

Supplementary file 2.

Alignment of Cpt 1 deduced amino acid sequences of Nile tilapia (Ti), Zebrafish (Zf), Human (Hu), Anole lizard (Al), Tetraodon (Te), and Japanese medaka (Me). The green letters represent 100% homology. CPT N-terminal is shown in underlined letters, transmembrane region domains (Transmembrane region 1 and Transmembrane region 2) boxed in yellow, acyltransferases choActase domains (Acyltransferases ChoActase 1 and Acyltransferases ChoActase 2) boxed in red.

		CPT N-Terminal	Transmembrane Region 1	Transmembrane Region 2	Acyltransferase ChoActase 1
Ti Cpt 1 Alpha1a	1	<u>MAEAHQAVAFQFTVT</u> PEGIDLHLSHEALRQVYLSGIHSWKKRFRVRFKNGIM	MTGVYPGSPA		
Zf Cpt 1 Alpha1a	1	<u>MAEAHQAVAFQFTV</u> TPDGDIDLHLCHEALRQIYLSGIHSWKKRFRIRFKNGV	MTGVYPGSPS		
Hu CPT 1Alpha1	1	<u>MAEAHQAVAFQFTV</u> TPDGDIDRLSHEALRQIYLSGLHSWKKKFRIRFKNGI	ITGVYPASP		
Al CPT 1Alpha1	1	<u>MAEAHQAVAFQFTV</u> TPDGDIDLRMSHEALRQIYLSGLYSWKKKFRIRFKNGI	ITGVYPASP		
Ti Cpt 1Alpha2a	1	<u>MAEAHQAVAFQFTV</u> TPDGDIDLQLSHQALTEIYLSGMRSWKKRIVRVKNS	VITGVYPASP		
Zf Cpt 1Alpha2a	1	<u>MAEAHQAVAFQFTI</u> TPEGIDLQLSHQALRQVYLSGLRSWKKRVTRLKNSV	ITGVYPASP		
Te Cpt 1Alpha2a	1	<u>MAEAHQAVGF</u> EFTVIPEGTDAQLSHQALTEIYLSAVHSWKKCIIRIKNSVIK	GVYPASP		
Ti Cpt 1Alpha2b	1	<u>MAEAHQAVAFQFTI</u> TPEGIDLQLSYQALNQIYLSGVRSWKKRVSRVRNS	SLIKGVYPASP		
Zf Cpt 1Alpha2b	1	<u>MAEAHQAVAFQFTI</u> SPEGINLHLSYQALNQIYLSGLRSWKKRISRIKRIK	AYPASP		
Me Cpt 1Alpha2b	1	<u>MAEAHQAVAFQFTI</u> TPEGIDLQLSYQALNQIYLSGVRSWKKRVSRMRNR	VIKGVYPASP		
Ti Cpt 1Beta	1	<u>MAEAHQAVGF</u> QFTVREDGVDFKLSQEVTKNIYLSGVTAWKKKAIQFKNG	VLAGVYPASP		
Zf Cpt 1Beta	1	<u>MAEAHQAVAFQFTV</u> TPDGDIDLQLSREVLKHIYISGVTSWKKRAIRFKN	SVLTGVYPASP		
Hu CPT 1Beta	1	<u>MAEAHQAVAFQFTV</u> TPDGDGVDFRLSREALKHVYLSGINSWKKRLIRIKN	GIIRGVYPGSET		
Consensus		MAEAHQAV F FT P G L S WKK N G P P			
		Transmembrane Region 1	Transmembrane Region 2		
Ti Cpt 1Alpha1a	61	GFSIVVGSYMAYNKFKQLDPSLG	LFTKLQHIP--ISRYMSTDSQK	IVGGILVGTSLWVT	
Zf Cpt 1Alpha1a	61	GLVVVLVGYSSTKYAKIDPSLG	ILTKLSTHLP--VSKYITEDGQR	IVGGVLVGTGLWIA	
Hu CPT 1Alpha1	61	<u>SWLIVVVGVMT-TMYAKIDPSLGI</u>	IAKINRTLE--TANCMSSTQTK	NVSGVLFGTGLWVA	
Al CPT 1Alpha1	61	<u>SWLIVVVGVMS-TMYAKIDPSLGLI</u>	IAKINRTLD--ITGYMSNQTON	IVSGVLFGTGLWVA	
Ti Cpt 1Alpha2a	61	<u>SWLFVVIAILA-TMYTRSDPSMGLI</u>	AKIQEHLVPSQ--SMSTQCQAV	VSAVLFSTMLWLM	
Zf Cpt 1Alpha2a	61	<u>SWLFVVIAILA-TMYTRSDPSMGLI</u>	AKIQEHLVSD--SLSVQCR	TMVSAVLFSTLLWFS	
Te Cpt 1Alpha2a	61	<u>SWLFVVIAILA-TMYTRSDPSMGLI</u>	AKIQENLPSQ--SLSTQCKV	LLSAVIFSTMLWLL	
Ti Cpt 1Alpha2b	61	<u>SWLFVAIGILA-TMYMQSDPSMGLI</u>	TKIQOHLPLSLHMSLSTQGQ	TMVSALVFSTLLWLS	
Zf Cpt 1Alpha2b	61	<u>SWLFVIVIAILA-TMYMQSDPSMGLI</u>	AKIQEHLPLSL--SLSPQGQ	TMLSALLFSTLLWMS	
Me Cpt 1Alpha2b	61	<u>SWLFVAIGILA-TIYMQSDPSMGLI</u>	AEIQORLPLSLHVSLSAQGQ	TMVSALVFSTLLWLS	
Ti Cpt 1Beta	61	<u>SWLIVVIAMMS-SLYIHIDPSLG</u>	MDAIKENLP--YRDCMSVQTR	AVLSAILEFATGLWLF	
Zf Cpt 1Beta	61	<u>SWLFVVIAIMS-TMYARIDPSMGT</u>	IDKIKTSLP--VSEFMTVQTQ	TVLSAILEFATGLWLS	
Hu CPT 1Beta	61	<u>SWLVVIMATVG-SSFCNVDISLGLV</u>	SCIQRCLPQCGPYQTPQTR	ALLSMAIFSTGVVVT	
Consensus		D S G		W	
		Transmembrane Region 2	Acyltransferase ChoActase 1		
Ti Cpt 1Alpha1a	119	<u>IIMIMRTVLKSL</u> LSWHGWMQERHGSLSWSSRIWMVLVKVFSGRKPMLYSFONS	LPRLPVP		
Zf Cpt 1Alpha1a	119	<u>VTFVMRNALKYLL</u> SWHGWMFNQHTLSLKTKIWLVLVKLFSGPKPMLYSFOSS	LPRLPVP		
Hu CPT 1Alpha1	118	<u>LIVTMRYSLKVL</u> LSYHGWMFTEHGKMSRATKIWMGMVKIFSGRKPMLYSFOTS	LPRLPVP		
Al CPT 1Alpha1	118	<u>LIFSMRYTLKML</u> LSYHGWMF AEHGKLSGTGKIWMTLVKLFSGRKPMLYSFOTS	LPRLPVP		
Ti Cpt 1Alpha2a	118	<u>LIFTMRLCLKQL</u> LSYHRWMFEQHGKMSSTTKIWMVALVRIFSGRKPMLYSYOGS	LPNLPVP		
Zf Cpt 1Alpha2a	118	<u>LIFTMRLCLKQL</u> LSYHGWMFQHGKVSNTTKIWAAMVRIFSGRQPLLYSYOGS	LPNLPVP		
Te Cpt 1Alpha2a	118	<u>LIFTMRLCLKQL</u> LSYHRWMFEPHGKMSSTTKVWMVALVRIFSGRKRPLLYSYOGS	LPNLPVP		
Ti Cpt 1Alpha2b	120	<u>LILALRFCLIKLL</u> LSYHQWMFEKHGRISNTTKVWVPLVRLLSSRKPLLYSYOGS	LPPLPVP		
Zf Cpt 1Alpha2b	118	<u>LILTLRFCLIKLL</u> LSYHRWMFEQHGKMSSTTKVWATLVKLLSSRKPLLYSYQTS	LPPLPVP		
Me Cpt 1Alpha2b	120	<u>LILALRFCLIKLL</u> LSYHQWMFEQHGKVSNTTKVWVTLRLSSRKPLLYSYQTS	LPPLPVP		
Ti Cpt 1Beta	118	<u>LIYLLRYTLKALL</u> SYHGWIFESHGKMSSTTKVWLCIVKMFSGRRPLLYSFOAS	LPRLPVP		
Zf Cpt 1Beta	118	<u>VIFLLRYLLKALL</u> SYHAWIFESHGKMSYSTKVWLSLVKLLSGRRPLLYSFOGS	LPPLPVP		
Hu CPT 1Beta	120	<u>GIFFFRQTLKLL</u> LCYHGWFMFEMHGKTSNLTRIWMACIRLLSSRHPLLYSFOGS	LPKLPVP		
Consensus		R L LL H W HG W S P LYS Q LP LPVP			

Acyltransferase
ChoActase 1

Ti Cpt 1Alpha1a	179	SIKDTICERYLESVRPLMDDQQFERMKGLTQDFEKNLGPRLQWYLKLSWWASNYVSDWWE
Zf Cpt 1Alpha1a	179	PVKDTVRRYLESARPLMDDEQYKRMEGLAKDFEKNLGPRLQWYLKLSWWTSNYVSDWWE
Hu CPT 1Alpha1	178	AVKDTVNRYLQSVRPLMKEEDFKRMTALAQDFAVGLGPRLQWYLKLSWWATNYVSDWWE
Al CPT 1Alpha1	178	SVKNTVNRYLESVHPLMNEEQFKRMEALGKDFATNLGPRLQWYLKLSWWAANYVSDWWE
Ti Cpt 1Alpha2a	178	TIKDTVKRYLESVRPLMDDKEYERMTKLAAEFESSLGNRLQWYLKLSWWASNYVSDWWE
Zf Cpt 1Alpha2a	178	AVKDTVKRYLESVRPLMNDSEYERMTLAREFESSLGNRLQWYLKLSWWASNYVSDWWE
Te Cpt 1Alpha2a	178	AVKDTVKRYLESVRPLMDDAQYERVAKLAAEFESSLGNRLQWYLKLSWWVVTNYVSDWWE
Ti Cpt 1Alpha2b	180	AIQDITVSRYLESVRPLLDLDFKRMTDLANEFESNLGNRLQRYLKLKALWATNYVSDWWE
Zf Cpt 1Alpha2b	178	PIKDTLERYLESVKPLLDLDGFQMRRLTSEFEKSLGNRLQRYLRKLKALWATNYVSDWWE
Me Cpt 1Alpha2b	180	AVRDTLTRYLESVRPLLDPEYKRMTDLANEFESSLGNRLQRYLKLKALWATNYVSDWWE
Ti Cpt 1Beta	178	SVDDTIHRYLESVRPLLDNEQYNKMELLASDFKENKAAQLQRCILKLSWWATNYVSDWWE
Zf Cpt 1Beta	178	SIDDTIRRYLESVRPLLDDEQYQMETVANDEKKDPAPKLQKHLKLSWWATNYVSDWWE
Hu CPT 1Beta	180	RVSATIORYLESVRPLLDDEEYYRMELLAKEFQDKTAPRLQKYLVLKLSWWASNYVSDWWE
Consensus		T RYL S PL F LQ L LK W NYVSDWWE

Acyltransferase
ChoActase 2

Ti Cpt 1Alpha1a	413	KAAFFLTLDDETEQRYDTKNPVKSLDIYAKSLLHGKCYDRWFDKSLNMIYVKNGTMGLNAE
Zf Cpt 1Alpha1a	414	KAAFFVTLDDESEQRYEPDNPIQSLDSYGKSLHKGKCYDRWFDKSLNLIVFKNGTMGLNAE
Hu CPT 1Alpha1	413	KAAFFVTLDDETEEGYRSEDPDTSMSYAKSLLHGCYDRWFDKSFTEFVVFKNKGKMGNAE
Al CPT 1Alpha1	413	KAAFFVTLDDETAQGYREEDPVTTMETYAKSLLHGKCYDRWFDKSFTEFVVFKNKGKMGINTTE
Ti Cpt 1Alpha2a	412	KAAFFVTLDDEEQGMMGDDPAASLDYAKSLLHGKCYDRWFDKSFTEFVVFKNKGKMGNAE
Zf Cpt 1Alpha2a	416	KAAFFVTLDDEEQGMMGDDPAGNLDYAKSLLHGKCYDRWFDKSFTEFVVFKNKGKMGNAE
Te Cpt 1Alpha2a	415	KAAFFVTLDDEEQGIMGDNLRSLDHYIKSLLHGKCYKRWFDKSFTEFVVFKNKGKSGINGE
Ti Cpt 1Alpha2b	415	RAAFFVTLDDEEQGMRGDDPEGNLDYAKSLLHGKCYDRWFDKSFTEFVVFKNKGKSGINGE
Zf Cpt 1Alpha2b	413	KAAFFVTLDDEAQEGMKGENPSENLDYAKSLLHGKCYDRWFDKSFTEFVVFKNKGKMGNAE
Me Cpt 1Alpha2b	415	KAAFFVTLDDEAQGMMGDDPTGNLDYAKSLLHGKCYDRWFDKSFTEFVVFKNKGKSGINGE
Ti Cpt 1Beta	412	SAAFFLTLDDEPQGYDPAK-SNSLDSYAKSLLHGKCYDRWFDKSFTEFVVFKNKGKMGVNVTE
Zf Cpt 1Beta	412	TAAFFLTLDDEAHGYDPEN-IRSLDLYAKSLLHGKCYDRWFDKSFNLIVYKNKGKMGVNVTE
Hu CPT 1Beta	414	RAAFFVALDEESYSYDPED-EASLSLYGKALLHGNCYNRWFDKSFTEFVVFKNKGKMGNAE
Consensus		AAFF LD Y K LLHG C RWFDKS NG G N E

Acyltransferase
ChoActase 2

Ti Cpt 1Alpha1a	473	HSWADAFIVGHLWEHVLSDMP-KLGYTEDGHCVGKPHPNLPGPQRLQWTIPAECEQEAIES
Zf Cpt 1Alpha1a	474	HSWADAFIVGHLWEQVLSSDPVRLGYTEEGHCKGNPHPNMPPGPQRLQWDIPEECQTVISS
Hu CPT 1Alpha1	473	HSWADAFIVGHLWEYVMSIDSLQLGYAEDGHCKGDINPNIPYPTRLQWDIPGECQEVIEET
Al CPT 1Alpha1	473	HSWADAFIVGHLWENVMFSDCLELGYTEDGHCKGESSSGIIMPSRLQWEILEECQEVIER
Ti Cpt 1Alpha2a	472	HSWADAFVLAHVWEYTLANDSFQLGYNAEGHCKGDVDPSPSLPRPVKLSWEIPPECEEQIAQ
Zf Cpt 1Alpha2a	476	HSWADAFIMAHLWEYVMTTDCFQLGYNEEGHCKGDVAPTLPPEPSRLTWDIPAQCQERVQR
Te Cpt 1Alpha2a	475	HSWGDAPVLSHLWEYTLATECFQLGYNAEGHCKGEVDASLPKPQKLNWEIPSECEEQICQ
Ti Cpt 1Alpha2b	475	HSWADAPTVAHLWEYTLATDAFQLGYTEDGHCKGEVEPSLPQBPQRLVWNIIPAEVQAQVSS
Zf Cpt 1Alpha2b	473	HSWADAFIVGHLWEFTLATDTFHLGYNSDGNCRGDVDHSLPHQRLSWDIPFEVQTQISE
Me Cpt 1Alpha2b	475	HSWADAPTVAHLWEYTLATDAFQLGYTEDGHCKGEVDRSLPPEHRLSWEIPSEVQDQIFS
Ti Cpt 1Beta	471	HSWADAFIVGHMWEYILATDCFHLGYTEEGHCKGDVNKNLPHPTRLQWQIPNECQNVIEET
Zf Cpt 1Beta	471	HSWADSPFIIGHMWEYVLATDCFHLGYTAEGHCKGDVNKTLPPTRLQWDIPKACQEIIEG
Hu CPT 1Beta	473	HAWADAFIIGHLWEFVLGTDSFHLGYTETGHCLGKPNPALAPETRLQWDIPKQCQAVIES
Consensus		H W D P H WE LGY G C G P L W I