
CLUSTAL W 2.0 multiple sequence alignment
TEN
GQ
HsaTERT
MmuTERT
MdoTERT
OanTERT
GgaTERT
AcaTERT
XleTERT
TruTERT

Figure S2


TRBD:
v-II
|--- VSR --|
v-III
HsaTERT
MmuTERT
MdoTERT
OanTERT
GgaTERT
AcaTERT
XleTERT
TruTERT
|------- CP -------|
QFP
T
RT
1
2
3

Figure S2

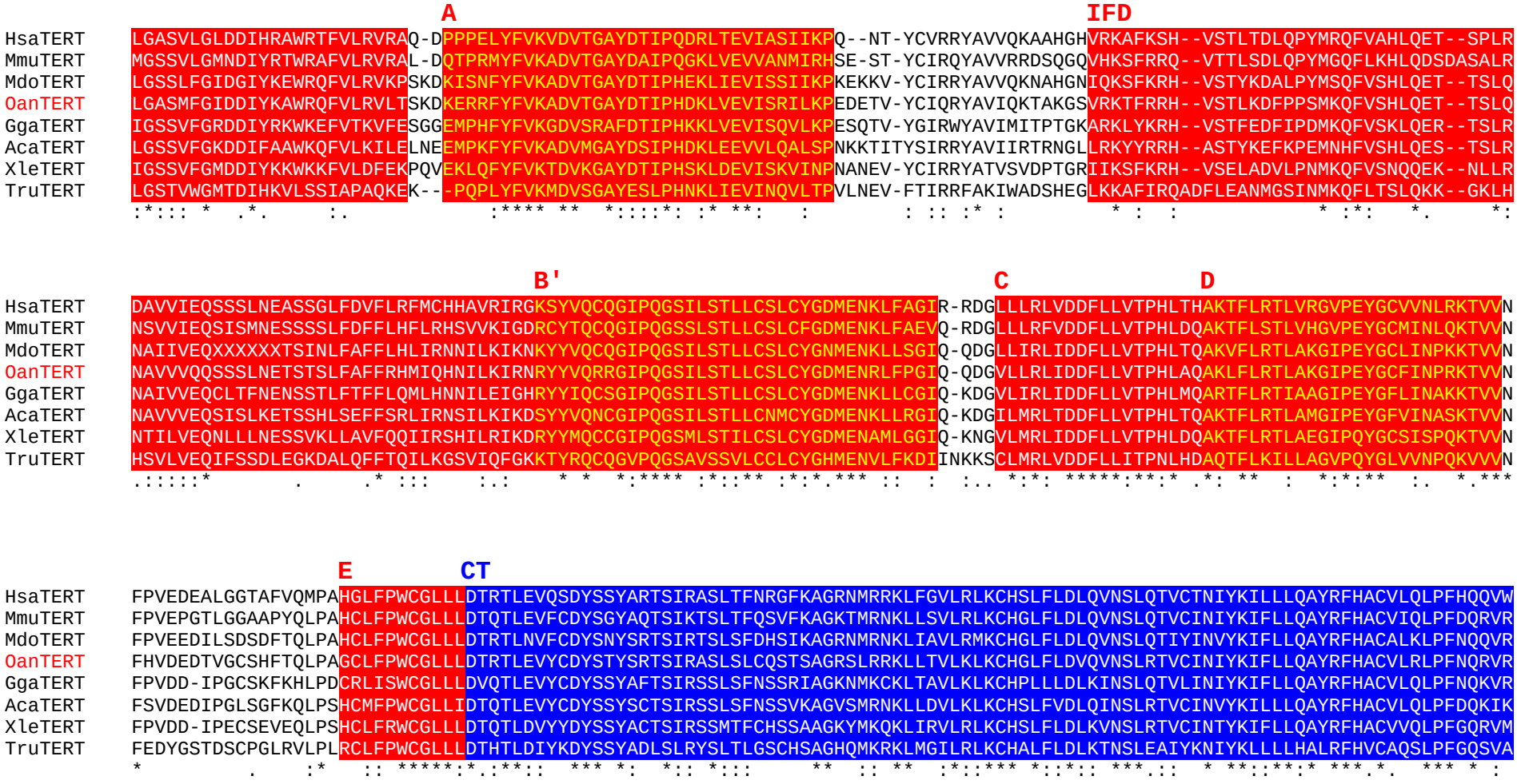
A
IFD
B'
C
D
E
CT
HsaTERT
MmuTERT
MdoTERT
OanTERT
GgaTERT
AcaTERT
XleTERT
TruTERT

Figure S2

Figure S2 The ClustalX sequence alignment of platypus TERT with the TERT proteins of selected vertebrates. This alignment serves as basis for the schematic representation of TERT proteins in Figure 1. To maximize the information available for the alignment, all 25 vertebrate TERT proteins specified in Materials and Methods section were aligned, but only sequences of those proteins presented in Figure 1 are shown here. For the abbreviations of species names see the legend to the Figure 1. The boundaries of the different domains and sequence motifs are indicated. The color code for the domains is the same as in the Figure 1. The TEN domain is shown as defined by [1] except that we did not include the variable region corresponding to the first 12 amino acids of human TERT that is shortened and modified in some TERT proteins. Other regions are shown as defined in the following references [2](GQ, CP, QFP), [3](VSR), [4](v-II, v-III, A, B', C, D, and E), [5](motifs 1, 2), [6](motif 3), [7](IFD), and [8](CT).

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