	Europe- Africa			***East Asia- Africa***			***Europe - East Asia***		
Chromosome	T_{LD} **0.1cM**	T_F **0.1cM**	T_F **0.25cM**	T_{LD} **0.1cM**	T_F **0.1cM**	T_F **0.25cM**	T_{LD} **0.1cM**	T_F **0.1cM**	T_F **0.25cM**
1	657	1391	1868	790	1768	2685	384	753	1338
2	657	1404	1887	800	1707	2599	358	814	1446
3	598	1351	1807	689	1578	2340	380	758	1300
4	707	1302	1761	839	1612	2446	353	728	1285
5	707	1458	1974	838	1654	2525	390	783	1393
6	765	1478	2001	958	1684	2591	423	866	1550
7	813	1460	1968	1005	1746	2680	367	776	1381
8	708	1482	2003	891	1836	2814	343	779	1385
9	809	1435	1936	910	1668	2556	403	723	1286
10	705	1381	1919	771	1649	2595	308	768	1407
11	666	1403	1894	657	1763	2688	390	771	1374
12	810	1440	1944	846	1758	2688	343	808	1440
13	768	1454	1969	904	1829	2795	391	771	1376
14	854	1426	1929	838	1748	2668	345	708	1264
15	676	1435	1938	911	1921	2926	408	795	1425
16	675	1474	1991	723	1886	2876	359	877	1568
17	801	1472	1987	845	1855	2829	385	815	1456
18	709	1475	1992	774	1808	2760	341	749	1343
19	711	1400	1893	749	1777	2718	364	814	1459
20	569	1369	1846	729	1602	2415	305	722	1261
21	719	1415	1903	801	1726	2624	368	786	1399
22	695	1510	2030	781	1824	2773	311	800	1422
MEAN	**717**	**1428**	**1929**	**820**	**1745**	**2663**	**365**	**780**	**1389**
SD	**72**	**50**	**68**	**87**	**94**	**149**	**32**	**43**	**82**
SE	**15.4**	**10.7**	**14.5**	**18.5**	**20**	**31.8**	**6.8**	**9.2**	**17.5**
95 CI +	**747**	**1449**	**1957**	**856**	**1784**	**2725**	**378**	**798**	**1423**
95 CI -	**687**	**1407**	**1901**	**784**	**1706**	**2601**	**352**	**762**	**1355**

Supplementary Table 3 Estimates of *T* by chromosome**.** To determine the statistical significance of differences in average *T* estimates between continental groups, we used the variation in those estimates across all autosomal chromosomes to derive the standard deviation (or standard error) on the distribution of mean differences (for example between Europe-Africa and East Asia- Africa divergence times) which can be used to place 95% confidence intervals (CIs) around the mean value and/or test directly test the significance level of a specific difference (using a standard *t*-test). The table reports chromosome 1-22 estimates of T_F using a N_e calculated over all recombination distance categories up 0.1cM or 0.25cM, and T_{LD} using the inter-population correlation (r_{pop}) in LD structure over 0.1cM. However, the number of LD observations in distances categories beyond 0.25cM for many of the smaller chromosomes is low leading to stochastic negative r_{pop} correlations. Therefore accurate calculation of T_{LD} for all chromosomes over the full range of 0.25cM is impossible.