

Supplemental Figures:

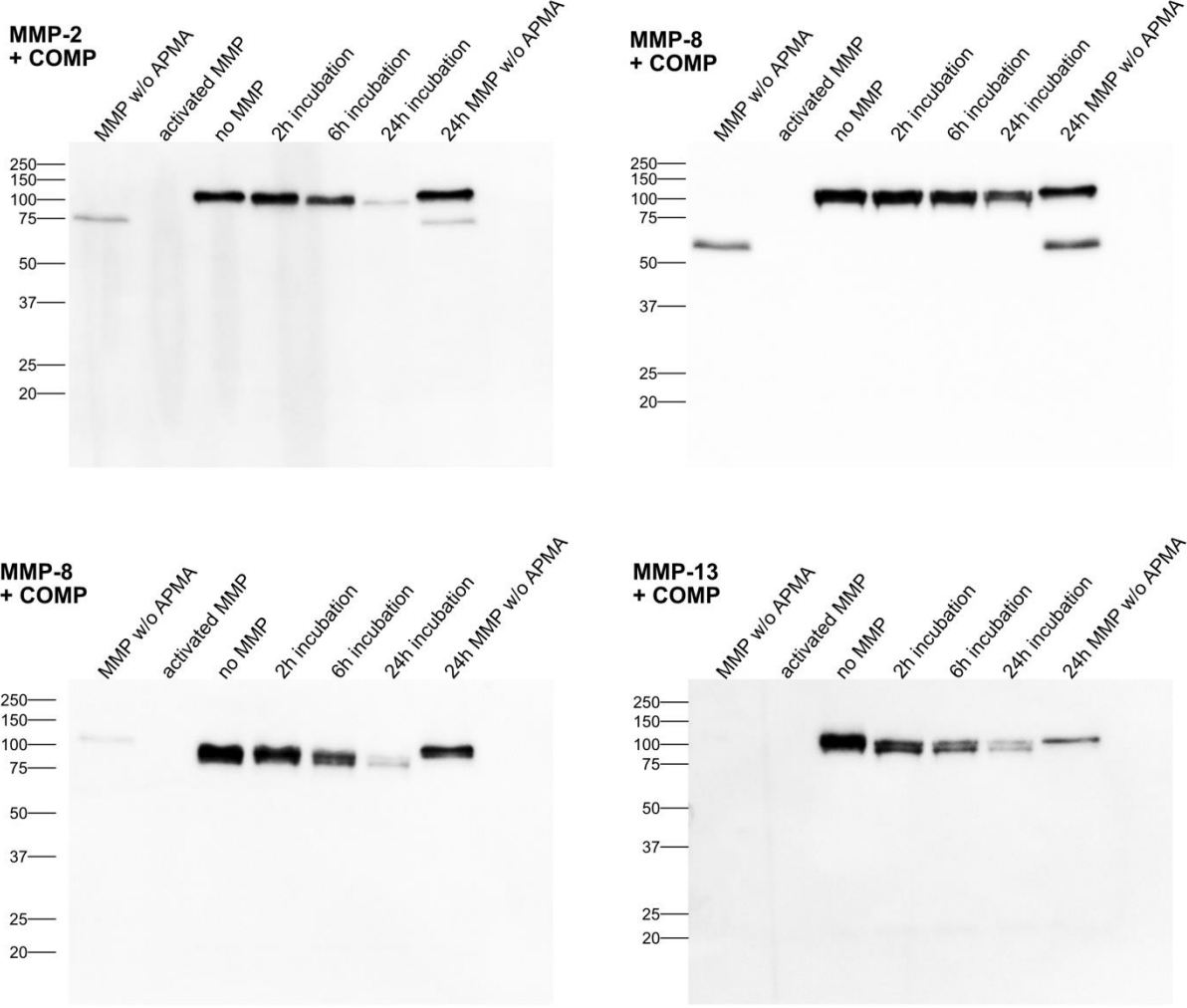


Figure S1: MMPs have to be activated by APMA for efficient proteolytic cleavage of COMP. COMP was incubated with activated or non-activated MMP for different time points. Efficient cleavage is indicated by a reduction of signal intensity and, in some cases, a shift towards a smaller size compared to the full-length protein without MMP (no MMP). Cleavage was observed with activated MMPs only.

Sequence ID	Start	Alignment	End	Organism
EAW95841.1	(+)	1	961	Homo sapiens
AAI25093.1	(+)	1	757	Homo sapiens

<input checked="" type="checkbox"/>	EAW95841.1	1	MLAPRGAAVLLHLVLRWLAAGAATPQVFDLLPSSSQLNPGALLPVLTDPALNDLYVISTFKLQTKSSATIFGLYSS	80
<input checked="" type="checkbox"/>	AAI25093.1		-----	
<input checked="" type="checkbox"/>	EAW95841.1	81	TDNSKYFEFTVMGRLNKAILRVLKNDGKVLVVFNNLQLADGRRRIRILLRSLNLRGAGSLELYLDCIQVDSVHNLPRAF	160
<input checked="" type="checkbox"/>	AAI25093.1		-----	
<input checked="" type="checkbox"/>	EAW95841.1	161	AGPSQKPEITELRTFQRKQDFLEELKLVVRGSLFQVASLQDCFLQQSEPLAATGTG-----DFNRQFLGQMTQLNQLL	234
<input checked="" type="checkbox"/>	AAI25093.1	1	-----MVPDTACVLLLLAALGASGQGQSPPLGSDLGPQMLRELQETNAAL	45
<input checked="" type="checkbox"/>	EAW95841.1	235	GEVKDLLRQVQKETSFLRNTIAECQACGPKLQSPSTPSTVPPAPPTRPFRRCDSNCFRGVQCTDSRDGFQCGPCP	314
<input checked="" type="checkbox"/>	AAI25093.1	46	QDVRELLRQVREITFLKNTVMECDACG---MQQSVRTGL-----PSVRPLLHCAPGFQPGVACIQTESGARCGPCP	115
<input checked="" type="checkbox"/>	EAW95841.1	315	EGYTGNGITCIDVDECKYHPCYPGVHCINLSPGFRCDAFVGTGPMVQGVGISFAKSNKQVCTDIDECRNGA--CVPNS	392
<input checked="" type="checkbox"/>	AAI25093.1	116	AGFTGNGSHCTDVNECNAHPCFRVRCINTSPGFRCEACPPGYSGPTHQGVGLAFKANKQVCTDINECETQGHNCVPNS	195
<input checked="" type="checkbox"/>	EAW95841.1	393	ICVNTLGSYRCGCKPGYTGDIQRC--KAERNCRNPELNPCSVNAQCIEERQGDVTCVCGVWAGDGYICGKDVDDISY	470
<input checked="" type="checkbox"/>	AAI25093.1	196	VCINTRGSFQCGPCQPGFVGDQASGCQRRARFCPDGSPSECHEHADCVLERDGSRSVCVAVGWAGNGLCGRDTDLDF	275
<input checked="" type="checkbox"/>	EAW95841.1	471	PDEELPCSARNCKKDNCKYVPNSGQEDADRDIQDADCEADADGDGILNEQDNCVLIHNVDQRNSDKDIFGDACDNCLSVL	550
<input checked="" type="checkbox"/>	AAI25093.1	276	PDEKLRCPERQCRKDNCKVTPNSGQEDVDRDGIQDADDPADGDGVPNEKDNCPVLRNPQQRNTDEDKWDACDNCRSQK	355
<input checked="" type="checkbox"/>	EAW95841.1	551	NNDQKDTDQDGRGDACDDDDMDGDIKNILDNCFKFPNRDQRKDGDCVGDACDSCPDSVSNPQSDVDNDLVGDSCTNQD	630
<input checked="" type="checkbox"/>	AAI25093.1	356	NNDQKDTDQDGRGDACDDDDIDGDIRNQADNCPRVNSDQKDSDDGIGDADCNCPKSNPDQADVDHDFVGDACDSDQD	435
<input checked="" type="checkbox"/>	EAW95841.1	631	SDGDGHQDSTDNCPVTIINSAQLDITKDGIGDECDDDDDNDGIPDLVPPGPDNCRVLPNPAQEDSNSDGVGDICESDFDQD	710
<input checked="" type="checkbox"/>	AAI25093.1	436	QDGDGHQDSDNCPVTVPNSAQEDSDHDGQGDACDDDDDDNDGVPD---SRDNCRLVPPGQEDADRQDGVGVCQDQDFDAD	511
<input checked="" type="checkbox"/>	EAW95841.1	711	QVIDRIDVCPENAEVTLTDFRAYQTVVLDPEGDAQIDPNWVVLNQGMEIVQTMNSDPGLAVGYTAFNGVDFEGTFHVNTQ	790
<input checked="" type="checkbox"/>	AAI25093.1	512	KVVDKIDVCPENAEVTLTDFRAYQTVVLDPEGDAQIDPNWVVLNQGREIVQTMNSDPGLAVGYTAFNGVDFEGTFHVNTV	591
<input checked="" type="checkbox"/>	EAW95841.1	791	TDDDYAGFIFGYQDSSSFYVVMWQTEQTYWQATPFRAVAEPIQLKAVKSKTGPGEHLRNSLWHTGDTESQVRLWWDKDS	870
<input checked="" type="checkbox"/>	AAI25093.1	592	TDDDYAGFIFGYQDSSSFYVVMWQMEQTYWQATPFRAVAEPIQLKAVKSKTGPGEQLRNALWHTGDTESQVRLWWDKDP	671
<input checked="" type="checkbox"/>	EAW95841.1	871	RNVGWKDKVSYRWFLQHRPQVGYIRVRFYEGSELVADSGVTIDTTMRGGRLGVFCFSQENI IWSNLKYRCNDTIPEDFQE	950
<input checked="" type="checkbox"/>	AAI25093.1	672	RNVGWKDKVSYRWFLQHRPQVGYIRVRFYEGSELVADSNVLDTTMRGGRLGVFCFSQENI IWANLRYRCNDTIPEDYET	751
<input checked="" type="checkbox"/>	EAW95841.1	951	FQTQNFDRFDN 961	
<input checked="" type="checkbox"/>	AAI25093.1	752	HQLRQA----- 757	

EAW95841.1 = Thrombospondin-4
 AAI25093.1 = COMP

Figure S2: Sequence alignment of COMP and TSP-4. Red amino acids are conserved, blue indicates differences in sequence.