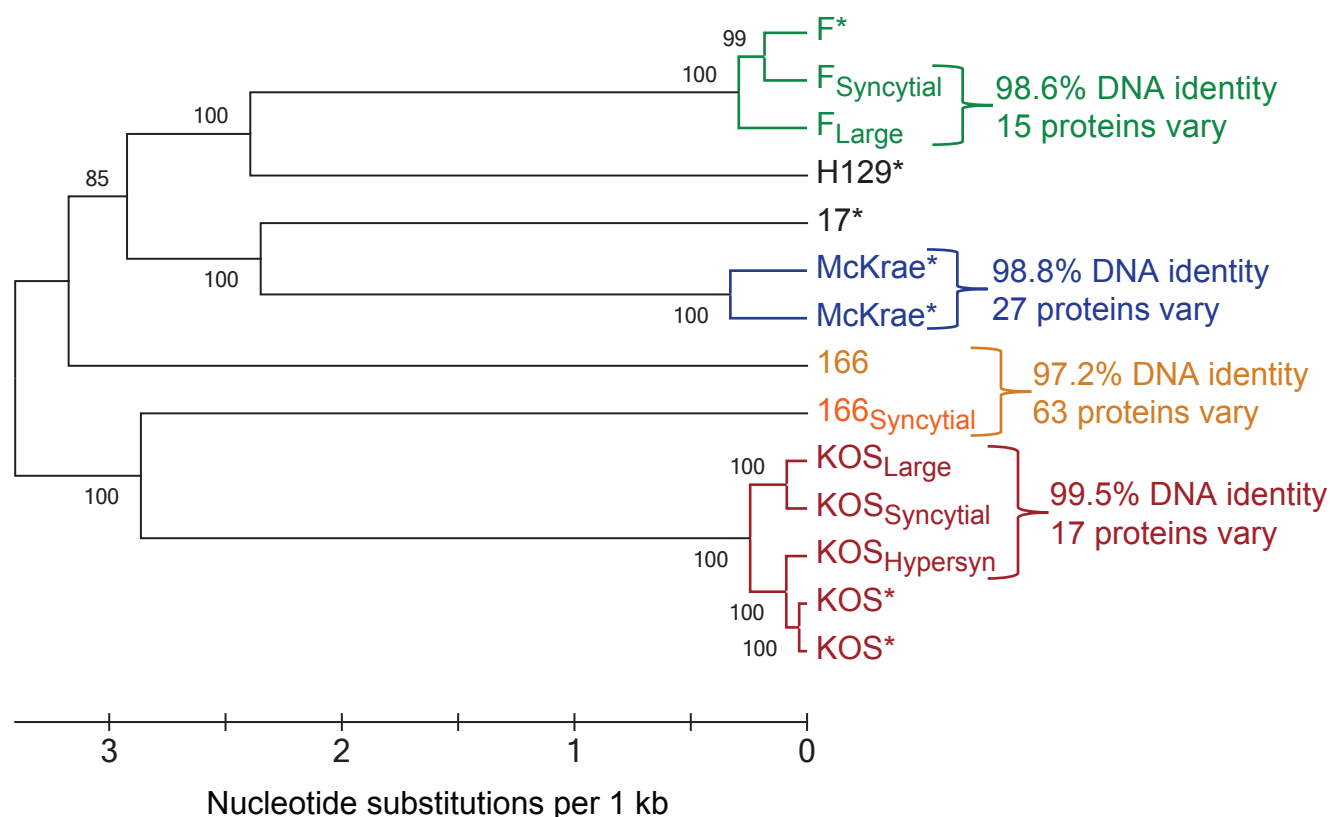


Supplemental Figure S6. Genetic distance diagram, DNA identity, and protein difference statistics summarize relatedness of HSV-1 strains and sub-clones.



Supplemental Figure S6. Genetic distance diagram, DNA identity, and protein difference

statistics summarize relatedness of HSV-1 strains and sub-clones. We followed the same approach as used previously (Szpara et al., 2014, *J. Virol*, 88: 1209–27) to generate a genetic distance tree from whole-genome alignments of the strains and sub-clones shown (see Methods for details). Branch-points show confidence values. We calculated the percent DNA identity and number of variant proteins for selected sets of sequences; these are shown on the right. NCBI Accessions for strains not sequenced in this paper (marked *) are as follows: H129, GU734772; 17, JN555585; McKrae, JQ730035 and JX142173; KOS, JQ780693 and JQ673480.