64.4	30	250	2	80	0.0	40.0	14.1	30	50
19	AP001674	340,000	232,907	118,654	11	870	0.7	79.1	109.3	30	310	0						
20	AP001675	340,000	226,083	226,083	24	1,620	0.7	67.5	75.6	30	310	0						
21	AP001676	340,000	230,149	130,659	2	60	0.0	30.0	0.0	30	30	0						
22	AP001677	340,000	224,240	224,240	19	810	0.4	42.6	27.7	30	130	0						
23	AP001678	340,000	224,518	83,612	10	1,040	1.2	104.0	118.2	30	350	0						
24	AP001679	340,000	219,760	1,000	0							0						
25	AP001680	340,000	253,203	253,203	23	1,930	0.8	83.9	96.8	30	370	0						
26	AP001681	340,000	239,425	239,425	27	1,650	0.7	61.1	52.4	30	190	9	590	0.2	65.6	46.7	30	170
27	AL163227	340,000	224,506	143,201	16	1,440	1.0	90.0	86.4	30	330	5	410	0.3	82.0	48.2	30	150
28	AP001683	340,000	211,972	165,714	12	1,200	0.7	100.0	85.5	30	270	0						
29	AP001684	340,000	206,761	148,553	11	730	0.5	66.4	54.3	30	190	0						
30	AP001685	340,000	222,301	189,430	15	990	0.5	66.0	62.0	30	250	0						
31	AP001686	340,000	224,148	0	0							0						
32	AP001687	340,000	227,376	0	0							0						
33	AP001688	340,000	230,350	127,833	16	1,220	1.0	76.3	64.0	30	230	0						
34	AP001689	340,000	230,628	161,846	15	830	0.5	55.3	65.2	30	270	0						
35	AP001690	340,000	222,804	0	0							0						
36	AP001691	340,000	234,688	2,422	2	140	5.8	70.0	56.6	30	110	0						
37	AP001692	340,000	232,936	232,936	40	2,553	1.1	66.0	65.2	30	310	0						

Supplemental Table 4

38	AP001693	340,000	213,176	213,176	29	1,670	0.8	57.6	42.9	30	170	5	373	0.2	74.6	42.6	30	130
39	AP001694	340,000	221,379	221,379	34	2,120	1.0	62.4	58.9	30	230	30	2,740	1.2	92.1	77.7	30	350
40	AP001695	340,000	249,138	189,534	31	1,290	0.7	41.6	26.7	30	130	12	1,500	0.8	125.0	99.9	30	310
41	AP001696	340,000	231,532	166,215	27	1,110	0.7	41.1	26.2	30	150	0						
42	AP001697	340,000	248,558	248,558	40	2,460	1.0	61.5	75.5	30	370	25	2,750	1.1	110.0	89.4	30	370
43	AP001698	340,000	255,124	255,124	32	1,260	0.5	39.4	22.7	30	130	2	260	0.1	130.0	141.4	30	230
44	AP001699	340,000	229,987	229,987	11	330	0.1	30.0	0.0	30	30	0						
45	AP001700	340,000	203,654	203,654	29	1,810	0.9	62.4	64.7	30	270	0						
46	AL163246	340,000	223,493	223,493	24	1,580	0.7	65.8	71.0	30	290	0						
47	AL163247	340,000	232,167	232,167	41	1,850	0.8	45.1	41.4	30	230	0						
48	AL163248	340,000	212,146	212,146	16	680	0.3	42.5	24.1	30	110	29	1,750	0.8	60.3	49.2	30	190
49	AL163249	340,000	233,426	233,426	50	2,780	1.2	55.6	68.0	30	370	46	4,980	2.1	108.3	87.3	30	390
50	AP001705	340,000	256,691	256,691	71	4,530	1.8	63.8	68.1	30	370	24	3,460	1.3	144.2	105.2	30	530
51	AP001706	340,000	265,896	250,556	56	3,420	1.4	61.1	64.0	30	330	8	1,100	0.4	137.5	164.2	30	510
52	AP001707	340,000	260,760	100,283	12	620	0.6	51.7	38.6	30	150	5	190	0.2	38.0	11.0	30	50
53	AP001708	340,000	227,772	227,772	12	520	0.2	43.3	32.3	30	130	10	940	0.4	94.0	46.0	30	170
54	AP001709	340,000	235,490	186,016	37	1,870	1.0	50.5	35.7	30	170	7	1,430	0.8	204.3	267.0	30	790
55	AP001710	340,000	238,296	177,885	50	2,340	1.3	46.8	35.1	30	190	27	4,350	2.4	161.1	195.8	30	990
56	AP001711	340,000	196,312	196,312	55	2,790	1.4	50.7	40.2	30	210	22	2,083	1.1	94.7	70.3	30	330
57	AP001712	340,000	211,508	95,063	14	560	0.6	40.0	18.8	30	90	13	633	0.7	48.7	25.1	30	110
58	AP001713	340,000	223,822	0	0							0						
59	AP001714	340,000	229,689	93,325	16	860	0.9	53.8	59.0	30	230	8	660	0.7	82.5	54.4	30	190
60	AP001715	340,000	239,768	239,768	60	5,020	2.1	83.7	116.4	30	710	24	3,600	1.5	150.0	107.5	30	390
61	AP001716	340,000	225,630	225,438	38	4,220	1.9	111.1	140.0	30	570	10	620	0.3	62.0	50.9	30	190
62	AP001717	340,000	203,626	178,366	34	1,580	0.9	46.5	38.6	30	170	70	10,740	6.0	153.4	352.2	30	2,690
63	AP001718	340,000	231,342	231,342	34	1,260	0.5	37.1	19.0	30	130	33	3,350	1.4	101.5	68.2	30	290
64	AP001719	340,000	245,941	206,619	42	1,840	0.9	43.8	28.5	30	150	12	2,880	1.4	240.0	532.7	30	1,890
65	AP001720	340,000	237,211	214,108	41	1,770	0.8	43.2	34.8	30	230	11	810	0.4	73.6	43.7	30	150
66	AP001721	340,000	276,360	159,588	46	2,960	1.9	64.3	80.3	30	450	6	540	0.3	90.0	52.2	50	190
67	AL163267	340,000	258,256	148,706	26	1,500	1.0	57.7	63.5	30	270	0						
68	AL163268	340,000	260,235	260,235	46	4,980	1.9	108.3	109.9	30	450	0						
69	AL163269	340,000	221,970	221,970	31	2,270	1.0	73.2	69.9	30	330	7	630	0.3	90.0	90.2	30	270
70	AL163270	340,000	172,248	172,248	6	180	0.1	30.0	0.0	30	30	27	1,390	0.8	51.5	28.2	30	130
71	AL163271	340,000	242,497	242,497	41	2,510	1.0	61.2	59.8	30	310	24	1,760	0.7	73.3	55.8	30	190
72	AL163272	340,000	211,483	211,483	36	4,140	2.0	115.0	168.3	30	950	17	1,690	0.8	99.4	105.9	30	350
73	AL163273	340,000	220,907	220,907	12	700	0.3	58.3	41.3	30	150	22	1,460	0.7	66.4	50.0	30	210
74	AL163274	340,000	246,216	246,216	17	870	0.4	51.2	55.4	30	250	18	5,060	2.1	281.1	307.6	30	1,310
75	AL163275	340,000	241,786	145,469	12	540	0.4	45.0	46.0	30	190	3	130	0.1	43.3	23.1	30	70
76	AL163276	340,000	260,779	254,578	13	690	0.3	53.1	57.6	30	230	9	530	0.2	58.9	40.1	30	150
77	AL163277	340,000	256,009	256,009	32	2,529	1.0	82.5	94.7	30	370	6	520	0.2	86.7	86.2	30	250
78	AL163278	340,000	239,600	109,073	6	180	0.2	30.0	0.0	30	30	4	300	0.3	75.0	52.6	30	150

Supplemental Table 4

79	AL163279	340,000	209,051	189,913	6	200	0.1	33.3	8.2	30	50	47	2,990	1.6	63.6	45.5	30	190
80	AL163280	340,000	216,079	1,000	0							0						
81	AL163281	340,000	262,096	262,096	32	1,280	0.5	40.0	24.9	30	150	19	1,810	0.7	95.3	66.3	30	210
82	AL163282	340,000	216,061	121,312	3	90	0.1	30.0	0.0	30	30	10	1,200	1.0	120.0	80.1	30	250
83	AL163283	340,000	218,624	185,141	23	1,250	0.7	54.3	36.2	30	190	4	620	0.3	155.0	123.7	50	330
84	AL163284	340,000	182,383	146,971	10	480	0.3	48.0	22.0	30	90	2	80	0.1	40.0	14.1	30	50
85	AL163285	340,000	201,788	74,863	9	450	0.6	50.0	46.9	30	170	8	300	0.4	37.5	10.4	30	50
86	AL163286	39,322	23,137	0	0							0						
88	AP001743	219,256	140,663	101,737	21	730	0.7	34.8	10.8	30	70	11	1,050	1.0	95.5	83.5	30	270
90	AP001745	336,578	238,876	238,876	17	530	0.2	31.2	4.9	30	50	22	1,040	0.4	47.3	40.6	30	190
91	AP001746	340,000	236,040	236,040	20	840	0.4	42.0	41.8	30	210	33	2,230	0.9	67.6	48.2	30	190
92	AP001747	340,000	203,680	203,680	11	350	0.2	31.8	6.0	30	50	23	1,570	0.8	68.3	45.1	30	170
93	AP001748	340,000	165,363	165,363	11	390	0.2	35.5	9.3	30	50	40	3,220	1.9	80.5	70.7	30	410
94	AP001749	27,076	15,921	15,921	0							0						
96	AP001751	340,000	230,811	122,267	14	520	0.4	37.1	21.6	30	110	9	730	0.6	81.1	53.0	30	150
97	AP001752	340,000	190,689	124,093	5	170	0.1	34.0	8.9	30	50	10	580	0.5	58.0	45.4	30	150
98	AP001753	340,000	219,412	140,568	6	180	0.1	30.0	0.0	30	30	34	1,780	1.3	52.4	34.7	30	170
99	AP001754	340,000	216,365	205,063	14	420	0.2	30.0	0.0	30	30	54	7,560	3.7	140.0	227.2	30	1,070
100	AL163300	340,000	220,741	220,741	11	510	0.2	46.4	41.8	30	170	34	3,460	1.6	101.8	120.6	30	550
101	AL163301	340,000	231,447	187,526	11	510	0.3	46.4	26.6	30	110	9	770	0.4	85.6	49.8	30	150
102	AL163302	340,000	242,470	49,451	4	300	0.6	75.0	64.0	30	170	0						
103	AL163303	340,000	188,977	188,977	3	230	0.1	76.7	30.6	50	110	10	1,380	0.7	138.0	81.8	30	270
104	AP001759	340,000	213,785	213,785	6	200	0.1	33.3	8.2	30	50	42	2,520	1.2	60.0	48.2	30	230
105	AP001760	340,000	194,165	194,165	11	450	0.2	40.9	25.9	30	110	25	1,490	0.8	59.6	42.9	30	190
106	AP001761	39,800	18,043	18,043	0							2	100	0.6	50.0	28.3	30	70
	Total	33,824,148	22,490,347	16,580,114	2,257	145,010	0.9	64.2	77.7	30	950	1,141	115,216	0.7	101.0	149.8	30	2,690
	>= 50 bp	33,824,148	22,490,347	16,580,114	762	100,160	0.6	131.4	105.1	50	950	716	102,463	0.6	143.1	176.2	50	2,690

Supplemental Table 4. Distribution and size analysis of conserved human-mouse elements on chromosome 21. For each of the 106 segments of chromosome 21, the GenBank accession number and size in base pairs is indicated. # Tiled bps = the number of non-repetitive base pairs tiled on the arrays (Hattori et al. 2000). Total bps hybridized = the number of tiled bps hybridized with orthologous mouse DNA. The conserved elements are classified as in identified exons (IE) and not in identified exons (NIE). For each of these classes: # of elements = the number of conserved elements identified, # of bps = the number of base pairs covered by all the conserved elements, % of hyb'd bps = percent of the hybridized base pairs that are conserved. For the length data: Mean = the mean length in base pairs of all conserved elements, S.D. = standard deviation of length, Min. = length of the smallest element, Max. = length of the largest element. At the bottom, >= 50 bp = the summary of the analysis for conserved elements ≥ 50 bp in length. *(To view the CONSEQ plot of a segment, click on the segment number.)*

CONSEQ plots: Conserved elements are shown (yellow rectangles) relative to their position in the human reference sequence (horizontal axes), and their percent conformances (0-100%) are indicated on the vertical axes. Peaks shaded red but not indicated by a yellow rectangle have $\geq 60\%$ conformance but are low complexity (see supplementary algorithm description). The locations of GenBank annotated exons on the Watson (blue rectangles) and Crick (green rectangles) strands, coding sequences identified by database searching (white rectangles with black outline) (see Material and Methods), and chromosome 21 cross-species markers (black with yellowed background) (Supplemental Table 1) are shown. Pseudogenes are indicated (p). Horizontal arrows indicate the direction of transcription for each gene.

Segment		Size (bp)	# Tiled bps	Total bps hybridized	NIE							IE						
					# of elements	# of bps	% of hyb'd bps	LENGTH (bp)				# of elements	# of bps	% of hyb'd bps	LENGTH (bp)			
								Mean	S.D.	Min.	Max.				Mean	S.D.	Min.	Max.
69	AL163269	340,000	221,970	167,957	81	5,590	3.3	69.0	103.8	30	670	11	1,410	0.8	128.2	128.5	30	470
70	AL163270	340,000	172,248	148,027	19	690	0.5	36.3	23.1	30	130	56	4,700	3.2	83.9	56.0	30	270
71	AL163271	340,000	242,497	242,497	120	10,660	4.4	88.8	108.6	30	570	27	2,870	1.2	106.3	99.2	30	470
72	AL163272	340,000	211,483	81,417	63	8,750	10.7	138.9	206.7	30	1,250	5	1,030	1.3	206.0	215.1	30	470
73	AL163273	340,000	220,907	0														
74	AL163274	340,000	246,216	191,158	116	7,380	3.9	63.6	70.3	30	430	11	2,350	1.2	213.6	195.3	30	570
75	AL163275	340,000	241,786	241,786	147	9,010	3.7	61.3	56.9	30	290	8	840	0.3	105.0	107.3	30	310
76	AL163276	340,000	260,779	208,093	109	7,501	3.6	68.8	57.4	30	370	17	2,270	1.1	133.5	159.3	30	710
77	AL163277	340,000	256,009	256,009	152	11,920	4.7	79.2	87.2	30	490	9	1,190	0.5	132.2	144.0	30	490
78	AL163278	340,000	239,600	118,514	35	2,350	2.0	67.1	69.0	30	290	9	830	0.7	92.2	50.4	30	190
79	AL163279	340,000	209,051	77,726	26	1,100	1.4	42.3	40.4	30	230	15	1,250	1.6	83.3	85.7	30	370
80	AL163280	340,000	216,079	109,804	27	990	0.9	36.7	30.9	30	190	10	580	0.5	58.0	42.4	30	130
81	AL163281	340,000	262,096	198,211	62	3,260	1.6	52.6	41.4	30	210	10	920	0.5	92.0	70.2	30	210
82	AL163282	340,000	216,061	121,312	28	1,800	1.5	64.3	73.4	30	270	11	2,330	1.9	211.8	112.6	30	430
83	AL163283	340,000	218,624	0														
84	AL163284	340,000	182,383	114,777	26	2,760	2.4	106.2	103.1	30	390	5	510	0.4	102.0	59.3	30	190
85	AL163285	340,000	201,788	138,353	12	800	0.6	66.7	51.8	30	170	17	1,170	0.8	68.8	57.7	30	210
86	AL163286	39,322	23,137	23,137	4	120	0.5	30.0	0.0	30	30	0						
88	AP001743	219,256	140,663	140,663	28	1,080	0.8	38.6	19.9	30	130	12	1,300	0.9	108.3	71.1	30	270
90	AP001745	336,578	23,676	23,676	0							7	370	1.6	52.9	35.5	30	130
	Total	6,375,156	3,942,825	2,597,732	1,052	75,571	2.9	71.8	91.2	30	1,250	240	25,920	1.0	108.0	106.0	30	710
	>= 50 bp	6,375,156	3,942,825	2,597,732	406	56,191	2.2	138.4	119.8	50	1,250	172	23,880	0.9	138.8	111.0	50	710

Supplemental Table 5. Distribution and size analysis of conserved human-dog elements on chromosome 21. For each analyzed segment of chromosome 21 (69-90), the GenBank accession number and size in base pairs is indicated. # Tiled bps = the number of non-repetitive base pairs tiled on the arrays (Hattori et al. 2000). Total bps hybridized = the number of tiled bps hybridized with orthologous dog DNA. The conserved elements are classified as in identified exons (IE) and not in identified exons (NIE). For each of these classes: # of elements = the number of conserved elements identified, # of bps = the number of base pairs covered by all the conserved elements, % of hyb'd bps = percent of the hybridized base pairs that are conserved. For the length data: Mean = the mean length in base pairs of all conserved elements, S.D. = standard deviation of length, Min. = length of the smallest element, Max. = length of the largest element. At the bottom, ≥ 50 bp = the summary of the analysis for conserved elements ≥ 50 bp in length. *(To view the CONSEQ plot of a segment click, on the segment number.)*

CONSEQ plots: Conserved elements are shown (yellow rectangles) relative to their position in the human reference sequence (horizontal axes), and their percent conformances (0-100%) are indicated on the vertical axes. Peaks shaded red but not indicated by a yellow rectangle have $\geq 60\%$ conformance but are low complexity. The locations of GenBank annotated exons on the Watson (blue rectangles) and Crick (green rectangles) strands, coding sequences identified by database searching (white rectangles with black outline) (see Material and Methods), and chromosome 21 cross-species markers (Supplemental Table 1) are shown. Pseudogenes are indicated (p). Horizontal arrows indicate the direction of transcription for each gene.