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S11 Fig. Phylogenetic tree of *TYMS* and its herpesviral homologs. The phylogenetic analysis used the Maximum Likelihood method based on the HKY85 model. The displayed tree is the resulting bootstrap consensus tree inferred from 1000 replicates. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test is shown next to the branches. The branch lengths indicate the number of substitutions per site at the scale shown below the tree. The primate species considered (in green) were: *Homo sapiens* (hs), *Pan troglodytes* (pt), *Pongo abelii* (po), *Macaca mulatta* (rm), *Papio anubis* (pa), *Callithrix jacchus* (cj), and *Otolemur garnettii* (og). Other mammal species included (in blue) were: *Bos taurus* (bt), *Ovis aries* (ov), *Sus scrofa* (ss), *Equus caballus* (ec), *Canis lupus familiaris* (cl), *Mustela putorius furo* (mp), *Spermophilus tridecemlineatus* (st), *Pteropus vampyrus* (pv), *Myotis lucifugus* (ml), *Loxodonta africana* (la), *Dasypus novemcinctus* (dn), *Oryctolagus cuniculus* (oc), *Cavia porcellus* (cp), *Mus musculus* (mm), *Rattus norvegicus* (rn), *Sarcophilus harrisii* (sh), and *Ornithorhynchus anatinus* (oa). Other vertebrates species (in yellow) were also considered: *Latimeria chalumnae* (lc), *Gallus gallus* (gg), *Anolis carolinensis* (ac), *Oryzias latipes* (ol), *Gasterosteus aculeatus* (ga), *Danio rerio* (dr), *Petromyzon marinus* (pm), and *Xenopus tropicalis* (xt). The herpesviruses included in the analysis (in purple) were: Macropodid herpesvirus 1 (MaHV1), Equid herpesvirus 2 (EHV2), Equid herpesvirus 5 (EHV5), Kaposi's sarcoma-associated herpesvirus (KSHV, strain GK18 and type M), Retroperitoneal fibromatosis-associated herpesvirus (RFHV), *Macaca nemestrina* rhadinovirus 2 (MneRV2), Rhesus macaque rhadinovirus (RRV, strains 12E2, 3A1, 17577, and 26-95), Varicella-zoster virus (VZV), Simian varicella virus (SVV), Herpesvirus saimiri (HVS, normal strain and strain C488), Ateline herpesvirus 2 (AtHV2), and Ateline herpesvirus 3 (AtHV3). *Caenorhabditis elegans* (ce) ortolog (tym1) was used as an outgroup.