Supplementary Figures S1 - S15

Substantial heritable variation in recombination rate on multiple scales in honeybees and bumblebees

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Chrom	Pos	D1	D2	D3	D4	D5	D6	D7	D8	D9	D10	Q_hap1	Q_hap2
Group1	823099	C	T	C	C	T	C	T	T	T	T	C	T
Group1	823129	C	T	C	C	T	C	T	T	T	T	C	T
Group1	823137	C	T	C	C	T	C	T	T	T	T	C	T
Group1	823145	T	A	T	T	A	T	A	A	A	A	T	A
Group1	823866	T	C	T	T	C	T	C	C	C	C	T	C
Group1	824431	G	A	G	G	A	G	A	A	A	A	G	A
Group1	824748	C	T	C	C	T	C	T	T	T	T	C	T
Group1	825395	C	T	C	C	T	C	T	T	T	T	C	T
Group1	829758	A	G	A	A	G	A	G	G	G	G	A	G
Group1	830251	C	C	C	C	G	C	G	G	G	G	C	G
Group1	830263	A	A	A	A	G	A	G	G	G	G	A	G
Group1	830274	G	G	G	G	A	G	A	A	A	A	G	A
Group1	830291	T	T	T	T	C	T	C	C	C	C	T	C
Group1	830592	T	T	T	T	A	T	A	A	A	A	T	A
Group1	830614	T	T	T	T	C	T	C	C	C	C	T	C
Group1	830624	C	C	C	C	T	C	T	T	T	T	C	T
Group1	830645	A	A	A	A	G	A	G	G	G	G	A	G
Group1	830652	T	T	T	T	C	T	C	C	C	C	T	C
Group1	831015	T	T	T	T	C	T	C	C	C	C	T	C
Group1	831016	A	A	A	A	G	A	G	G	G	G	A	G

Figure S1 An example case of crossover event between the position 829758 and 830251 on chromosome 1 (Group1) identified in drone 2 (D2). A total of ten drones (D1-D10) were sequenced in this colony (FB_B12). Linkage between adjacent markers allows reconstruction of the queen haplotypes (Q_hap1 and Q_hap2).
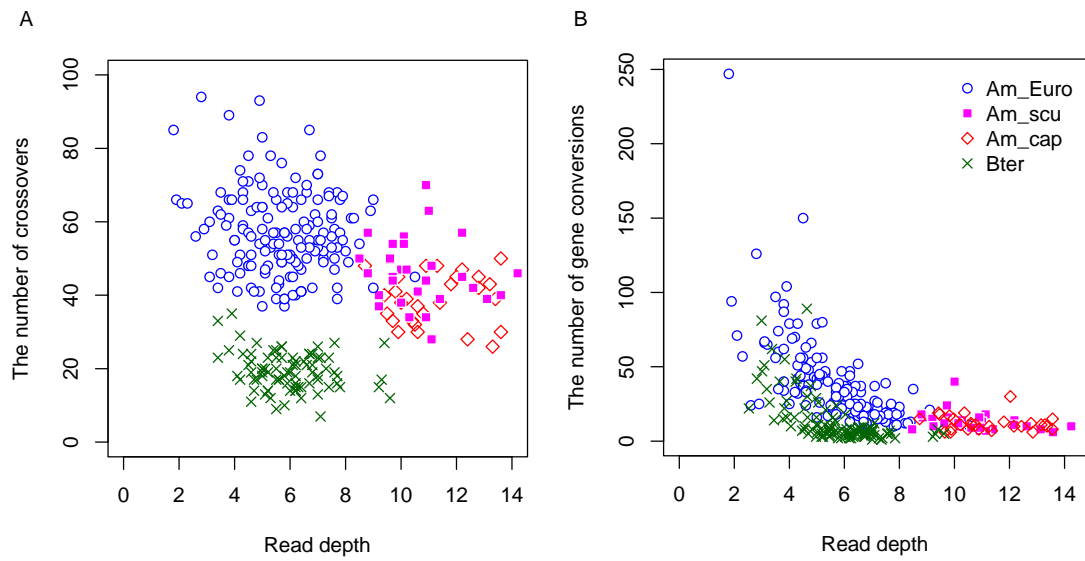
Figure S2 Relationship between the number of putative gene conversions and genome-wide sequence read depth per drone. European *A. mellifera* (blue circle), African *A. m. scutellata* (magenta square), African *A. m. capensis* (red diamond), and *B. terrestris* (green cross).
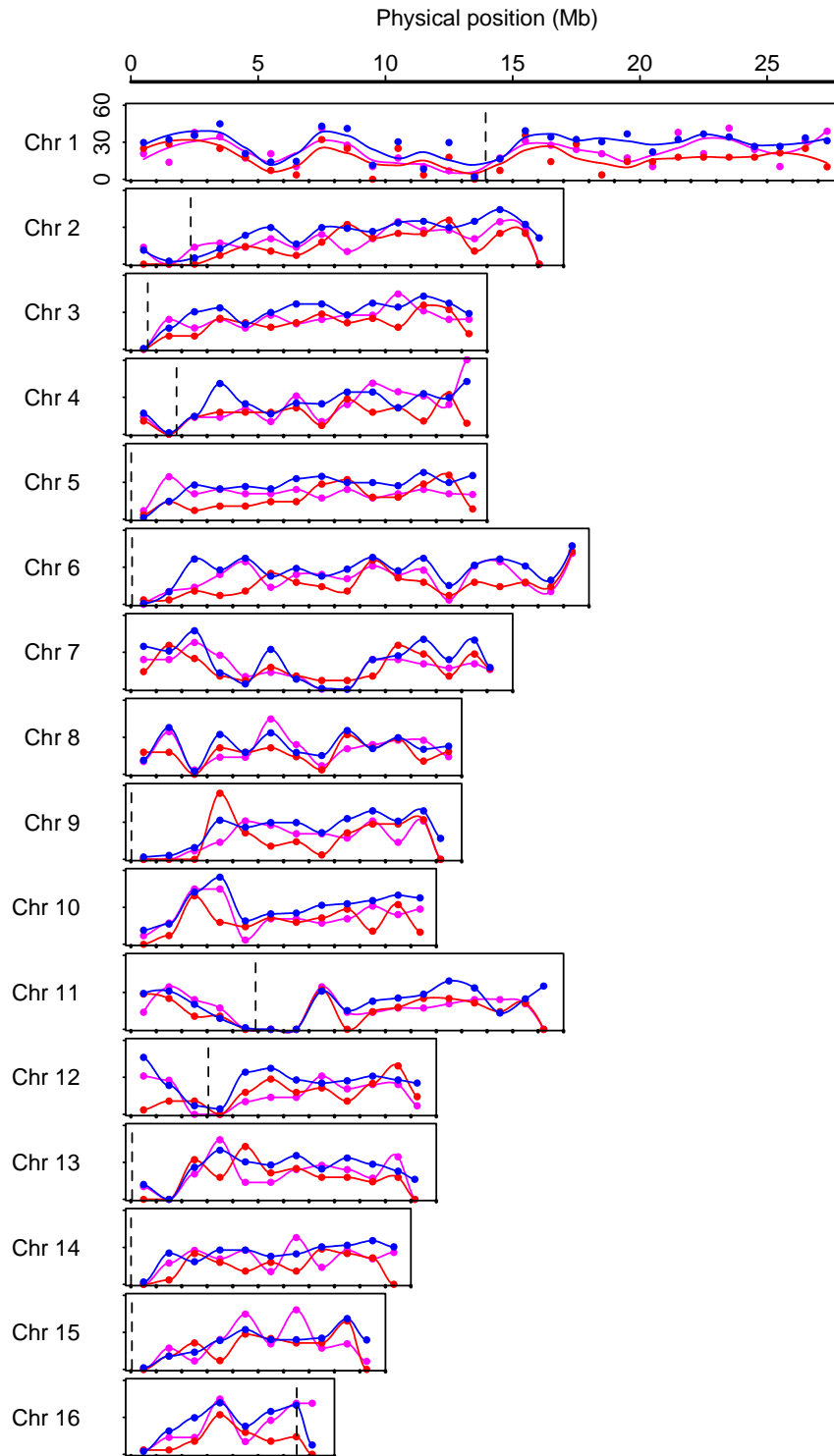
Figure S3 Mean CO density (/100 Mb) in 1-Mb windows along a chromosome in three populations of *A. mellifera*: European *A. mellifera* (blue) African *A. m. scutellata* (magenta), and African *A. m. capensis* (red). Vertical dotted lines indicate predicted centromere locations. Centromere locations are not predicted on chromosome 7, 8, and 10 due to the lack of Ava I cluster. CO density / 100 Mb is the average density of crossovers in the genome inferred across drones and is directly comparable to cM/Mb.

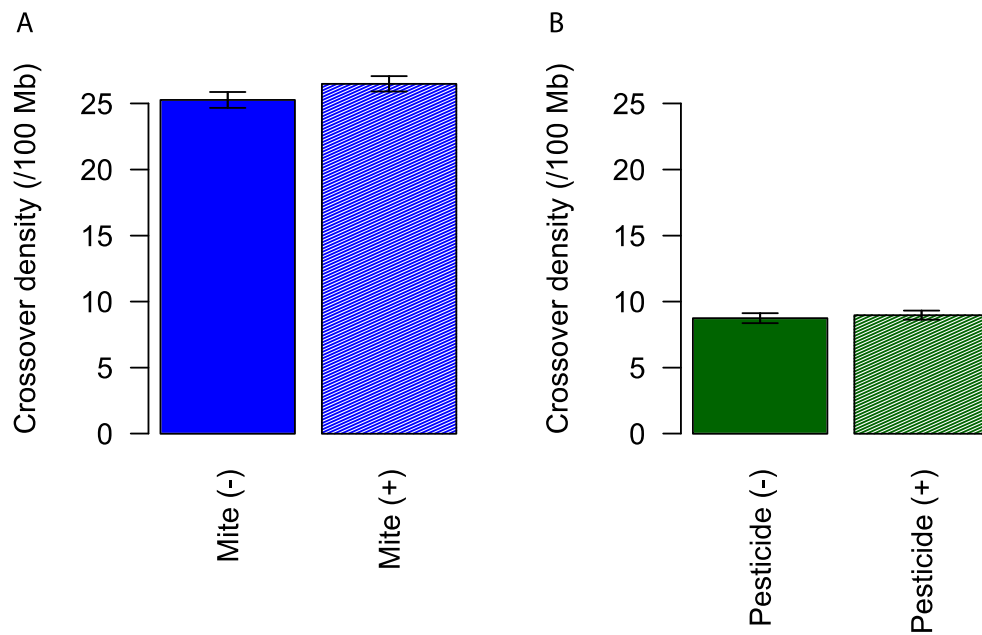**Figure S4** (A) CO density in three populations of *A. mellifera* (European *A. mellifera* [Am_Euro, blue], African *A. m. scutellata* [Am_scu, magenta], and African *A. m. capensis* [Am_cap, red]) and one population of *B. terrestris* [Bter, green]. (B) Density of NCO-associated gene conversions. (C) CO density per colony of honeybees and bumblebees. Data are represented as boxplots. CO density / 100 Mb is the average density of crossovers in the genome inferred across drones and is directly comparable to cM/Mb.

Figure S5 Effect of environmental factors on CO rate. A) Mean CO density of European *A. mellifera* colonies exposed or not exposed to parasitic mite *Varroa destructor* [Mite (+) and Mite (-), respectively]. B) Mean CO density of *B. terrestris* colonies exposed or not exposed to Neonicotinoid pesticide [Pesticide (+) and Pesticide (-), respectively]. Error bars represent standard errors of the mean.
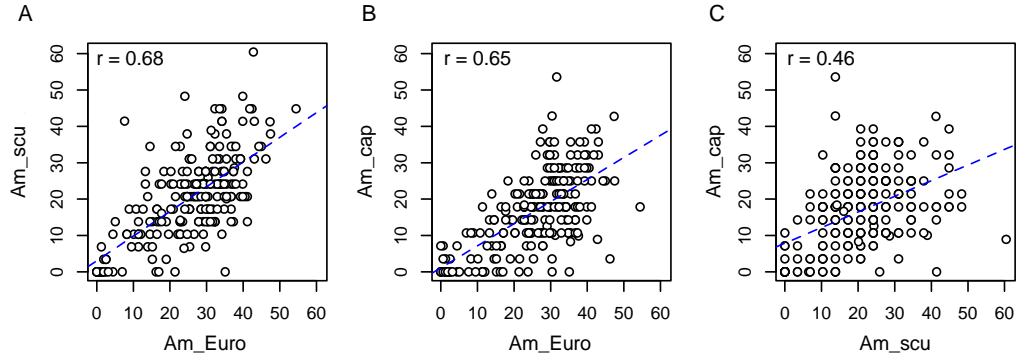
Figure S6 Correlation of CO density (/100 Mb) in 1-Mb windows between European *A. mellifera* (Am_Euro) and African *A. m. scutellata* (Am_scu) (A), between European *A. mellifera* and African *A. m. capensis* (Am_cap) (B), and between *African A. m. scutellata* and *African A. m. capensis* (C). Pearson's correlation coefficient r is indicated.
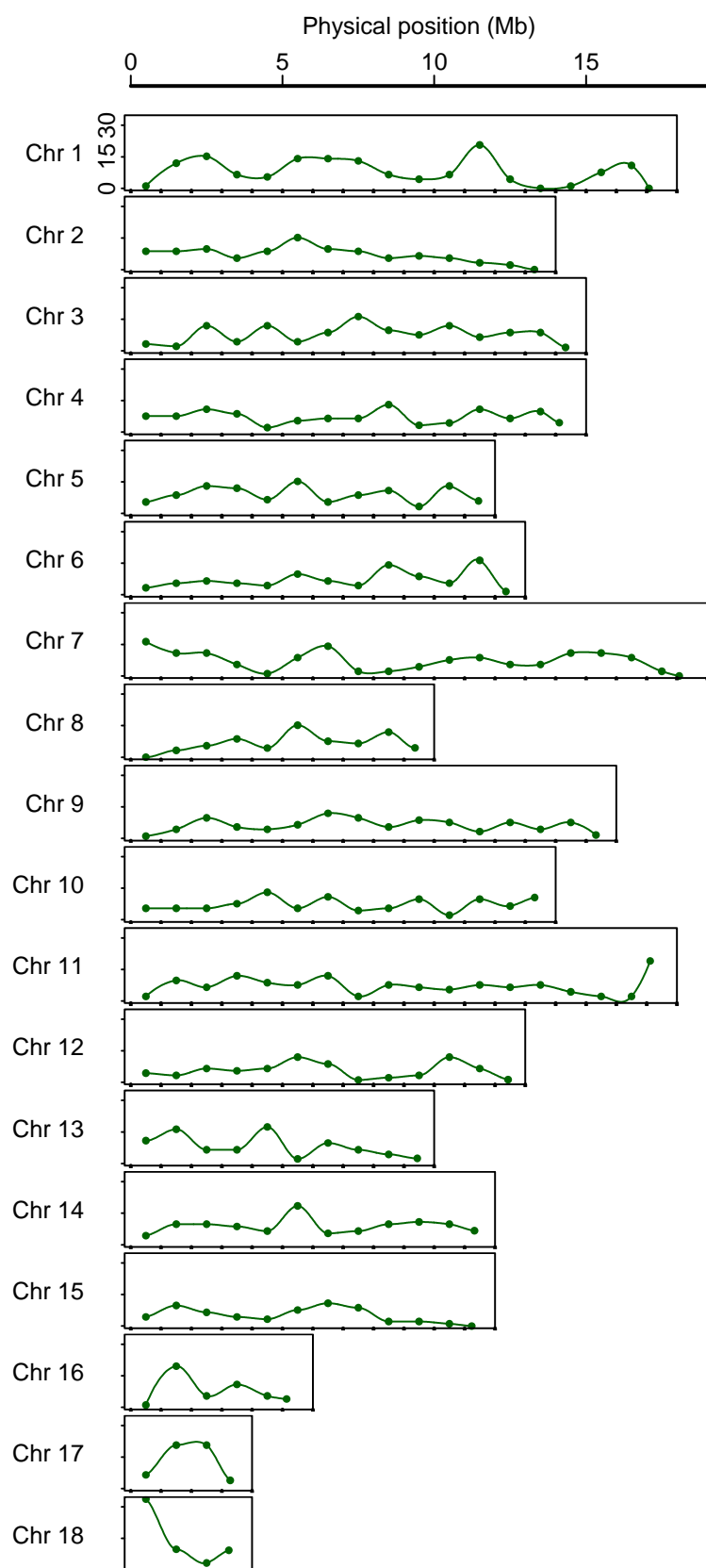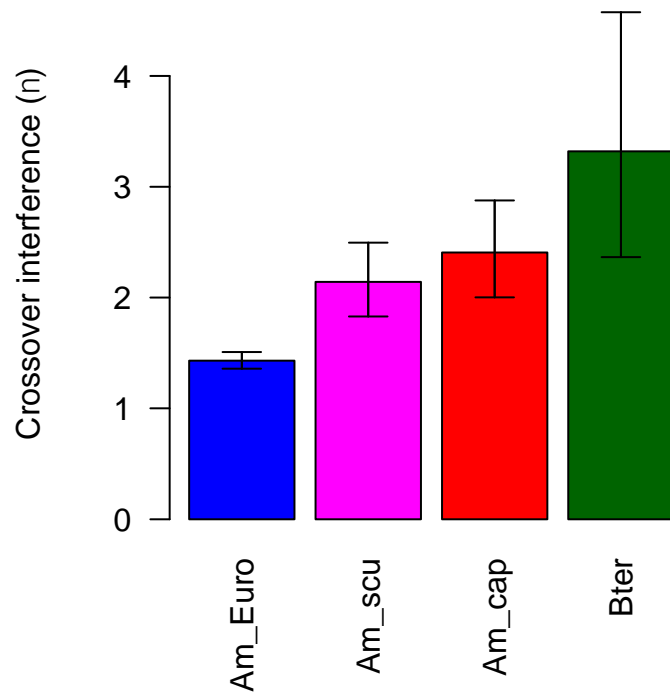
Figure S7 Mean CO density (/100 Mb) in 1-Mb windows along a chromosome of *B. terrestris.* CO density / 100 Mb is the average density of crossovers in the genome inferred across drones and is directly comparable to cM/Mb.

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Figure S8 Strength of crossover interference measured as gamma shape parameter (v) in three populations of *A. mellifera* (European *A. mellifera*, African *A. m. scutellata*, and African *A. m. capensis*) and one population of *B. terrestris*. Error bars represent log-likelihood supporting interval.

Figure S9 Frequency of CO events in a 28-kb region in three populations of *A. mellifera* (European *A. mellifera*, African *A. m. scutellata*, and African *A. m. capensis*). A 28-kb window, corresponding to the size of Sex Determining Locus (SDL), was chosen at random positions in the honeybee genome for 10,000 times.
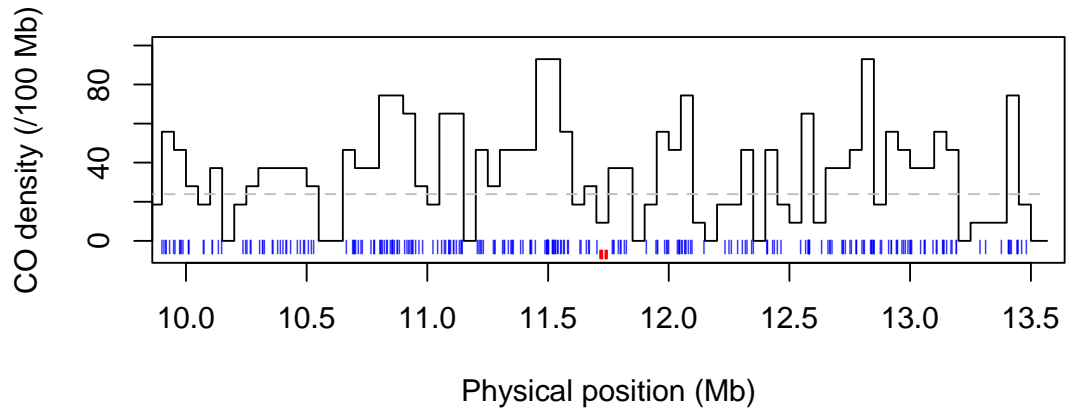
Figure S10 CO density (/100 Mb) near Sex Determining Locus (SDL) on chromosome 3 in honeybees. Black line indicates CO density in 50-kb windows in three populations of *A. mellifera* (European *A. mellifera*, African *A. m. scutellata*, and African *A. m. capensis*). Blue ticks indicate the CO breakpoints. The grey dashed line indicates mean genome-wide CO density. Two red rectangles indicate *csd* and *fem* genes at SDL.
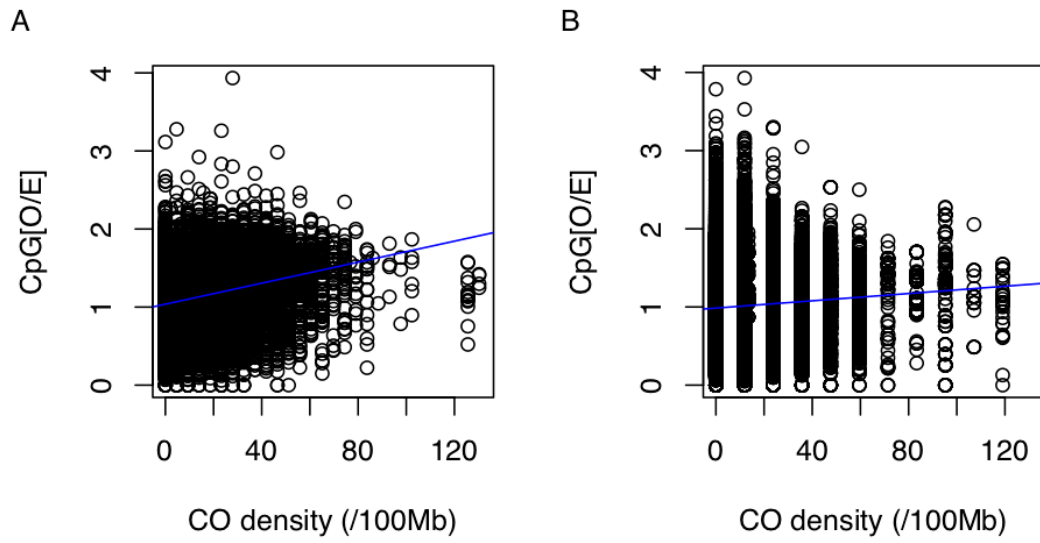
Figure S11 Correlations between CO density (/100 Mb) and CpG observed/expected (o/e) ratio in genic regions in honeybees (A) and bumblebees (B). 100-kb genomic windows are used in each comparison.
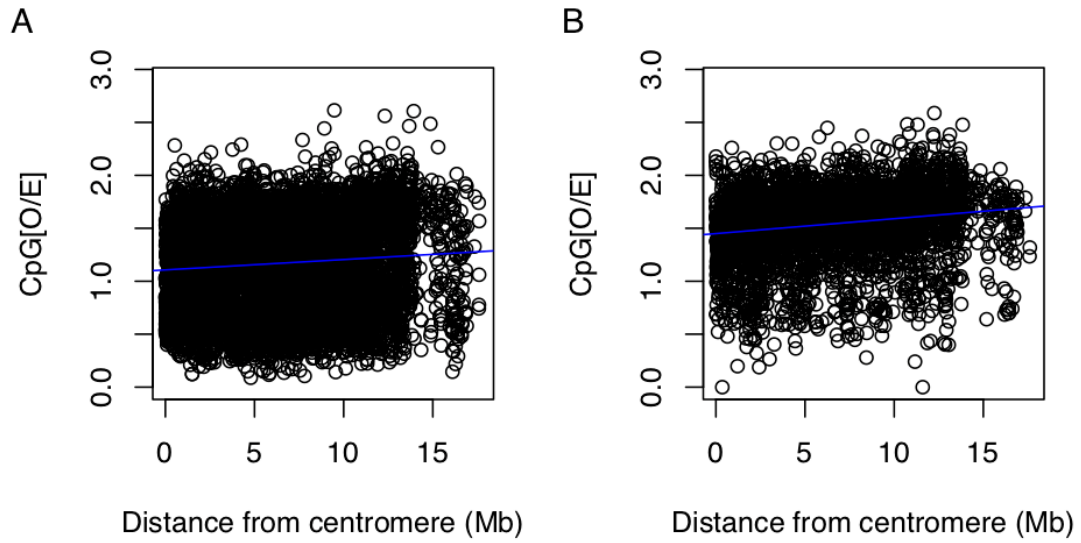
Figure S12 Correlations between CO density (/100 Mb) and CpG observed/expected (o/e) ratio in genic (A) and intergenic regions (B) and distance from the centromere in honeybees. Only chromosomes with predicted centromere positions were used (Group 1, 2, 3, 4, 5, 6, 9, 11, 12, 14, and 15).
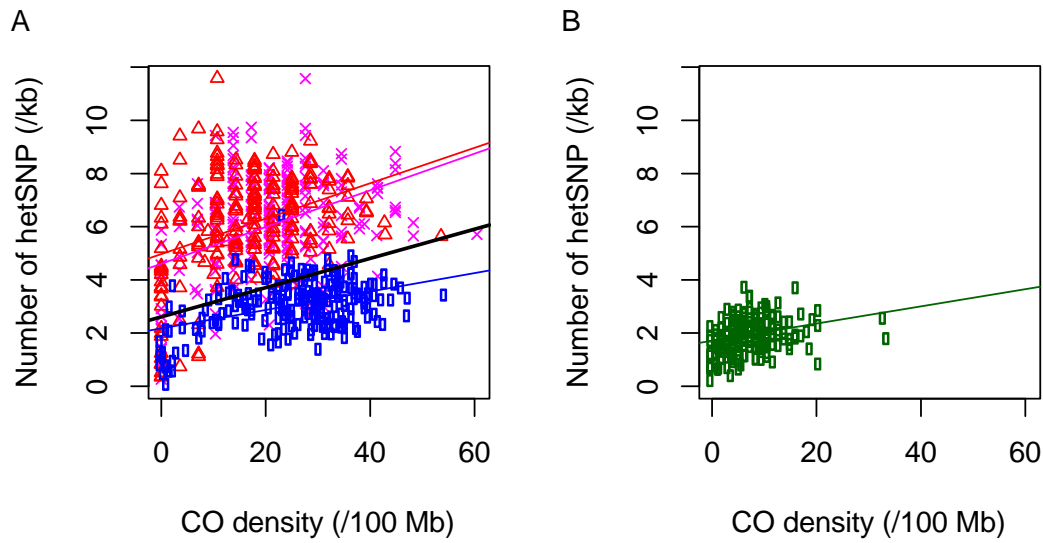
Figure S13 The density of heterozygous SNPs in queens (hetSNP) plotted against CO density (/100 Mb) in 1-Mb window in three populations of *A. mellifera* (European *A. mellifera*: blue circles, African *A. m. scutellata*: magenta crosses, and African *A. m. capensis*: red triangles) (A), and one population of *B. terrestris* (B). Lines with corresponding colours are regression for each population, while the black line indicates regression analysis using all three honeybee populations.
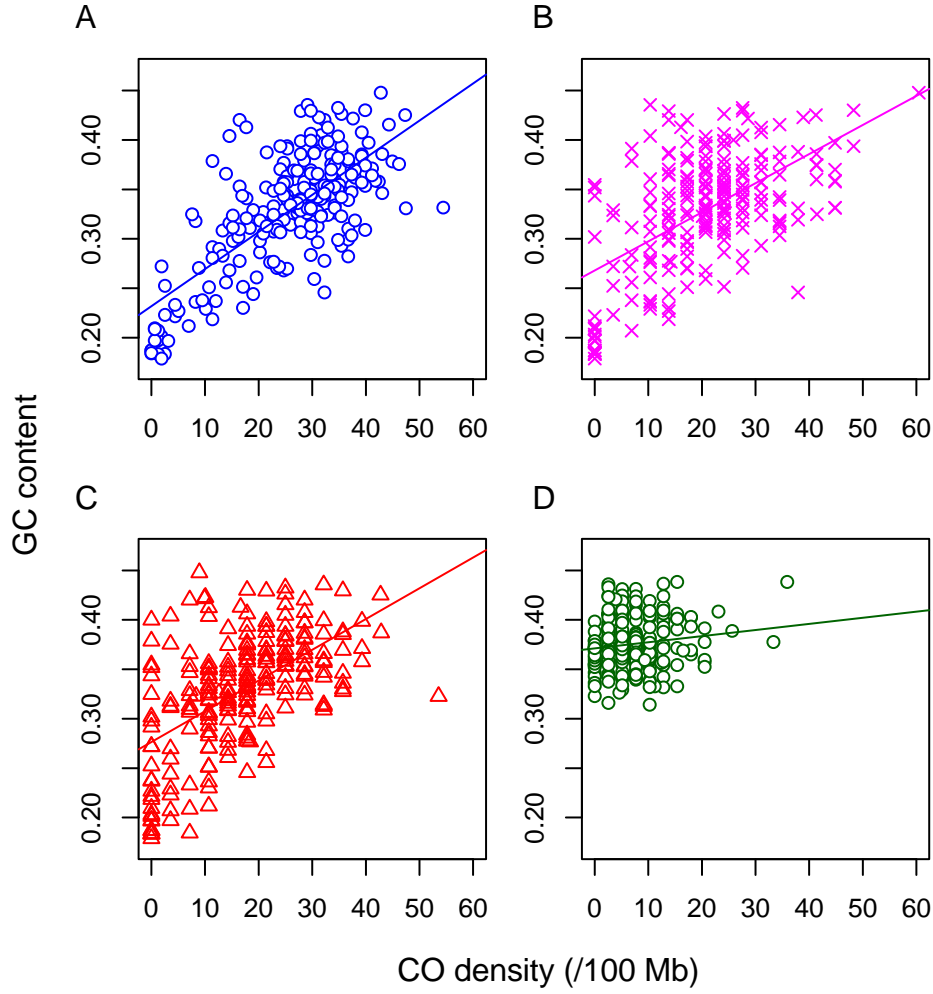
Figure S14 Correlation between GC content and CO density (/100 Mb) in 1-Mb windows in European *A. mellifera* (A), African *A. m. scutellata* (B), African *A. m. capensis* (C), and *B. terrestris* (D). Pearson's correlation coefficients are $r = 0.72$ in European *A. mellifera* ($p < 10^{-16}$), $r = 0.57$ in African *A. m. scutellata* ($p < 10^{-16}$), $r = 0.56$ in African *A. m. capensis* ($p < 10^{-16}$), and $r = 0.14$ in *B. terrestris* ($p = 0.04$).
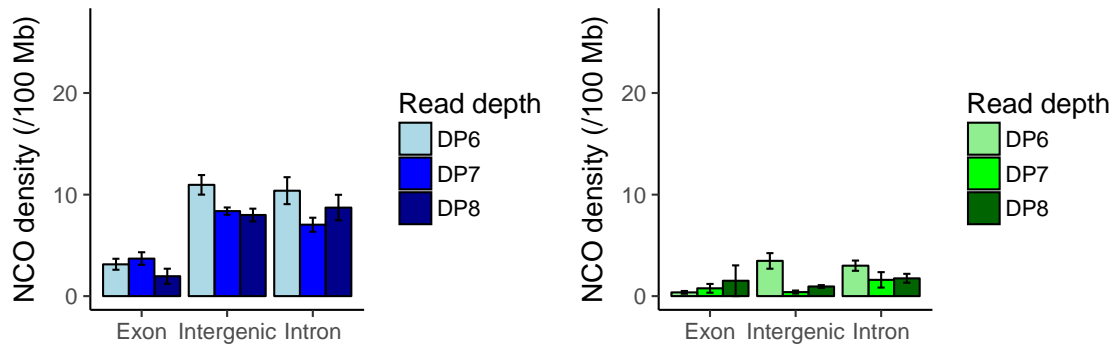
Figure S15 A) Mean density of NCO-associated gene conversions in exonic, intronic and intergenic regions in European *A. mellifera*. A subset of individuals (drones) was selected based on the average sequence read depth (DP) per SNP (DP = 6, 7 and 8). B) Mean density of NCO-associated gene conversions in exonic, intronic and intergenic regions in *B. terrestris*.