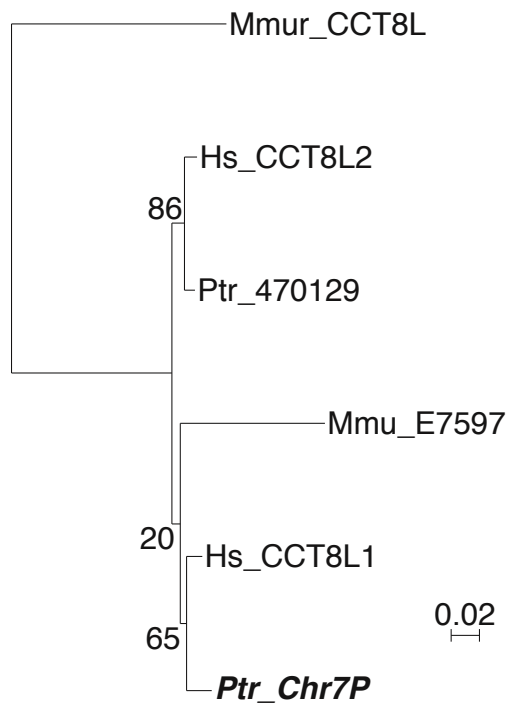
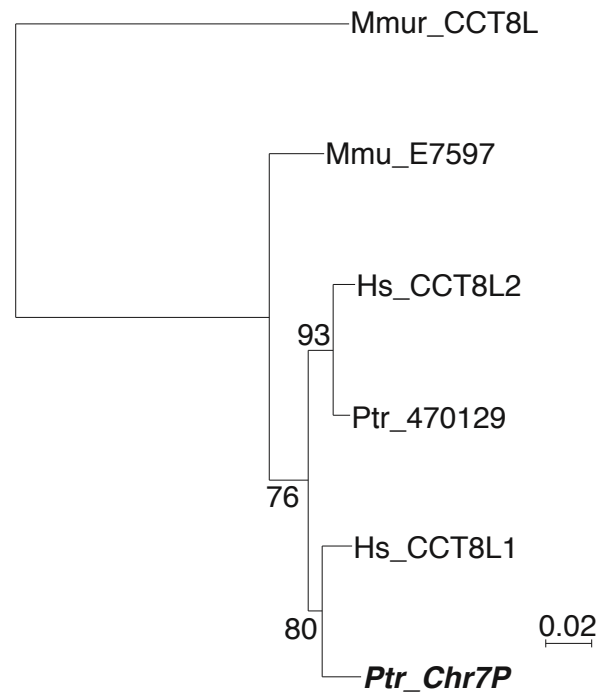


**a****b****c**

Mmur_CCT8L	GAGLPRPQLREAYAAAMA EVLST-LPTLAIRS-----LG-PL-ED-PSWALYSVMNTH TLS SH THYLTKLV AHACWAAREL
Mmu_E7597	KAGLPR-RTREA <b>THS-TAEYCHTALPGHPI-SGAFGRSVLGS PFCDEY PHPVLHG-----PP----DQAGGPC</b> CWAIKEL
Hs_CCT8L2	KAGLPRPQLREAYATATAEVLAT-LPSLAIQS-----LG-PL-ED-PSWALHSVMNTH TLS PMDHLTKLV AHACWAIKEL
Ptr_470129	KAGLPRPQLLEAYATATAEVLAT-LPSLAIQS-----LG-PL-ED-PSWALHSVMNTH TLS PMDHLTKLV AHACWAIKEL
Hs_CCT8L1	KFGLPRPQLREAYATATAEVLAT-LPSLAIQS-----LG-PL-ED-PSWALHSVMNTH TLP MNHLTKLV AHACWAIKEL
Ptr_Ch7P	KAGLPRPQLREAYSTATAEVLAT-LPSLAIQS-----LG-PL-ED-PSWALHSVMNTY TLP PMDHLTKLV AHAC-AIKEL

Figure S6. Evolutionary trees of primate CCT8L sequences obtained: **(a)** from the alignment of the complete sequence; **(b)** removing a 50 amino acid region highly diverged in the sequence from rhesus monkey (Mmu) **(c)** Alignment of CCT8L sequence segments from different primate species showing in yellow diverged positions 132-181 from the rhesus monkey sequence. See legend to Figure 2 for species name abbreviations.