Figure S1. Unsupervised hierarchical clustering of novel sRNAs and samples from the Illumina MPS data. The heat map contained 37 novel and unique sRNAs, which were differentially expressed in patients with ASM and ASP human T-lymphotropic virus type I. The sample clustering tree is displayed to the left and the sRNA clustering tree is above. The color scale at the top indicates the relative expression levels of novel sRNA across all samples. Red indicates that the expression levels are higher compared with the mean, whereas blue indicates that the expression levels are lower compared with the mean. Each column represents one novel sRNA and each row represents one sample. Clustering was performed using one-way analysis of variance P(Corr) cut-off ≤0.05 and fold-change cut-off=2.0. ASM, asymptomatic carriers with monoclonal T cell receptor γ gene rearrangement; ASP, asymptomatic carriers with polyclonal T cell receptor γ gene rearrangement; miR, microRNA; trna, transfer RNA; ASM_ASP_HC, ASM vs. ASP vs. HC; HC, healthy control.