

Figure S1. Multiple alignments of DNA sequences in late 3'UTR fragment. Sequence alignments of 8 PVs were performed using Clustal Omega (29) and visualized with Jalview (30). 3'UTR, 3' untranslated region; PV, papillomavirus.

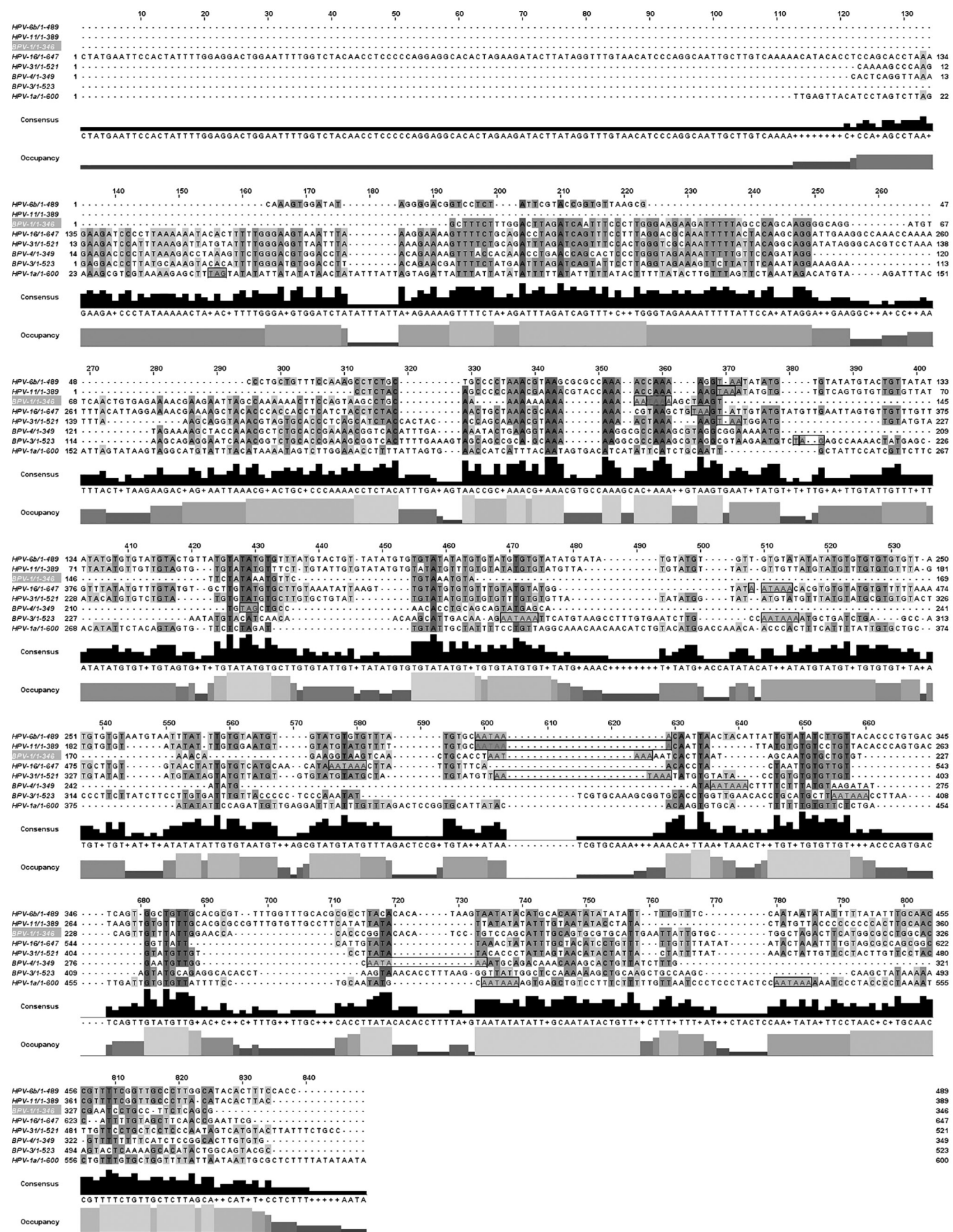
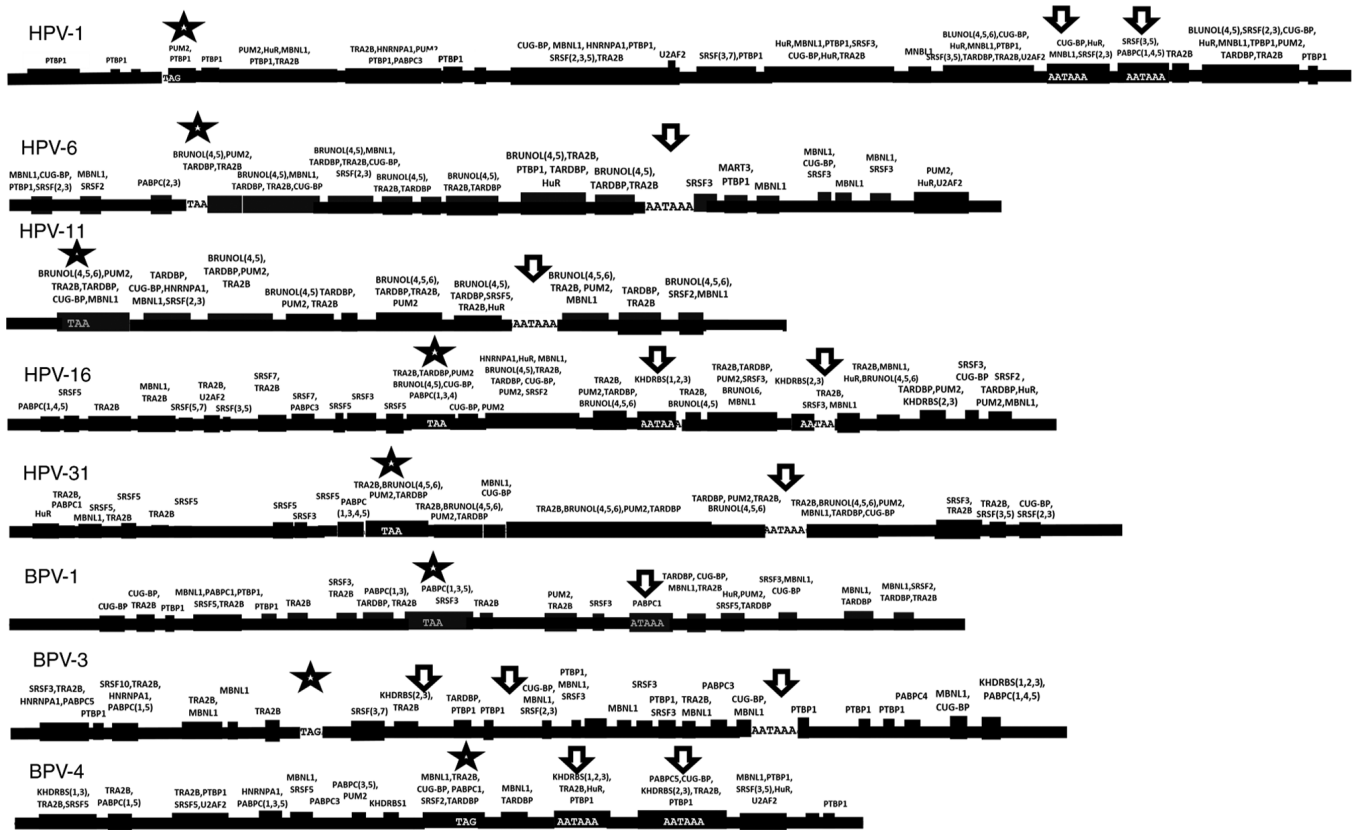


Figure S2. Diagram of RNA binding protein sites commonly found in eight PV late 3'UTRs predicted by using RBPmap version 1.1 at high stringency level, P-value (significant) <0.001 and P-value (suboptimal) <0.01. PV, papillomavirus; 3'UTR, 3' untranslated region.



★ Indicates L1 stop codon (TAG, TAA), ⇩ Indicates poly A signal (AAUAAA)

Figure S3. Predicted RNA binding proteins and binding site numbers that have functions related to mRNA splicing, translation and stress granules by using RBPmap version 1.1 (<http://rbpmap.technion.ac.il/>) (31), at high stringency level [P-value (significant) <0.001 and P-value (suboptimal) <0.01].

