

The expression of retroviral genes depends on the establishment of the provirus – the DNA copy of retroviral genome integrated into the host genome. The transcriptional state of provirus is then influenced by the environment at the site of integration. The phenomenon of proviral silencing is an obstacle to the usage of retroviral vectors and a barrier to the eradication of human immunodeficiency virus type 1 (HIV-1) from infected individuals. Taking advantage of single cell clones bearing one provirus, this diploma thesis investigates the distribution of (epi)genomic features at the sites occupied by stably expressed proviruses. In total, long-term expression profiles of 245 and 255 clones carrying avian sarcoma-leucosis virus (ASLV) and HIV-1, respectively, were obtained. The database-based analysis of 42 integration sites of ASLV and three integration sites of HIV-1 proviruses shows that proviral stable expression highly correlates with the transcriptional start sites (TSS) at the sites of integration. Histone marks characteristic for the proximity of active TSSs and regulatory elements at the sites of integration of stably expressed proviruses confirm this finding. The results presented in this thesis could inspire other analyses investigating the relationship between the integration site and the expression of retroviruses and should be noted by future analyses of retroviral expression.