Table 3 Population estimates on percentage polymorphism, number of private alleles, gene diversity on expected and observed heterozygosity and inbreeding index

Population Name	N	%PL	N^P	N^S	Na (SE)	H_o (SE)	uH_e (SE)	F_{is} (SE)
Gash Barka (ErGa)	48	100.0	13	9	4.8 (0.3)	0.21 (0.03)	0.61 (0.03)	0.6 (0.05)
South (ErSo)	24	96.6	5	4	4.4 (0.2)	0.25 (0.03)	0.55 (0.03)	0.5 (0.06)
Anseba (ErAn)	14	100.0	2	1	3.8 (0.2)	0.21(0.03)	0.54 (0.03)	0.6 (0.06)
Northern Red Sea	10	100.0	2	1	3.6 (0.2)	0.21(0.04)	0.56 (0.03)	0.6 (0.08)
National (ErNat)	2	56.6	0	0	1.6 (0.1)	0.12 (0.04)	0.38 (0.06)	0.7 (0.11)
Ethiopia (Eth)	5	83.3	1	1	2.5 (0.1)	0.20 (0.04)	0.48 (0.04)	0.6 (0.08)
Kenya (Ken)	16	96.6	5	4	3.6 (0.2)	0.17 (0.02)	0.53 (0.03)	0.7 (0.05)
South Sudan (SSU)	6	86.6	8	6	2.6 (0.2)	0.13 (0.03)	0.49 (0.04)	0.7 (0.07)
Sudan (Sud)	6	83.3	0	0	2.5 (0.1)	0.13 (0.04)	0.45 (0.04)	0.7 (0.09)
Tanzania (Tan)	5	83.3	0	0	2.5 (0.1)	0.09 (0.03)	0.54 (0.05)	0.8 (0.07)
Uganda (Uga)	4	63.3	1	1	1.9 (0.1)	0.11 (0.03)	0.33 (0.05)	0.7 (0.08)

Note: Where, N = Population size; N^P = No. of private alleles; N^S = No. samples contributed to private alleles; % PL = percentage of Polymorphic loci; Na = Number of different alleles; uH_e = Unbiased expected heterozygosity, H_o = Observed heterozygosity and F_{is} = inbreeding index, SE = standard error in parenthesis