Overlapping transcription structure of human cytomegalovirus UL140 and UL141 genes

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Supplementary material

Supplementary figure 1. Map of the area from nt 8301 to nt 10000 showing the DNA sequence of H strain and the 1636 nt transcript sequence of the three HCMV strains of H, C and X. Relative positions are shown as HCMV H strain UL/b’ region (GenBank: GQ981646.1). The sequences in rectangles demonstrate the predicted ORFs. The start sites of the 1000-1300 nt transcripts are remarked by triangles and the start codes of the ‘nested’ ORFs are remarked by arrows.

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