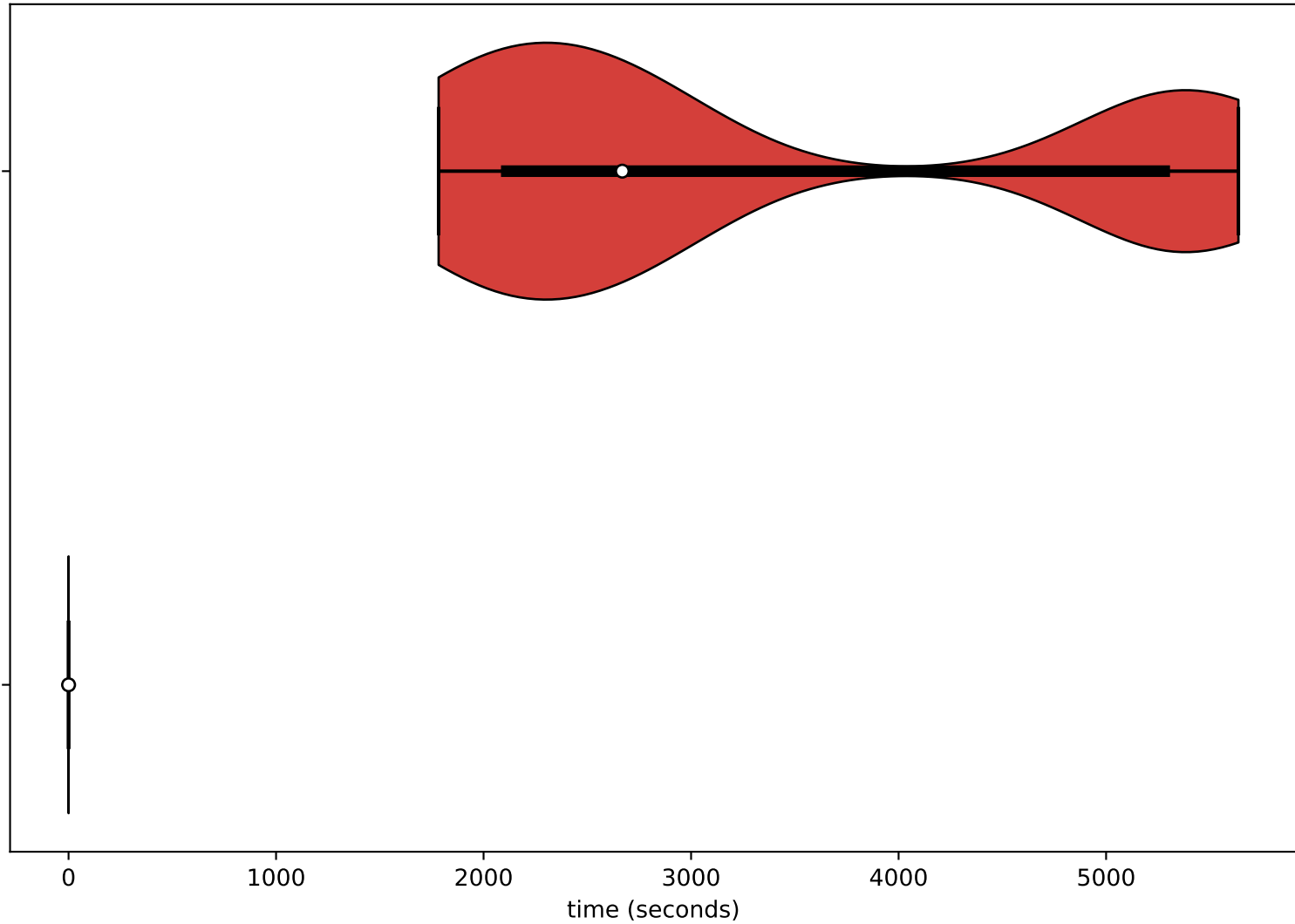


Run time.

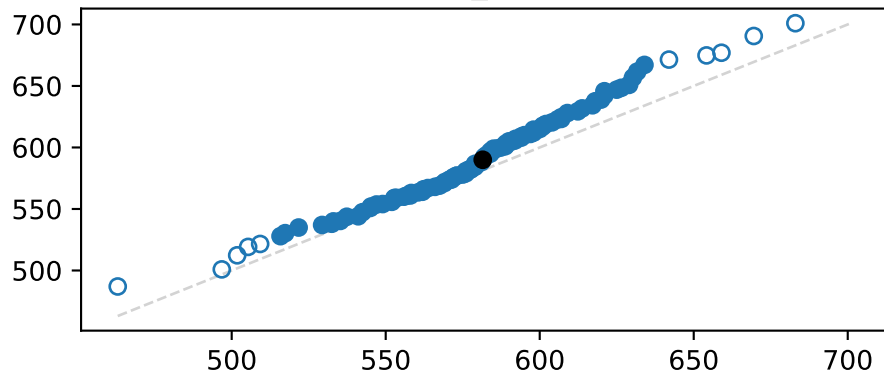
AmericanAdmixture_4B11_slim1

AmericanAdmixture_4B11_msprime1

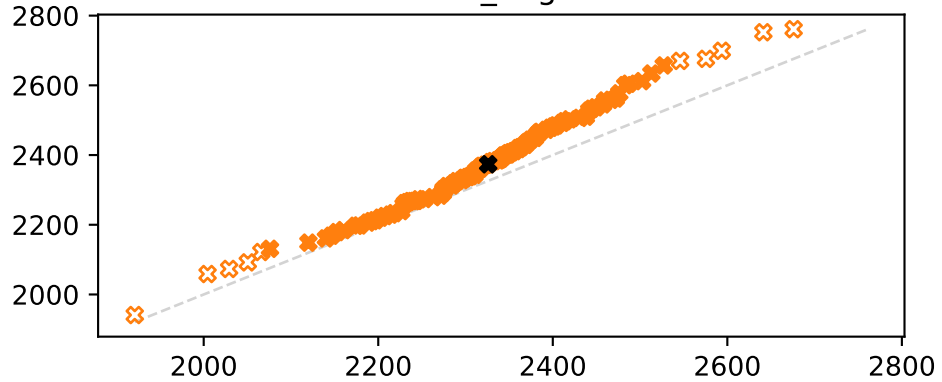


ts_properties:
TreeSequence properties.

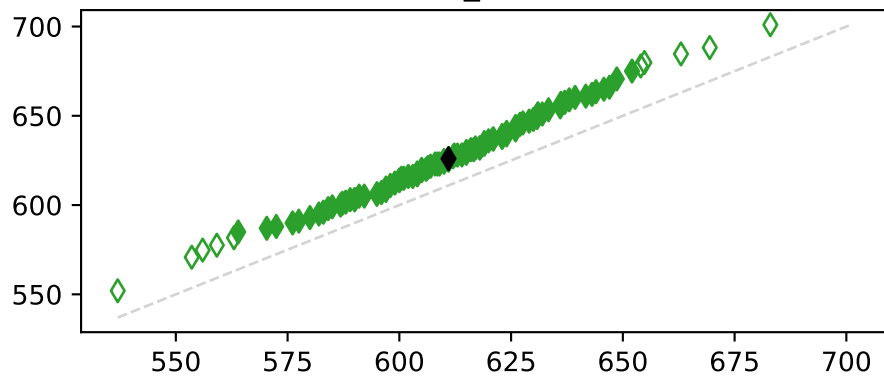
num_trees



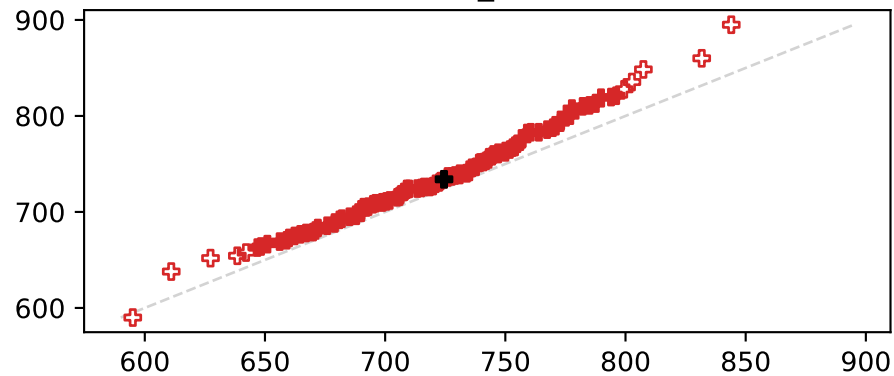
num_edges



num_nodes



num_sites



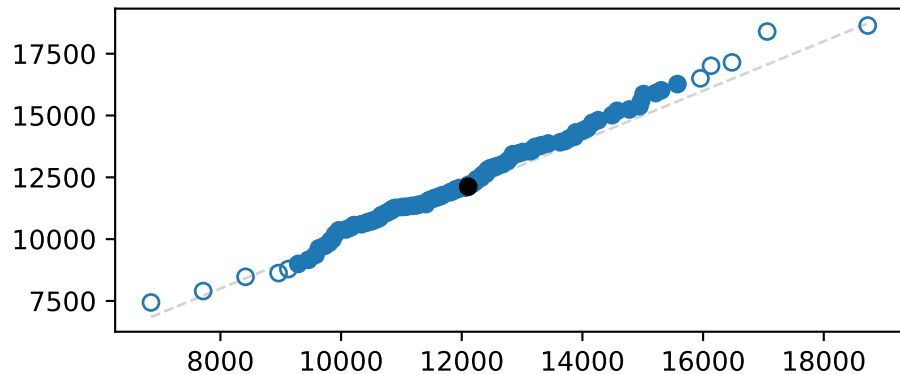
AmericanAdmixture_4B11_msprime1

AmericanAdmixture_4B11_slim1

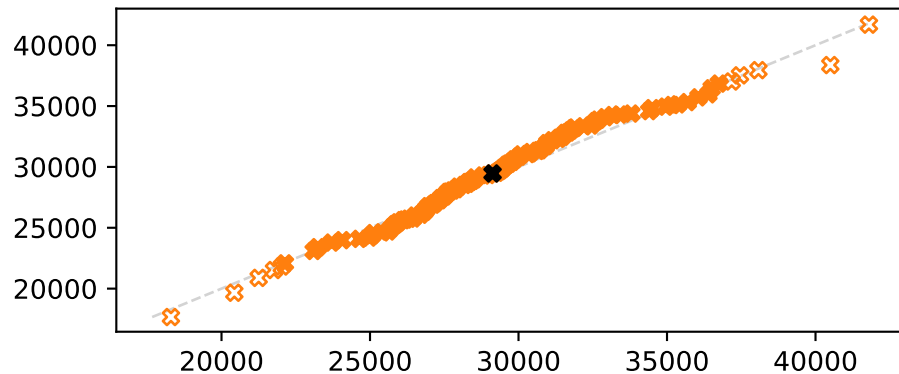
tmrca:

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

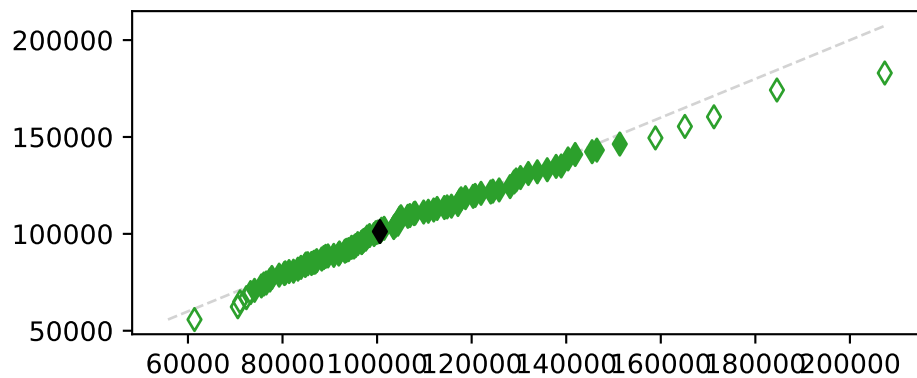
min(tmrca)



median(tmrca)

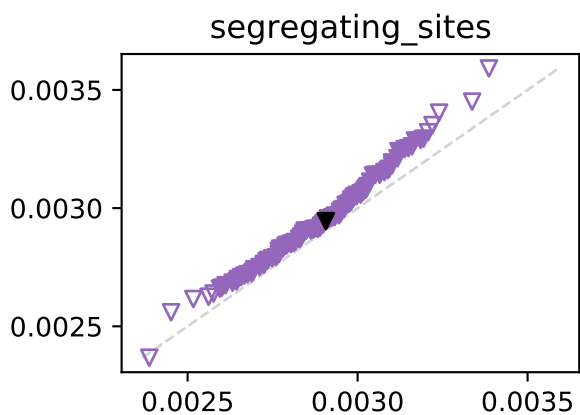
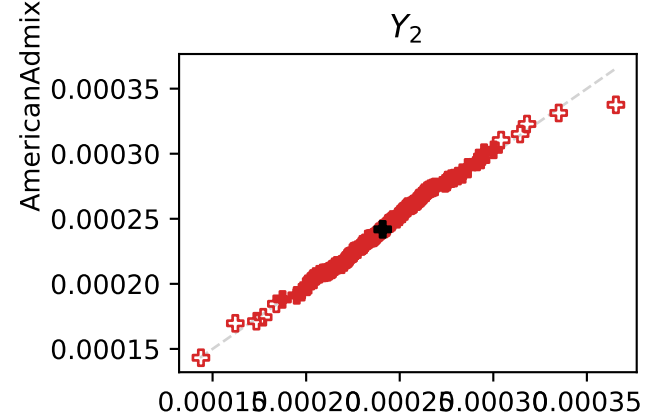
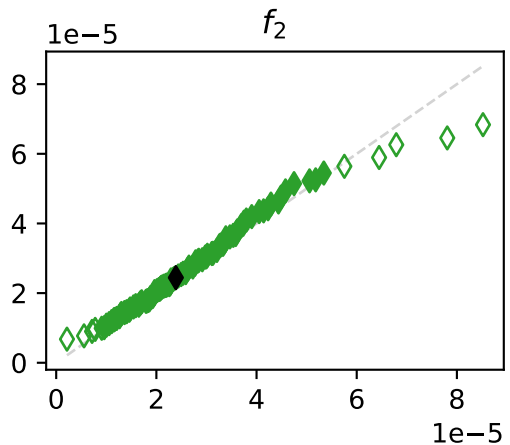
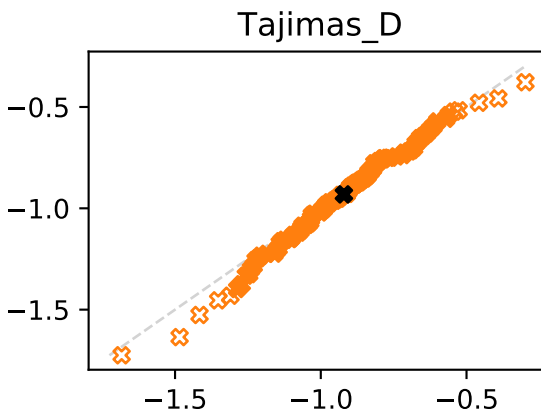
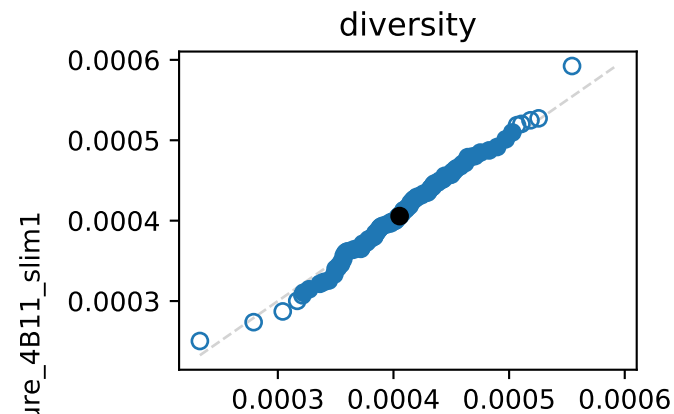


max(tmrca)



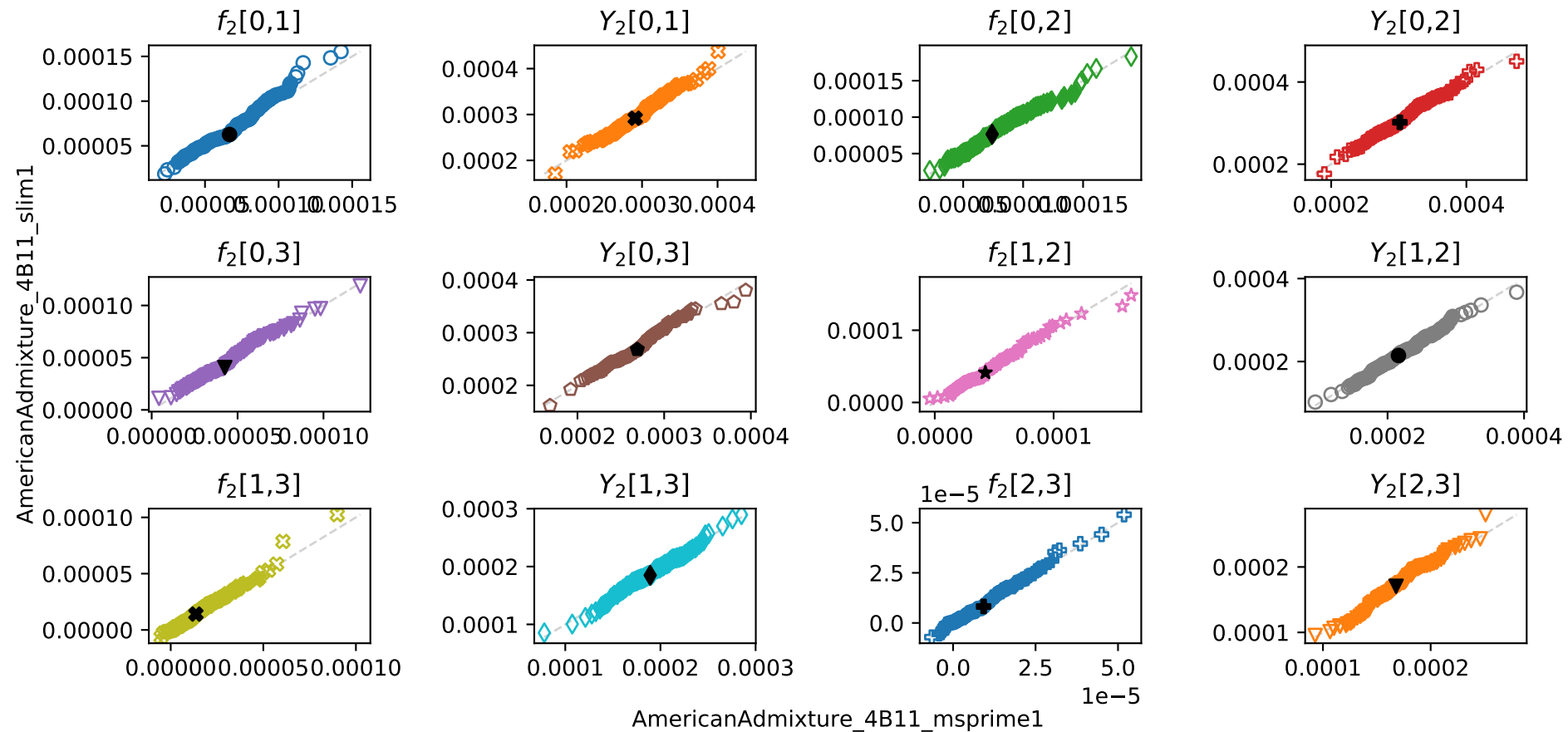
AmericanAdmixture_4B11_msprime1

pooled_pop_stats:
Population statistics, with samples pooled from all populations.

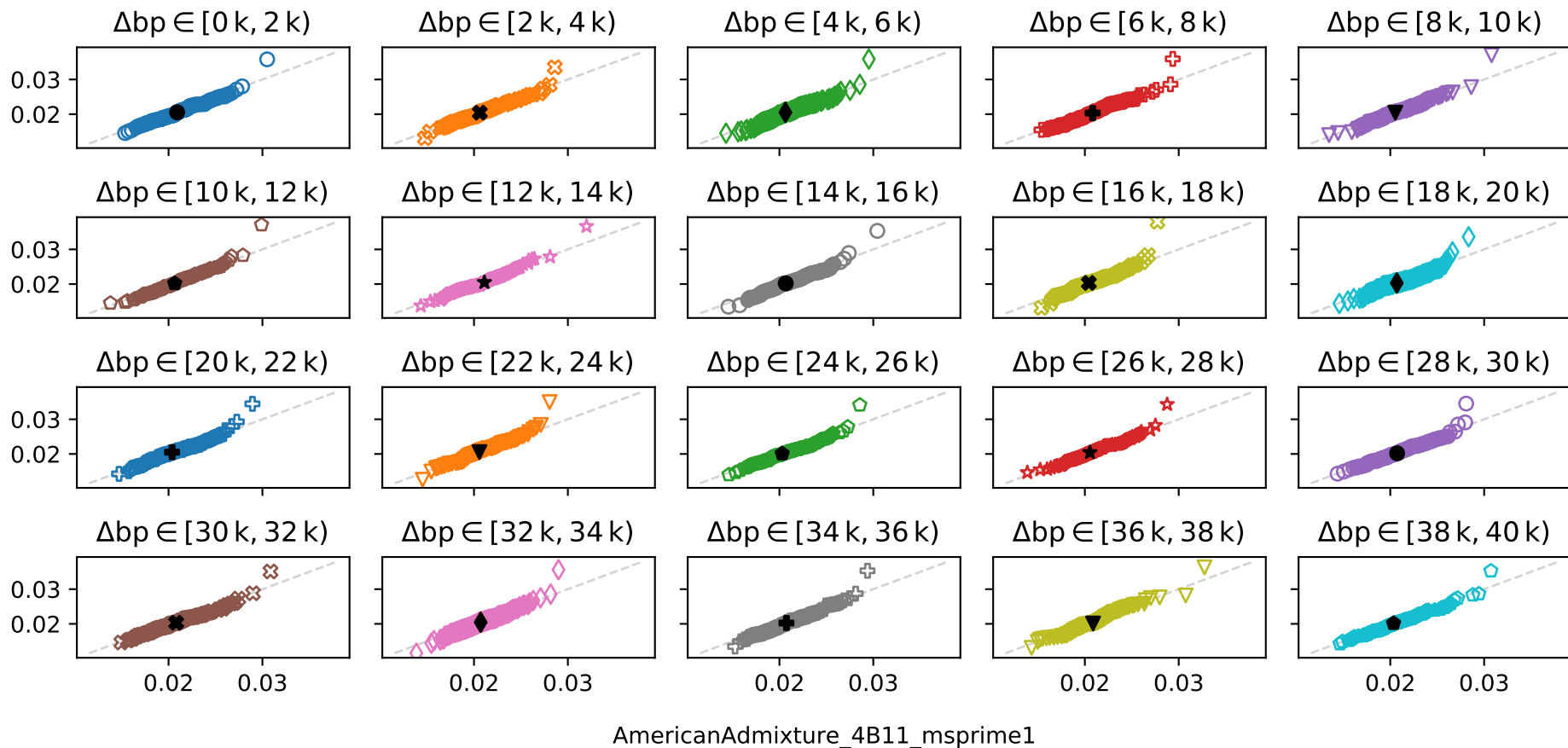


AmericanAdmixture_4B11_msprime1

pairwise_pop_stats:
Pairwise population statistics, calculated for all pairs of populations.

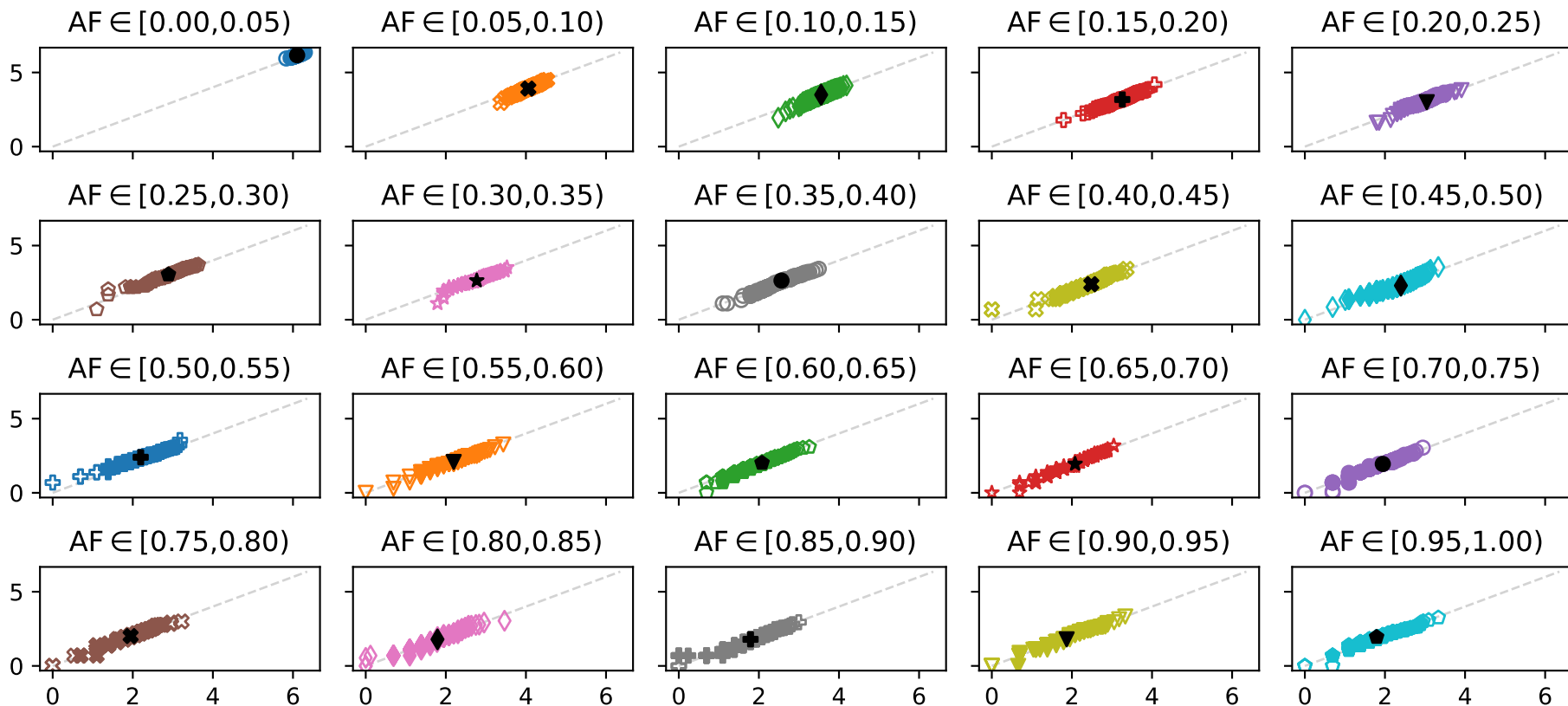


linkage disequilibrium:
 R^2 as a function of site-separation distance, for `bins` bins up to a
site-separation distance of `span` bp.



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

AmericanAdmixture_4B11_slim1



AmericanAdmixture_4B11_msprime1