

Linkage Disequilibrium and Inversion-Typing of the *Drosophila melanogaster* Genome Reference Panel

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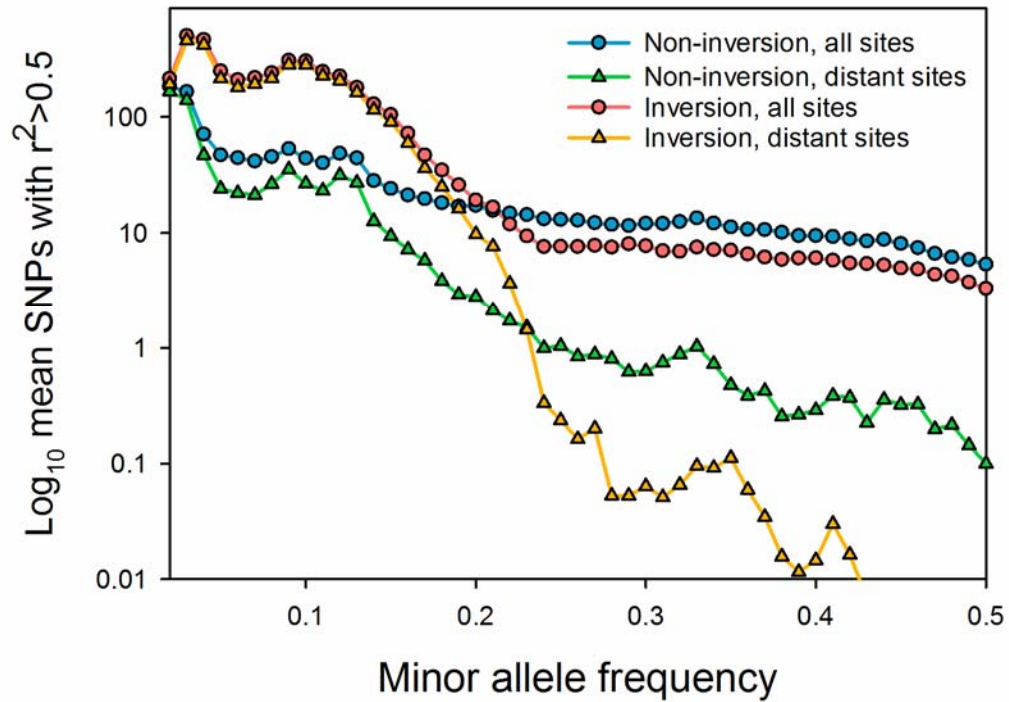


Figure S1 Mean number of sites correlated with variant sites at $r^2 > 0.5$ as a function of minor allele frequency for sites within and outside common inversions. We treated the distal segment of chromosome 3R as part of In(3R)Mo (Corbett-Detig and Hartl 2012).

Supporting Files

All supporting files are archived and available at <http://dx.doi.org/10.5061/dryad.06jt7>

File S1

HouleMarquezSASfiles.zip . Zip file with two SAS programs and example data set. Gcorrlimits.sas is a stand-alone program that demonstrates how we calculated the limits on which allele frequencies can be correlated at $r^2 \geq 0.5$. CalcHighCorr.sas reads the SAS data set gcorrexampledatsas7bdat to demonstrate the calculation of correlations as a measure of linkage disequilibrium. Programs are written in SAS 9.3 (SAS Institute 2011).

File S2

LD205results.zip. Correlations of all SNP pairs with $r^2 \geq 0.5$ in the Freeze2 of the DGRP. Zip file contains separate csv files for each chromosome arm.

File S3

HouleMarquezF3_PCscores.csv. Supporting Table: Inversion-typing of DGRP lines for the three common inversions In(2L)t, In(2R)NS, and In(3R)Mo, and heterozygosity of chromosome regions.

Table S1 Inferred kilobase pairs of African ancestry in homozygous inverted regions.

| Chromosome | Predicted Karyotype | Consensus* | | Mismatch† | |
|------------|---------------------|--------------|-----|----------------|---|
| | | Mean ± S.D. | N | Mean ± S.D. | N |
| 2L | Standard | 2,022 ±1,081 | 161 | -- | |
| | In(2L)t | 13,605±2,494 | 19 | 14,713 ± 1,098 | 4 |
| 2R | Standard | 412 ±194 | 161 | 5,840 | 1 |
| | In(2R)NS | 6,385±3,057 | 7 | 874 | 1 |
| 3R | Standard | 1,504 ±3,459 | 175 | 1,051± 466 | 2 |
| | In(3R)MO | 80 ± 67 | 16 | 64 ± 40 | 4 |

* Consensus lines are assigned the same inversion type by our LD-based PC classification and by previous studies (Corbett-Detig and Hartl 2012; Huang et al. 2012).

† Mismatch lines are assigned an LD PC classification that disagrees with one of the previous studies.

Literature Cited

- Corbett-Detig, R.B., and D.L. Hartl, 2012 Population Genomics of Inversion Polymorphisms in *Drosophila melanogaster*. *PLoS Genetics* 8: e1003056.
- Huang, W., S. Richards, M.A. Carbone, D. Zhu, R.R.H. Anholt *et al.*, 2012 Epistasis dominates the genetic architecture of *Drosophila* quantitative traits. *Proceedings of the National Academy of Sciences of the United States of America* 109: 15553-15559.
- SAS Institute, Inc., 2011 *The SAS System for Windows*, Release 9.3. SAS Institute, Cary, NC.