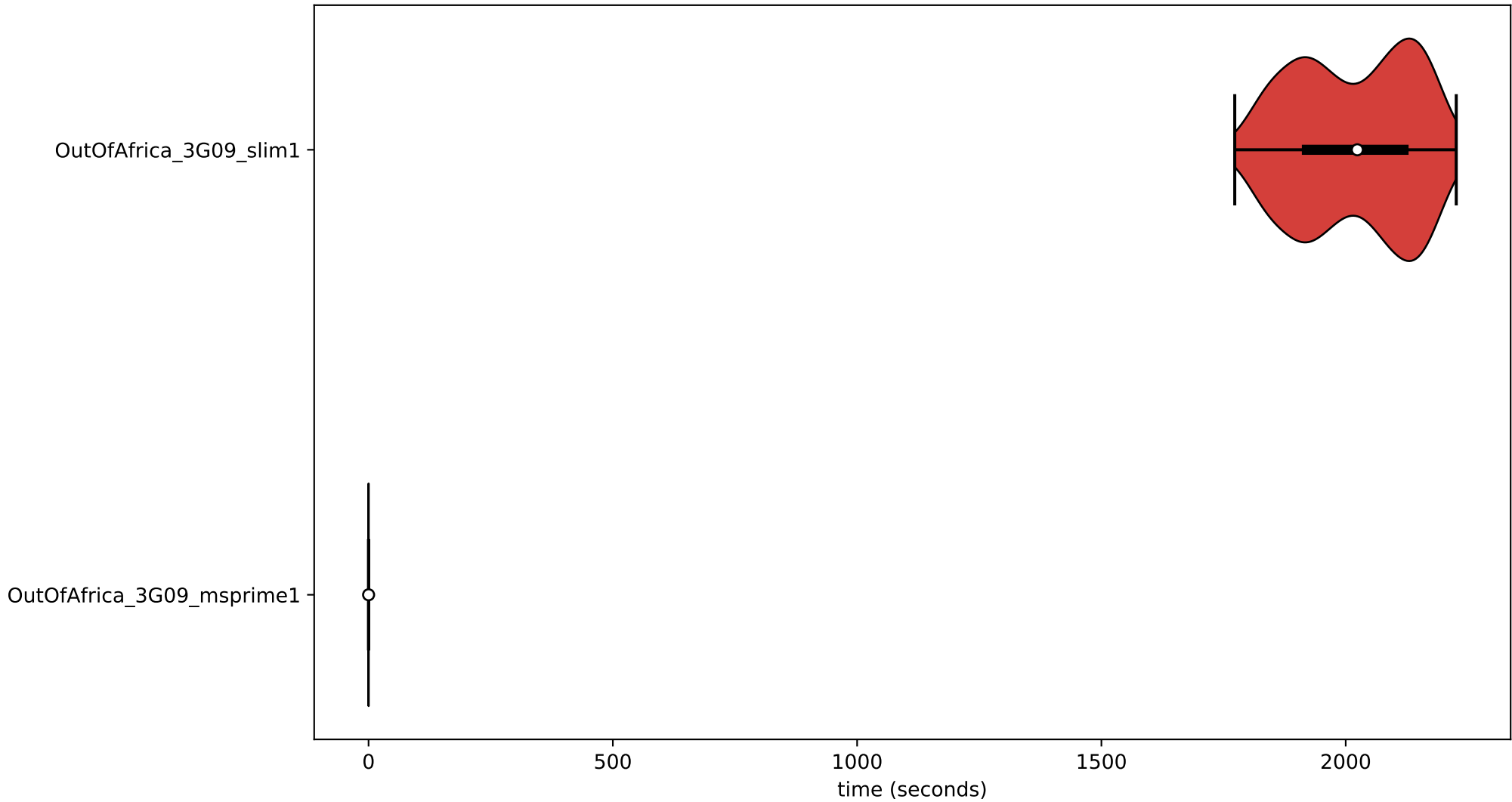
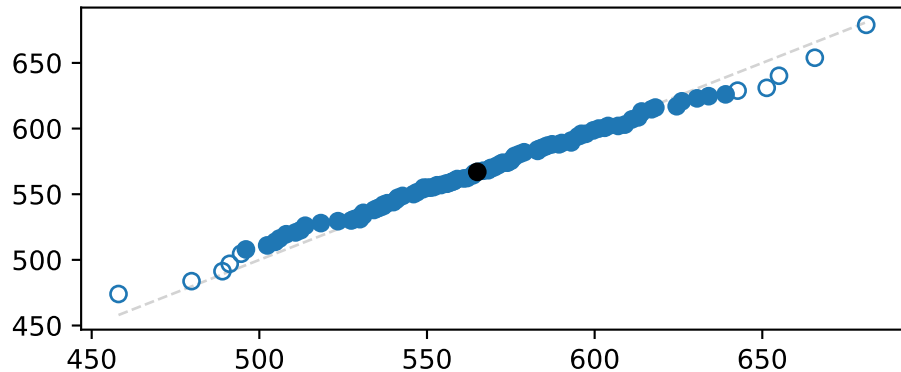


# Run time.

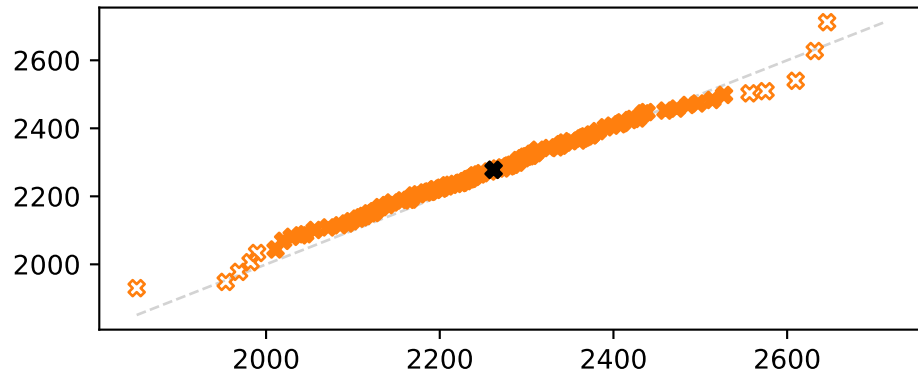


ts\_properties:  
TreeSequence properties.

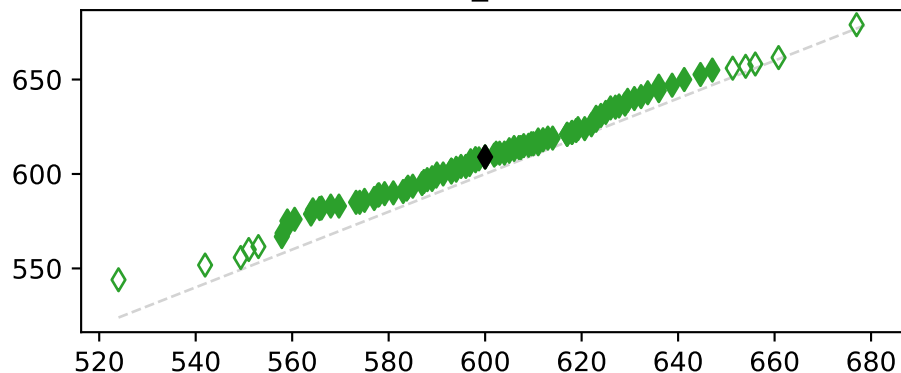
num\_trees



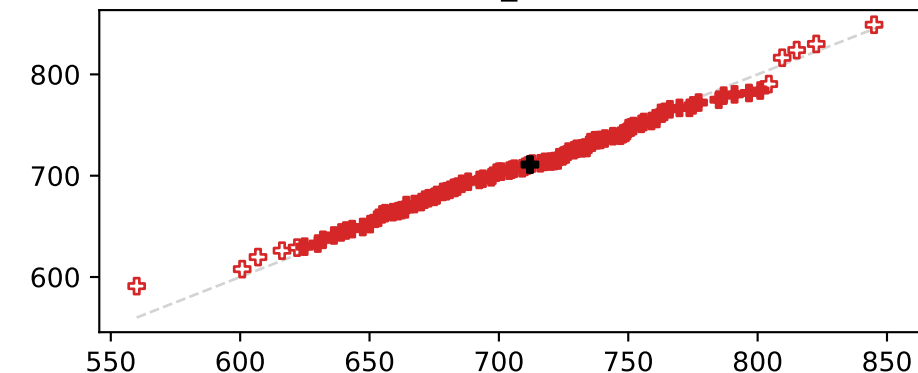
num\_edges



num\_nodes



num\_sites



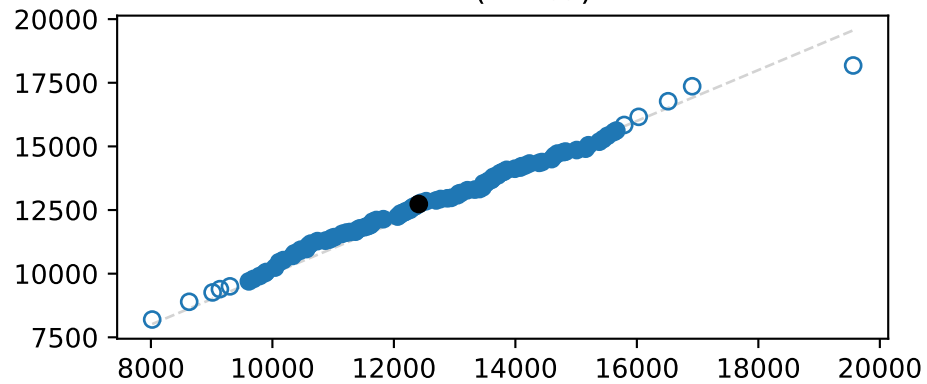
OutOfAfrica\_3G09\_msprime1

OutOfAfrica\_3G09\_slim1

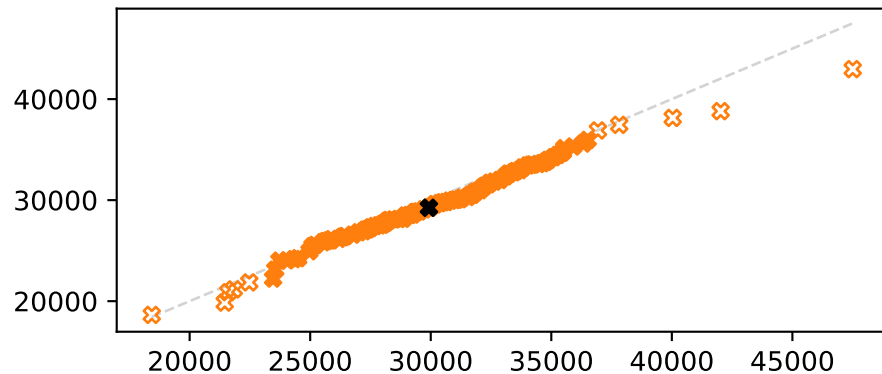
tmrca:

Time to most recent common ancestor of sample, aka tree height.

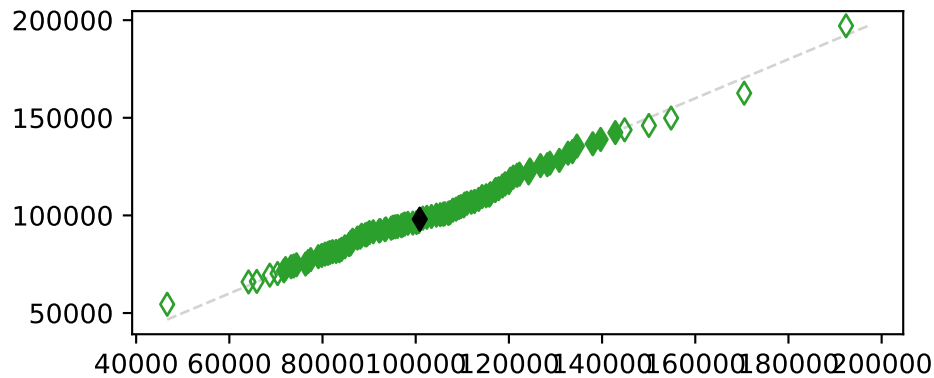
min(tmrca)



median(tmrca)

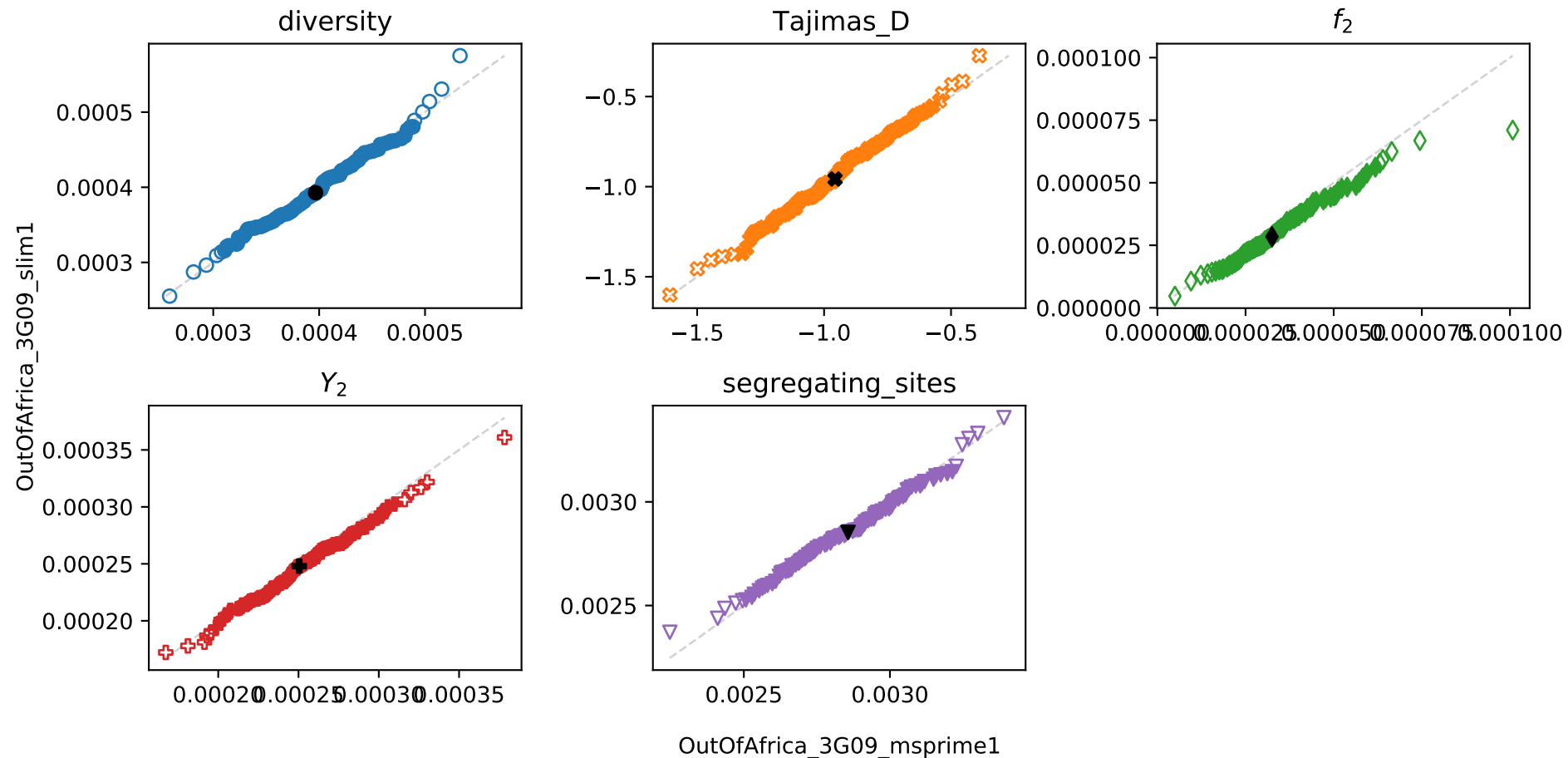


max(tmrca)

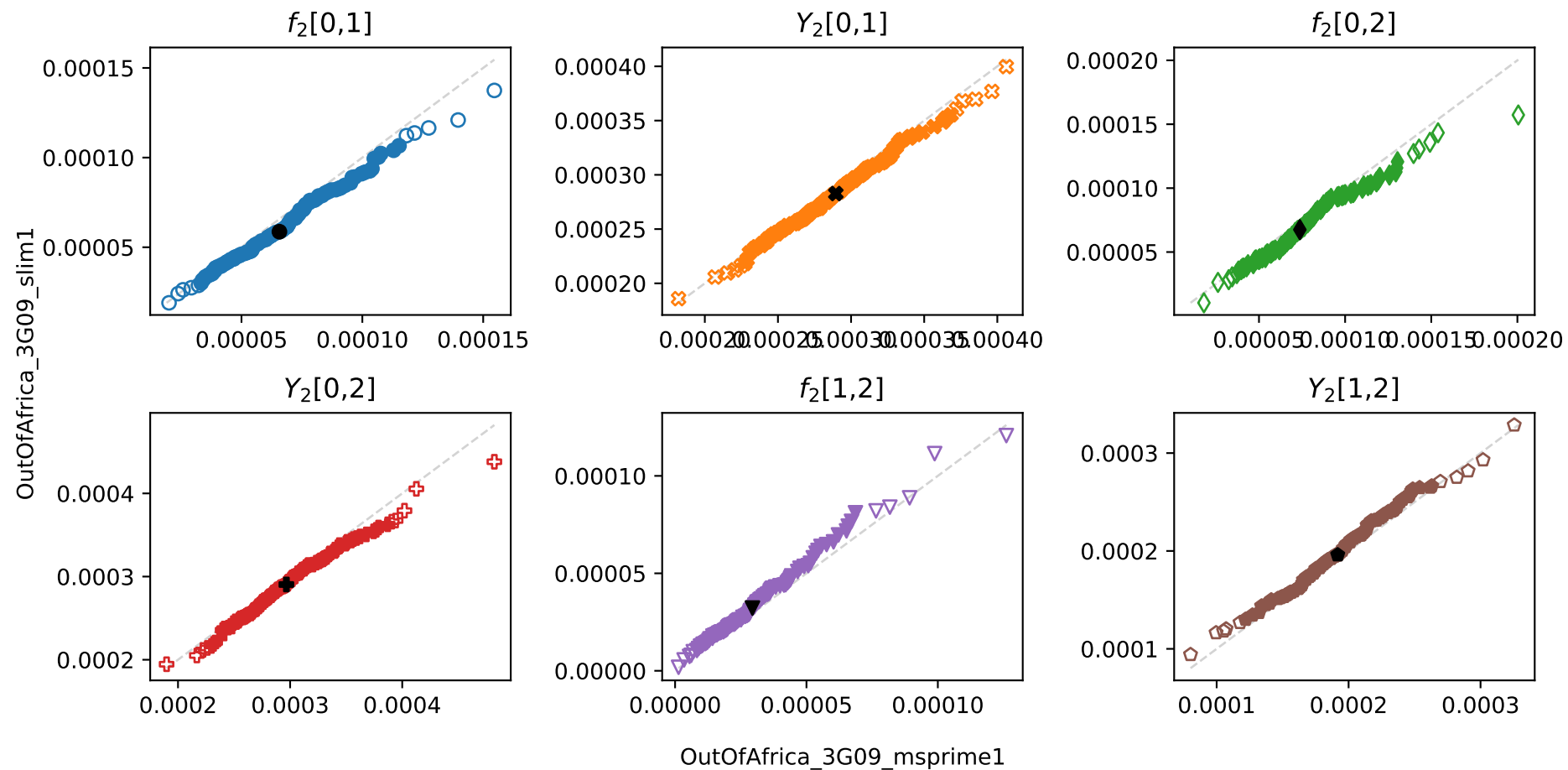


OutOfAfrica\_3G09\_msprime1

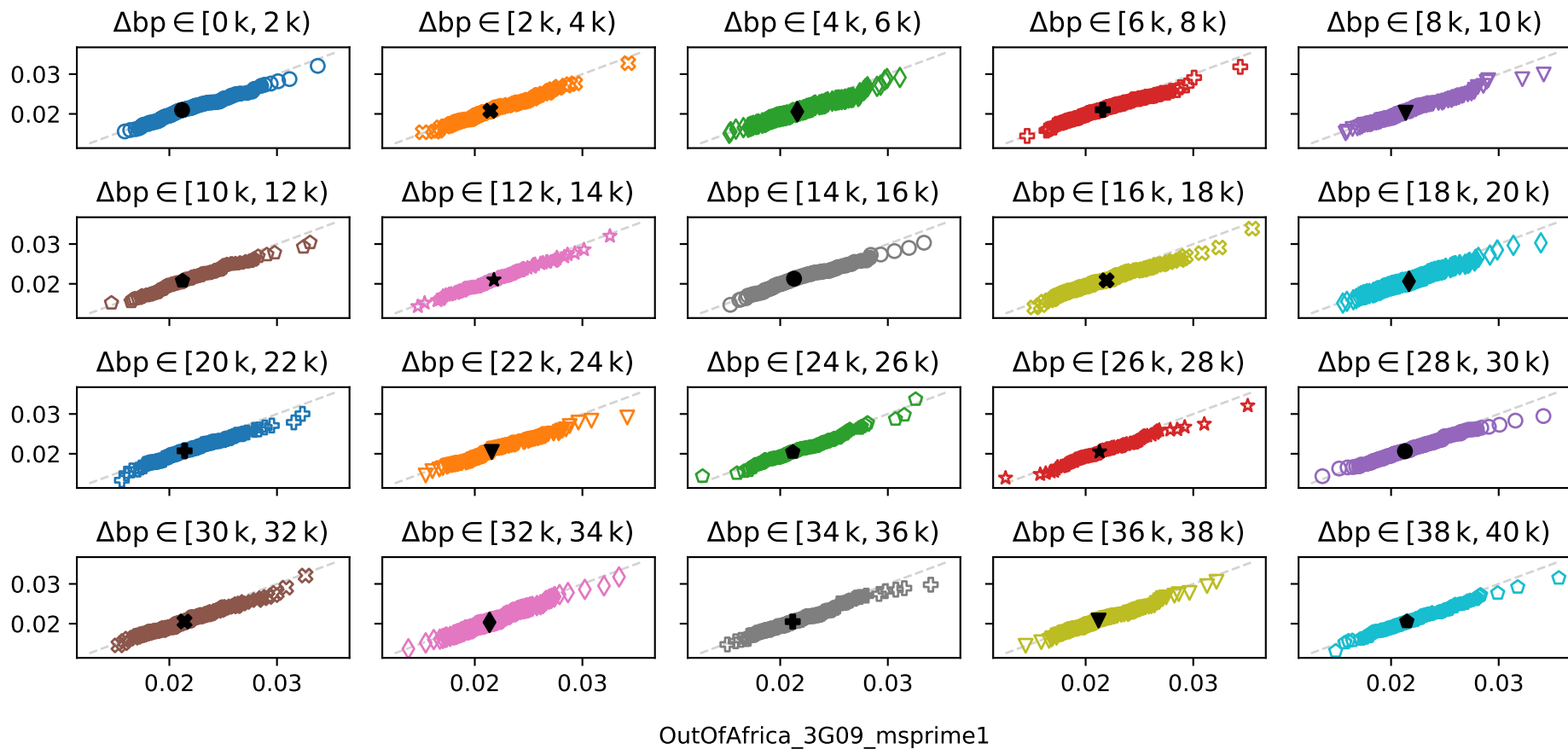
pooled\_pop\_stats:  
Population statistics, with samples pooled from all populations.



pairwise\_pop\_stats:  
Pairwise population statistics, calculated for all pairs of populations.



linkage disequilibrium:  
 $R^2$  as a function of site-separation distance, for `bins` bins up to a  
site-separation distance of `span` bp.



allele\_frequency\_spectrum:  
Allele frequency spectrum for `bins` allele frequency bins.  
Values are log(1+counts) for each bin.

