Supplemental data:

Supplemental Table 1. Genome-wide recombination rates of multicellular animals that are based on the overall genetic length and the genome size in Mb.

Taxon	**Physical genome size (Mb) (Estimation method)**	**Recomb. genome size (cM) (Estimation method)**	**Recomb. rate (cM/Mb) (Estimation method unless simple ratio)**	**Haploid Chromo-some # (incl. sex chr.)**	**Comments**
<u>Nematoda</u>					
Caenorhabditis elegans	100 (*1*) Physical map based on integration from fingerprint bands, contigs and YAC bridges	298 (*1*) Marey map construction based on ACEDB database (multiple mapping experiments)	2.94 (*1*)	6	Range: 0.5 – 10.0 cM/Mb; Marey maps available, based on females, male recombination reduced (*1*)
Heterodera glycines	92.5 (*2*) Flow cytometry	630-743 (*3*) ML-estimation based on AFLP linkage map (Kosambi)	6.67 – 8.33 (*3*)	9	Recomb. genome size estimated from partial map, sex average
<u>Arthropoda</u>					
Ixodes scapularis (deer tick, Acari)	2100 (*4*) Re-association kinetics	616 (*5*) RAPD, SNP, microsatellite linkage map (Kosambi)	0.29	14	Linkage map preliminary, sex average
Acyrthosiphon pisum (pea aphid, Hemiptera)	303 (*6*) Micro-densitometric analysis of Feulgen-staining	360 (*7*) Integrated AFLP linkage map	1.19	4	
Rhyzopertha dominica (lesser grain borer, Coleoptera)	476 (*8*) Flow cytometry	390.1 (*8*) RAF linkage map (Morgan)	0.82 (*8*)	9	Sex average
Leptinotarsa	450 (*9*)	1032 (*10*)	2.29	18	Female

decemlineata (Potato beetle, Coleoptera)	Micro-densitometric analysis of Feulgen-stained sperm	AFLP linkage map (Kosambi)			recombination
Tribolium castaneum (red flour beetle, Coleoptera)	200 (*11*) Micro-densitometric analysis of Feulgen-stained sperm	573 (*12*) AFLP linkage map (Kosambi)	2.87	10	Sex average
Tribolium confusum (confused flour beetle, Coleoptera)	250 (*11*) Micro-densitometric analysis of Feulgen-stained sperm	968.5 (*13*) RAPD linkage map (Morgan)	3.87	9	Sex average
Anopheles gambiae (malaria mosquito, Diptera)	257 (*14*) Whole genome assembly	215 (*15*) Microsatellite linkage map (Kosambi)	0.84	3	Sex average, recombination frequencies between sexes comparable
Aedes aegypti (yellow fever mosquito, Diptera)	780 (*16*) Combined data from flow cytometry	168 (*17*) RAPD-SSCP linkage map (Kosambi)	0.48 (*16*) Cosmid and cDNA FISH mapping	3	Sex average
Drosophila melanogaster (vinegar fly, Diptera)	180 (*18*) Whole genome assembly	284.2 (*19*) Genetic map based on classic mutations and chromosome banding	1.59 (*20*)	4	See (*20*) for more data on recombination rates in protests, fungi and plants
Apis mellifera (honey bee, Hymenoptera)	238 (*this study*)	4553 (*this study*)	19 (*this study*)	16	Female recombination
Bombus terrestris (bumble bee, Hymenoptera)	274 (*21*) Flow cytometry	1073 (*21*) Extrapolation from RAPD, microsatellite linkage map	3.92	18	Female recombination
Pogonomyrmex rugosus (harvester ant, Hymenoptera)	255 (*22*) Flow cytometry	3558 (*22*) AFLP linkage map (Kosambi)	14.0 (*22*)	16	Female recombination
Acromyrmex echinatior (leaf-cutting ant,	335 (*22*) Flow cytometry	2076 (*22*) AFLP linkage map (Kosambi)	6. 2 (*22*)	18	Female recombination

Hymenoptera)					
Nasonia vitripennis (parasitoid jewel wasp, Hymenoptera)	312 (*23*) Micro-densitometric analysis of Feulgen-stained hemocytes	764.5 (*24*) RAPD linkage map (Kosambi)	2.45	5	Genetic map constructed from hybrid (*N. vitripennis* and *N. giraulti*) female recombination
Trichogramma brassicae (parasitic wasp, Hymenoptera)	246 (*25*) Flow cytometry	1330 (*26*) Composite RAPD linkage map (Haldane)	5.41	5	Female recombination
Bracon hebetor (parasitic wasp, Hymenoptera)	156 (*23*) Micro-densitometric analysis of Feulgen-stained hemocytes	1156 (*17*) RAPD-SSCP linkage map (Kosambi)	7.41	10	Female recombination
Bombyx mori (silkworm, Lepidoptera)	429 (*27*) Whole genome draft sequence	2000 (*28*) RAPD linkage map	4.66	28	Male only (female Lepidoptera have no intra-chromosomal recombination [28])
Heliconius melpomene (Postman butterfly, Lepidoptera)	292 (*29*) Flow cytometry	1616 (*29*) AFLP, SNP, microsatellite linkage map	5.56 (*29*)	21	Male only
Heliconius eratio (erato heliconian, Lepidoptera)	396 (*30*) Flow cytometry	2400 (*30*) AFLP, SNP, microsatellite inter-specific linkage map (Haldane)	6.06 (*30*)	21	Male only
Vertebrata					
Takifugu rubripes (fugu, pufferfish)	365 (*31*) Whole genome shotgun assembly	1214 ♀ / 697 ♂ (*32*) Microsatellite linkage maps	3.00 (*33*)	22	Genetic maps lack parts of the telomeric regions(*33*), sex average
Danio rerio (zebrafish)	1700 (*34*)	2445 (*34*) Microsatellite linkage map	1.35 (*34*)	25	Over 2-fold reduction of recombination in males(*35*) sex average

Oncorhynchus mykiss (rainbow trout)	2680 (*36*) Average of multiple estimates, including flow cytometry	4590 ♂ (*37*) Integrated map with multiple markers (Morgan)	1.71	30	Male-specific recombination rate, females 7x lower (*37*)
Salmo salar, (atlantic salmon)	3050 (*36*) Average of multiple estimates, including flow cytometry	901 ♀ / 103 ♂ (*38*) Microsatellite, AFLP linkage map (Kosambi)	0.16	30	Unsaturated genetic maps ➔ min. estimate of cM/Mb, sex average
Gallus gallus (chicken)	1200 (*39*) Whole genome shotgun assembly	3800 (*40*) Integrated estimate from multiple maps	3.17	39	Range: 2.5 – 21.0 cM/Mb(*39*), sex average, male/female difference only 1.15%
Mus musculus (house mouse)	2500 (*41*) Euchromatic genome sequence based on contigs	1600 (*42*) Integrated estimate from multiple maps (inter-specific maps smaller)	0.56 (*43*) Correction for chromosome ends	20	Sex average, female recombination ususally 40% higher than in males
Rattus norvegicus (laboratory rat)	2750 (*44*) Whole genome assembly	1503 (*45*) Microsatellite linkage map (Kosambi)	0.60 (*43*) Correction for chromosome ends	21	Sex average
Porcine (pigs x boars)	2800 (*46*) Flow cytometry	1873 (*47*) Extrapolation from recombination rate in selected parts of genome	0.67 (*47*) Comparison of genetic distance and FISH physical estimates	19	Extrapolation of genetic map size, sex average
Papio hamadryas (Baboon)	3450 (*48*) Micro-densitometric analysis of Feulgen-stained lymphocytes	2375 (*49*) Microsatellite linkage map	0.69	20	Sex average
Homo sapiens (human)	2910 (*50*) Whole genome shotgun	3449, calculated from (*50*)	1.22 (*50*) Genethon microsatellite linkage map	23	Range: 0 – 8.8 cM/Mb (*51*), sex average, females 76%

	assembly		comparison to physical distance in 3Mb-windows.		more recombination than males, though not uniform map expansion

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The following oligonucleotides were designed for this study:

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RR07-rev1:CTGTGTCTAAGCTGTACTCTCTG

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RR08-rev1:AACGATTTACCATGCTTTCCACGG

RR09-fwd1:TACACGACGCTACGAGAGACGTTA

RR09-rev1:TTTTCAATTTATCCATTCGTCTTCTCAAAC

RR11-fwd1:CAAGATCGAAATGATGATGCCCC

RR11-rev1:AAAGATTATTTATTCGCGAAACGATTC

RR14-fwd1:GCAGTATCTGAACACACCGTTGA

RR14-rev1:CGTTCGACGTGAAAGAATATAGCTAAT

RR17-fwd1:ATTTTATGTGCATTATCAACAAGAAGCTG

RR17-rev1:CGTTCTACACCTATCTCAAGCTGTT

RR19-fwd1:TATGTTTTCATTTTCTGCCTATGGATAG

RR19-rev1:GGAACAACGGATTTTCTTGTGTGAA

RR21-fwd1:CTGGACCCTCAGCTTGTATTACTA

RR21-rev1:ATGAACATTTTGATTGCGCTTTGCG

RR22-fwd1:ATGTCAAAACAGCCAACCAGAATGAA

RR22-rev1:TCGTTGATAAAGCAATATTTAGTAACAAGA

RR23-fwd1:ATTATTTGCATACGACTGCCCCGAT

RR23-rev1:ATCGTTACTGTTACACTTCCGCTAAA

RR25-fwd1:CATAGGTTGGCCACGAATAACAATA

RR25-rev1:ATGAAACCGAGAAACGGAGTAGTAAAA

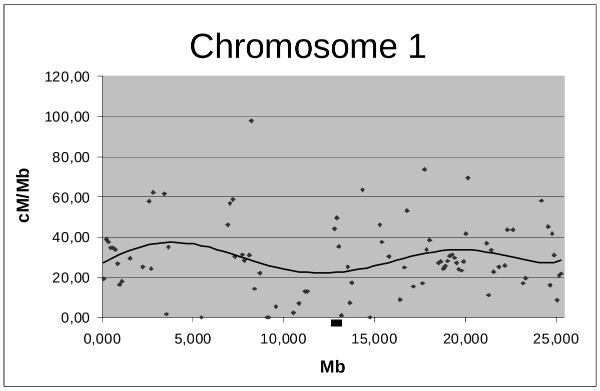
RR28-fwd1:CGGGATAAAAACTTGACTAGAAATCTAT

RR28-rev1:TTGACTAAAGTATCATCACGACACTG

RR29 fw1: TACGATTGGCAGACACGAAGG

RR29 rev1: CTGTGCAAGCAACACAAGTCC

Supplemental Figure 1: Scatter plots of local recombination rate (cM/Mb of 125 kb windows) versus position on the chromosome (Mb) for all the bee chromosomes. The orientation of the chromosomes (bars indicate the centromere) was previously determined using half-tetrad analysis, made possible by the central fusion during meiosis of thelytokous workers of *A. mellifera capensis* bees (Baudry et al. 2004). Fith to six term polynomial regressions show the overall trend of recombination activity across the chromosome.



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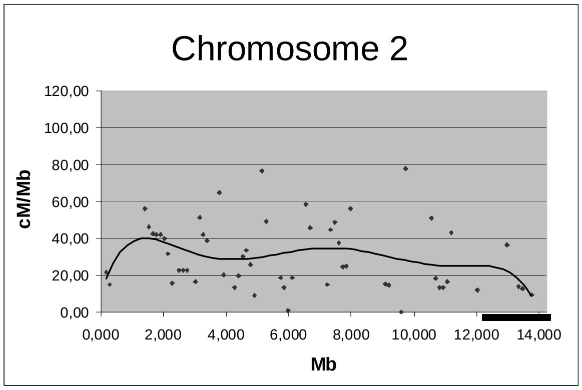

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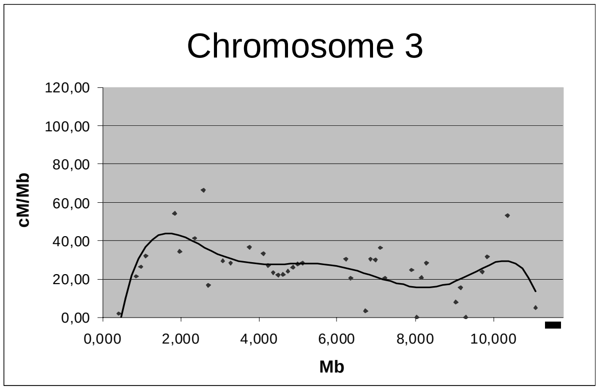

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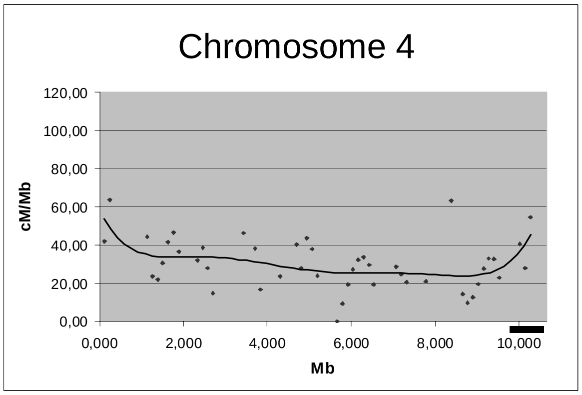

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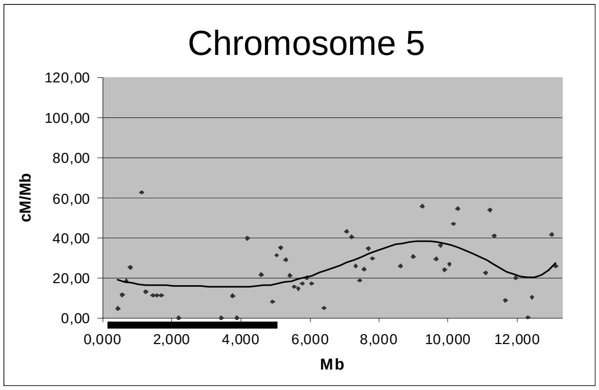

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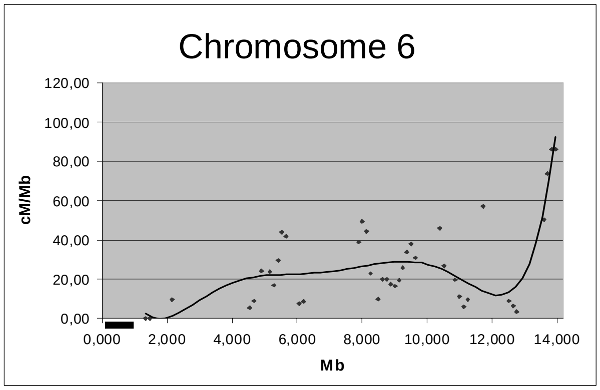

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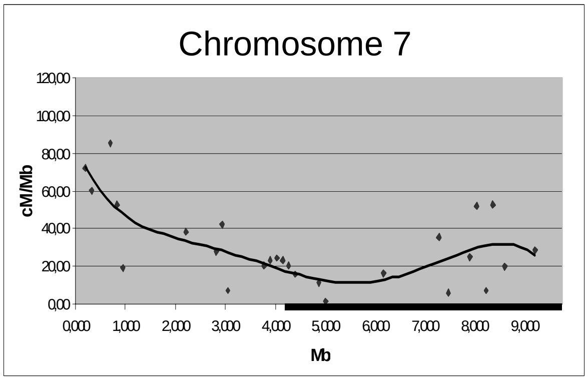

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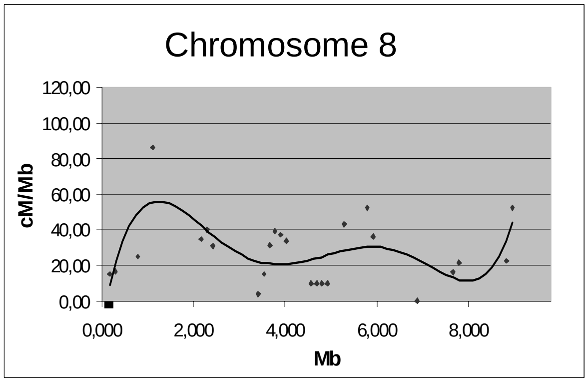

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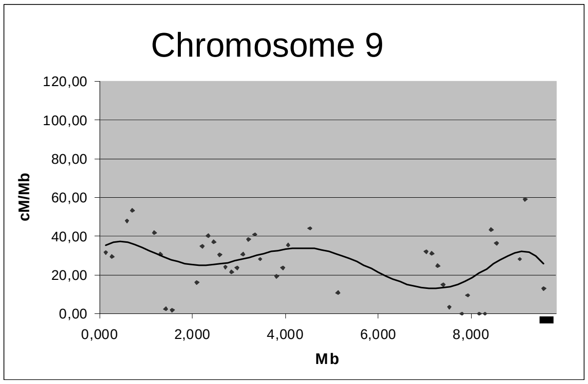

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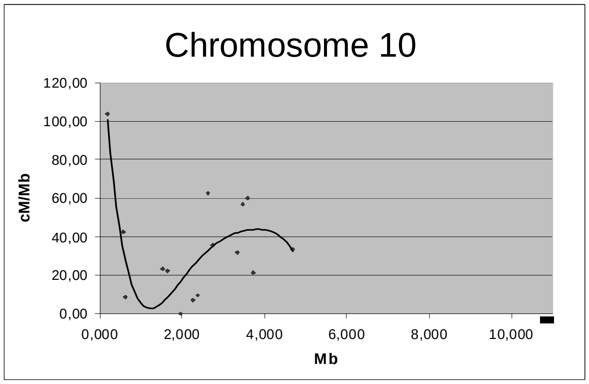

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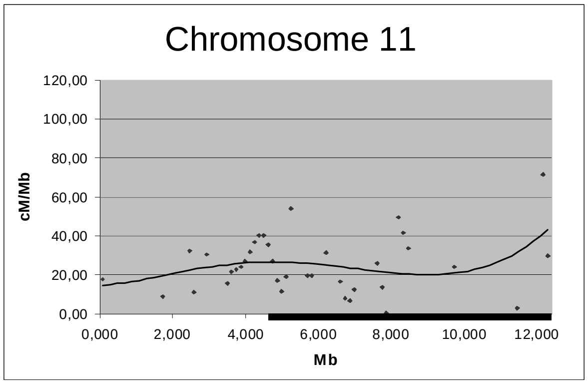

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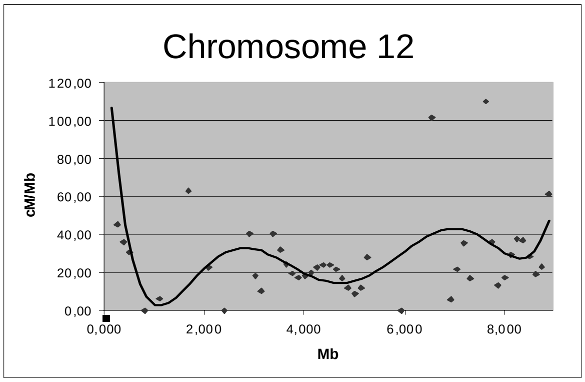

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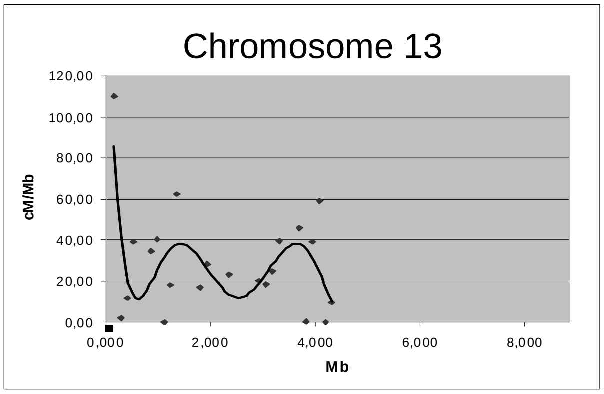

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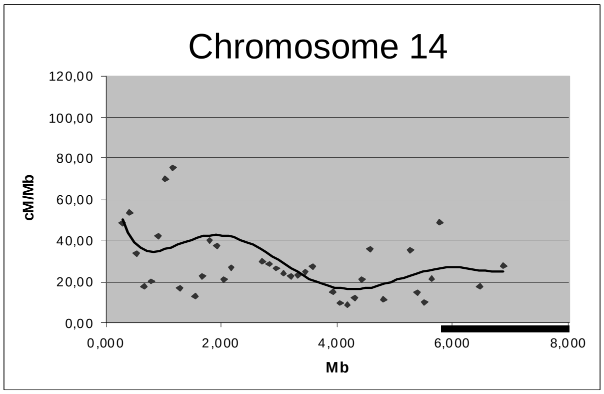

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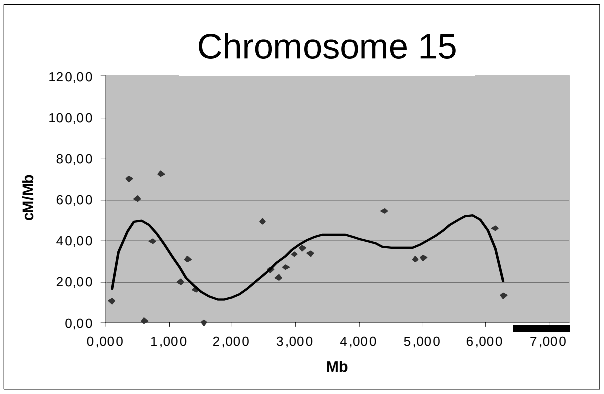

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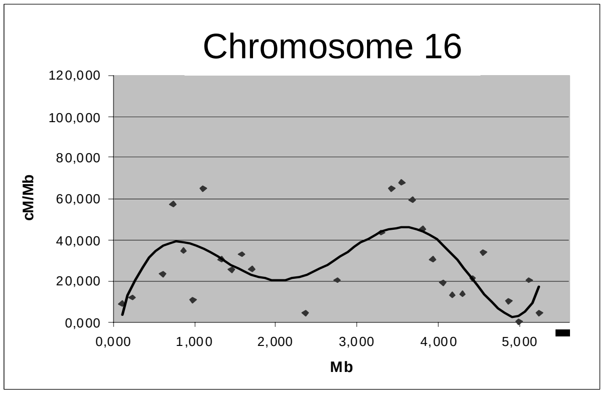

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