

Supplementary Informations for :

**Facilitating genome navigation: survey sequencing and dense radiation-hybrid gene mapping**

Christophe Hitte<sup>1</sup>, Jennifer Madeoy<sup>2</sup>, Ewen F. Kirkness<sup>3</sup>, Catherine Priat<sup>1</sup>, Travis D. Lorentzen<sup>2</sup>, Fabrice Senger<sup>1</sup>, Dan Thomas<sup>4</sup>, Thomas Derrien<sup>1</sup>, Christina Ramirez<sup>2</sup>, Carol Scott<sup>4</sup>, Gwenaëlle Evanno<sup>1</sup>, Barbara Pullar<sup>2</sup>, Edouard Cadieu<sup>1</sup>, Vinay Oza<sup>2</sup>, Kristelle Lougant<sup>1</sup>, David B. Jaffe<sup>5</sup>, Sandrine Tacher<sup>1</sup>, Stéphane Dréano<sup>1</sup>, Nadia Berkova<sup>1</sup>, Catherine Andre<sup>1</sup>, Panagiotis Deloukas<sup>4</sup>, Claire Fraser<sup>3</sup>, Kerstin Lindblad-Toh<sup>5</sup>, Elaine A. Ostrander<sup>2,6</sup>, and Francis Galibert<sup>1</sup>

<sup>1</sup> UMR 6061 CNRS, Génétique et développement, Faculté de Médecine, 35043 Rennes Cédex, France.

<sup>2</sup> Divisions of Human Biology and Clinical Research, Fred Hutchinson Cancer Research Center, Seattle WA 98109-1024.

<sup>3</sup> The Institute for Genomic Research, 9712 Medical Center Drive, Rockville, MD, USA 20850.

<sup>4</sup> Wellcome Trust Sanger Institute, Hixton, Cambridgeshire, UK.

<sup>5</sup> Broad Institute of MIT and Harvard, 320, Charles Street, Cambridge, MA 02141.

<sup>6</sup> NHGRI/NIH, 50 South Drive, MSC 8000, Building 50, Room 5351, Bethesda MD 208928000.

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## Supplementary Information : S1

*The Canine Genome: Survey Sequencing and a Dense Gene Map for Genome Navigation  
(Hitte et al. 2005)*

### **Methods : The RH panel construction.**

A high resolution dog/hamster radiation hybrid panel has been constructed by fusing dog primary fibroblasts, irradiated at 9000 rads, with thymidine kinase-deficient hamster cells HTK3.

I) Cells: Dog primary fibroblasts were derived from two male mongrel dogs. Hamster HTK3-cells (thymidine kinase deficient) were derived from the A2H strain after 6BrdU selection.

II) Irradiation/Fusion:

A) 20X106 Dog fibroblasts were irradiated by exposure to a 9000-rad gamma ray. B) Fusion of 20X106 and HTK3-cells was chemically induced using PEG2000+10% DMSO (Dog/ Hamster cell ratio = 1.0).

III) Results: Five identical fusions were done, producing 400 clones. Average fusion efficiency was 4 clones for every 106 dog fibroblasts. All 400 clones were tested for retention frequency using a set of 96 defined BAC end-based markers. Eighty-eight clones were selected and expanded, resulting in a panel with an average retention frequency of 29% and a resolution of 300 kb.

### **Cell Line Retention (percentages are derived from 10,500 RH genotypes)**

Cell Line n.1 = 23.0071 %	Cell Line n.45 = 23.7318 %
Cell Line n.2 = 16.3397 %	Cell Line n.46 = 43.2022 %
Cell Line n.3 = 18.6298 %	Cell Line n.47 = 23.21 %
Cell Line n.4 = 38.3902 %	Cell Line n.48 = 16.533 %

Cell Line n.5 = 45.3957 %	Cell Line n.49 = 22.2534 %
Cell Line n.6 = 19.1613 %	Cell Line n.50 = 48.2655 %
Cell Line n.7 = 23.8477 %	Cell Line n.51 = 18.5718 %
Cell Line n.8 = 20.0019 %	Cell Line n.52 = 10.5904 %
Cell Line n.9 = 22.0118 %	Cell Line n.53 = 33.5395 %
Cell Line n.10 = 25.2005 %	Cell Line n.54 = 38.1486 %
Cell Line n.11 = 28.4858 %	Cell Line n.55 = 22.5722 %
Cell Line n.12 = 32.0224 %	Cell Line n.56 = 38.738 %
Cell Line n.13 = 35.7909 %	Cell Line n.57 = 21.1711 %
Cell Line n.14 = 17.7215 %	Cell Line n.58 = 30.1092 %
Cell Line n.15 = 24.5531 %	Cell Line n.59 = 15.0449 %
Cell Line n.16 = 18.4559 %	Cell Line n.60 = 21.9152 %
Cell Line n.17 = 40.0425 %	Cell Line n.61 = 27.1041 %
Cell Line n.18 = 30.7952 %	Cell Line n.62 = 22.0118 %
Cell Line n.19 = 37.8104 %	Cell Line n.63 = 20.6687 %
Cell Line n.20 = 16.7552 %	Cell Line n.64 = 34.0613 %
Cell Line n.21 = 28.4279 %	Cell Line n.65 = 19.1323 %
Cell Line n.22 = 23.5578 %	Cell Line n.66 = 23.3936 %
Cell Line n.23 = 18.1177 %	Cell Line n.67 = 21.7992 %
Cell Line n.24 = 27.8771 %	Cell Line n.68 = 20.8909 %
Cell Line n.25 = 18.0501 %	Cell Line n.69 = 30.5827 %
Cell Line n.26 = 26.0798 %	Cell Line n.70 = 17.7215 %
Cell Line n.27 = 49.3091 %	Cell Line n.71 = 29.3458 %
Cell Line n.28 = 26.7949 %	Cell Line n.72 = 20.3015 %

Cell Line n.29 = 24.2246 %	Cell Line n.73 = 44.4487 %
Cell Line n.30 = 25.4517 %	Cell Line n.74 = 16.2335 %
Cell Line n.31 = 35.4334 %	Cell Line n.75 = 35.2401 %
Cell Line n.32 = 23.2969 %	Cell Line n.76 = 30.3701 %
Cell Line n.33 = 51.0387 %	Cell Line n.77 = 30.1962 %
Cell Line n.34 = 28.5148 %	Cell Line n.78 = 32.0128 %
Cell Line n.35 = 25.674 %	Cell Line n.79 = 13.9434 %
Cell Line n.36 = 37.5882 %	Cell Line n.80 = 38.2452 %
Cell Line n.37 = 43.5791 %	Cell Line n.81 = 21.9152 %
Cell Line n.38 = 47.8404 %	Cell Line n.82 = 41.2407 %
Cell Line n.39 = 41.8688 %	Cell Line n.83 = 22.1084 %
Cell Line n.40 = 27.0268 %	Cell Line n.84 = 27.7708 %
Cell Line n.41 = 15.3445 %	Cell Line n.85 = 23.9443 %
Cell Line n.42 = 25.7996 %	Cell Line n.86 = 32.3799 %
Cell Line n.43 = 37.965 %	Cell Line n.87 = 20.6977 %
Cell Line n.44 = 23.5965 %	Cell Line n.88 = 37.0374 %

**RH panel average retention : 29 %**

## **Supplementary Information : S2**

*The Canine Genome: Survey Sequencing and a Dense Gene Map for Genome Navigation  
(Hitte et al. 2005)*

### **Supplementary Information for Marker Identification**

All canine gene sequences were chosen by the best BLASTn mutual alignment with the human genome. The human genome was divided into 75 kb segments. Human genes with representative dog sequence were assigned to a genomic segment creating 11,818 bins. If multiple genes fell within the same 75 kb segment they were assigned to the same bin. A single gene marker from each bin was chosen based on the following criteria. All selected dog sequences were either contigs or singletons, derived from the assembly of 6.22 million reads.

Selection criteria :

1. Blastn alignment with human genome yields mutually-best HSPs (High Scoring Pairs). HSPs are defined as mutually-best when the segment of aligned dog sequence has no higher-scoring hit elsewhere on the human genome and the segment of aligned human sequence has no higher-scoring alignment with another dog sequence.
2. The dog/human alignment overlaps at least one human exon defined by the 24,567 genes of Ensembl version 13.31.1.
3. The dog sequence is not a processed pseudogene. A dog sequence was considered a potential pseudogene if the HSPs were <25 base pairs on the dog sequence but >300 base pairs on the human sequence. Aligned sequences fitting this criterion were eliminated.
4. After applying criteria 1-3, selection of a single dog sequence for each human gene was based on the highest blastn score.

## Supplementary Information : S3

*The Canine Genome: Survey Sequencing and a Dense Gene Map for Genome Navigation  
(Hitte et al. 2005)*

### Supplementary for RH Map Construction

Map construction was carried out using the `rh_tsp_map2` package (Agarwala et al. 2001) that incorporates the state of art CONCORDE algorithm as applied to the Traveling Salesman Problem (TSP) (Applegate et al. — 1998). The RH vectors were analyzed by pairwise analysis using the `pairlods_dists` option to construct linkage groups. The TSP method uses the CONCORDE chained Lin-Kernighan algorithm of the `rh_tsp_map2` package to order each of the linkage groups. Parametric and non-parametric analyses are systematically completed, resulting in 5 independent maps. A consensus map is derived from the 5 independent maps. Mapping support is expressed in percentages assigned to each marker.

### Supplementary : Map characteristics :

(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)	(13)
CFA01	137	124,9	5385	23	637	459	12	298	272	414	31	25
CFA02	99	87,7	4335	20	458	350	12	283	251	306	20	15
CFA03	105	95,1	3934	24	322	280	14	375	340	224	15	8
CFA04	100	91,3	3837	24	395	330	12	303	277	304	20	15
CFA05	99	92,1	4879	19	426	376	13	263	245	366	21	14
CFA06	87	79,1	3898	20	398	342	11	254	231	305	16	9
CFA07	94	83,0	4076	20	383	340	12	276	244	308	19	13
CFA08	86	77,4	3723	21	282	263	14	327	294	214	17	13
CFA09	77	53,6	6041	9	440	399	15	193	134	359	16	12
CFA10	80	72,7	4383	17	310	295	15	271	246	263	13	10
CFA11	86	75,8	2760	27	316	285	10	302	266	261	18	14
CFA12	85	75,5	3786	20	265	258	15	329	292	215	21	13
CFA13	75	66,2	2905	23	216	207	14	362	320	199	13	10
CFA14	72	63,5	2041	31	273	227	9	317	280	215	20	12
CFA15	75	67,2	3342	20	291	260	13	288	259	247	13	8
CFA16	73	60,3	2470	24	237	212	12	344	284	209	8	4
CFA17	80	66,9	3540	19	303	275	13	291	243	264	13	8
CFA18	66	66,2	3292	20	302	288	11	229	230	235	14	12
CFA19	66	56,9	1429	40	83	81	18	815	703	791	0	5
CFA20	66	61,2	2560	24	412	299	9	221	205	255	11	7
CFA21	61	53,0	3121	17	229	214	15	285	248	202	14	11
CFA22	61	64,2	1649	39	157	139	12	439	462	136	9	8
CFA23	61	55,6	1879	30	202	176	11	347	316	153	8	5
CFA24	73	50,7	3345	15	236	229	15	319	222	176	12	9
CFA25	60	54,4	2812	19	240	214	13	280	254	178	11	5
CFA26	48	41,0	2784	15	229	214	13	224	192	185	12	8

CFA27	57	49,1	2376	21	254	235	10	243	209	230	9	7
CFA28	55	42,5	2848	15	258	248	11	222	171	233	15	12
CFA29	51	44,9	2111	21	135	129	16	395	348	121	12	10
CFA30	47	43,2	2542	17	265	239	11	197	181	209	8	7
CFA31	50	41,2	1387	30	98	88	16	568	468	88	6	5
CFA32	51	41,8	1855	23	130	122	15	418	343	118	10	7
CFA33	41	34,5	1261	27	152	140	9	293	246	134	11	10
CFA34	50	45,2	1283	35	147	119	11	420	380	109	12	8
CFA35	38	29,5	1601	18	115	107	15	355	276	102	8	7
CFA36	41	34,0	1862	18	119	115	16	357	295	103	10	8
CFA37	40	33,9	2215	15	143	138	16	290	246	114	12	10
CFA38	38	26,5	1193	22	109	94	13	404	282	65	6	5
CFAX	139	126,9	2735	46	381	295	9	471	430	254	11	4
TOTAL	2770	2428,7	113475	22	10348	9081	12.8	305	267	8152	525	373

columns :

- (1) Chromosome name
- (2) Size in Mb (estimated by cytogenetics measures)
- (3) Size in Mb (estimated by the sequence assembly Release 1.0)
- (4) Size in cR (cR9000 = RH map unit)
- (5) Value of the cR9000 expressed in kb (based on sequence assembly size)
- (6) Number of Markers
- (7) Number of Unique Positions
- (8) Inter-Marker Distance in cR9000
- (9) Inter-Marker Distance (calculated from cytogenetics values)
- (10) Inter-Marker Distance (calculated from the sequence assembly Release 1.0 values)
- (11) Number of Markers with High Statistical Support
- (12) Number of Markers Used to Assign Linkage Groups to Chromosomes
- (13) Number of Markers Used to Assign Linkage Groups to Chromosomes and also FISHeD

## Supplementary Information : S4

*The Canine Genome: Survey Sequencing and a Dense Gene Map for Genome Navigation (Hitte et al. 2005)*

### Supplementary for canine markers design and RH genotyping success rate

dog markers distribution per HSA

	(1)	(2)	(3)	(4)	(5)	(6)
HSA01	1380	1291	93,6%	1083	83,9%	78,5%
HSA02	1137	1057	93,0%	776	73,4%	68,2%
HSA03	844	802	95,0%	685	85,4%	81,2%
HSA04	715	685	95,8%	505	73,7%	70,6%
HSA05	702	665	94,7%	577	86,8%	82,2%
HSA06	800	729	91,1%	562	77,1%	70,3%
HSA07	680	644	94,7%	573	89,0%	84,3%
HSA08	533	496	93,1%	404	81,5%	75,8%
HSA09	549	508	92,5%	448	88,2%	81,6%
HSA10	615	581	94,5%	500	86,1%	81,3%
HSA11	806	743	92,2%	586	78,9%	72,7%
HSA12	761	711	93,4%	585	82,3%	76,9%
HSA13	277	267	96,4%	239	89,5%	86,3%
HSA14	428	390	91,1%	303	77,7%	70,8%
HSA15	454	424	93,4%	367	86,6%	80,8%
HSA16	449	408	90,9%	316	77,5%	70,4%
HSA17	675	601	89,0%	454	75,5%	67,3%
HSA18	275	258	93,8%	203	78,7%	73,8%
HSA19	536	494	92,2%	423	85,6%	78,9%
HSA20	414	382	92,3%	254	66,5%	61,4%
HSA21	136	123	90,4%	82	66,6%	60,2%
HSA22	252	219	86,9%	178	81,3%	70,6%
HSAX	480	449	93,5%	398	88,6%	82,9%
HSAY	7	7	100,0%	2	28,6%	28,6%

subTOTAL

genes	13905	12934	93,0%	10503	81,2%	75,5%
BAC	567	567	100,0%	545	96,1%	96,1%

TOTAL 14472 13501 93,20% 11048 81,80% 76,30%

#### Legend:

- (1) Number of Canine Gene Sequences Used
- (2) Number of Primers Designed
- (3) Ratio of Primers to Sequences
- (4) Number of RH Vectors Obtained
- (5) Ratio of Vectors to Primers
- (6) Ratio of Vectors to Sequences



Supplementary Information : S5

*The Canine Genome: Survey Sequencing and a Dense Gene Map for Genome Navigation (Hitte et al. 2005)*

Supplementary information for the Comparative Genome Analysis: A Canine/Human Oxford Grid

HSA	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	X	CS	
CFA01					8				3									3	1					15	
CFA02	3				3					4						2									12
CFA03				6	3										6										15
CFA04	2				5					3															10
CFA05	4									2						2	1								9
CFA06	1						3									3									7
CFA07	1																		5						6
CFA08	1													6											7
CFA09									1								8								9
CFA10		2										5											3		10
CFA11					4				4																8
CFA12						8																			8
CFA13				3				3							3										9
CFA14	1							12																	13
CFA15	3			2								2		2											9
CFA16				2			3	2																	7
CFA17	3	2																							5
CFA18							3			4															7
CFA19		3		2																					5
CFA20				7																2					9
CFA21										5															5
CFA22													5												5
CFA23				4																		1			5
CFA24																					6				6
CFA25		1		2				1						4											8
CFA26									1		1												2		4
CFA27													6												6
CFA28									4																4
CFA29								5																	5
CFA30															5										5
CFA31			2																			1			3
CFA32				6																					6
CFA33				6																					6
CFA34				1	1																				2
CFA35						2																			2
CFA36		4																							4
CFA37		5						1																	6
CFA38	1																								1
CFA39																								1	1

Legend:

The Oxford Grid is a schematic representation of the conserved segments (CS) >500

kb between canine and human genome. CS are defined as having two or more conserved

markers on the corresponding dog/human chromosomes, without interruption. CS between

canine and human genomes are represented by blue squares. Number of CS are indicated in the square. The total number of CS >500 kb is reported in the last line, last column of the grid.

## Supplementary Information : S6

*The Canine Genome: Survey Sequencing and a Dense Gene Map for Genome Navigation  
(Hitte et al. 2005)*

### Supplementary for : Marker Chromosomal Assignment Comparison between RH Map and Draft Dog Sequence Assembly (Release1.0)

(1)	(2)	(3)	(4)
CFA01	546	546 (100,0%)	0 (0,0%)
CFA02	413	410 (99,3%)	3 (0,7%)
CFA03	271	267 (98,5%)	4 (1,5%)
CFA04	345	343 (99,4%)	2 (0,6%)
CFA05	368	366 (99,5%)	2 (0,5%)
CFA06	352	351 (99,7%)	1 (0,3%)
CFA07	351	347 (98,9%)	4 (1,1%)
CFA08	241	238 (98,8%)	3 (1,2%)
CFA09	386	386 (100,0%)	0 (0,0%)
CFA10	274	271 (98,9%)	3 (1,1%)
CFA11	269	267 (99,3%)	2 (0,7%)
CFA12	218	217 (99,5%)	1 (0,5%)
CFA13	183	182 (99,5%)	1 (0,5%)
CFA14	235	229 (97,4%)	6 (2,6%)
CFA15	260	257 (98,8%)	3 (1,2%)
CFA16	196	194 (99,0%)	2 (1,0%)
CFA17	278	277 (99,6%)	1 (0,4%)
CFA18	259	255 (98,5%)	4 (1,5%)
CFA19	57	54 (94,7%)	3 (5,3%)
CFA20	359	357 (99,4%)	2 (0,6%)
CFA21	186	186 (100,0%)	0 (0,0%)
CFA22	141	140 (99,3%)	1 (0,7%)
CFA23	166	165 (99,4%)	1 (0,6%)
CFA24	196	196 (100,0%)	0 (0,0%)
CFA25	202	201 (99,5%)	1 (0,5%)
CFA26	193	192 (99,5%)	1 (0,5%)
CFA27	228	227 (99,6%)	1 (0,4%)
CFA28	213	211 (99,1%)	2 (0,9%)
CFA29	108	108 (100,0%)	0 (0,0%)
CFA30	227	225 (99,1%)	2 (0,9%)
CFA31	75	75 (100,0%)	0 (0,0%)
CFA32	112	111 (99,1%)	1 (0,9%)
CFA33	131	129 (98,5%)	2 (1,5%)
CFA34	122	122 (100,0%)	0 (0,0%)
CFA35	92	91 (98,9%)	1 (1,1%)
CFA36	93	92 (98,9%)	1 (1,1%)
CFA37	109	109 (100,0%)	0 (0,0%)
CFA38	100	99 (99,0%)	1 (1,0%)
CFA39	334	333 (99,7%)	1 (0,3%)

Total        8889    8826 (99.3%)    63 (0.7%)

**Legend :**

(1) Chromosome number

(2) Number of marker compared between the RH map and the assembly

(3) Number of markers assigned to the same chromosome on the RH Map and the canine sequence assembly (expressed in % in parenthesis).

(4) Number of markers assigned to different chromosomes on the RH map and the canine sequence assembly (expressed in % in parenthesis)

### Supplementary Information : S7

*The Canine Genome: Survey Sequencing and a Dense Gene Map for Genome Navigation (Hitte et al. 2005)*

**Supplementary informations for :  
Conserved segment size analysis : Comparison of the canine CS and their human counterparts**

(1)	(2)	(3)	(4)	(5)	(6)	(7)		
cfa01	0	1270	3,9	27,8	1270	29,21	HSA18	30,13
cfa01	1282	3605	28,1	71,7	2323	53,429	HSA06	52,68
cfa01	3673	4543	72,8	101,85	870	20,01	HSA09	42,23
cfa01	4559	5385	101,91	124,37	826	18,998	HSA19	33,73
cfa02	0	2125	6,52	35,1	2125	42,5	HSA10	36,59
cfa02	2132	2821	35,32	57,87	689	13,78	HSA05	28,56
cfa02	2836	3262	58,61	66,83	426	8,52	HSA16	10,3
cfa02	3347	4335	69	87,5	988	19,76	HSA01	22,61
cfa03	0	931	3,08	34,05	931	22,344	HSA05	37,86
cfa03	1059	2208	35,01	61,49	1149	27,576	HSA15	33,47
cfa03	2345	3933	61,9	95,05	1588	38,112	HSA04	40,11
cfa04	0	139	3,06	3,63	139	3,336	HSA10	1,09
cfa04	149	738	3,63	13,01	589	14,136	HSA01	10,77
cfa04	768	2256	13,5	37,6	1488	35,712	HSA10	29,36
cfa04	2363	3837	38,03	91,03	1474	35,376	HSA05	67,37
cfa05	0	2188	3,71	32,95	2188	41,572	HSA11	34,92
cfa05	2288	2612	41,85	45,84	324	6,156	HSA17	6,13
cfa05	2624	3503	46,21	66,48	879	16,701	HSA01	23,47
cfa05	3525	4847	66,08	89,84	1322	25,118	HSA16	29,11
cfa06	0	752	3,05	18,3	752	15,04	HSA07	31
cfa06	774	2453	18,67	41,96	1679	33,58	HSA16	31,4
cfa06	2461	3897	42,25	78,77	1436	28,72	HSA01	43,62
cfa07	0	2291	3,03	46,16	2291	45,82	HSA01	48,4
cfa07	2309	4076	46,39	82,35	1767	35,34	HSA18	40,86
cfa08	16	35	3,12	3,23	19	0,399	HSA01	0,11
cfa08	79	3723	3,79	76,08	3644	76,524	HSA14	86,11
cfa09	0	614			614	5,526	HSA17	6,25
cfa09	695	701			6	0,054	HSA01	0,86
cfa09	735	2038	3,19	14,18	1303	11,727	HSA17	10,06
cfa09	2160	2172			12	0,108	HSA11	1,21
cfa09	2315	5221	14,4	40,6	2906	26,154	HSA17	28,53
cfa09	5227	6020	40,7	53,59	793	7,137	HSA09	16,25

cfa10	0	1126	3,1	18,98	1126	19,142	HSA12	19,07
cfa10	1164	2352	19,7	34,4	1188	20,196	HSA22	18,16
cfa10	2459	2477	37,5	37,7	18	0,306	HSA02	1,4
cfa10	2480	2535	35,23	37,13	55	0,935	HSA12	2,36
cfa10	2561	4383	38,3	72,55	1822	30,974	HSA02	39,24
cfa11	0	1190	3,1	27,9	1190	32,13	HSA05	31,57
cfa11	1197	2759	28,29	75,65	1562	42,174	HSA09	56,97
cfa12	0	3786	3,16	75,2	3786	75,72	HSA06	87,2
cfa13	0	1799	3,4	41,25	1799	41,377	HSA08	47,08
cfa13	1808	1832	41,46	41,56	24	0,552	HSA15	0,1
cfa13	1855	2904	41,8	66,05	1049	24,127	HSA04	34,34
cfa14	0	65	3,17	3,77	65	2,015	HSA01	10,9
cfa14	113	2041	5,8	63,5	1928	59,768	HSA07	65,3
cfa15	0	543	3,45	12,46	543	10,86	HSA01	5,75
cfa15	582	610	11,21	11,39	28	0,56	HSA16	0,18
cfa15	661	970	11,67	19,95	309	6,18	HSA01	9,2
cfa15	980	1091	20,52	21,88	111	2,22	HSA14	1,32
cfa15	1112	2369	22,3	45,53	1257	25,14	HSA12	28,31
cfa15	2376	3341	45,75	67,04	965	19,3	HSA04	24,82
cfa16	32	609	4,86	15,77	577	13,848	HSA07	11,26
cfa16	626	644	4,2	4,2	18	0,432	HSA01	0,02
cfa16	664	719	3,16	3,75	55	1,32	HSA07	1,2
cfa16	764	965	15,95	22,71	201	4,824	HSA07	10,71
cfa16	1015	2045	23,54	42,91	1030	24,72	HSA08	20,7
cfa16	2077	2470	44,181	55,47	393	9,432	HSA04	12,53
cfa17	0	2939	3,15	53,46	2939	55,841	HSA02	71,4
cfa17	2966	3540	54,27	66,72	574	10,906	HSA01	16,68
cfa18	0	897	3,03	31,83	897	17,94	HSA07	21,17
cfa18	924	3292	35,91	65,96	2368	54,464	HSA11	36,72
cfa19	0	383	15,04	22,21	383	15,32	HSA04	7,91
cfa19	514	1429	23,52	49,06	915	36,6	HSA02	30,15
cfa20	0	1724	3,01	46,36	1724	41,376	HSA03	47,84
cfa20	1727	2559	46,54	61,1	832	19,968	HSA19	19,44
cfa21	0	3121	7,79	52,99	3121	53,057	HSA11	50,24
cfa22	0	1648	3,04	64,19	1648	64,272	HSA13	73,05
cfa23	0	97	3,05	4,57	97	2,91	HSA20	1,54
cfa23	155	1873	4,97	55,15	1718	51,54	HSA03	57,07
cfa24	0	3344	3,2	50,61	3344	50,16	HSA20	63,4

cfa25	2	851	3,1	21,75	849	16,131	HSA13	21,31
cfa25	885	1238	22,12	28,16	353	6,707	HSA04	6,23
cfa25	1261	2009	29,14	40,12	748	14,212	HSA08	10,35
cfa25	2036	2811	40,84	54,28	775	14,725	HSA02	17,27
cfa26	0	1498	3,09	21,75	1498	22,47	HSA12	24,87
cfa26	1562	2483	22,14	33,32	921	13,815	HSA22	13,36
cfa26	2567	2784	34,43	40,9	217	3,255	HSA10	7,86
cfa27	0	2363	3,38	48,23	2363	49,623	HSA12	53,74
cfa28	0	2652	3,65	42,44	2652	39,78	HSA10	43,15
cfa29	17	2110	3,04	44,51	2093	43,953	HSA08	49,5
cfa30	35	2541	3,29	43,12	2506	42,602	HSA15	44,98
cfa31	0	234	3,09	11,53	234	7,02	HSA03	9,51
cfa31	291	1235	14,16	40,91	944	28,32	HSA21	30,76
cfa32	0	1826	3,02	41,21	1826	41,998	HSA04	42,75
cfa33	0	1249	3,99	34,43	1249	33,723	HSA03	40,79
cfa34	0	346	3,06	14,75	346	12,11	HSA05	14,26
cfa34	352	1282	15,61	43,69	930	32,55	HSA03	33,62
cfa35	0	1600	3,53	29,414	1600	28,8	HSA06	30,12
cfa36	0	1862	3,97	33,7	1862	33,516	HSA02	34,8
cfa37	0	2056	3,28	32,68	2056	30,84	HSA02	34,4
cfa37	2128	2215	33,09	33,86	87	1,305	HSA08	
cfa38	41	1192	3,06	26,42	1151	25,322	HSA01	25,52
cfaX	51	2735	1,85	126,79	2684	123,464	HSAX	149,76
TOTAL				110413	2429,086			2690,36
ratio Dog/Human						90,29%		

**Legend:**

- (1) Canine chromosome
- (2) Canine conserved segment coordinate in cR9000 (data from RH map) : start - end
- (3) Canine conserved segment coordinate in Mbp (from the sequence assembly) : start - end
- (4) Canine conserved segment size in cR9000
- (5) Canine conserved segment size expressed in Mbp : (size in cR x value of the cR in Mb per chromosome) - \*Value of cR (genome-wide ave = 22kb range : [9 – 48.6]).
- (6) Human counterparts segments
- (7) Human counterparts segments size (ncbi build 34)

**Supplementary informations for : Detail of the comparative dog/human conserved segments analysis**

(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)
	(10)	(11)	(12)					
cfa01	hsa18	<b>30.13</b> (79.3%)	13.2	13.8	<u>0.6</u>	46.57	47.24	<u>0.67</u>
	48.34	77.2 <u>28.86</u>						
cfa01	hsa06	<b>52.68</b> (82.8%)	116.7	169.38	<u>52.68</u>			
cfa01	hsa09	<b>42.23</b> (68.8%)	0.2	5.79	<u>5.59</u>	34.23	39.14	<u>4.91</u>
	63.17	94.9 <u>31.73</u>						
cfa01	hsa19	<b>33.73</b> (66.6%)	29.94	63.67	<u>33.73</u>			
cfa02	hsa10	<b>36.59</b> (78.1%)	0.22	36.81	<u>36.59</u>			
cfa02	hsa05	<b>28.56</b> (79.0%)	54.41	74.07	<u>19.66</u>	138.7	147.6	<u>8.9</u>
cfa02	hsa16	<b>10.3</b> (79.8%)	46.78	57.08	<u>10.3</u>			
cfa02	hsa01	<b>22.61</b> (81.8%)	10.84	33.45	<u>22.61</u>			
cfa03	hsa05	<b>37.86</b> (81.8%)	74.41	112.27	<u>37.86</u>			
cfa03	hsa15	<b>33.47</b> (79.1%)	20.55	30.04	<u>9.49</u>	71.48	72.37	<u>0.89</u>
	76.02	76.36 <u>0.34</u>	76.79	99.54	<u>22.75</u>			
cfa03	hsa04	<b>40.11</b> (82.6%)	1.06	41.17	<u>40.11</u>			
cfa04	hsa10	<b>1.09</b> (52.3%)	37.82	38.4	<u>0.58</u>	46.46	46.97	<u>0.51</u>
cfa04	hsa01	<b>10.77</b> (87.1%)	226.34	237.11	<u>10.77</u>			
cfa04	hsa10	<b>29.36</b> (82.1%)	59.12	88.48	<u>29.36</u>			
cfa04	hsa05	<b>67.37</b> (78.7%)	16.52	54.29	<u>37.77</u>	112.41	112.51	<u>0.1</u>
	147.67	177.17 <u>29.5</u>						
cfa05	hsa11	<b>34.92</b> (83.7%)	100.8	135.72	<u>34.92</u>			
cfa05	hsa17	<b>6.13</b> (65.1%)	15.34	21.47	<u>6.13</u>			
cfa05	hsa01	<b>23.47</b> (86.4%)	1.07	10.04	<u>8.97</u>	52.74	67.24	<u>14.5</u>
cfa05	hsa16	<b>29.11</b> (81.6%)	61.77	90.88	<u>29.11</u>			
cfa06	hsa07	<b>31</b> (49.2%)	0.28	6.43	<u>6.15</u>	55.76	75.72	<u>19.96</u>
	96.78	101.67 <u>4.89</u>						
cfa06	hsa16	<b>31.4</b> (74.2%)	0.17	31.57	<u>31.4</u>			



cfa06	hsa01	<b>43.62</b> (83.7%)	67.53	111.15	<u>43.62</u>			
cfa07	hsa01	<b>48.4</b> (89.1%)	150.83	155.11	<u>4.28</u>	164.01	184.18	<u>20.17</u>
	194.21	200.43 <u>6.22</u>	204.15	212.31 <u>8.16</u>	220.92	224.41	<u>3.49</u>	237.67
	243.75	<u>6.08</u>						
cfa07	hsa18	<b>40.86</b> (88.0%)	0.19	12.97	<u>12.78</u>	18.03	46.04	<u>28.01</u>
	48.05	48.12 <u>0.07</u>						
cfa08	hsa01	<b>0.11</b> (100.0%)	244.43	244.54	<u>0.11</u>			
cfa08	hsa14	<b>86.11</b> (84.0%)	16.63	18.5	<u>11.88</u>	20.83	105.06	<u>84.23</u>
cfa09	hsa17	<b>6.25</b> (-%)	70.71	76.96	<u>6.25</u>			
cfa09	hsa01	<b>0.86</b> (-%)	12.04	12.9	<u>0.86</u>			
cfa09	hsa17	<b>10.06</b> (109.2%)	11.4	13.5	<u>2.1</u>	60.95	68.7	<u>7.75</u>
	45.89	46.1 <u>0.21</u>						
cfa09	hsa11	<b>1.21</b> (-%)	74.07	75.28	<u>1.21</u>			
cfa09	hsa17	<b>28.53</b> (91.8%)	0.5	4.16	<u>3.66</u>	25.77	36.26	<u>10.49</u>
	37	39.4 <u>2.4</u>	48.25	60.23 <u>11.98</u>				
cfa09	hsa09	<b>16.25</b> (79.3%)	119.67	135.92	<u>16.25</u>			
cfa10	hsa12	<b>19.07</b> (83.3%)	54.31	61.82	<u>7.51</u>	62.48	74.04	<u>11.56</u>
cfa10	hsa22	<b>18.16</b> (80.9%)	31.1	49.26	<u>18.16</u>			
cfa10	hsa02	<b>1.4</b> (14.3%)	108.5	109.9	<u>1.4</u>			
cfa10	hsa12	<b>2.36</b> (80.5%)	103.24	105.6	<u>2.36</u>			
cfa10	hsa02	<b>39.24</b> (87.3%)	108.5	96.96	<u>11.54</u>	43.5	71.2	<u>27.7</u>
cfa11	hsa05	<b>31.57</b> (78.6%)	181.67	175.56	<u>6.11</u>	113	138.46	<u>25.46</u>
cfa11	hsa09	<b>56.97</b> (83.1%)	5.88	38.3832.5	<u>95</u>	119.47	<u>24.47</u>	
cfa12	hsa06	<b>87.2</b> (82.6%)	30.02	116.64	<u>86.62</u>	169.87	170.45	<u>0.58</u>
cfa13	hsa08	<b>47.08</b> (80.4%)	98.95	146.03	<u>47.08</u>			
cfa13	hsa15	<b>0.1</b> (100.0%)	76.5	76.6	<u>0.1</u>			
cfa13	hsa04	<b>34.34</b> (70.6%)	41.44	75.78	<u>34.34</u>			
cfa14	hsa01	<b>10.9</b> (5.5%)	214.67	225.57	<u>10.9</u>			
cfa14	hsa07	<b>65.3</b> (88.4%)	133.1	122.8	<u>10.3</u>	85.56	97.09	<u>11.53</u>
	7.06	37.09 <u>30.03</u>	107.77	106.68 <u>1.09</u>	110.32	122.67	<u>12.35</u>	
cfa15	hsa01	<b>5.75</b> (156.7%)	38.84	33.54	<u>5.3</u>	51.62	52.07	<u>0.45</u>

cfa15	hsa16	<b>0.18</b> (100.0%)	46.72	46.54	<u>0.18</u>			
cfa15	hsa01	<b>9.2</b> (90.0%)	43.32	52.52	<u>9.2</u>			
cfa15	hsa14	<b>1.32</b> (103.0%)	18.63	19.95	<u>1.32</u>			
cfa15	hsa12	<b>28.31</b> (82.1%)	74.7	103.01	<u>28.31</u>			
cfa15	hsa04	<b>24.82</b> (85.8%)	145.03	169.85	<u>24.82</u>			
cfa16	hsa07	<b>11.26</b> (96.9%)	43.89	46.67	<u>2.78</u>	134.08	142.56	<u>8.48</u>
cfa16	hsa01	<b>0.02</b> (0.0%)	245.93	245.95	<u>0.02</u>			
cfa16	hsa07	<b>1.2</b> (49.2%)	44.85	43.65	<u>1.2</u>			
cfa16	hsa07	<b>10.71</b> (63.1%)	147.53	158.24	<u>10.71</u>			
cfa16	hsa08	<b>20.7</b> (93.6%)	8.69	9.05	<u>0.36</u>	12.58	19.69	<u>7.11</u>
		29.84	43.07	<u>13.23</u>				
cfa16	hsa04	<b>12.53</b> (90.1%)	177.62	190.15	<u>12.53</u>			
cfa17	hsa02	<b>71.4</b> (70.5%)	0.21	42.77	<u>42.56</u>	71.27	96.64	<u>25.37</u>
		110.44	113.91	<u>3.47</u>				
cfa17	hsa01	<b>16.68</b> (74.6%)	111.28	119.8	<u>8.52</u>	142	150.16	<u>8.16</u>
cfa18	hsa07	<b>21.17</b> (102.3%)	47.67	55.65	<u>7.98</u>	76.43	84.28	<u>7.85</u>
		102	107.34	<u>5.34</u>				
cfa18	hsa11	<b>36.72</b> (81.8%)	0.27	2.98	<u>2.71</u>	30.3	49.17	<u>18.87</u>
		55.09	59.19	<u>4.1</u>	60.15	71.19	<u>11.04</u>	
cfa19	hsa04	<b>7.91</b> (90.6%)	130.24	122.33	<u>7.91</u>			
cfa19	hsa02	<b>30.15</b> (84.7%)	114.76	144.91	<u>30.15</u>			
cfa20	hsa03	<b>47.84</b> (90.6%)	0.42	15.09	<u>14.67</u>	43.8	43.85	<u>0.05</u>
		44.77	74.33	<u>29.56</u>	127.04	130.63	<u>3.56</u>	
cfa20	hsa19	<b>19.44</b> (74.9%)	0.38	19.82	<u>19.44</u>			
cfa21	hsa11	<b>50.24</b> (90.0%)	3.69	28.29	<u>24.6</u>	49.31	50.36	<u>1.05</u>
		59.34	59.99	<u>0.65</u>	71.36	95.3	<u>23.94</u>	
cfa22	hsa13	<b>73.05</b> (83.7%)	39.31	50.43	<u>11.12</u>	51.07	113	<u>61.93</u>
cfa23	hsa20	<b>1.54</b> (98.7%)	23.85	25.39	<u>1.54</u>			

cfa23	hsa03	<b>57.07</b> (87.9%)	15.26	44.36	<u>29.1</u>	131.76	159.73	<u>27.97</u>
cfa24	hsa20	<b>63.4</b> (74.8%)	0.11	63.51	<u>63.4</u>			
cfa25	hsa13	<b>21.31</b> (87.5%)	18.03	39.1	<u>21.07</u>	50.52	50.76	<u>0.24</u>
cfa25	hsa04	<b>6.23</b> (97.0%)	170.04	176.27	<u>6.23</u>			
cfa25	hsa08	<b>10.35</b> (106.1%)	10.32	11.65	<u>1.33</u>	19.82	28.84	<u>9.02</u>
cfa25	hsa02	<b>17.27</b> (77.8%)	225.62	242.89	<u>17.27</u>			
cfa26	hsa12	<b>24.87</b> (75.0%)	107.1	131.97	<u>24.87</u>			
cfa26	hsa22	<b>13.36</b> (83.7%)	17.29	30.65	<u>13.36</u>			
cfa26	hsa10	<b>7.86</b> (82.3%)	51.3	57.46	<u>6.16</u>	88.93	90.63	<u>1.7</u>
cfa27	hsa12	<b>53.74</b> (83.5%)	0.26	54	<u>53.74</u>			
cfa28	hsa10	<b>43.15</b> (89.9%)	49.28	50.92	<u>1.64</u>	90.85	132.36	<u>41.51</u>
cfa29	hsa08	<b>49.5</b> (83.8%)	48.74	98.24	<u>49.5</u>			
cfa30	hsa15	<b>44.98</b> (88.6%)	30.64	75.62	<u>44.98</u>			
cfa31	hsa03	<b>9.51</b> (88.7%)	78.6	88.11	<u>9.51</u>			
cfa31	hsa21	<b>30.76</b> (87.0%)	14.47	45.23	<u>30.76</u>			
cfa32	hsa04	<b>42.75</b> (89.3%)	76.86	119.61	<u>42.75</u>			
cfa33	hsa03	<b>40.79</b> (74.6%)	89.31	126.56	<u>37.25</u>	195.39	198.93	<u>3.54</u>
cfa34	hsa05	<b>14.26</b> (82.0%)	0.48	14.74	<u>14.26</u>			
cfa34	hsa03	<b>33.62</b> (83.5%)	160.9	194.52	<u>33.62</u>			
cfa35	hsa06	<b>30.12</b> (85.9%)	0.12	30.24	<u>30.12</u>			
cfa36	hsa02	<b>34.8</b> (85.4%)	155.31	190.11	<u>34.8</u>			
cfa37	hsa02	<b>34.4</b> (85.5%)	190.64	225.04	<u>34.4</u>			

cfa38	hsa01	<b>25.52</b> (91.5%)	155.47	163.73	<u>8.26</u>	187.35	193.93	<u>6.58</u>
		200.56	203.84	<u>3.28</u>	212.83	220.23	<u>7.4</u>	
cfaX	hsaX	<b>149.76</b> (83.4%)	3.16	152.92	<u>149.76</u>			

Legend :

(1) Canine chromosome

(2) Human conserved segment (CS) counterpart

(3) Size in Mbp of the Human CS

(4-12) CS are composed of inverted or interrupted sub-segments, sub-segments of each CS are detailed as : start (4)(7)(10), end (5)(8)(11) and sub-total (underlined) (6)(9)(12)

## Supplementary Information : S8

*The Canine Genome: Survey Sequencing and a Dense Gene Map for Genome Navigation  
(Hitte et al. 2005)*

### Supplementary information for :

#### Optimization and Application of the Survey-Sequence/RH Map Approach

The theoretical coverage of a genome is 39%, 63% and 78% after sequencing to 0.5x, 1.0x and 1.5x, respectively (Lander and Waterman, 1988). For an average sequence read of 800 bases, the probability of including a specific 100 base segment of the genome within a sequence read is 0.36, 0.59 and 0.74, after sequencing to 0.5x, 1.0x and 1.5x, respectively. We assume that identification of a gene fragment requires alignment of a read to at least 100 bases of at least one exon per gene of the reference genome. For the collection of 23,269 human RefSeqs, 23,233 contain at least one exon of 100 bases or longer (mean, 7.4; median 6; <http://genome.ucsc.edu/cgi-bin/hgTables>). The mean probability of sequencing at least 100 bases from at least one exon for each of 23,269 homologous genes is 0.84, 0.94 and 0.97 after 0.5x, 1.0x and 1.5x coverage, respectively. However, it is acknowledged that approximately 25% of reference human genes will lack 1:1 orthology with genes in the surveyed mammalian genome (and will therefore fail to provide mutual best blastn matches). Consequently, our estimate for the number of orthologues that could be detected after 0.5x, 1.0x, and 1.5x coverage is 14,700 (i.e.  $23,269 \times 0.75 \times 0.84$ ), 16,400 and 16,900, respectively. These values do not consider the homology between intronic regions of orthologous genes, which can often be used to further increase the number of identifiable gene fragments after survey-sequencing (Kirkness et al., 2003).

The 1.5x survey-sequence described more than 89,000 SNPs (and di-, tri-, and

tetranucleotide polymorphisms) mapped near or within the coding sequences of 14,679 distinct human genes. Nine percent (1,299) of the gene-based marker sequences contained single tandem repeat sequence (STR). Of those, 25% demonstrate size polymorphisms when the 7.5x boxer and 1.5x poodle sequences are compared, making them an optimal resource for genetic linkage studies, and further demonstrating the utility of the survey sequence/dense RH map approach for providing genomic resources in species of interest.

#### References:

Lander ES, Waterman MS. Genomic mapping by fingerprinting random clones : a mathematical analysis. *Genomics*. 1988 Apr, 2(3) :231-9.