

Appendix 1 to:

Meta-analysis of chromosome-scale crossover rate variation in eukaryotes and its significance to evolutionary genomics

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Table S1.

References used to obtain information on centromere position in the organisms indicated in Table 1 in the main paper. The references are sorted alphabetically by species name.

Aedes aegypti

Sharakhova, M. V. et al. (2011) Imaginal discs - A new source of chromosomes for genome mapping of the yellow fever mosquito *Aedes aegypti*. PLoS Negl. Trop. Dis. 5, 1–9.

Beta vulgaris

Paesold, S., Borchardt, D., Schmidt, T. & Dechyeva, D. (2012) A sugar beet (*Beta vulgaris* L.) reference FISH karyotype for chromosome and chromosome-arm identification, integration of genetic linkage groups and analysis of major repeat family distribution. Plant J. 72, 600–611.

Bos taurus

Di Berardino, D., Di Meo, G. P., Gallagher, D. S., Hayes, H. & Iannuzzi, L. (co-ordinator) (2001). ISCNDB 2000 International System for Chromosome Nomenclature of Domestic Bovids. Cytogenet. Cell Genet. 299, 283–299.

Caenorhabditis briggsae*, *C. elegans

Hillier, L. D. W. et al. (2007) Comparison of *C. elegans* and *C. briggsae* genome sequences reveals extensive conservation of chromosome organization and synteny. PLoS Biol. 5, 1603–1616.

Canis lupus familiaris

Yang, F. et al. (2000) Chromosome identification and assignment of DNA clones in the dog using a red fox and dog comparative map. Chromosom. Res. 8, 93–100.

Cervus elaphus

Johnston, S. E., Huisman, J., Ellis, P. A. & Pemberton, J. M. (2017) A high-density linkage map reveals sexually-dimorphic recombination landscapes in red deer (*Cervus elaphus*). *G3: Genes|Genomes|Genetics* 7, 2859–2870.

Felis catus

Yang, F. et al. (2000) Reciprocal chromosome painting illuminates the history of genome evolution of the domestic cat, dog and human. Chromosom. Res. 8, 393–404.

Gasterosteus aculeatus

Urton JR, McCann SM, Peichel CL (2011) Karyotype differentiation between two stickleback species (Gasterosteidae). Cytogenet. Genome Res. 135, 150-159.

Heliconius melpomene

Ahola, V. et al. (2014) The Glanville fritillary genome retains an ancient karyotype and reveals selective chromosomal fusions in Lepidoptera. Nat. Commun. 5, 4737.

Homo sapiens

http://www.ensembl.org/Homo_sapiens/Location/Genome

Mus musculus

http://www.ensembl.org/Mus_musculus/Location/Genome

Nasonia vitripennis

Rutten, K. B. et al. (2004) Chromosomal anchoring of linkage groups and identification of wing size QTL using markers and FISH probes derived from microdissected chromosomes in *Nasonia* (Pteromalidae: Hymenoptera). *Cytogenet. Genome Res.* 105, 126–133.

Ovis aries

Di Berardino, D., Di Meo, G. P., Gallagher, D. S., Hayes, H. & Iannuzzi, L. (co-ordinator) (2001). ISCNDB 2000 International System for Chromosome Nomenclature of Domestic Bovids. *Cytogenet. Cell Genet.* 299, 283–299.

Goldammer, T. et al. (2009) Molecular cytogenetics and gene mapping in sheep (*Ovis aries*, 2n = 54). *Cytogenet. Genome Res.* 126, 63–76.

Pan troglodytes verus

Lin, C. C., Chiarelli, B., Cohen, M. & Boer, L. E. M. de. (1973) A comparison of the fluorescent karyotypes of the chimpanzee (*Pan troglodytes*) and man. *J. Hum. Evol.* 2, 311–321.

Phaseolus vulgaris

Fonsêca, A. et al. (2010) Cytogenetic map of common bean (*Phaseolus vulgaris* L.). *Chromosom. Res.* 18, 487–502.

Rattus norvegicus

Hamta, A. et al. (2006) Chromosome ideograms of the laboratory rat (*Rattus norvegicus*) based on high-resolution banding, and anchoring of the cytogenetic map to the DNA sequence by FISH in sample chromosomes. *Cytogenet. Genome Res.* 115, 158–168.

Figure S1

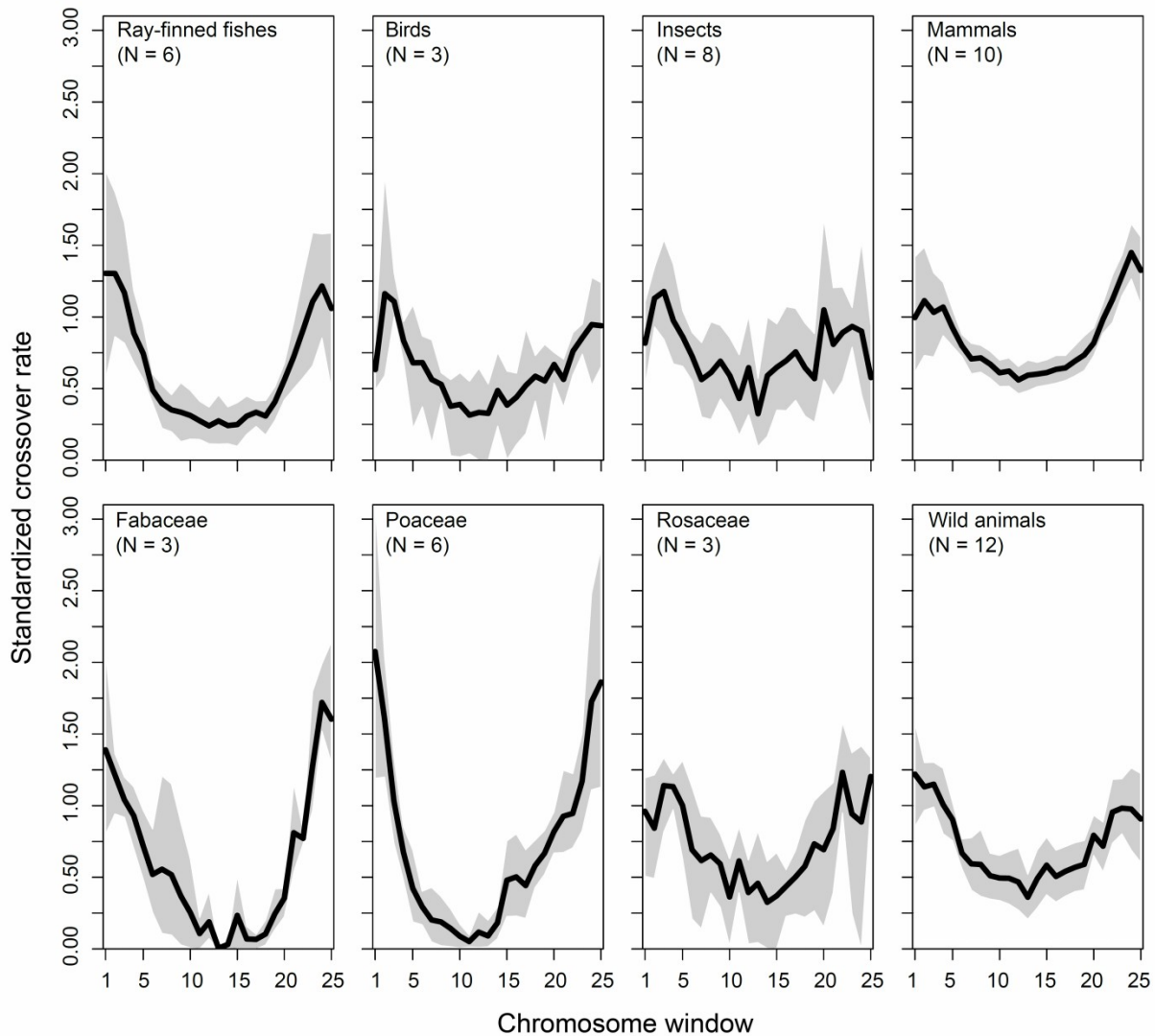


Fig. S1. A reduced crossover (CO) rate around chromosome centers is well supported across taxonomic groups within our focal eukaryote kingdoms, as shown by average CO rate profiles generated separately for selected animal classes (top row) and plant families (bottom row, first three panels from the left). A similar CO distribution also emerges when restricting the analysis to wild species only (i.e., domesticated species excluded), shown in the bottom right panel (for animals only; wild plant species were too few in our data base). Sample sizes (i.e., number of species) are given in parentheses. All plotting conventions follow Figure 1 in the main paper.

Figure S2

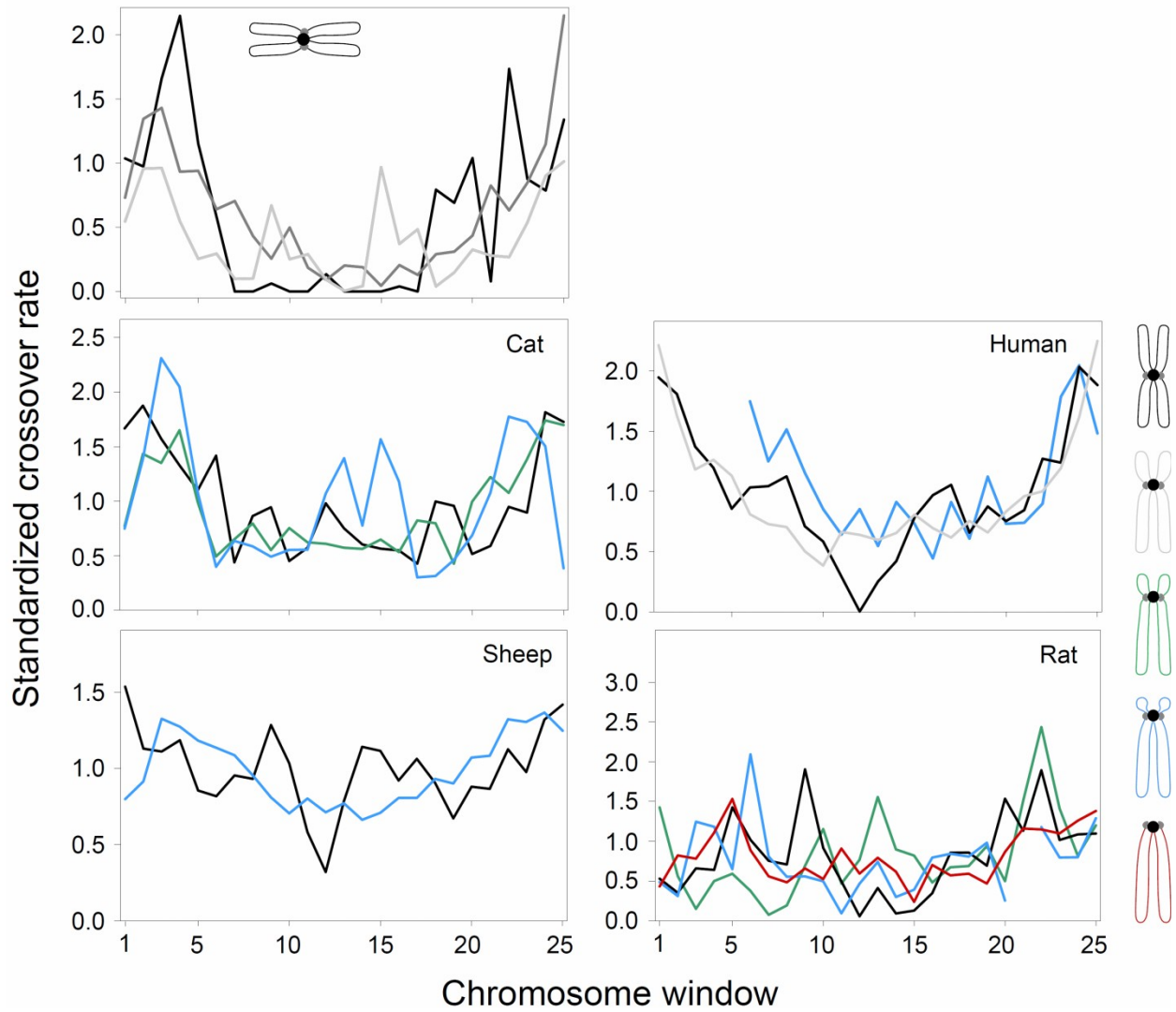


Fig. S2. The top left panel shows the distribution of CO rate in three species with metacentric chromosomes (*Nasonia* wasp, Sugar beet, and Yellow fever mosquito in light gray, dark gray and black), the other panels show CO rate profiles separately for different chromosome morphologies within four species. Color coding and plotting conventions follow Figure 2 in the main paper.

Figure S3

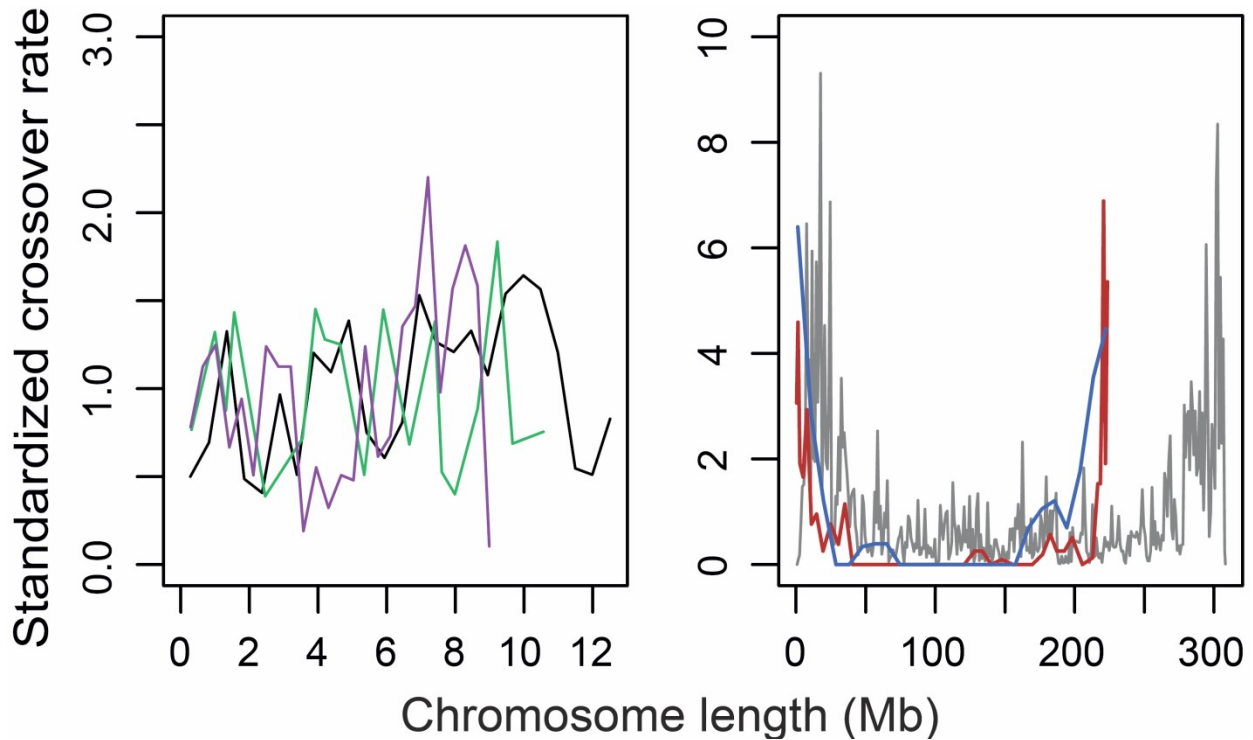


Fig. S3. Short chromosomes generally display a relatively uniform CO distribution, as illustrated by a single representative chromosome from three species with short chromosomes (left panel; black profile: Honeybee, chromosome 5; green: Monkey flower, chromosome 11; purple: Postman butterfly, chromosome 3). By contrast, long chromosomes typically cross over primarily toward their tips and thus exhibit a vast region of very low CO around their center, exemplified in three species with long chromosomes (right panel; gray: Pig, chromosome 1; red: Pepper, chromosome 5; blue: Maize, chromosome 5). The profiles show mean-standardized CO rates for marker intervals along the chromosome at the original physical scale. Note that the scale of the X-axis is more than 25 times larger in the right than the left panel! The references to the specific studies are provided in Table 1.