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**Hillary E. Sussman, Ph.D.**  
Executive Editor  
Genome Research  
Cold Spring Harbor Laboratory Press  
One Bungtown Road  
Cold Spring Harbor, NY 11724

22 December 2015

Dear Ms Sussman,

I hereby submit the manuscript “Genome variation and meiotic recombination in *Plasmodium falciparum*: insights from deep sequencing of genetic crosses” for your consideration.

Resistance to front-line anti-malarial drugs has emerged and spread in South-East Asia and is a major threat to malaria control. Evolution of anti-malarial resistance in parasite populations is influenced by the processes of mutation and sexual recombination, and by the presence of standing genetic variation. In this paper we show that the architecture of core genome variation in *P. falciparum* is extreme, with an exceptionally high density of INDELs throughout, and tightly localised regions of intense SNP polymorphism. We also provide a definitive analysis of sexual recombination, and show for the first time how recombination can modify amplifications spanning known drug resistance genes. These data provide a reference resource for deeper studies of evolutionary processes in natural parasite populations.

This manuscript has been seen and approved by all listed authors.

Potential referees:

* TODO

All sequence read data have been submitted to the European Nucleotide Archive. All genome variation data are available from a public FTP site hosted by the Wellcome Trust Sanger Institute. Further details of data released are available from <http://www.malariagen.net/data/pf-crosses-1.0>.

Gene/protein names used in the paper: TODO

Yours sincerely,  
Alistair Miles