Human Immunodeficiency Virus is a major public health problem, socio-economic burden and a serious threat to development globally. HIV exhibits an extremely high capacity for genetic variation with rapid turnover of virions. The heterogeneity of HIV may ultimately lead to increased viral fitness in the face of pharmacological, immunological or other environmental selection pressures. The high genetic diversity of HIV-1 continues to complicate measures for the design of an effective vaccine. An effective HIV-1 vaccine would have to stimulate a range of host defenses, including mucosal, innate immunity, neutralizing antibodies and cell-mediated immunity. The variability of the HIV-1 envelope region and the inaccessibility of potentially neutralizing epitopes on primary isolates continue to hamper the development of vaccines for HIV. The focus has shifted to the induction of CD8+ cytotoxic T-lymphocytes (CTLs), which have been shown to play an important role in the control of HIV infection. The ability of a vaccine to induce responses directed at a particular group of epitopes is of interest because it is easier to assess the possible efficacy of any resultant immune response. The knowledge of epitopes is critical in the precise evaluation of the strength and quality of CTL responses that could be induced by vaccine candidates and it would be helpful in identifying immunologically silent regions of a vaccine so that they can be omitted from future constructs. The use of epitopes that are conserved across clades could improve the breadth of induced responses. In this study, the aim was to identify the HIV-1 subtypes circulating in Northern Kenya and to identify conserved immunogenic epitopes that can be used to design a multiepitope cross-clade candidate vaccine to be used in Kenya. Phylogenetic analysis of the generated gp41 sequences showed that 44% of the sequences generated from the three districts were HIV-1 subtype Al, 45% were HIV-1 subtype C and 11% were HIV-1 subtype D. Samples from Moyale indicated 36% of subtype A1, 55% were HIV-1 subtype C and 9% were HIV-1 subtype D while from Mandera 67% were HIV-1 subtype Al, 33% were HIV-1 subtype C. In Turkana the most dominant HIV-1 subtype was Al (58%), HIV-1 subtype C was 25% and HIV-1 subtype D was 17.%. There was a significant difference in the pattern of subtypes circulating in the three regions in that both Turkana and Mandera had subtype Al as the predominant subtype while subtype C was the dominant subtype in Moyale. For epitope determination, sequences generated from the *env* gp41, *env* gp120 (CM) and the p24 gag regions of the HIV-1 genome were analysed. The generated sequences were translated to amino acid sequences using the Translation for publication software and aligned using ClustalW version 1.81 software to determine the areas of the sequences that were conserved and therefore relevant for design of a candidate vaccine. The identified conserved epitopes were further analyzed using the SYFPEITHI bioinformatics tool to identify class 1 restricted T-cell epitopes and their immunogenicity. A total of 80 epitopes from gp 120, 41 from gag and 37 from gp 41 were identified. The identified epitopes were used to construct a super-epitope that can be used to design a HIV-1 candidate vaccine. Information generated from this study can be used to address the challenges of HIV-1 viral diversity in the development of vaccine candidates. This can be part of the long term effort to build a panel of subunit vaccines that can be used in design of an efficacious vaccine.