Table S2 Comparison between computer simulations and diffusion approximations (E[] in bold face) for different gene frequency and allelic diversity variables.

u = 0.00001								
Nm	A_S	E[A_S]	D_A	E[D_A]	A_{ST}	E[A_{ST}]	K_T	E[K_T]
0	0.299	**0.301**	1.152	**1.146**	0.794	**0.792**	12.36	**68.198**
0.01	0.512	**0.547**	1.203	**1.174**	0.701	**0.682**	10.50	**37.366**
0.05	0.923	**1.059**	1.028	**0.969**	0.527	**0.478**	7.31	**16.269**
0.1	1.444	**1.277**	0.935	**0.749**	0.393	**0.370**	6.57	**11.208**
0.5	1.652	**1.483**	0.533	**0.385**	0.244	**0.206**	5.45	**6.223**
1	1.628	**1.574**	0.436	**0.330**	0.211	**0.173**	4.94	**5.515**
5	1.961	**1.909**	0.365	**0.280**	0.157	**0.128**	4.75	**4.928**
10	2.218	**2.080**	0.337	**0.269**	0.132	**0.115**	4.76	**4.853**
50	2.431	**2.464**	0.265	**0.248**	0.098	**0.092**	4.64	**4.792**
100	2.592	**2.598**	0.283	**0.236**	0.098	**0.083**	4.72	**4.785**
500	3.009	**2.782**	0.233	**0.180**	0.072	**0.061**	4.87	**4.779**
1000	3.110	**2.802**	0.217	**0.136**	0.065	**0.046**	4.91	**4.778**
u = 0.0002								
0	5.605	**4.887**	5.945	**4.382**	0.515	**0.473**	66.05	**112.854**
0.01	5.784	**5.058**	6.049	**4.435**	0.511	**0.467**	65.16	**110.190**
0.05	6.370	**5.782**	6.402	**4.683**	0.501	**0.448**	64.84	**101.763**
0.1	7.323	**6.552**	6.854	**4.872**	0.483	**0.427**	63.67	**94.500**
0.5	11.942	**10.520**	7.653	**5.352**	0.391	**0.337**	61.33	**74.240**
1	15.569	**13.205**	7.768	**5.389**	0.333	**0.290**	61.87	**68.030**
5	23.456	**20.803**	7.196	**5.249**	0.235	**0.202**	61.55	**61.392**
10	26.924	**24.416**	6.750	**5.222**	0.200	**0.176**	60.98	**60.419**
50	33.847	**32.129**	5.857	**4.880**	0.147	**0.132**	60.08	**59.614**
100	36.821	**34.941**	5.323	**4.777**	0.126	**0.120**	58.88	**59.511**
500	40.904	**38.592**	4.822	**3.610**	0.105	**0.086**	58.87	**59.429**
1000	43.009	**38.968**	4.649	**2.707**	0.098	**0.065**	59.92	**59.419**

The scenario considered refers to a subdivided population with n = 10 subpopulations, each of size N = 1000 individuals, mutation rate u, variable migration rate (m), and no sampling (all subpopulation individuals are analysed). See main text for definitions.