



Figure S4: F_{ST} for 100 10kb regions where only 10% of the sites are variable in the population. F_{ST} is computed using the estimated global 2D-SFS (first row) or the true 2D-SFS as a prior (second row) (see Material and Methods). Dotted line represents the diagonal while the continuous line is the regressed line between true and estimated F_{ST} . We simulated a total of 1M sites at 2X, 6X and 20X sequencing coverage and 20 individuals for each population.