

**Figure S1 The tree topology of ACPT used to conduct the selective pressure analysis in PAML.** The phylogeny is based on OrthoMaM and some previous researches (Celine et al., 2019; Waddell et al., 2001; Sergey et al., 2007; Zhou et al., 2012; Gatesy et al., 2013; Kuntner et al., 2011; OrthoMaM)

**a.**

*H. sap* ATGGCCGGCCTGGGTTTGGGCCACCTGCTGGACCTCTCCTGCTGCTGCTGGTGTGCCACCCGGCCCTGCCAGAAGGA  
*C. hof* -----CCCAGGCCCTGGCGGCAGGA

*H. sap* CCCCTGGTGGTCTGGCTCTGGTATTCCGCCATGGCGACCAGGGCCCCGCTGGCCTCCTACCCCATGGACCCACACAAGGAGGTGGCCTCC  
*C. hof* CCCCTGG-GITCAGGGCTCTGG-----

*H. sap* ACCCTGTGGCACGAGGCCTGGCCAGCTGACCACGGAGGGGTCCGCCAGCAGCTGGAGCTGGCCGCTTCCTGAGGAGCCGTACGAG  
*C. hof* -----

*H. sap* GCCTTCCTGAGTCGGAGTACCGCGGGAGGAGGTGTACATCCGAGCACGGACTTGACCGCACGCTGGAGAGTGCCCAGGCCAACCTT  
*C. hof* -----

*H. sap* GCCGGGCTGTTCCGAGGCTGCTCCAGGGAGCCCCGAGGCCGCTGG-AGGCCGATCCGGTGCACACGGTGCCGTGGCTGAGGATAA  
*C. hof* -----CCCGCGGCTGC-CCAGGGAGCCCCCAGGGCCGCTGGCGGCCCTTCCCGG-----A

*H. sap* GCTGCTGAGGTTCCCCATGCGCAGCTGCCCCGATACCACGAGCTGCTGGGAGGCCACCGAGGCCGCGAGTACCAAGGAGGCCCTGGA  
*C. hof* GCTGCCAGGCTCCCCATGTGCCACTGCCCCACTGCCGGAGCTGCTGCAGGGCTCCCCAGAGGTGCCACGCACCAGGCAGCTCTGGA

*H. sap* GGGCTGGACGG---GCTTCCTGAGT-----CGCCTGGAGAACTTCACGGACTGTCGCTGGTGGAGAGCCACTGCGCAGGGCATGGA  
*C. hof* GGGCTGGATGGGAGCGGGCTGGGTGTGGTGGAGCAGGGAGCGCTCATGGGCTCTCACTGGTCGGGAAGCCACTCAGCAGCGTGTGGA

*H. sap* AGGTTCTGGACACCCATGTGCCAGCAAGCCCACGGCTTCACTACCAGCCTGGCCTCCCCAGATGTCCTGCGACTCTGCCAGA  
*C. hof* AAGTTCTGGACACACT-----CCAGCAGGCCAGGGCTGCCCTCCCATCCTGGG-----TGTCCCTGC--ATCCTCACCCAGA

*H. sap* TCTCGGTTGGATATTGGAGCCCACGTGGGCCACCCGGCAGCAGAGAAGGCCAGCTGACAGGGGGATCCTGCTGAATGCTATCC  
*C. hof* CCTCGGTTGGA-----

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*H. sap* TTGCAAACCTCTCCGGTCCAGCGCTGGGCTGCCCTCAAGATGGTCATGTACTCAGCTCATGACAGCACCCCTGCTGGCCCTCCAGG  
*C. hof* -----

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*H. sap* GGGCCCTGGGCCTATGATGGACACACCCCCGCCATATGCTGCCTGCCTCGGTTGAGTTCCGGAAGCACCTGGGAATCCGCCAAAG  
*C. hof* -----

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*H. sap* ATGGAGGGAATGTCACCGTCTCCCTCTTCTACCGCAATGACTCCGCCACCTGCCCTGCCTCTCAGCCTCCCCGGTGCCGGCCCT  
*C. hof* -----

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*H. sap* GTCCACTAGGCCGTTCTACCAGCTGACTGCCCGGCCGCCATGGGTCTCCTGCCATGCCCTATGAGGCTGCCATCC  
*C. hof* -----

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*H. sap* CCCCAGCTCCAGTGGTGCCCCGCTGGCCGGAGCTGTAGCTGTGCTGGTGGCACTCAGCTTGGGCTGGCCTGCTGGAGACCAAG  
*C. hof* -----

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*H. sap* GGTGCCTGCCGCCCTGGGGGCCCGTGTGA  
*C. hof* -----

b.

*H. sap* ATGGCCGGCTGGGTTTGGGCCACCTGCTGGACCTCTCCTGCTGCTGCTGCTGGTGTGCCACCCGGGCCCTGCCAGAAGGA

*M. jav* -----GCCCTGACGGAAGG-

*M. pen* -----

*P. tri* -----GGAGG-

*H. sap* CCCCTGGTGGCTCTGGTATTCCGCCATGGCGACCAGGCCCCGCTGGCCTCCTACCCCATGGACCCACACAAGGAGGTGGCCTCC

*M. jav* CCCCTGGTGGTCATGGCTGTGGT-----

*M. pen* -----

*P. tri* -----GTGTCCGC-----

*H. sap* ACCCTGTGGCACGAGGCCTGGCCAGCTGACCACGGAGGGGTCCGCCAGCAGCTGGAGCTGGCCGCTCCTGAGGA----GCCGCTA

*M. jav* -----CTGCAGCTGAACAGCTTCCTGAGGA----GCCCTC

*M. pen* -----CTTGGGTTTCAGGGCCTCCCCTGGACGGCGCTCTT

*P. tri* -----CCGCAGCTGGACAGCTTCCTGAGGA----GCCCTC

*H. sap* CGAGGCCTCCTGAGTCCGGAGTACCGCGGGAGGGAGGTGTACATCCGAGCACGGACTTGACCGCACGGCTGGAGAGTGCCCCAGGCCAA

*M. jav* CCAGACCTCTCTGAGCCTGGAGTACCAAGAGGGAGGGAGGTGCATGTTCGCAGCC--GACTTGGCCGGATGCTGGAGGGCGCTCAGTCCGA

*M. pen* CCTG---TTGCTGCTCC---AGCCCTGACGGAA-----

*P. tri* CCAGACCTTTTGAGCCGGAGTACCAAGAGGGAGGGAGGT-----

*H. sap* CCTTGCCGGCTTTCCCGAGGCTGCTCCAGGGAGCCCCGAGGCCGCTGGAGGCCGATCCGGTGCACACGGTGCCGTGGCTGAGGA

*M. jav* CCT-----

*M. pen* -----

*P. tri* -----

*H. sap* TAAGCTGCTGAGGTCCCCA---TGCAGCTGTCCCCGATACCACGAGCTGCTGGGAGGCCACCGAGGCCGAGTACCAAGGAGGC  
*M. jav* --GGCTAGTCTGGTCCC-----CGAGGCCGC-----TACCCCCAGCTGCTGAGGGAGGCCACCGAGGCTACGGAGTACAAGGCGGG  
*M. pen* -----GCTCCCTGGTGTCTGGCTGT----GGTACCCCCAGCTGCTGAGGGAGGCCACCGAGGCTACGGAGTACAAGGCGGG  
*P. tri* --AGCTGCTGAGGCTCCCCA---CGCGTGGCGGTCCCTCGATACCGTGAGCTGCTGAGGGAGGCCACCGAGGCTACGGAGTACAAGGGGA

*H. sap* CCTGGAGGGCTGGACGGCTTCCCTGAGTCGCCTGGAGAACTTCACGGACTGTCGTTGGAGAGGCCACTGCGCAGGGCATGGAAGGT  
*M. jav* CCTGAAGGCCTGGACG-----GAATTTCACGGGCCGGCGTGGTCTGGGAGGCCCTCCGAGAGCGGGGAAGGT  
*M. pen* CCTGAAGGGCTGGAGGGACTTCCCAGCTGGGGGAGAACTTCACGAGGCCGTCGTTGGCTGGGAGGCCCTCCGAGGGCGGGGAAGGT  
*P. tri* CCTGAAGGGCTGGACGGATTCCCAGCGCGCTGGAGAACTTCACGAGCCTGTTGCTGGCTGGGAGGCCCTCCGCAAGGCGTGGGAGGT

*H. sap* TCTGGACACCCCTCATGTGCCAGCAAGCCCACGGTCTTCACTACCAGCCTGGCCTCCCCAGATGTCCTGGGACTCTGCCAGATCTC  
*M. jav* TCTGGACACCCCTCATGCGCCA-----GTCCTCCCCCTCCCATCCTGGCTCCCCCAAACGCCCTACAGACGCTAGCCCAGATCTC  
*M. pen* TCTGGACACCCCTGATGCGCCA-----GTCCTCCCCCTCCCATCCTGGCTCCCCCAAATGCCCTACAGACACTAGCCTGGATCTC  
*P. tri* TCTGGACACCCCTGATGCGCCAGCAGGCC-----GTCTTCCCCCTCCCATCCTGGCTCCCCGAATGCCCTACGGACACTAGCCCAGATCTC

*H. sap* GGCTTGGATATTGGAGCCCACGTGGGCCACCCCGGGCAGCAGAGAAGGCCAGCTGACAGGGGGATCCTGCTGAATGCTATCCTTGC  
*M. jav* AGCTTGGATATTAGGCTCATGTGGGCCATCCCGGGCAGCAG---AGGCCAGCCG---AGGGGG---CCTGCTGGATGCCATCCTTCC  
*M. pen* AGCTTGGATATTAGGCTCATGTGGGCCACCCCGGGCAGCAG---AGGCCAGCTG---AGGGGGGATCCTGCTGGATACCA-CCTTCC  
*P. tri* AGCTTGGATATTAGGCTCATGTGGGCCACCCGGGTAGCAAAGGAGGCCAGCTGAGTGTGGG-----

*H. sap* AAACTTCTCCGGTCC-AGCGCTGGGCTGCCCTCAAGATGGTACTCAGCTCATGACAGCACCTGCTGCCCTCCAGGGGG  
*M. jav* CAACTTCT--CAAGTCT-AGCACCTGGGCTGCCCTCAAGATGGTACCTACTCAGCTCATGACAGCA--CTACCAGCCGCCCTGGGG  
*M. pen* CAACTTCT--CAAGTCTAAGCACCCGGGCTGCCCTCAAGATGGTACGTACTCAGCTCATGACAGCA--CTACCGGCCGCCCTGGGG  
*P. tri* -----GGTCT-AGCACCTGGGCTGCCCTCAAGATGGTACTCAGC--CATGACAGCACACTGCCAGCCGCCCTGGGAG

*H. sap* CCCTGGCCTATGATGGACACACCCGCCATATGCTGCCTGCCTGGCTTGAGTCCGGAAGCACCTGGGAATCCGCCAAAGATG

*M. jav* TCC-GGGTCTCTATGATGGCACACCCCACCATATGCCACCTGCCTCGGC  
*M. pen* CCC-GGGTCTCTATGATGGCACACCCCACCATAGGCCACCTGCCTGGC  
*P. tri* CCT-GGGTCTCTGTGATGGCACA-CCCGCCGTACGCCCTGCCTCGGC



*H. sap* GAGGAATGTACCGTCTCCCTTTCTACCGCAATGACTCCGCCACCTGCCCTGCCTTCAGCCTCCCCGGTGCCGGCCCCCTGTC  
*M. jav* ---GGAATGTACAATCTCCCTTTCTACTGCAATGACTGCACCGGCCTGCCCTGCCCTCAGCCTCCCTGGTGCCAGACCCCTGCC  
*M. pen* ---GGAATGTACCACATCTCCCTTTCTACTGCAATGACTGCACCGGCCTGCCCTGCCCTCAGCCTCCCTGGAGGCCAGACCCCTGCC  
*P. tri* ---GGAATGTACAATCTCCCTTTCTACTGCAATGGCTGCACTGGCCTGCCCTGCCCTCAGCCTCCGTAGTGTGAGACCCCTGCC

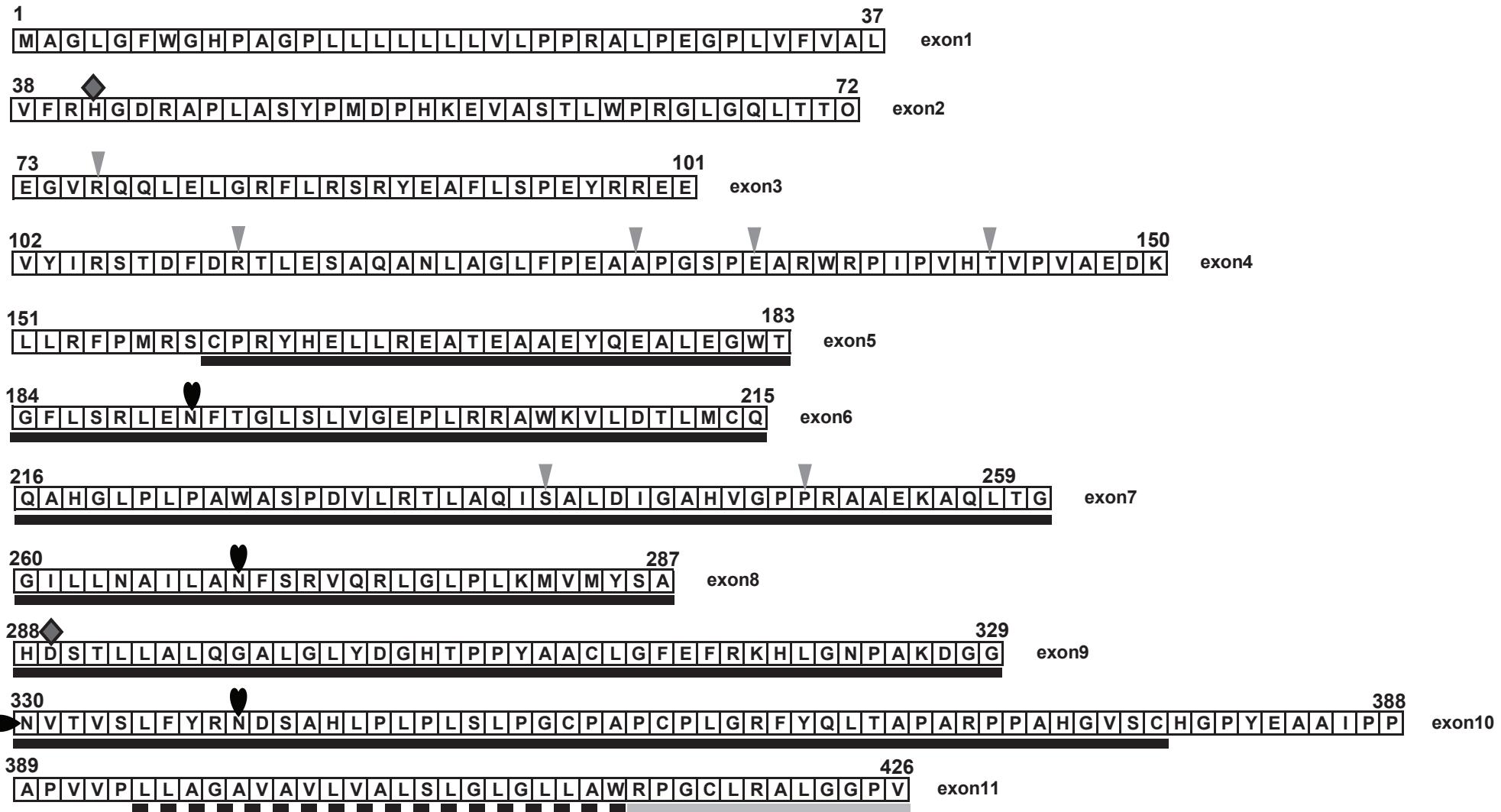
*H. sap* CACTAGGCCGTTCTACCAGCTGACTGCCCGGCCGCTCCGCCATGGGTCTCCTGCCATGGCCCTATGAGGCTGCCATCCCC  
*M. jav* CACTAGGCCACTTCTGCCGGCTGACTGCCCT-GCCCGGTCTCCAGCTCGTGGGTGCCCTGCTACGACTCCCATGAGTTGCAATCCCC  
*M. pen* CACTAGGCCACTTCCGCCGGCTGACTGCCCT-GCCCGCCCTCCAGCTCGTGGGTGCCCATGACTCCCATGAGTTGCCATCCCTG  
*P. tri* CACTAGGCCACTTCTGCCAGCTGACTGCCCTGGCCTCCAGCTCGTGGAGTCCCTGCCACGGCTCCCATGAGCTTGCCA

*H. sap* CAGCTCCAGTGGTCCCCCTGCTGGC-CGGAGCTGTAGCTGTGCTGGTGGCACTCAGCTTGGGCTGGCCTGCTGGCTGGAGACCAGGG  
*M. jav* CAGCCACCGTCCTGCCCGCTGGCTGGGTATGCCCTGAGCGCTCAGTGTGGGCTTA-----CGAACTGGAGACCTGGC  
*M. pen* CAGGT-----  
*P. tri* -----

*H. sap* TGCCTGCCGGCCTTGGGGGGCCCGTGTGA  
*M. jav* TGCCTGCCGGCCTGGGAGGGCCTATGTGA  
*M. pen* -----GGTGGCCCTGTCTGG  
*P. tri* -----

**Figure S2 a. ACPT sequence comparison between human and sloth;**  
**b. ACPT sequence comparison among human and 3 pangolins**

**Figure S3 The detailed information about inactivated mutation of ACPT among relative cetaceans.** Orange represents initiation codon mutation, yellow represents deletion, green represents insertion, and blue represents two common deletion sites among all baleen whales.



▼ Mutation in these sites will lead to hypoplastic AI (Seymen et al. 2016 and Smith et al. 2017)

◆ These sites are used for enzymes and indicates the residues directly involved in catalysis.

♥ Glycosylation

— Disulfide bond

— — — Transmembrane

— Intracellular

Figure S4 The information of mutation sites about amelogenesis imperfecta in ACPT protein sequence.

## References

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