Supplementary Information

Experimental evidence for rapid genomic adaptation to a new niche in an adaptive radiation

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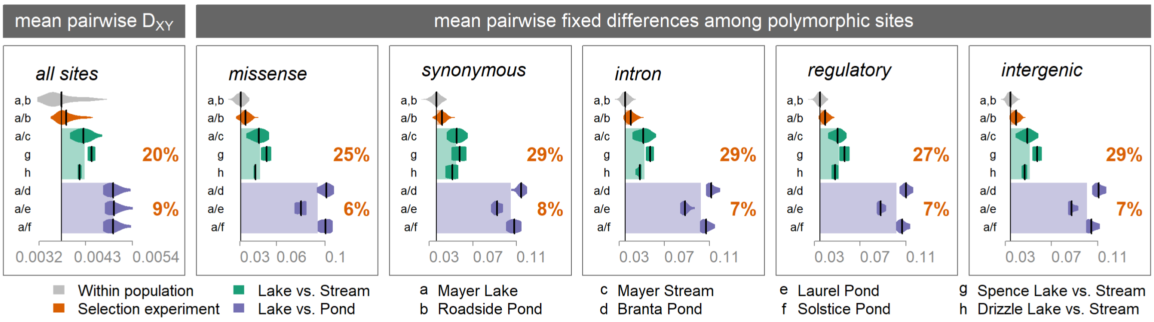
Table of contents

Supplementary Results

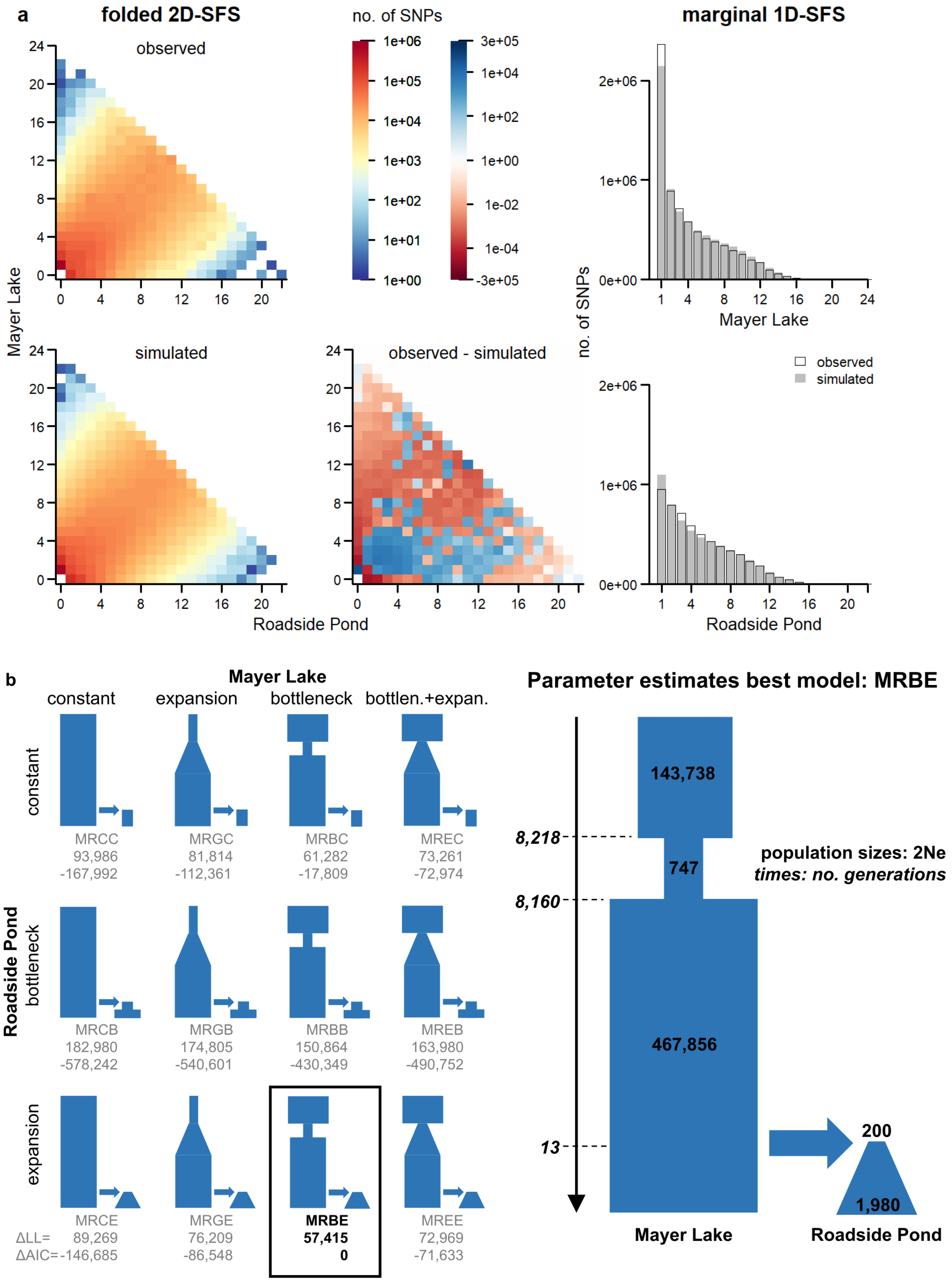
Genomic change at sites of different functional categories. Absolute divergence measured by the proportion of fixed differences among polymorphic sites between pairs of individuals in the selection experiment increased 25-29% compared to lake and stream ecotypes and 6-8% compared to Mayer Lake vs. small pond populations, in similar magnitude for non-synonymous, synonymous, intron, regulatory and intergenic sites (Supplementary Fig. 1).

Supplementary Figures

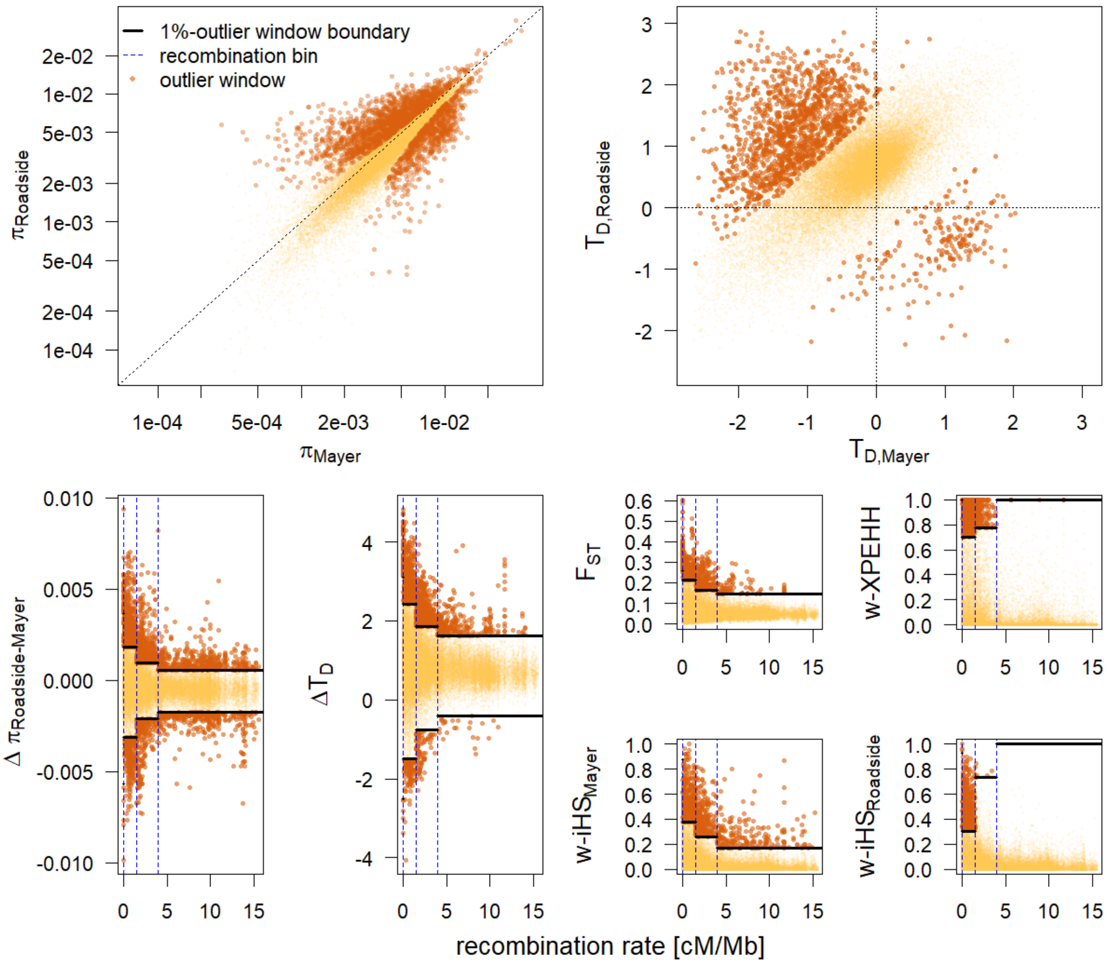
Supplementary Figure 1 | Proportion of fixed differences between two individuals for different SNP categories. The left panel shows the distribution of mean absolute divergence as in Fig. 4 for comparison. The other panels depict the percentage of fixed differences for missense mutations, synonymous mutations, intron, regulatory and intergenic variation.



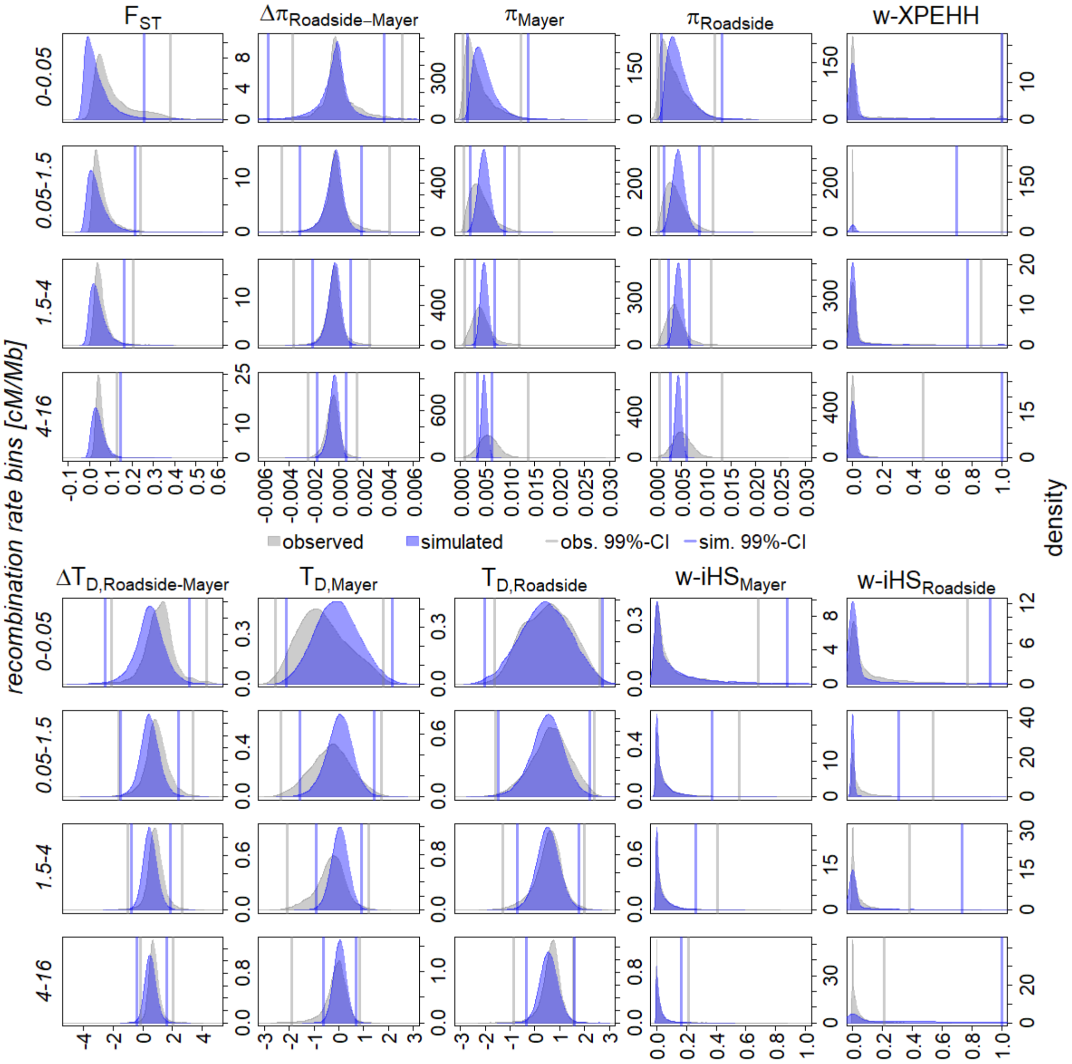
Supplementary Figure 2 | Reconstruction of demographic history based on the 2D-site-frequency spectrum (SFS). a Observed and simulated 2D-SFS under the best demographic model (see below) and marginal 1D-SFS for each population, with entries containing the sum of entries over the folded 2D-SFS for each population. **b** We fit twelve demographic models to the observed folded 2D-SFS between Mayer Lake and Roadside Pond to estimate maximum-likelihood parameters for the simulation of neutral data. The best-fitting demographic model features a bottleneck corresponding to the timing of postglacial colonization and a recent expansion of the transplant population, in line with biogeographic predictions and census data. ΔLL: log-likelihood difference for each model between observed and expected 2D-SFS; ΔAIC: differences between models for the Akaike information criterion.



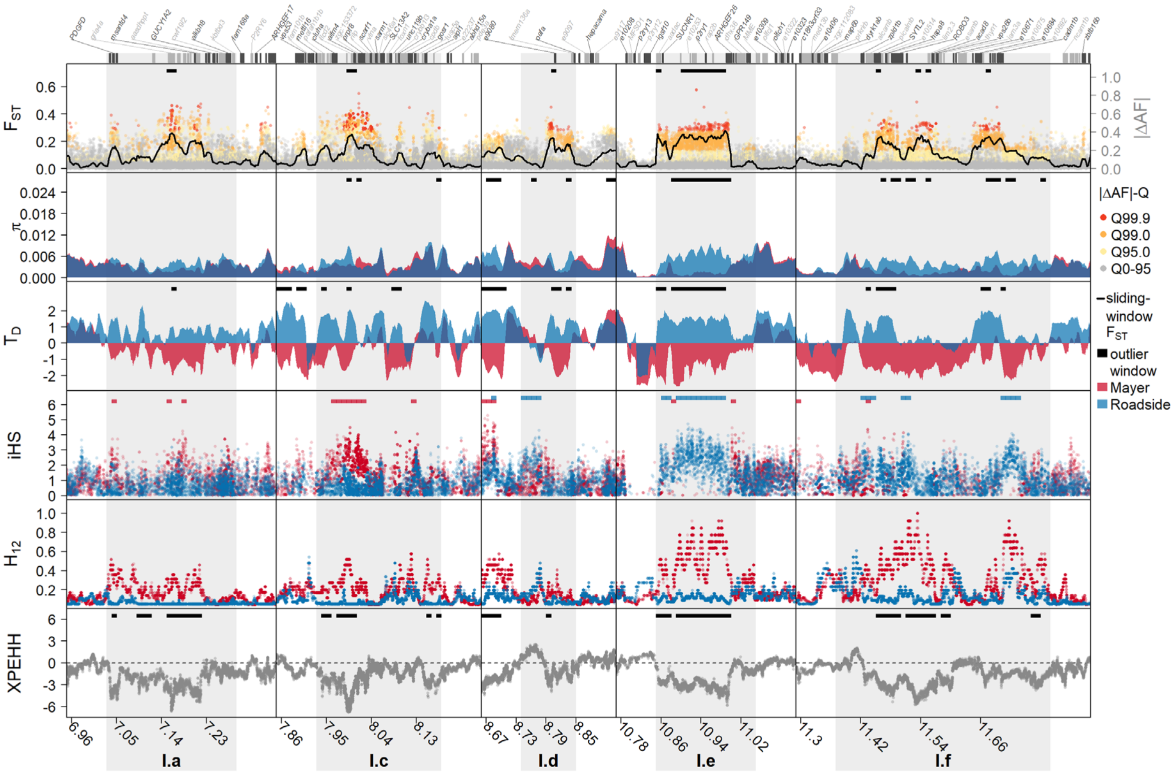
Supplementary Figure 3 | Recombination-rate based cut-offs to identify outlier windows. The lower panels show the distribution of differentiation (F_{ST}), change in diversity ($\Delta\pi$) and Tajima's D (ΔT_D), iHS and XP-EHH and the respective recombination-rate bin based (0–0.05, 0.05–1.5, 1.5–4, >4 cM/Mb) one- or two-sided cut-offs to identify outlier windows (dark brown dots) at the 1%-alpha level against neutral distributions of these statistics (see Supplementary Fig. 4). The upper panels show the correlation of nucleotide diversity and Tajima's D 10 kb window statistics between the two populations with outlier windows highlighted in dark brown. Note the strongly -shifted Tajima's D distribution in Roadside Pond.



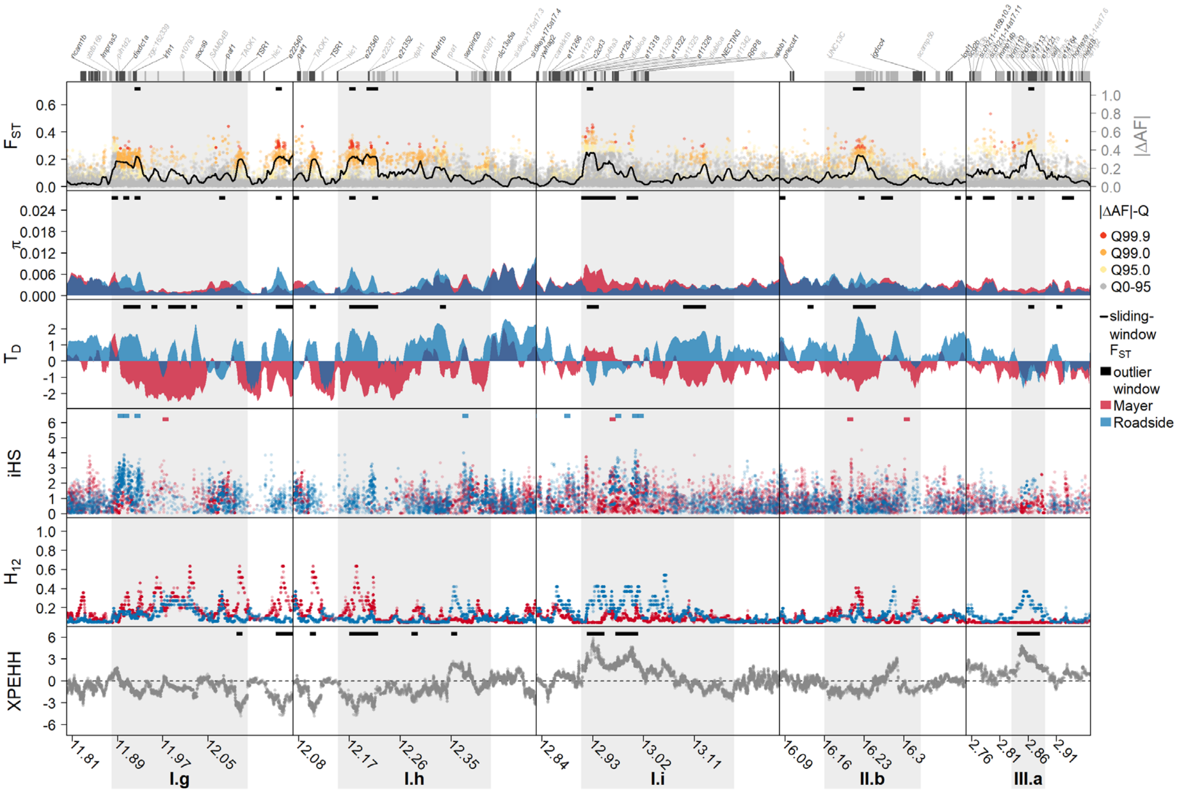
Supplementary Figure 4 | Distribution of observed and simulated summary statistics under the best demographic model. Shown are distributions of 10kb-window statistics in observed and simulated data, for each of four recombination rate bins: differentiation (F_{ST}) between Mayer Lake and Roadside Pond, nucleotide diversity in both populations (π_{Mayer}, $\pi_{Roadside}$) and between populations ($\Delta\pi_{Roadside\text{-}Mayer}$), Tajima's D in both populations ($T_{D,Mayer}$, $T_{D,Roadside}$) and between populations ($\Delta T_{D,Roadside\text{-}Mayer}$), as well as the haplotype-based selection statistics iHS in each population (w-iHS$_{Mayer}$, w-iHS$_{Roadside}$) and XP-EHH between populations (w-XP-EHH). Vertical lines depict boundaries for the 1% most extreme windows in the simulated (blue) and observed (grey) data.



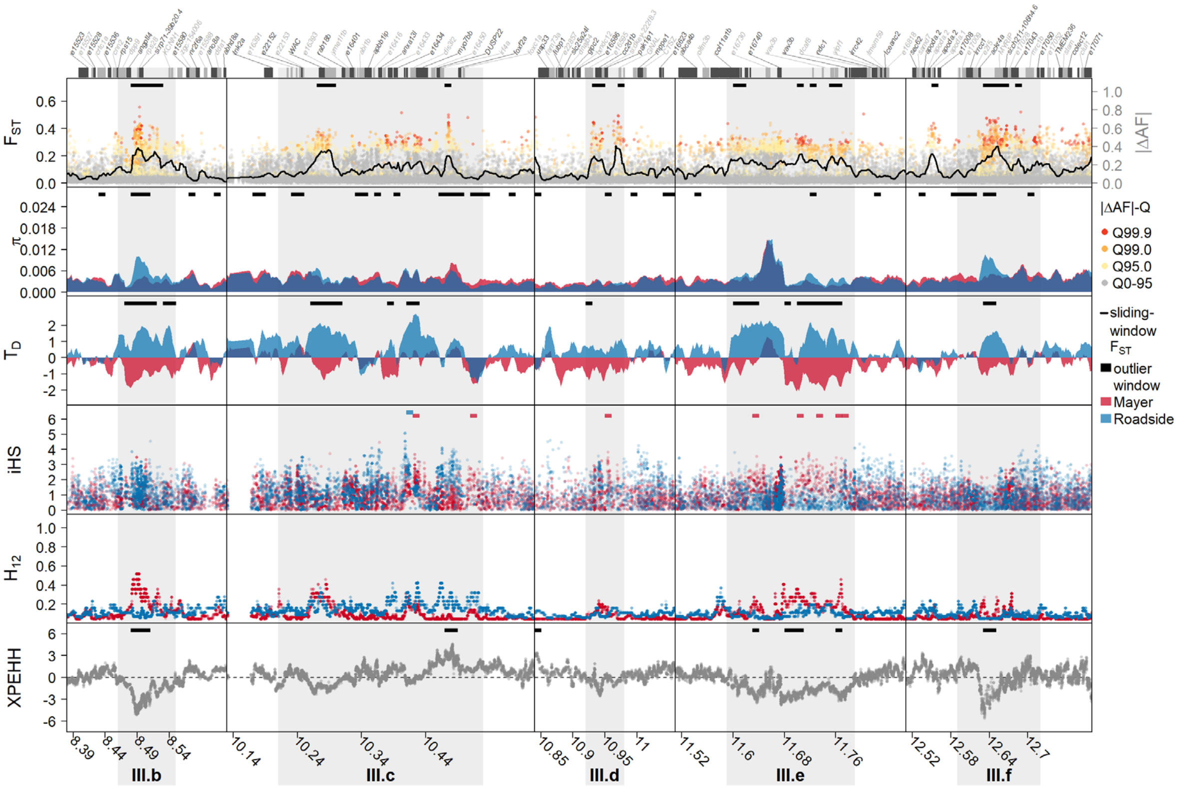
Supplementary Figure 5 | Local signatures of divergent selection on candidate genes. See Fig. 3 legend.



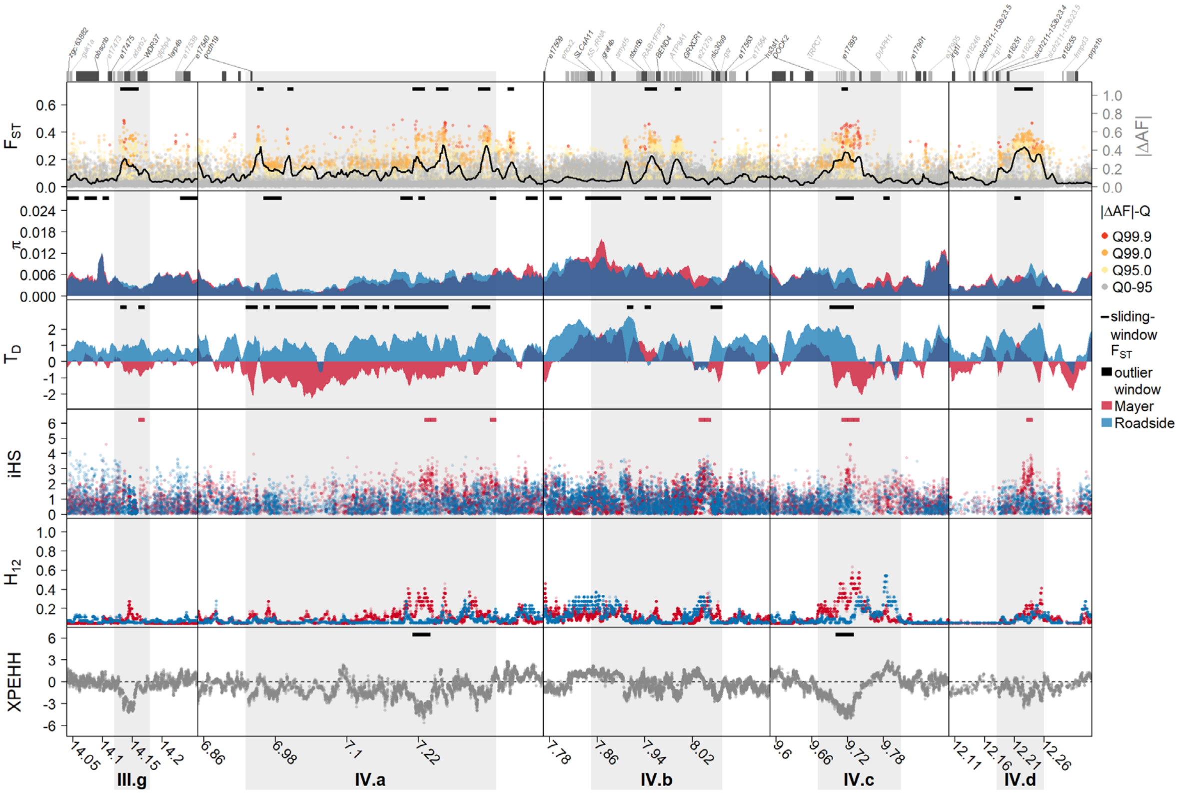
Supplementary Figure 6 | Local signatures of divergent selection on candidate genes. See Fig. 3 legend.



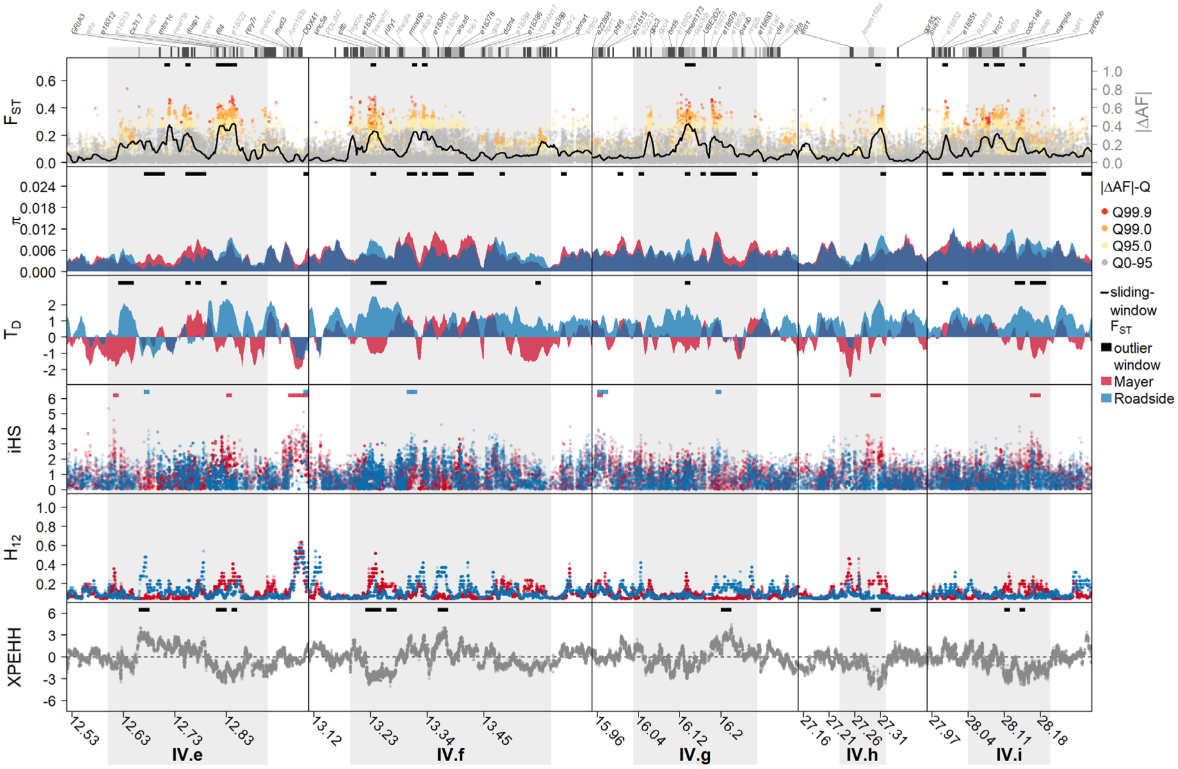
Supplementary Figure 7 | Local signatures of divergent selection on candidate genes. See Fig. 3 legend.



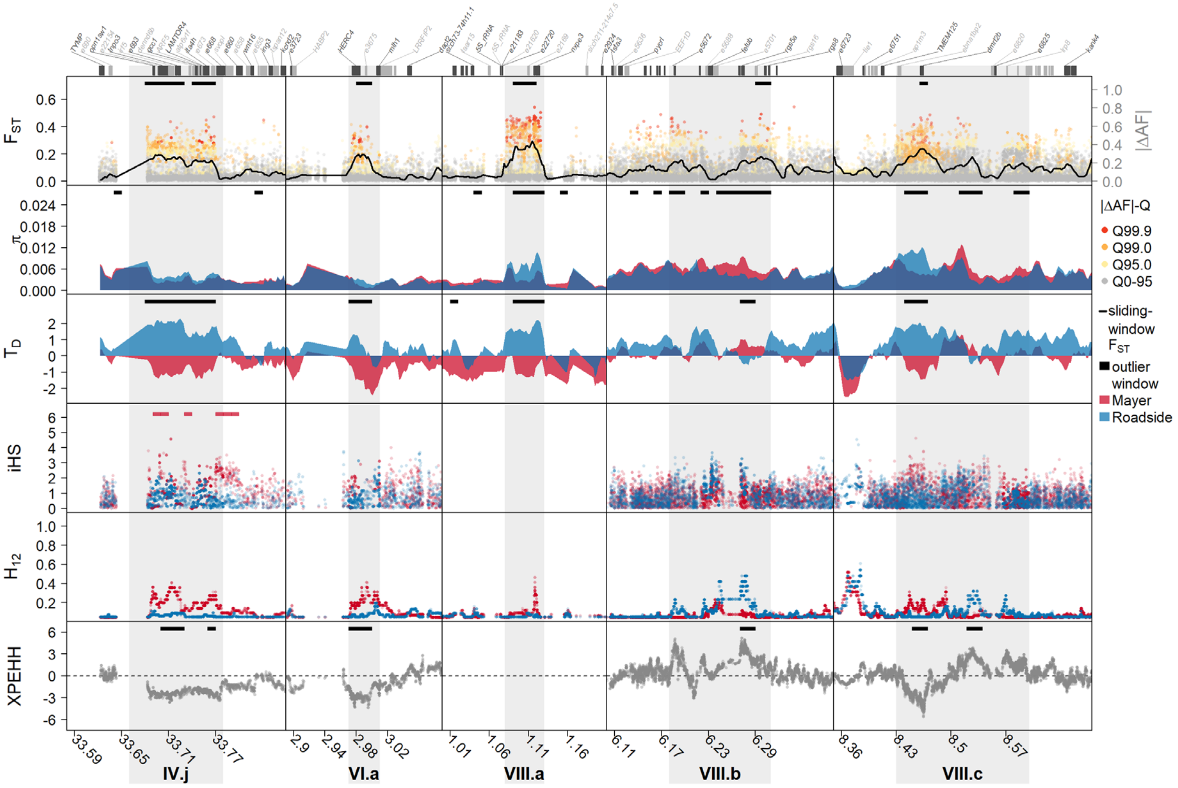
Supplementary Figure 8 | Local signatures of divergent selection on candidate genes. See Fig. 3 legend.



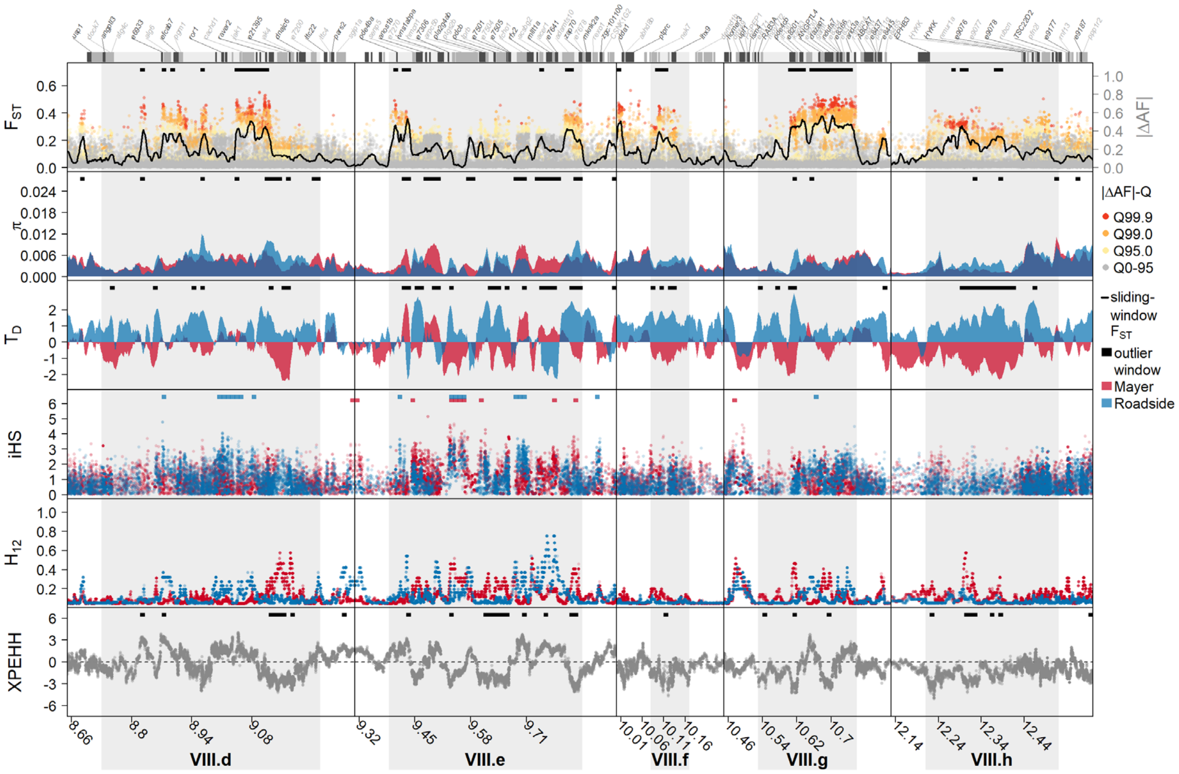
Supplementary Figure 9 | Local signatures of divergent selection on candidate genes. See Fig. 3 legend.



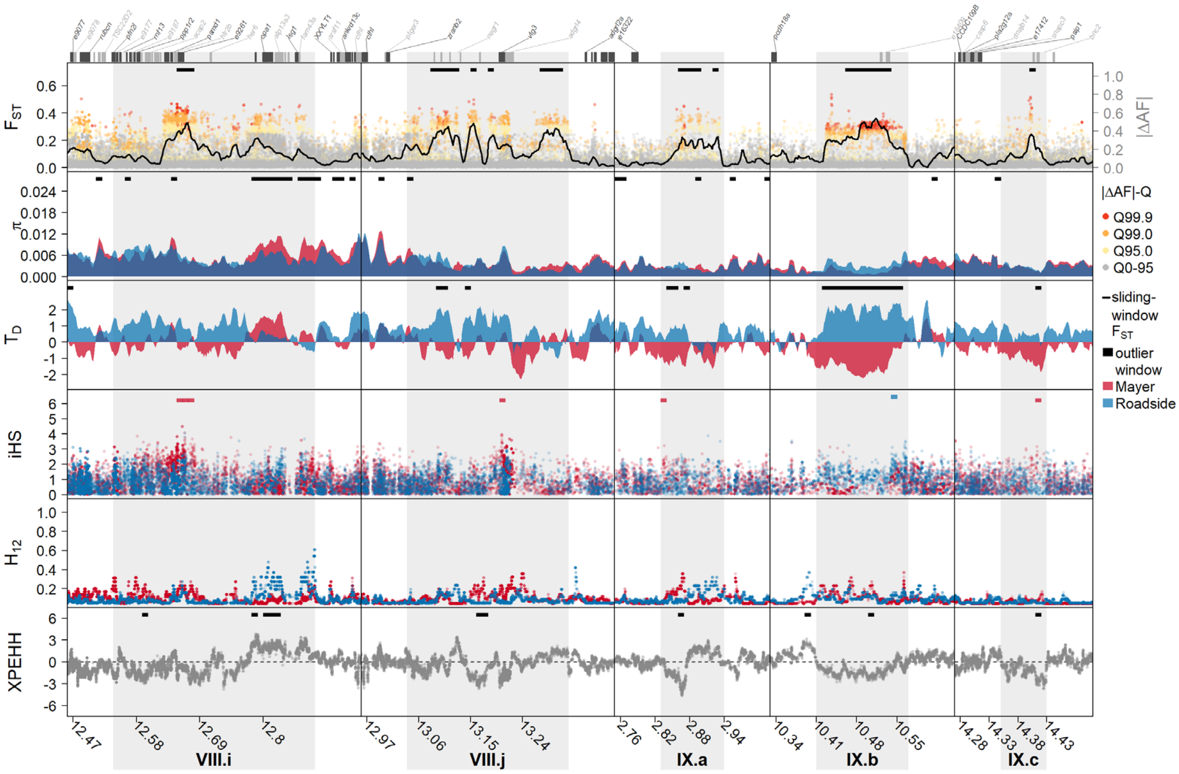
Supplementary Figure 10 | Local signatures of divergent selection on candidate genes. See Fig. 3 legend.



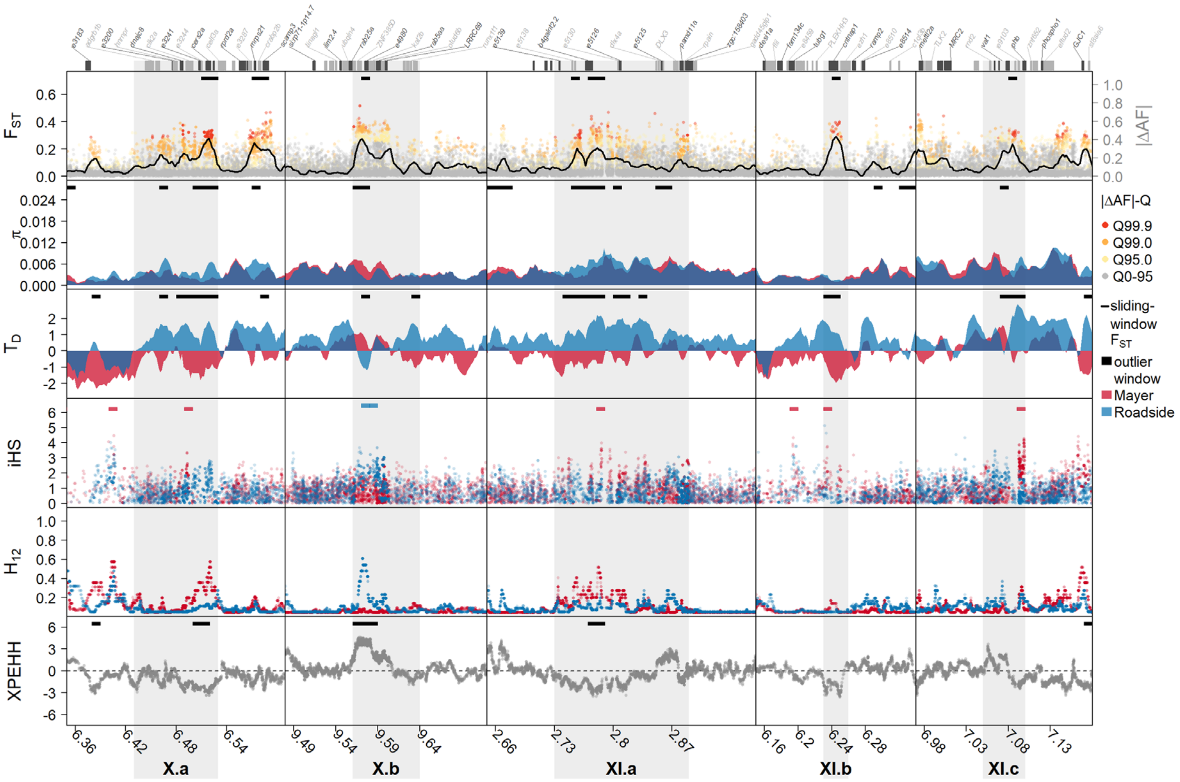
Supplementary Figure 11 | Local signatures of divergent selection on candidate genes. See Fig. 3 legend.



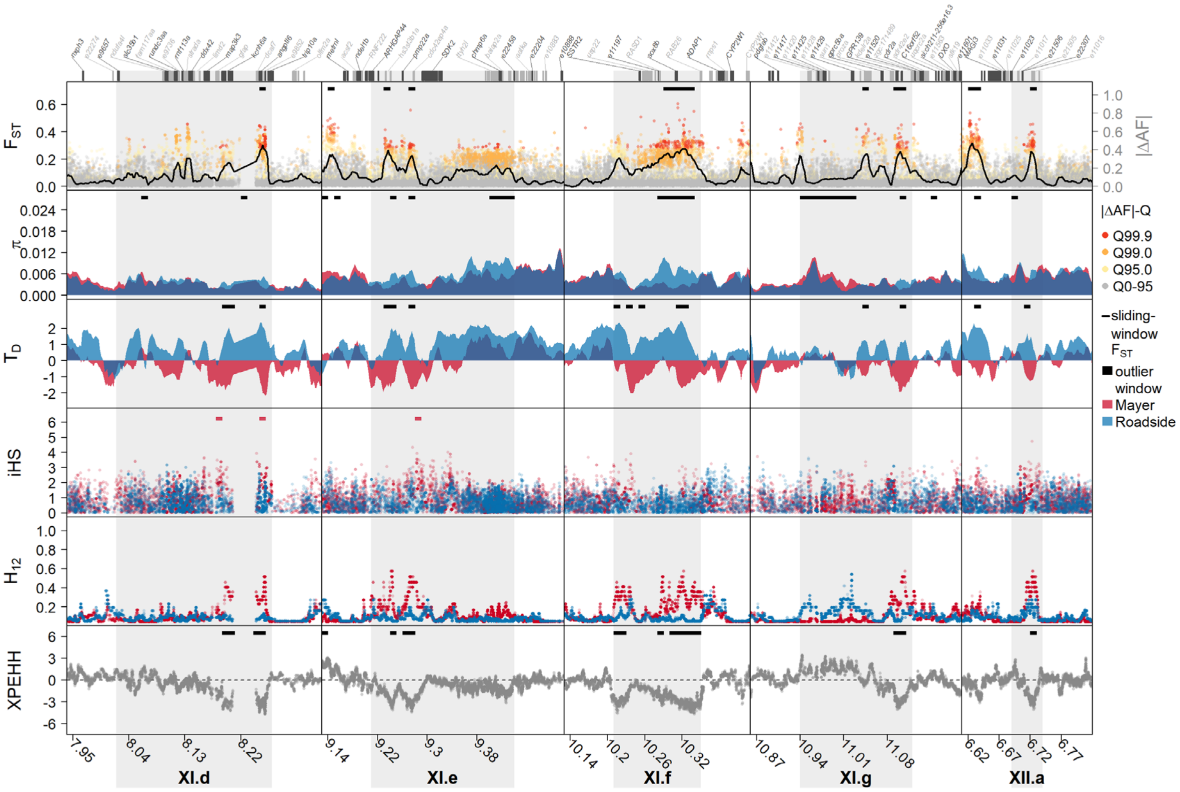
Supplementary Figure 12 | Local signatures of divergent selection on candidate genes. See Fig. 3 legend.



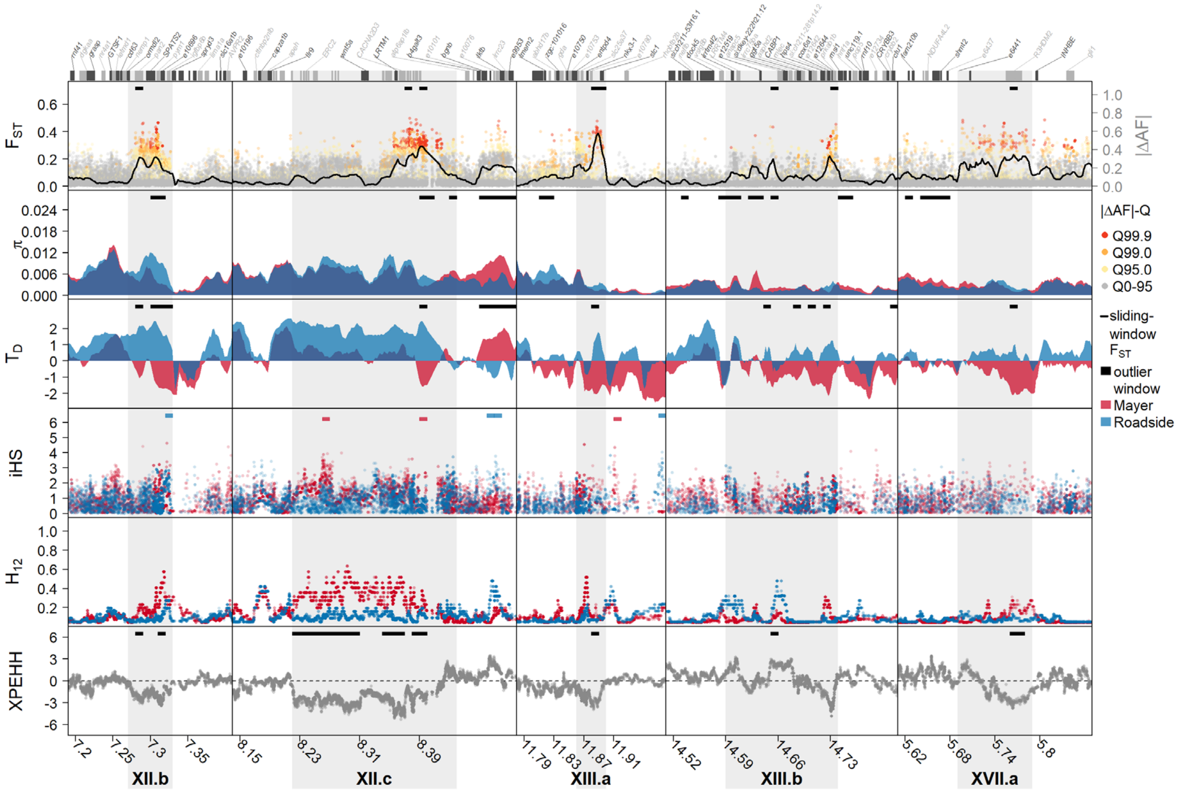
Supplementary Figure 13 | Local signatures of divergent selection on candidate genes. See Fig. 3 legend.



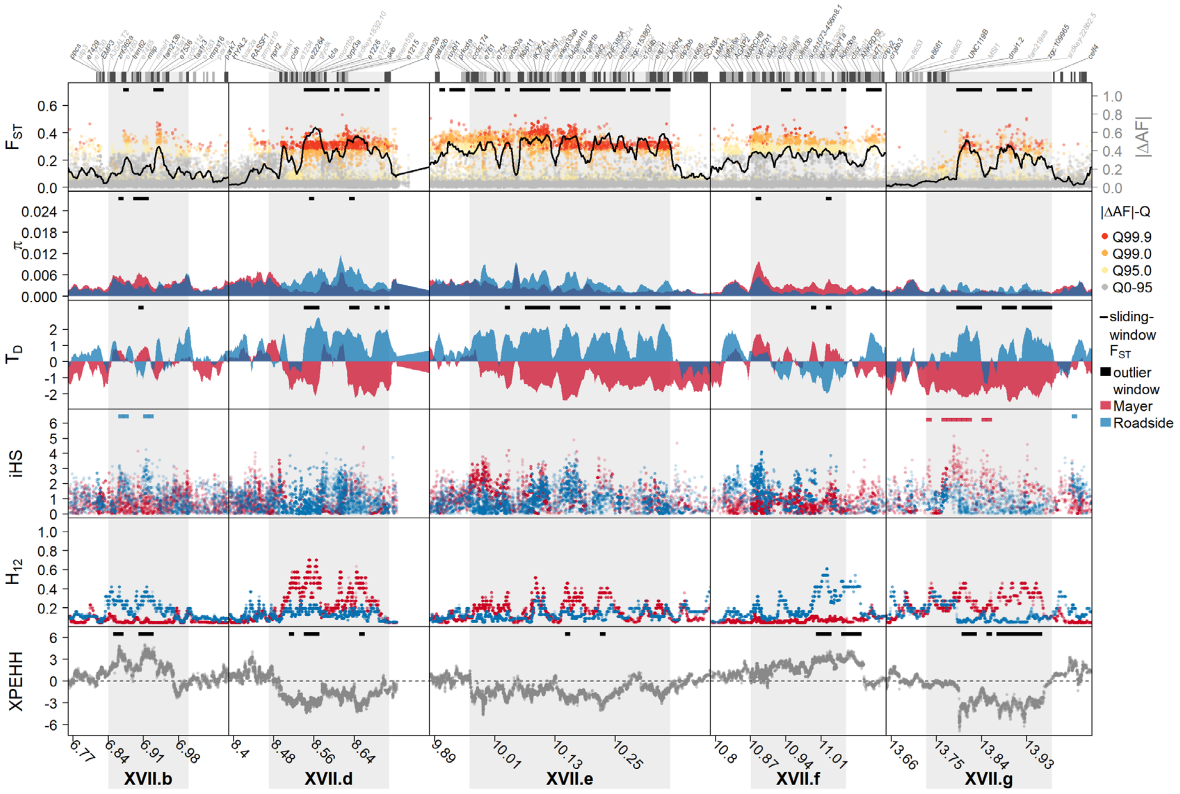
Supplementary Figure 14 | Local signatures of divergent selection on candidate genes. See Fig. 3 legend.



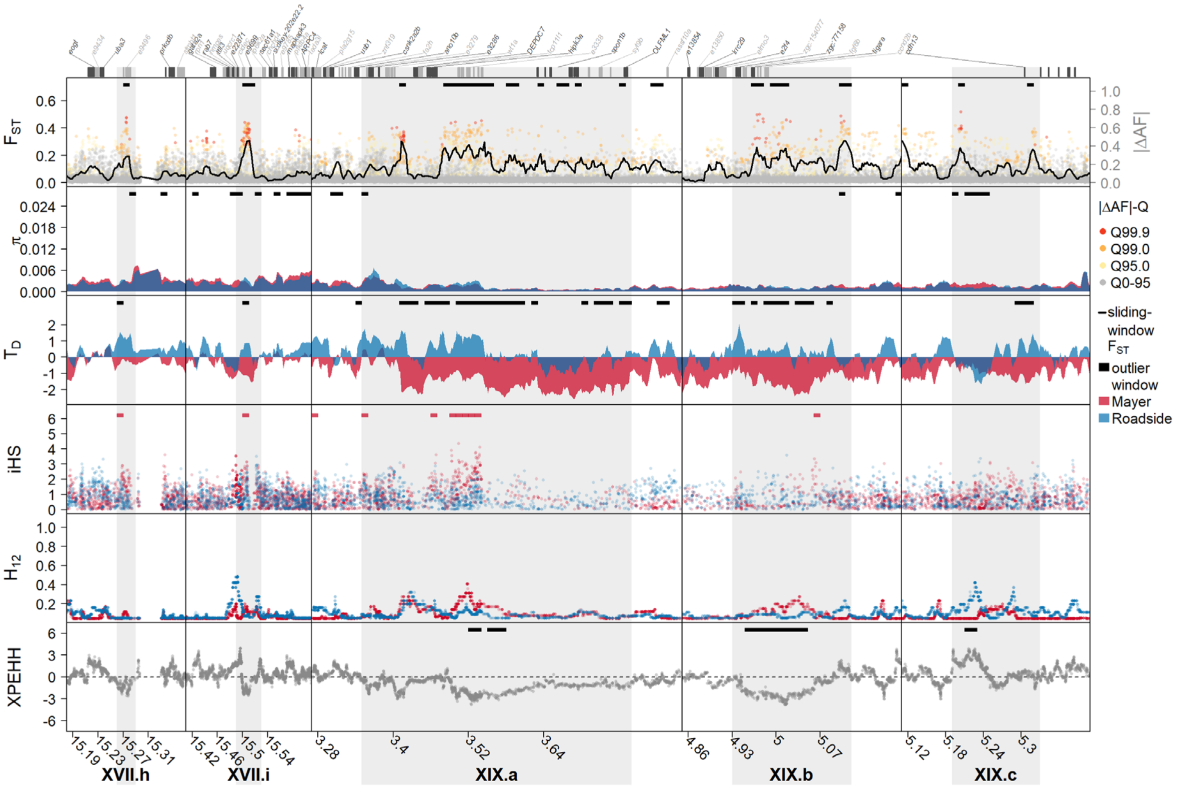
Supplementary Figure 15 | Local signatures of divergent selection on candidate genes. See Fig. 3 legend.



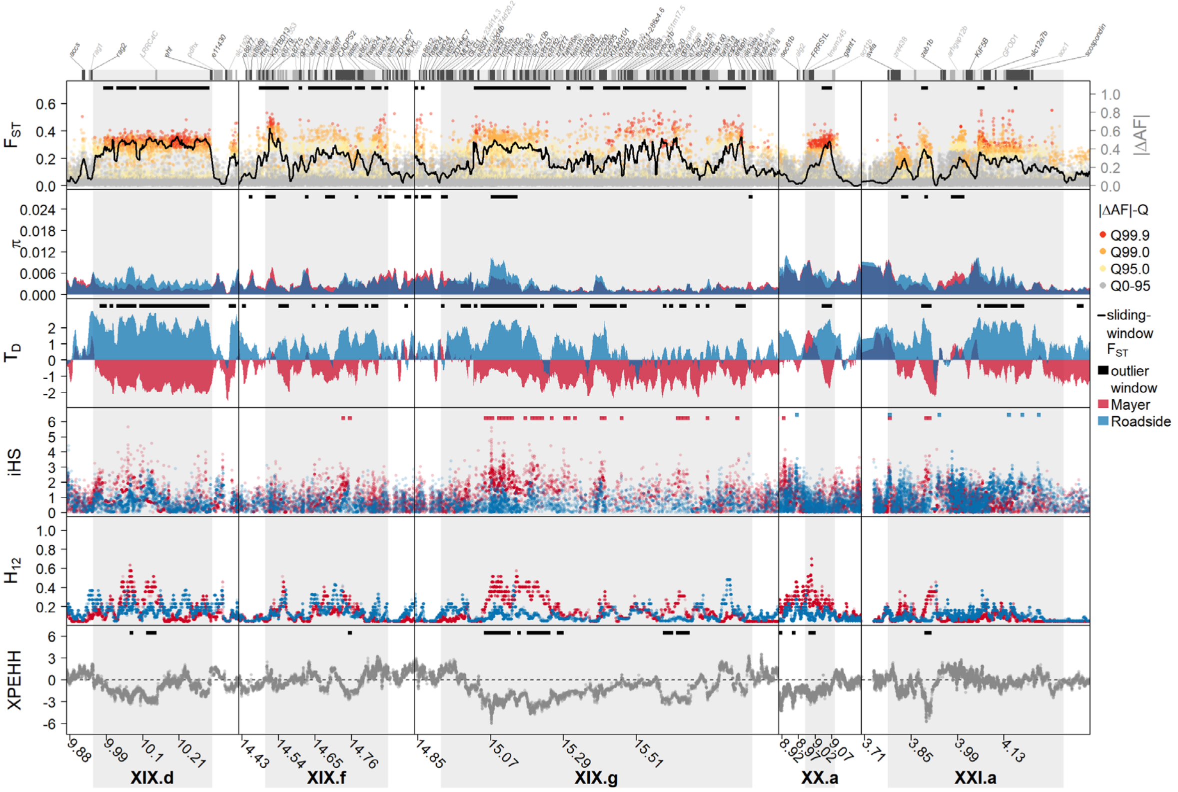
Supplementary Figure 16 | Local signatures of divergent selection on candidate genes. See Fig. 3 legend.



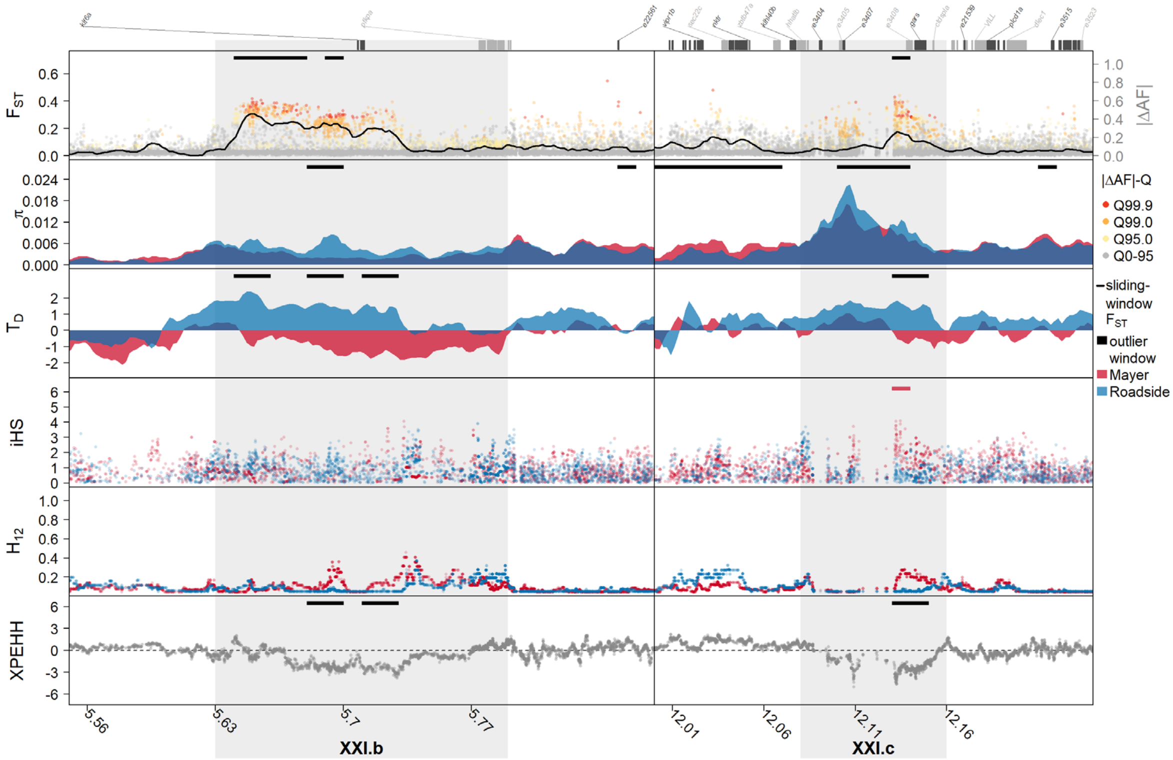
Supplementary Figure 17 | Local signatures of divergent selection on candidate genes. See Fig. 3 legend.



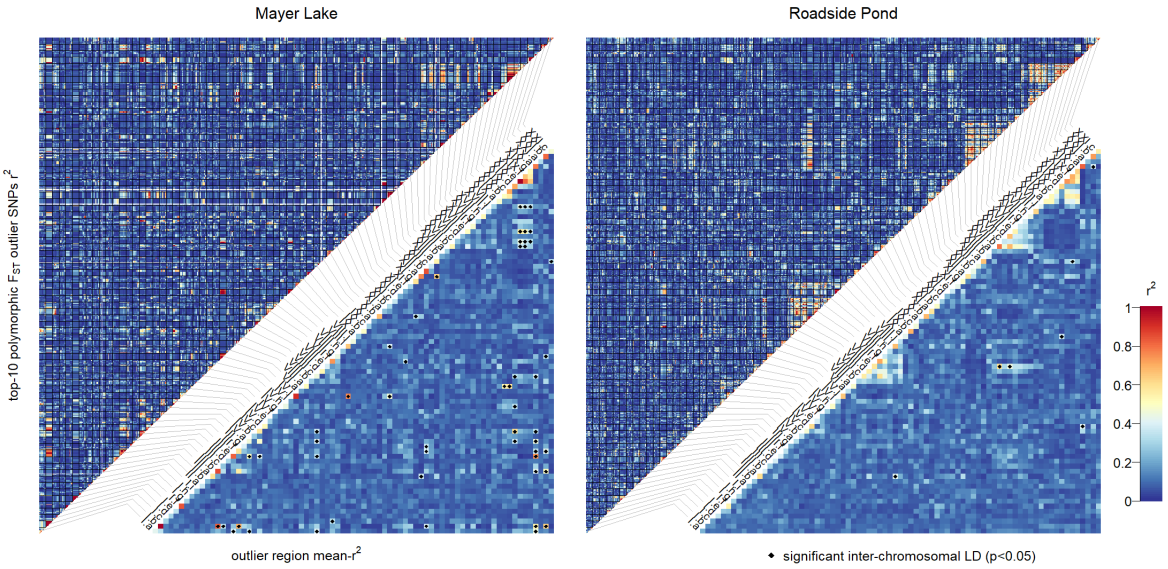
Supplementary Figure 18 | Local signatures of divergent selection on candidate genes. See Fig. 3 legend.



Supplementary Figure 19 | Local signatures of divergent selection on candidate genes. See Fig. 3 legend.



Supplementary Figure 20 | Linkage disequilibrium (LD) between outlier regions in the selection experiment. Several outlier regions in the source population, Mayer Lake, show higher LD between unlinked outlier regions than expected by chance from inter-chromosomal LD between neutral SNPs. In contrast, only a few outlier regions show inter-chromosomal LD in the transplant population, suggesting selection on many genomic regions instead of selection on one genomic region and a hitchhiking genomic background.



Supplementary Data

Supplementary Data 1 | Twelve demographic models fit to the observed data. Specification of the models (.tpl) and parameter (.est) for each of the 12 tested demographic models used with fastsimcoal2 v2.6 (see Methods section). See Supplementary Fig. 2 for a visual representation of the models.

MRCC.tpl

```
//Parameters for the coalescence simulation program : simcoal.exe
2
//Population effective sizes (number of genes)
NMAYR
200
//Samples sizes and samples age
24 5
22
//Growth rates: negative growth implies population expansion
0
0
//Number of migration matrices : 0 implies no migration between demes
0
//historical event: time, source, sink, migrants, new deme size, new growth rate, migration
matrix index
1 historical event
13 1 0 1 1 0 0
//Number of independent loci [chromosome]
1 0
//Per chromosome: Number of contiguous linkage Block: a block is a set of contiguous loci
1
//per Block:data type, number of loci, per generation recombination and mutation rates and
optional parameters
FREQ 1 0 1.7e-8 OUTEXP
```

MRCC.est

```
// Priors and rules file
// *********************
[PARAMETERS]
//#isInt? #name #dist.#min #max
//all Ns are in number of haploid individuals
1 NMAYR unif 1000 100000 output
[RULES]
[COMPLEX PARAMETERS]
```

MRCB.tpl

```
//Parameters for the coalescence simulation program : simcoal.exe
2
//Population effective sizes (number of genes)
NMAYR
NRDSP
//Samples sizes and samples age
24 5
22
//Growth rates: negative growth implies population expansion
0
0
//Number of migration matrices : 0 implies no migration between demes
0
//historical event: time, source, sink, migrants, new deme size, new growth rate, migration
matrix index
2 historical event
7 1 1 1 RES1 0 0
13 1 0 1 1 0 0
//Number of independent loci [chromosome]
1 0
//Per chromosome: Number of contiguous linkage Block: a block is a set of contiguous loci
1
//per Block:data type, number of loci, per generation recombination and mutation rates and
optional parameters
FREQ 1 0 1.7e-8 OUTEXP
```

MRCB.est

```
// Priors and rules file
// *********************
[PARAMETERS]
//#isInt? #name #dist.#min #max
//all Ns are in number of haploid individuals
1 NMAYR unif 1000 100000 output
1 NRDSP unif 1000 10000 output
[RULES]
[COMPLEX PARAMETERS]
0 RES1 = 200/NRDSP
```

MRCE.tpl

```
//Parameters for the coalescence simulation program : simcoal.exe
2
//Population effective sizes (number of genes)
NMAYR
NRDSP
//Samples sizes and samples age
24 5
22
//Growth rates: negative growth implies population expansion
0
RRAT
//Number of migration matrices : 0 implies no migration between demes
0
//historical event: time, source, sink, migrants, new deme size, new growth rate, migration
matrix index
2 historical event
13 1 1 1 1 0 0
13 1 0 1 1 0 0
//Number of independent loci [chromosome]
1 0
//Per chromosome: Number of contiguous linkage Block: a block is a set of contiguous loci
1
//per Block:data type, number of loci, per generation recombination and mutation rates and
optional parameters
FREQ 1 0 1.7e-8 OUTEXP
```

MRCE.est

```
// Priors and rules file
// *********************
[PARAMETERS]
//#isInt? #name #dist.#min #max
//all Ns are in number of haploid individuals
1 NMAYR unif 1000 100000 output
1 NRDSP unif 1000 10000 output
[RULES]
[COMPLEX PARAMETERS]
0 RATBB = 200/NRDSP hide
0 RCOF = log(RATBB) hide
0 RRAT = RCOF/13 hide
```

MRGC.tpl

```
//Parameters for the coalescence simulation program : simcoal.exe
2
//Population effective sizes (number of genes)
NMAYR
200
//Samples sizes and samples age
24 5
22
//Growth rates: negative growth implies population expansion
0
0
//Number of migration matrices : 0 implies no migration between demes
0
//historical event: time, source, sink, migrants, new deme size, new growth rate, migration
matrix index
```

```
3 historical event
13 1 0 1 1 0 0
TMAX 0 0 1 1 GRAT 0
TCOL 0 0 1 1 0 0
//Number of independent loci [chromosome]
1 0
//Per chromosome: Number of contiguous linkage Block: a block is a set of contiguous loci
1
//per Block:data type, number of loci, per generation recombination and mutation rates and optional parameters
FREQ 1 0 1.7e-8 OUTEXP
```

MRGC.est

```
// Priors and rules file
// *********************
[PARAMETERS]
//#isInt? #name #dist.#min #max
//all Ns are in number of haploid individuals
1 NMAYR unif 1000 100000 output
1 NANC unif 1000 100000 output
1 TCOL unif 3000 10000 output
0 PROP unif 0.1 0.9 hide
[RULES]
[COMPLEX PARAMETERS]
1 TMAX = TCOL*PROP output
1 TDIV = TCOL-TMAX hide
0 RATIO = NANC/NMAYR hide
0 RTEA = log(RATIO) hide
0 GRAT = RTEA/TDIV hide
```

MRGB.tpl

```
//Parameters for the coalescence simulation program : simcoal.exe
2
//Population effective sizes (number of genes)
NMAYR
NRDSP
//Samples sizes and samples age
24 5
22
//Growth rates: negative growth implies population expansion
0
0
//Number of migration matrices : 0 implies no migration between demes
0
//historical event: time, source, sink, migrants, new deme size, new growth rate, migration matrix index
4 historical event
7 1 1 1 RES1 0 0
13 1 0 1 1 0 0
TMAX 0 0 1 1 GRAT 0
TCOL 0 0 1 1 0 0
//Number of independent loci [chromosome]
1 0
//Per chromosome: Number of contiguous linkage Block: a block is a set of contiguous loci
1
//per Block:data type, number of loci, per generation recombination and mutation rates and optional parameters
FREQ 1 0 1.7e-8 OUTEXP
```

MRGB.est

```
// Priors and rules file
// *********************
[PARAMETERS]
//#isInt? #name #dist.#min #max
//all Ns are in number of haploid individuals
1 NMAYR unif 1000 100000 output
1 NRDSP unif 1000 10000 output
1 NANC unif 1000 100000 output
1 TCOL unif 3000 10000 output
0 PROP unif 0.1 0.9 hide
```

```
[RULES]
[COMPLEX PARAMETERS]
1 TMAX = TCOL*PROP output
1 TDIV = TCOL-TMAX hide
0 RATIO = NANC/NMAYR hide
0 RTEA = log(RATIO) hide
0 GRAT = RTEA/TDIV hide
0 RES1 = 200/NRDSP
```

MRGE.tpl

```
//Parameters for the coalescence simulation program : simcoal.exe
2
//Population effective sizes (number of genes)
NMAYR
NRDSP
//Samples sizes and samples age
24 5
22
//Growth rates: negative growth implies population expansion
0
RRAT
//Number of migration matrices : 0 implies no migration between demes
0
//historical event: time, source, sink, migrants, new deme size, new growth rate, migration
matrix index
4 historical event
13 1 1 1 1 0 0
13 1 0 1 1 0 0
TMAX 0 0 1 1 GRAT 0
TCOL 0 0 1 1 0 0
//Number of independent loci [chromosome]
1 0
//Per chromosome: Number of contiguous linkage Block: a block is a set of contiguous loci
1
//per Block:data type, number of loci, per generation recombination and mutation rates and
optional parameters
FREQ 1 0 1.7e-8 OUTEXP
```

MRGE.est

```
// Priors and rules file
// *********************
[PARAMETERS]
//#isInt? #name #dist.#min #max
//all Ns are in number of haploid individuals
1 NMAYR unif 1000 100000 output
1 NRDSP unif 1000 10000 output
1 NANC unif 1000 100000 output
1 TCOL unif 3000 10000 output
0 PROP unif 0.1 0.9 hide
[RULES]
[COMPLEX PARAMETERS]
1 TMAX = TCOL*PROP output
1 TDIV = TCOL-TMAX hide
0 RATIO = NANC/NMAYR hide
0 RTEA = log(RATIO) hide
0 GRAT = RTEA/TDIV hide
0 RATBB = 200/NRDSP hide
0 RCOF = log(RATBB) hide
0 RRAT = RCOF/13 hide
```

MRBC.tpl

```
//Parameters for the coalescence simulation program : simcoal.exe
2
//Population effective sizes (number of genes)
NMAYR
200
//Samples sizes and samples age
24 5
22
//Growth rates: negative growth implies population expansion
```

```
0
0
//Number of migration matrices : 0 implies no migration between demes
0
//historical event: time, source, sink, migrants, new deme size, new growth rate, migration matrix index
3 historical event
13 1 0 1 1 0 0
TEND 0 0 1 RES2 0 0
TBOT 0 0 1 BTST 0 0
//Number of independent loci [chromosome]
1 0
//Per chromosome: Number of contiguous linkage Block: a block is a set of contiguous loci
1
//per Block:data type, number of loci, per generation recombination and mutation rates and optional parameters
FREQ 1 0 1.7e-8 OUTEXP
```

MRBC.est

```
// Priors and rules file
// *********************
[PARAMETERS]
//#isInt? #name #dist.#min #max
//all Ns are in number of haploid individuals
1 NMAYR unif 10000 100000 output
1 NANC unif 10000 1000000 output
1 BTST unif 2 100 output
1 TBOT unif 3000 10000 output
1 LEBO unif 20 200
[RULES]
[COMPLEX PARAMETERS]
1 TEND = TBOT-LEBO output
1 NCOL = NANC/BTST output
0 RES2 = NCOL/NMAYR hide
0 RES1 = NMAYR/NCOL hide
```

MRBB.tpl

```
//Parameters for the coalescence simulation program : simcoal.exe
2
//Population effective sizes (number of genes)
NMAYR
NRDSP
//Samples sizes and samples age
24 5
22
//Growth rates: negative growth implies population expansion
0
0
//Number of migration matrices : 0 implies no migration between demes
0
//historical event: time, source, sink, migrants, new deme size, new growth rate, migration matrix index
4 historical event
7 1 1 1 RES1 0 0
13 1 0 1 1 0 0
TEND 0 0 1 RES2 0 0
TBOT 0 0 1 BTST 0 0
//Number of independent loci [chromosome]
1 0
//Per chromosome: Number of contiguous linkage Block: a block is a set of contiguous loci
1
//per Block:data type, number of loci, per generation recombination and mutation rates and optional parameters
FREQ 1 0 1.7e-8 OUTEXP
```

MRBB.est

```
// Priors and rules file
// *********************
[PARAMETERS]
//#isInt? #name #dist.#min #max
```

```
//all Ns are in number of haploid individuals
1 NMAYR unif 1000 100000 output
1 NRDSP unif 1000 10000 output
1 NANC unif 1000 100000 output
1 BTST unif 2 100 output
1 TBOT unif 3000 10000 output
1 LEBO unif 20 200
[RULES]
[COMPLEX PARAMETERS]
1 TEND = TBOT-LEBO output
1 NCOL = NANC/BTST output
0 RES2 = NCOL/NMAYR hide
0 RES1 = 200/NRDSP hide
```

MRBE.tpl

```
//Parameters for the coalescence simulation program : simcoal.exe
2
//Population effective sizes (number of genes)
NMAYR
NRDSP
//Samples sizes and samples age
24 5
22
//Growth rates: negative growth implies population expansion
0
RRAT
//Number of migration matrices : 0 implies no migration between demes
0
//historical event: time, source, sink, migrants, new deme size, new growth rate, migration
matrix index
4 historical event
13 1 1 1 1 0 0
13 1 0 1 1 0 0
TEND 0 0 1 RES2 0 0
TBOT 0 0 1 BTST 0 0
//Number of independent loci [chromosome]
1 0
//Per chromosome: Number of contiguous linkage Block: a block is a set of contiguous loci
1
//per Block:data type, number of loci, per generation recombination and mutation rates and
optional parameters
FREQ 1 0 1.7e-8 OUTEXP
```

MRBE.est

```
// Priors and rules file
// *********************
[PARAMETERS]
//#isInt? #name #dist.#min #max
//all Ns are in number of haploid individuals
1 NMAYR unif 10000 100000 output
1 NRDSP unif 1000 10000 output
1 NANC unif 10000 1000000 output
1 BTST unif 2 100 output
1 TBOT unif 3000 10000 output
1 LEBO unif 20 200
[RULES]
[COMPLEX PARAMETERS]
1 TEND = TBOT-LEBO output
1 NCOL = NANC/BTST output
0 RES2 = NCOL/NMAYR hide
0 RATBB = 200/NRDSP hide
0 RCOF = log(RATBB) hide
0 RRAT = RCOF/13 hide
```

MREC.tpl

```
//Parameters for the coalescence simulation program : simcoal.exe
2
//Population effective sizes (number of genes)
NMAYR
200
```

```
//Samples sizes and samples age
24 5
22
//Growth rates: negative growth implies population expansion
0
0
//Number of migration matrices : 0 implies no migration between demes
0
//historical event: time, source, sink, migrants, new deme size, new growth rate, migration
matrix index
3 historical event
13 1 0 1 1 0 0
TMAX 0 0 1 1 GRAT 0
TBOT 0 0 1 BTST 0 0
//Number of independent loci [chromosome]
1 0
//Per chromosome: Number of contiguous linkage Block: a block is a set of contiguous loci
1
//per Block:data type, number of loci, per generation recombination and mutation rates and
optional parameters
FREQ 1 0 1.7e-8 OUTEXP
```

MREC.est

```
// Priors and rules file
// *********************
[PARAMETERS]
//#isInt? #name #dist.#min #max
//all Ns are in number of haploid individuals
1 NMAYR unif 10000 100000 output
1 NANC unif 10000 1000000 output
1 BTST unif 2 100 output
1 TBOT unif 3000 10000 output
0 PROP unif 0.1 0.9 hide
[RULES]
[COMPLEX PARAMETERS]
1 TMAX = TBOT*PROP output
1 NCOL = NANC/BTST output
0 RES1 = NMAYR/(NANC/BTST) hide
1 TDIV = TBOT-TMAX hide
0 RATIO = (NANC/BTST)/NMAYR hide
0 RTEA = log(RATIO) hide
0 GRAT = RTEA/TDIV hide
```

MREB.tpl

```
//Parameters for the coalescence simulation program : simcoal.exe
2
//Population effective sizes (number of genes)
NMAYR
NRDSP
//Samples sizes and samples age
24 5
22
//Growth rates: negative growth implies population expansion
0
0
//Number of migration matrices : 0 implies no migration between demes
0
//historical event: time, source, sink, migrants, new deme size, new growth rate, migration
matrix index
4 historical event
7 1 1 1 RES1 0 0
13 1 0 1 1 0 0
TMAX 0 0 1 1 GRAT 0
TBOT 0 0 1 BTST 0 0
//Number of independent loci [chromosome]
1 0
//Per chromosome: Number of contiguous linkage Block: a block is a set of contiguous loci
1
//per Block:data type, number of loci, per generation recombination and mutation rates and
optional parameters
FREQ 1 0 1.7e-8 OUTEXP
```

MREB.est

```
// Priors and rules file
// *********************
[PARAMETERS]
//#isInt? #name #dist.#min #max
//all Ns are in number of haploid individuals
1 NMAYR unif 10000 100000 output
1 NRDSP unif 1000 10000 output
1 NANC unif 10000 1000000 output
1 BTST unif 2 100 output
1 TBOT unif 3000 10000 output
0 PROP unif 0.1 0.9 hide
[RULES]
[COMPLEX PARAMETERS]
1 TMAX = TBOT*PROP output
1 NCOL = NANC/BTST output
1 TDIV = TBOT-TMAX hide
0 RATIO = (NANC/BTST)/NMAYR hide
0 RTEA = log(RATIO) hide
0 GRAT = RTEA/TDIV hide
0 RATBB = 200/NRDSP hide
0 RCOF = log(RATBB) hide
0 RRAT = RCOF/13 hide
0 RES1 = 200/NRDSP
```

MREE.tpl

```
//Parameters for the coalescence simulation program : simcoal.exe
2
//Population effective sizes (number of genes)
NMAYR
NRDSP
//Samples sizes and samples age
24 5
22
//Growth rates: negative growth implies population expansion
0
RRAT
//Number of migration matrices : 0 implies no migration between demes
0
//historical event: time, source, sink, migrants, new deme size, new growth rate, migration
matrix index
4 historical event
13 1 1 1 1 0 0
13 1 0 1 1 0 0
TMAX 0 0 1 1 GRAT 0
TBOT 0 0 1 BTST 0 0
//Number of independent loci [chromosome]
1 0
//Per chromosome: Number of contiguous linkage Block: a block is a set of contiguous loci
1
//per Block:data type, number of loci, per generation recombination and mutation rates and
optional parameters
FREQ 1 0 1.7e-8 OUTEXP
```

MREE.est

```
// Priors and rules file
// *********************
[PARAMETERS]
//#isInt? #name #dist.#min #max
//all Ns are in number of haploid individuals
1 NMAYR unif 10000 100000 output
1 NRDSP unif 1000 10000 output
1 NANC unif 10000 1000000 output
1 BTST unif 2 100 output
1 TBOT unif 3000 10000 output
0 PROP unif 0.1 0.9 hide
[RULES]
[COMPLEX PARAMETERS]
1 TMAX = TBOT*PROP output
1 NCOL = NANC/BTST output
```

```
0 RES1 = NMAYR/(NANC/BTST) hide
1 TDIV = TBOT-TMAX hide
0 RATIO = (NANC/BTST)/NMAYR hide
0 RTEA = log(RATIO) hide
0 GRAT = RTEA/TDIV hide
0 RATBB = 200/NRDSP hide
0 RCOF = log(RATBB) hide
0 RRAT = RCOF/13 hide
```