Abstract
Genetic analysis of molecular markers is critical in tracking the emergence and/or spread of artemisinin resistant parasites. Clinical isolates collected in western Kenya pre- and post-introduction of artemisinin combination therapies (ACTs) were genotyped at SNP positions in regions of strong selection signatures on chromosome 13 and 14, as described in Southeast Asia (SEA). Twenty five SNPs were genotyped using Sequenom MassArray and pfmdr1 gene copy number by real-time PCR. Parasite clearance half-life and in vitro drug sensitivity testing were performed using standard methods. One hundred twenty nine isolates were successfully analyzed. Fifteen SNPs were present in pre-ACTs isolates and six in post-ACTs. None of the SNPs showed association with parasite clearance half-life. Post-ACTs parasites had significantly higher pfmdr1 copy number compared to pre-ACTs. Seven of eight parasites with multiple pfmdr1 were post-ACTs. When in vitro IC50s were compared for parasites with single vs. multiple gene copies, only amodiaquine and piperaquine reached statistical significance. Data showed SNPs on chromosome 13 and 14 had different frequency and trend in western Kenya parasites compared SEA. Increase in pfmdr1 gene copy is consistent with recent studies in African parasites. Data suggests genetic signature of artemisinin resistance in Africa might be different from SEA.