

[illegible]

		+	°
TERT con	S LRFIPK G		
AmexTERT	DVAALKQ---NPLISRLRFIPKPNG		842
hTERT	EVRQHREARPALITSRLRFIPKPDG		629
mTERT	EVRHHQDOWLAMPICRLRFIPKPNG		619
PmtTERT	EIEKVQQKKCVPMASKLRFIPKPNG		845
VtTERT	EIKTLQQQCKVPLASKLRFIPKPNG		822
xTERT	ELENMQQWKNVPLVSRLRFIPKTNG		684
ZfTERT	QALKVPN---SAVTSRIIRFIPKTSS		609
OlaTERT	QVASLPK---GTVISQLRFIPKTDG		593
TtTERT	-----SFQIQPQGKLRIIPKGS		541
AtTERT	E-----SSRKKLSKFRLFIPKANG		620
Sc_Est2p	NHNS--YTLNFNFNHSKMRIIPKKS		446
HIV-1	EGKISKIGPENPYNTPVFAIKKDS		223
RT con	p h hh K		

	o	+	
TERT con	RPI		
AmexTERT	LRPIVKVQNVLDVQLHSKEKRD	KMQYFN	871
hTERT	LRPIVNM DYVGARTFRRE---	KRAERLT	655
mTERT	LRPIVNMSYSMGTRALGRR---	KQAQHT	645
TmtTERT	LRPIVKVNSVGAKTLNRKSRD	KKVHYFN	874
PvTERT	LRPVVQKQNGVGAETFSRKAGE	KKIQYFN	851
xTERT	LRPISKISSTLSSQ-QSKENQE	KKIHHFS	712
ZfTERT	MRPITRLSGSR-----	DTLQYFQ	627
OlaTERT	MRPITRVIGAD-----	SNTRLHH	611
TtTERT	FRPIMTFLRKDKQKN-----	IKLNLN	562
AtTERT	VRMVLDFSSSSRSQ-----		634
Sc_Est2p	FRIIAIPCRGADG---	EEFTIYKENHKNA	472
HIV-1 RT	WRKLVDFRELNKRTQDFWEV	QLGIPHPAG	254
RT con	hr h	K	

TERT con	YFVK DV GAYD IP KL EV	P
AmexTERT	KEKQY ^Y FVK ^D VTGAY ^D TIP ^H AKL ^E EV ^S KIL ^N P	952
hTERT	PPPEL ^Y FVK ^D VTGAY ^D TIP ^Q DR ^L TEVIAS ^I IK ^P	735
mTERT	QTPRM ^Y FVK ^A VTGAY ^D AI ^P Q ^G KL ^E V ^V AN ^M IR ^H	725
TmtTERT	KIPRF ^Y YVK ^A DVTGAY ^D TIP ^H DK ^L EV ^V SQIL ^D P	955
PvTERT	VLP ^R F ^Y FVK ^A DVIGAY ^D SIP ^H NKL ^E VEI ^L QAL ^S P	932
xTERT	EKLQ ^F YFVK ^T DVKGAY ^D TIP ^H SKL ^E DEVIS ^K VIN ^P	793
ZfTERT	SPRPL ^Y FVK ^D VSGAY ^D SLPH ^L KL ^E VEVL ^K EV ^L GP	705
OlaTERT	KPQPL ^Y FVK ^D VSGAY ^D SLPH ^D KL ^E KEV ^I TEAL ^S P	689
TtTERT	GRPQL ^Y YV ^T L ^D IKKCY ^D SIDQ ^M KL ^L N ^V FN ^F QSD ^L I	641
AtTERT	ELP ^L YFV ^A DVFKAF ^D SV ^D QK ^L LH ^V IQ ^S FL ^K D	714
Sc_Est2p	ALPEL ^Y FMK ^F DV ^K SKCY ^D SIP ^R MECM ^R IL ^K DAL ^K N	553
HIV-1 RT	LKKK ^S SV ^T VLDV ^G DY ^A FSV ^P LDED ^F RKY ^T AF ^T IP	288
RT con	h hDh GY h	
	AF	

TERT con	K	V	D	M	F	LQ	
AmexTERT	IRKSYKRV	ATM---	DDF-----	LPNTKMFVS	-----	HLQON-----	1000
hTERT	VRKAFKSH	VSTL---	TDL-----	QPYMRQFVA	-----	HLQET-----	783
mTERT	VHKSFRRQ	VTTL---	SDL-----	QPYMGQFLK	-----	HLQSDA-----	776
TmtTERT	IRKYYRRH	VSTF---	KDF-----	MSHMLRFVS	-----	HLQES-----	1005
PvTERT	IRRYRRHV	VSTY---	KEF-----	ISDMKEFIN	-----	HLQEV-----	982
xTERT	IIKSKFRH	VSEL---	ADV-----	LPNMKQFVS	-----	NQQEK-----	843
ZfTERT	LRKRFC	TKAEMS---	E-----	PLNMKGFFV	-----	DEQVS-----	753
OlaTERT	LKKAFARQ	VDFS---	DGSM-----	GSTSMKGFVM	-----	SLQKS-----	741
TtTERT	LQIQQTNN	INSAMEIEE	EKKINKKPFKMDNIN	FPYYFNLKERQIAYS	SLYDDDDQILQGFKEI		722
AtTERT	-RSNVVNK	LVS---	SDK-----	NSNFSRFTS	-----	TVPVN-----	756
Sc Est2p	L-KLFNVVN	-A---	SRV-----	P-----			584

TERT con	L	VEQ	L	F	
AmexTERT	-GSLKHA	ILVEQALHLNENSR	LLQFFQ	QMITNNIL	KVGD 1039
hTERT	-SPLRD	AVVIEQSSSLNEASS	GLFDVFLR	FMCCHAV	IRIG 822
mTERT	-SALRNV	VIEQISNMNESS	LLDFDLHFLHRS	VVKIGD	815
TmtTERT	-TSLQNA	IVVEQSLSLNETSS	LLFAFFLQ	MIHNNILE	IEG 1044
PvTERT	-TSLRNA	VVVEQSVSLKESNT	SLAEFFLKF	QISNLIK	IKD 1021
xTERT	-NLLRNT	ILVEQNLLNNESS	VKLLAVFQ	QIIRSHL	IRIKD 882
ZfTERT	-GRLHD	AAILVER-HSSEVR	GDVDFQ	FKMLCSYV	IHYDQ 791
OlaTERT	-SKVHH	AVLVEQAFGSNLR	KKDALQFF	TQMLTGSV	VQHKG 780
TtTERT	QSDRD	PFPIVNDKQKPRC	ITDKIITHNHL	KNMLKSN	VNISFNK 762
AtTERT	---	ALQISVVDKGNHVR	KDKLMVMW	IGNMLKNN	LQDK 793
Sc Est2p	---	KPYELYIDNVRTV	HLNSQDVINV	VEMEIFKTA	LWVED 621

Motif B'

		*		+	°		+	+	+	
TERT con	Y	Q	G	I	P	G	S	I	S	LCY G ME
AmexTERT	KCFV	Q	C	R	G	I	P	G	S	ILSTVLCSLCYGD MENNFSGI
hTERT	KSYV	Q	C	Q	G	I	P	G	S	ILSTLLCSLCYGD MENKLFAGI
mTERT	RCYT	Q	C	Q	G	I	P	G	S	SLSTLLCSLCFGD MENKLF AEV
TmtTERT	RYYL	Q	C	Q	G	I	P	G	S	ILSTLLCSLCYGD MENKLF CGI
PvTERT	RYVY	Q	R	C	G	I	P	G	S	ILSTLLCNLCYGD MENKLLQGV
xTERT	RYYM	Q	C	Q	G	I	P	G	S	MLSTILCSLCYGD MENAMLGGI
ZfTERT	QMFR	Q	V	C	G	I	P	G	S	SVSSLLCNLCYGHMEKALLKDI
OlaTERT	KTYR	Q	C	R	G	I	P	G	S	VVSSLLCCLCYGHMENVLFRDI
TtTERT	VKFR	Q	K	R	G	I	P	G	S	GLNISGVLC SFYFGKLEEEYTQFL
AtTERT	SFYV	Q	I	A	G	I	P	G	S	HRLLSLLCCFYFYGHLERTLIYPF
Sc_Est2p	KCYI	R	E	D	G	L	F	Q	S	SLSAPIVDLVYDDLLEF-YSEF
HIV-1 RT	GIRY	Q	Y	N	V	L	P	G	S	WKGSPAIFQSSMTKILEPFRKQN
RT con					h	P	Q	G		pP hh h

Motif C

			+	°	°	+	
TERT con	L	RL	DD	FL	L	TP	
AmexTERT	FMRLI	DD	FL	LV	TP	PYL DK	1096
hTERT	LLRLV	DD	FL	LV	TP	PHL TH	879
mTERT	LLRFV	DD	FL	LV	TP	PHL DQ	872
TmtTERT	LIRLI	DD	FL	LV	TP	PHL TL	1101
PvTERT	LMRLT	DD	FL	LV	TP	PHL TQ	1078
xTERT	LMRLI	DD	FL	LV	TP	PHL DQ	939
ZfTERT	LMRLI	DD	FL	LV	TP	PHL SK	848
OlaTERT	LMRLV	DD	FL	LV	TP	DRN Q	837
TtTERT	LMRLT	DD	Y	L	F	ISDSQ QN	826
AtTERT	LLRFT	DD	Y	L	F	VSTSRDQ	871
Sc_Est2p	ILKLA	DD	FL	I	I	STD RQ Q	681
HIV-1 RT	IYQYM	DD	Y	L	V	SGDLEIG	350
RT con			h	F	DD	hhh	
				Y			

Motif D

TERT con	A	FL	L	G	P	YG	N	K	
AmexTERT	AETFLRT	LA	E	G	I	P	Q	Y	GCSISLSKTMV
hTERT	AKTFLRT	LV	R	G	V	P	E	Y	GCVVNL RKT VV
mTERT	AKTFLST	LV	H	G	V	P	E	Y	GCMINL QKT VV
TmtTERT	AKTFLRT	LA	G	I	P	E	Y	G	FLINPKK TMM
PvTERT	AKMFLRT	LA	M	G	V	P	E	Y	GFVINP AKTVV
xTERT	AKTFLRT	LA	E	G	I	P	Q	Y	GCSISL PQT VV
ZfTERT	ATEFLT	LL	S	G	V	P	D	Y	GCQINP QKVAV
OlaTERT	AQSFLS	ILL	A	G	V	P	Q	Y	GVVANP QKV VV
TtTERT	ALNLIV	Q	L	Q	N	C	A	N	NGFMFNDQ KIT T
AtTERT	ASSFYH	R	L	K	H	G	F	K	DYNCFMNETK FCI
Sc_Est2p	VINIKK	L	A	M	G	G	F	Q	KYNAKANRD KILA
HIV-1 RT	HRTKIE	E	L	R	Q	H	L	L	WGLTTPDKKHQK
RT con						G	h		cK h

Motif E

			+	°	+	
TERT con	P	W	C	G	L	L
AmexTERT	RSVFP	W	C	G	V	L F
hTERT	HGLFP	W	C	G	L	L L
mTERT	HCLFP	W	C	G	L	L L
TmtTERT	CGVIP	W	C	G	L	L L
PvTERT	HGVIP	W	C	G	L	L I
xTERT	HCLFR	W	C	G	L	L L
ZfTERT	SCLFP	W	C	G	L	M I
OlaTERT	HCLFP	W	C	G	L	L L
TtTERT	QNECQ	W	I	G	K	S I
AtTERT	VPFVR	W	T	G	L	L I
Sc_Est2p	DTVIQ	F	C	A	M	H I
HIV-1 RT	EPPFL	W	M	G	Y	E L
RT con			L	G		h

CTE

			*		*		*	*	
TERT con	DTQT	LEVY	DYSS	YA	TSIR	SLTF	S	AG	MR
AmexTERT	DTQT	LEVY	C	DYSS	YACT	SIRSS	LT	ISHKA	ETG
hTERT	DTRT	LEVY	C	DYSS	YART	SIRAS	LT	FN	R
mTERT	DTQT	LEVY	C	DYSS	YACT	SIKTS	SLTF	Q	S
TmtTERT	DIQT	LEVY	C	DYSS	YACT	SIRSS	LA	FN	S
PvTERT	DTQT	LEVY	C	DYSS	YACT	SIRSS	LS	FN	S
xTERT	DTQT	LDVY	C	DYSS	YACT	SIRSS	MT	FC	S
ZfTERT	HFHT	LDVY	C	DYSS	YACT	SLRYS	LT	LS	A
OlaTERT	DTRS	LDVY	C	DYSS	YAGL	SLRYS	LT	LS	A

TERT con	ININ	YNI	LLQAY	R	F	H	A	C	V	QLPF	G	V	K	N	P	F	L	ISD	A	CCY
AmexTERT	FINI	YNI	LLQAY	R	F	H	A	C	V	QLPF	N	G	V	R	K	N	P	S	F	L
hTERT	CTNI	YNI	LLQAY	R	F	H	A	C	V	QLPF	H	Q	V	W	K	N	P	T	F	L
mTERT	CINI	YNI	LLQAY	R	F	H	A	C	V	QLPF	D	Q	V	R	K	N	P	T	F	L
TmtTERT	FINI	YNI	LLQAY	R	F	H	A	C	V	QLPF	N	Q	V	R	K	N	P	C	F	L
PvTERT	CINI	YNI	LLQAY	R	F	H	A	C	V	QLPF	N	Q	K	I	K	S	N	P	R	F
xTERT	CINT	YNI	LLQAY	R	F	H	A	C	V	QLPF	G	Q	V	M	N	P	P	F	L	T
ZfTERT	YRS	L	YNI	LLQAL	R	F	H	A	C	V	R	S	L	P	L	G	S	V	N	R
OlaTERT	YKNI	H	LV	LLQAC	R	F	H	V	C	V	Q	S	L	P	F	A	T	V	A	K

			*		*	
TERT con	LK	KN	G	LG	EAV	QWL
AmexTERT	ILKSK	N	I	G	I	A
hTERT	ILKAK	N	A	G	S	L
mTERT	ILKVK	N	P	G	M	T
TmtTERT	ILKTK	N	T	G	I	A
PvTERT	VLKTK	N	K	D	V	S
xTERT	TFKAK	N	K	D	L	T
ZfTERT	LLTHI	N	K	G	L	P
OlaTERT	LIRRS	N	T	G	L	V

		*		*	
TERT con	L	R	L	T	L
AmexTERT	QLSK	I	H	K	A
hTERT	QLSR	K	L	P	G
mTERT	LLCR	K	L	P	E
TmtTERT	QLFK	K	I	P	K
PvTERT	RLLR	Q	I	P	E
xTERT	QLSR	R	L	S	Q
ZfTERT	ALQRE	L	C	G	I
OlaTERT	RLER	L	G	D	L

Figure S2. Comparison of different TERT motifs of representative species using MSA: Conserved amino acid residues are colored, similar amino acid residues are highlighted in yellow. Consensus sequence is shown at the highest row, RT consensus [35] is shown at the lowest row. Residues that have been shown to be essential for enzyme activity [36] are indicated by open circles (o), telomerase-specific signatures [34] are indicated by plus (+). Amino acid residues deviate from TERT consensus are marked by asterisk (*).

MSA of conserved regions among vertebrate TERTs of the N-terminal half (v-I to v-IV) [40].

MSA of RT motifs, motif T and the IFD. Motif T and the IFD are TERT-specific so that the alignment was performed without HIV-1 RT. Hydrophobic conserved residues in the IFD are highlighted in blue and charged/hydrophilic positions are highlighted in pink [37].

MSA of CTE. CTE-like regions are found in RTs and in TERTs, but significant sequence-similarities are conserved within vertebrate TERTs only.