Supplemental Data for Cutter & Choi "Natural selection shapes nucleotide polymorphism across the genome of the nematode *Caenorhabditis briggsae*"

Supplemental Table 1. ANOVA results for lineage-specific, synonymous-site divergence in *C. briggsae* ($\log_{10}[d_S+0.001]$) as a function of recombination rate ($\log_{10}$-transformed "intermediate scale 5-loci estimates"), codon bias (F_{op}), background nucleotide composition (intron G+C), and chromosome of origin (and first-order interactions; $r^2_{adj} = 0.16$).

Model test	DF	Sum of Squares	Mean Square	F	P
Model	26	133.9358	5.15138	51.7291	<.0001
Error	6991	696.1897	0.09958		
C. Total	7017	830.1254			

Effect tests	DF	Sum of Squares	Sign	F	P
log10(Fop+0.001)	1	119.6604	-	1200.015	<.0001
log10(recRate5+0.001)	1	2.68317	+	26.9082	<.0001
Chr	5	3.86769		7.7574	<.0001
Chr*log10(recRate5+0.001)	5	2.20121		4.415	0.0005
Chr*log10(Fop+0.001)	5	1.16774		2.3421	0.0391
Chr*IntronGC	5	0.71483		1.4337	0.2085
log10(recRate5+0.001)*log10(Fop+0.001)	1	0.03049	+	0.3057	0.5803
IntronGC	1	0.0138	+	0.1383	0.7099
IntronGC*log10(Fop+0.001)	1	0.00396	-	0.0398	0.842
log10(recRate5+0.001)*IntronGC	1	0.00209	-	0.021	0.8848

Supplemental Table 2. ANOVA results for lineage-specific, replacement-site divergence in *C. briggsae* ($\log_{10}[d_N+0.001]$) as a function of recombination rate ($\log_{10}$-transformed "intermediate scale 5-loci estimates"), synonymous-site divergence ($\log_{10}[d_S+0.001]$), codon bias (F_{op}), background nucleotide composition (intron G+C), and chromosome of origin (and first-order interactions; $r^2_{adj} = 0.24$).

Model test	DF	Sum of Squares	Mean Square	F	P
Model	35	367.7895	10.5083	65.1951	<.0001
Error	6989	1126.5	0.1612		
C. Total	7024	1494.29			

Effect tests	DF	Sum of Squares	Sign	F	P
log10(dS+0.001)	1	143.594	+	890.882	<.0001
log10(Fop+0.001)	1	48.04274	-	298.0655	<.0001
log10(recRate5+0.001)	1	7.46393	+	46.3075	<.0001
IntronGC *log10(dS+0.001)	1	5.01968	+	31.143	<.0001
IntronGC *log10(Fop+0.001)	1	2.7918	+	17.3208	<.0001
Chr *log10(Fop+0.001)	5	6.22955		7.7298	<.0001
IntronGC	1	1.12213	+	6.9619	0.0083
Chr	5	2.46911		3.0638	0.0091
Chr *log10(dS+0.001)	5	2.31116		2.8678	0.0137
log10(recRate5+0.001)*log10(dS+0.001)	1	0.28439	+	1.7644	0.1841
Chr *log10(recRate5+0.001)	5	1.37052		1.7006	0.1308
log10(Fop+0.001)*log10(dS+0.001)	1	0.16899	+	1.0485	0.3059
log10(recRate5+0.001)*log10(Fop+0.001)	1	0.15492	+	0.9611	0.3269
Chr *IntronGC	5	0.59909		0.7434	0.5909
log10(recRate5+0.001)*IntronGC	1	0.00012	+	0.0007	0.9786

Supplemental Table 3. Summary of polymorphism and divergence for 24 autosomal loci (Excel file).

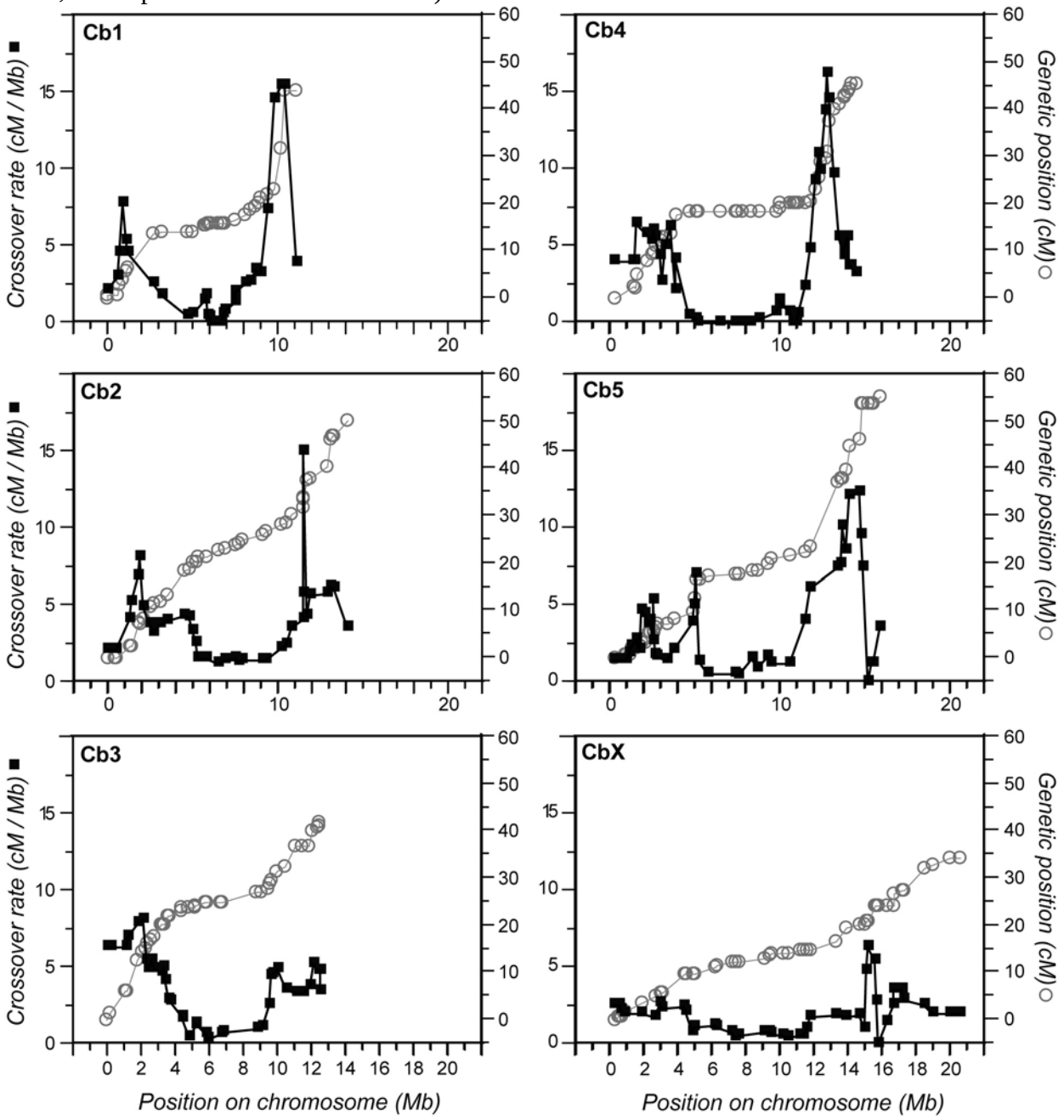
Supplemental Table 4. Summary of primers used for amplification and sequencing (Excel file).

Supplemental Table 5. Summary of a subset of explicit recurrent hitchhiking simulations that match the observed π and π-recombination correlation with corresponding simulation percentiles for the Innan and Stephan [2002] $R_{p\text{-}pr}$ statistic*.

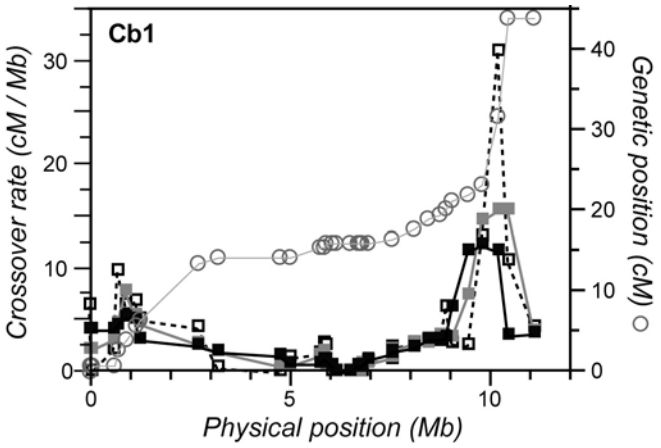
π_0	s	λ	scale of recombination	median simulated polymorphism (π, averaged across loci)	median of simulated Spearman correlation of π and crossover rate	$R_{p\text{-}pr}$ at 97.5th percentile of simulated distribution	Percentile of observed $R_{p\text{-}pr}$	P
0.030	0.0050	0.000000010	fine (3-loci)	0.001872	0.6828	0.8853	99.5	0.005
0.035	0.0010	0.000001000	intermediate (5-loci)	0.001790	0.6310	0.8260	100.0	<0.001
0.045	0.0025	0.000000075	coarse (7-loci)	0.001875	0.6309	0.9092	99.4	0.006
0.010	0.0075	0.000000001	fine (3-loci)	0.001851	0.6443	0.8559	99.7	0.003
0.040	0.0010	0.000001000	fine (3-loci)	0.002073	0.6420	0.8412	100.0	<0.001
0.010	0.0100	0.000000001	fine (3-loci)	0.001455	0.6409	0.8647	99.9	0.001
0.010	0.0008	0.000000100	fine (3-loci)	0.001560	0.6350	0.8618	99.8	0.002
0.035	0.0010	0.000001000	fine (3-loci)	0.001790	0.6310	0.8260	100.0	<0.001
0.030	0.0010	0.000001000	fine (3-loci)	0.001537	0.6203	0.8327	100.0	<0.001
0.015	0.0010	0.000000100	intermediate (5-loci)	0.001818	0.6873	0.8681	100.0	<0.001
0.010	0.0025	0.000000010	intermediate (5-loci)	0.001541	0.6756	0.8866	99.8	0.002
0.025	0.0050	0.000000010	intermediate (5-loci)	0.001569	0.6816	0.8964	99.8	0.002
0.035	0.0050	0.000000010	intermediate (5-loci)	0.002160	0.6915	0.9044	99.1	0.009
0.030	0.0050	0.000000010	intermediate (5-loci)	0.001872	0.6828	0.8853	99.5	0.005
0.030	0.0050	0.000000010	coarse (7-loci)	0.001765	0.6393	0.8971	82.0	0.18
0.035	0.0010	0.000000500	coarse (7-loci)	0.002014	0.6285	0.8602	95.5	0.045
0.040	0.0010	0.000000500	coarse (7-loci)	0.002308	0.6265	0.8701	95.2	0.048
0.030	0.0025	0.000000050	coarse (7-loci)	0.001633	0.6376	0.9209	76.9	0.231
0.020	0.0010	0.000000250	coarse (7-loci)	0.001523	0.6299	0.8676	93.8	0.062
0.040	0.0025	0.000000075	coarse (7-loci)	0.001636	0.6235	0.9125	77.9	0.221

*Top three rows indicate best parameter combinations for each scale of recombination (red points in Supplemental Figure 3).

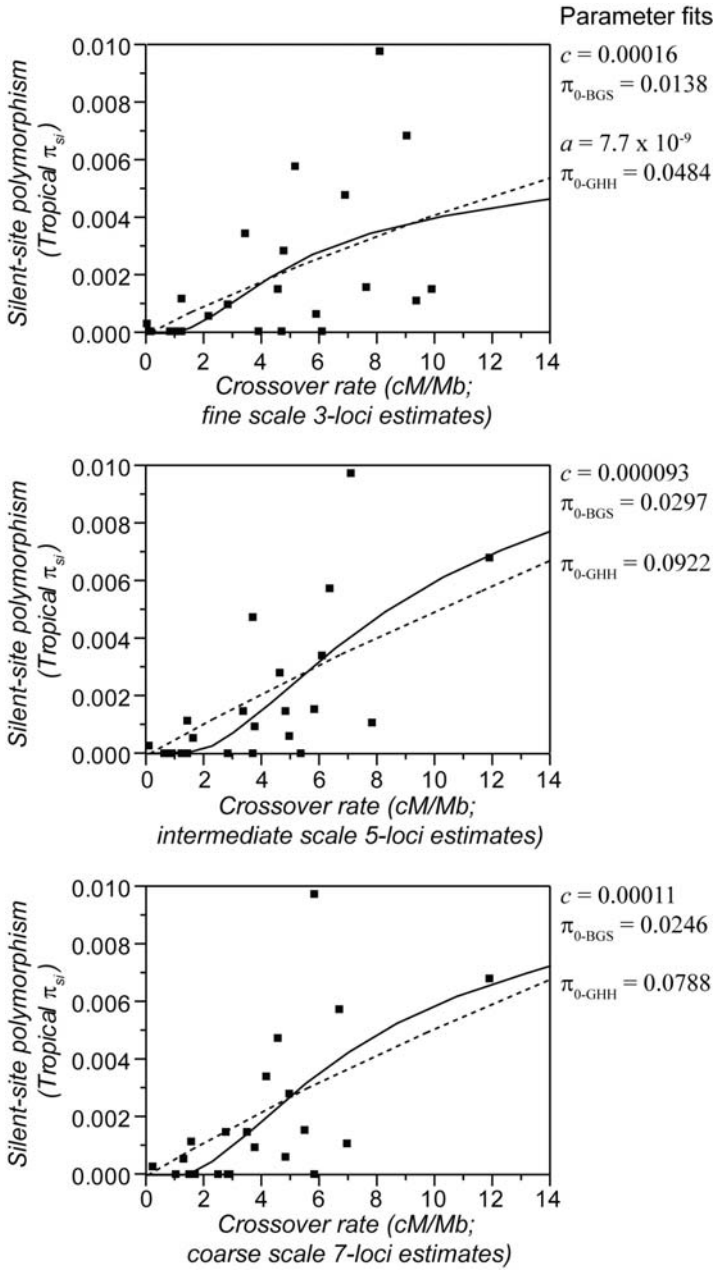
Supplemental Figure 1A. Recombination maps for *C. briggsae*'s six chromosomes (intermediate scale; 5 loci per crossover-rate estimate).



Supplemental Figure 1B. Recombination maps for *C. briggsae* chromosome I for three scales of recombination. Crossover rates indicated along the left axis with squares (fine-scale 3-locus estimates = unfilled; intermediate-scale 5-locus estimates = gray filled; coarse-scale 7-locus estimates = black filled). Genetic map positions indicated with circles with right axis.



Supplemental Figure 2. Nonlinear fits of analytical approximations for recurrent genetic hitchhiking (RGH) and background selection (BGS) to *C. briggsae* Tropical-strain nucleotide polymorphism, for three scales of crossover rate estimates. BGS models (solid lines) assume per-site deleterious mutation rate $\mu = 1.7\times10^{-9}$/ gen (given 32% constrained sites in the genome and mutation rate twice that of *C. elegans*) and infer outcrossing rate c and baseline polymorphism π_0. RGH models (dashed lines) assume the *c* values estimated from the BGS models (for the corresponding scale of recombination) as a fixed parameter and infer selection parameter *a* and baseline polymorphism π_0. For the cases of intermediate and coarse scale recombination, RGH models converged on biologically irrelevant parameter values, so we input the value of *a* from the fine-scale case as a fixed parameter.



Supplemental Figure 3. Comparison of summary statistics from explicit simulations of recurrent genetic hitchhiking to observed values. Horizontal lines indicates the mean observed polymorphism of Tropical strains. Vertical line indicates the observed correlation coefficient between polymorphism and recombination rate estimates. Input parameters in (A) include 392 factorial combinations of π_0 = {0.005, 0.01, 0.015, 0.02, 0.025, 0.03, 0.035, 0.04}, s = {0.0005, 0.00075, 0.001, 0.0025, 0.005, 0.0075, 0.01}, λ = {0.000000001, 0.00000001, 0.0000001, 0.000001, 0.00001, 0.0001, 0.001}, and assume c = 0.000158 and N_e = 190000. Input parameters in (B) include 378 factorial combinations of π_0 = {0.005, 0.01, 0.015, 0.02, 0.025, 0.03, 0.035, 0.045}, s = {0.0005, 0.00075, 0.001, 0.0025, 0.005, 0.0075, 0.01}, λ = {0.0000000001, 0.000000001, 0.00000001, 0.0000001, 0.000001, 0.00001}. Input parameters in (C) include 657 factorial combinations of π_0 = {0.005, 0.01, 0.015, 0.02, 0.025, 0.03, 0.035, 0.04}, s = {0.0005, 0.00075, 0.00085, 0.001, 0.0025, 0.005, 0.0075, 0.01}, λ = {0.000000001, 0.00000001, 0.00000005, 0.000000075, 0.0000001, 0.00000025, 0.0000005, 0.00000075, 0.000001, 0.000005}. The red dot in (A) identifies the combination of parameter values used to generate Figure 7C. Summaries of simulation output for several parameter combinations near the intersection of the horizontal and vertical lines are given in Supplemental Table 5.