

Figure 6-figure supplemental 1. Model output for all three gene flow scenarios. Simulated tree topology proportions (left) and D-statistics (right) under models of (a) symmetric, (b) asymmetric, and (c) unidirectional gene flow. Left: Tree topologies are simulated under 100 different combinations of m and N (represented as M on the x-axis) and 10 different combinations of t_1 (four values of which are shown in the legend). The difference between each of the 1000 simulated and observed tree topology proportions is estimated using euclidean distance where observed and simulated proportions of sib-japon and japon-oxy topologies specify point 1 and point 2, respectively (sib-japon refers to red tree while japon-oxy refers to blue tree in **Fig. 6a**). Quantified as such, a difference of zero (y-axis) points at the best parameter combination that matches observed allele sharing proportions genomewide. Right: Given the "species" tree (**Fig. 6b**), D-statistics (y-axis) are calculated for different combinations of m (x-axis) and N (legend; top left) which cover the parameter space of interest (**Fig. 6c** and **Supplementary Table 7**). Note that simulations are carried out with $t_1=1$ and only five out of twelve N values are shown in the legend. Filled circles on the y-axis denote observed chromosome-specific D statistic estimates and horizontal black lines denote the range of these values

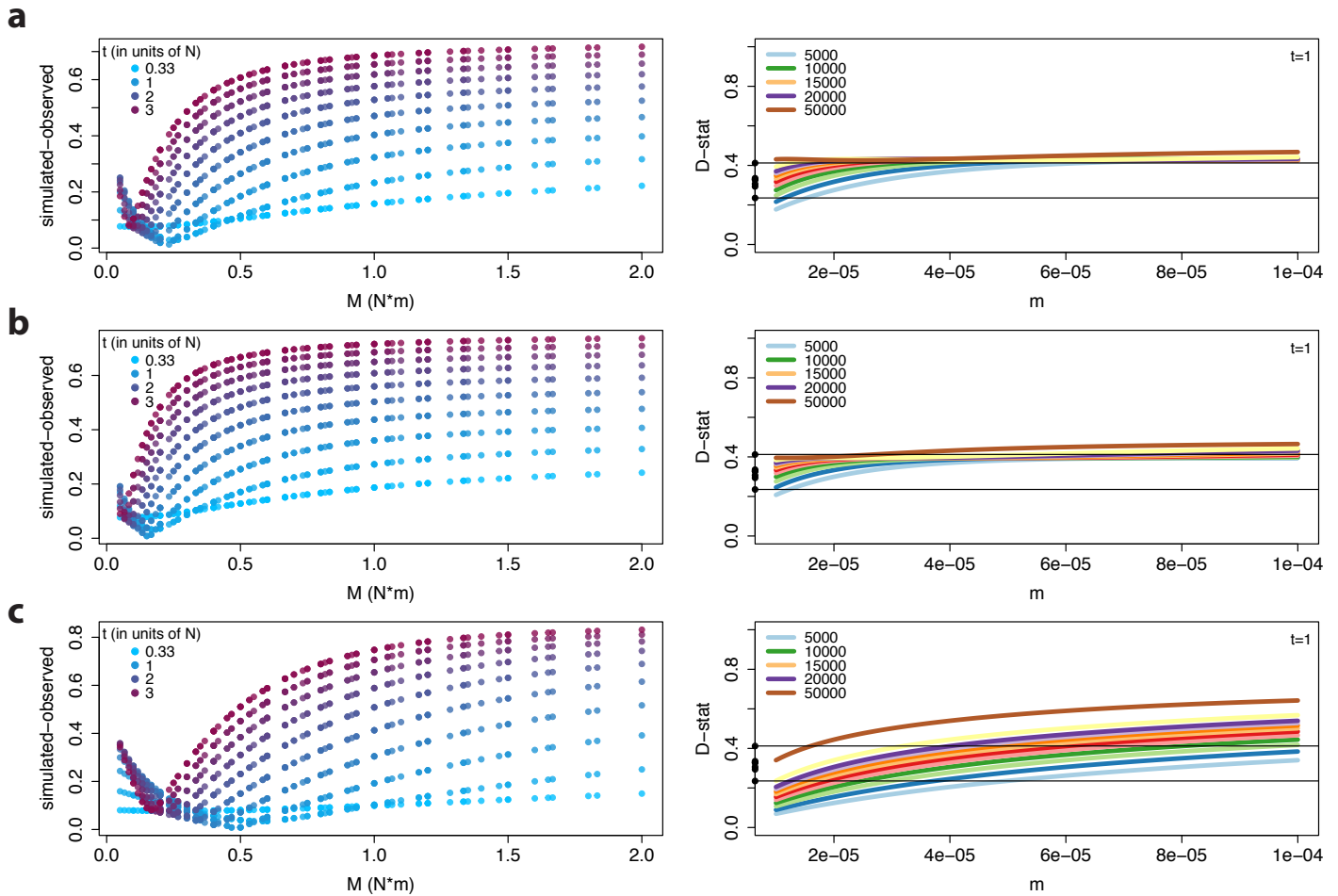


Figure 3-figure supplemental 2. P-values of proportion tests by chromosome for significantly-different trees - corrected for 70 tests

Subtree	Corrected p-value						
	Chr_01	Chr_02	Chr_03	Chr_04	Chr_05	Chr_06	Chr_07
japon/sib	1	1	1	9.2E-19	1	0.95	1
aur/japon/sib/vul	1	1	1	2.3E-13	1	1	1
japon/oxy	1	1	1	7.5E-10	1	1	1
oxy basal	0.3	1	1	6.7E-09	1	1	1
oxy/sib	1	1	1	3.1E-05	1	1	1
N.America	1	1	1	3.9E-04	1	1	1
aur/japon/oxy	1	1	1	7.5E-04	1	1	1
japon/oxy/sib	0.7	1	1	9.9E-03	1	1	1
japon/sib/vul	1	1	1	8.9E-02	1	1	1
bar/pub	0.002	1	1	1	1	1	1