Electronic Supplementary Material (ESI) for RSC Advances.

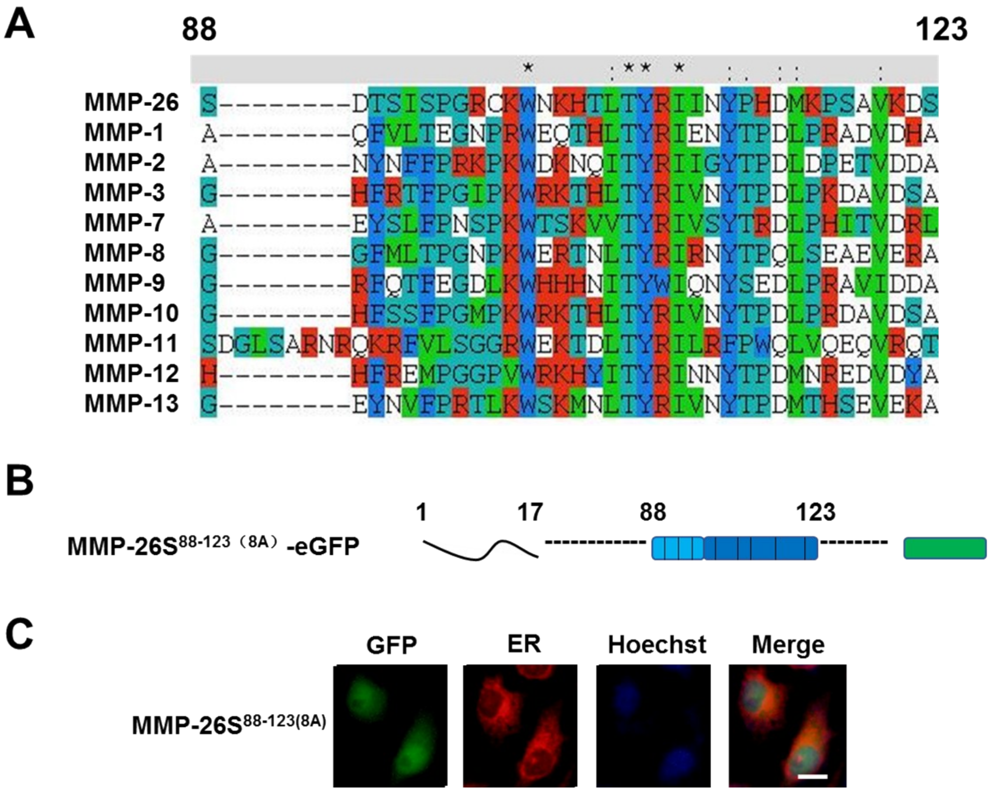

Figure. S1 Positively charged residues in the 88–123 region are vital for the ER retention of MMP-26. (A) Multi-sequence alignment of all secreted MMPs. Positively charged residues are coloured in red. Symbols denote the degree of conservation observed in each column: “*” (identical residues in all sequences), “:” (highly conserved column), and “.” (weakly conserved column). (B) Schematic of MMP-26S$^{88–123\ (8A)}$-GFP. (C) Hela cells were transfected with plasmid of MMP-26S$^{88–123\ (8A)}$-GFP, ER-Tracker Red was added into cell culture media after 24 h and nuclei were co-stained with Hoechst. The scale bar is 10 µm.

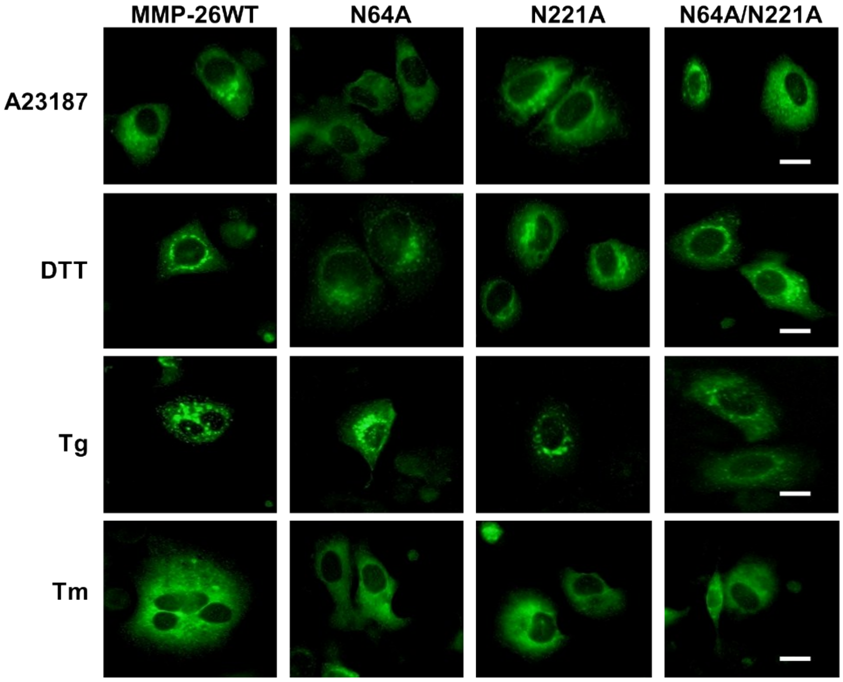

Figure. S2 Subcellular localization of MMP-26-GFP and its N-glycosylation deficient mutants under ER stress. Hela cells were transfected with plasmids of MMP-26 and its N-glycosylation-deficient mutants (N64A, N221A, N64A/N221A). After 24 h transfection, A23187 (1 μmol/L), DTT (200 μmol/L), Tg (2 μmol/L), and Tm (5 μg/L) were added to the cell culture media. The scale bar is 10 μm.

Primers design

MMP-26(signal peptide)	SP-for	CCAAGCTTATGCAGCTCGTCATCTTAAGAGTTA
	SP-rev	TCGGAGGCGAAACACCAGGGCAAGA
MMP-26(87-125)	87-125-for	TCGCCGGGTCCGACACCTCCATCT
	87-125-rev	GGGTACCAATATATATACTGTCTTTCACTGCGGATGGC
MMP-26(88-125)	88-125-for	TCGCCTCCGACACCTCCATCTCGCCAG
	88-125-rev	GGGTACCAATATATATACTGTCTTTCACTGCGGATGGC
MMP-26(89-125)	89-125-for	TCGCCGACACCTCCATCTCGCCAG

	89-125-rev	GGGTACCAATATATATACTGTCTTTCACTGCGGATGGC
MMP-26(90-125)	90-125-for	TCGCCACCTCCATCTCGCCAG
	90-125-rev	GGGTACCAATATATATACTGTCTTTCACTGCGGATGGC
MMP-26(88-124)	88-124-for	TCGCCTCCGACACCTCCATCTCGCCAG
	88-124-rev	GGGTACCAATTATACTGTCTTTCACTGCGGATGGC
MMP-26(88-123)	88-123-for	TCGCCTCCGACACCTCCATCTCGCCAG
	88-123-rev	GGGTACCAATACTGTCTTTCACTGCGGATGGC
MMP-26(88-122)	88-122-for	TCGCCTCCGACACCTCCATCTCGCCAG
	88-122-rev	GGGTACCAATGTCTTTCACTGCGGATGGC
MMP-26(88-121)	88-121-for	TCGCCTCCGACACCTCCATCTCGCCAG
	88-121-rev	GGGTACCAATTTTCACTGCGGATGGC
MMP-26△88-123	1-87-for	CCAAGCTTATGCAGCTCGTCATCTTAAGAGTTA
	1-87-rev	CATTATATATCCCATCAGGCACCCCACAGT
	124-261-for	GTGCCTGATGGGATATATAATGCAGTTTCCATCTGGAGCAAT
	124-261-rev	GGGTACCAATAGGTATGTCAGATGAACATTTTTCTCCATAC
MMP-26S88-123 (8A)	R96A-for	CTCCATCTCGCCAGGAGCATGCAAGTGGAA
	R96A-rev	TGCTCCTGGCGAGATGGAGGTGTCGGAGGC
	K98A-for	TCGCCAGGAAGATGCGCTTGGAATAAGCAC
	K98A-rev	GTGCTTATTCCAAGCGCATCTTCCTGGCGA
	K101A-for	TGCAAGTGGAATGCTCACACTCTAACTTAC
	K101A-rev	AAGTTAGAGTGTGTGCATTCCACTTGCATC
	H102A-for	ATGCAAGTGGAATAAGGCCACTCTAACTTA
	H102A-rev	GGCCTTATTCCACTTGCATCTTCCTGGCGA
	R107A-for	ACACTCTAACTTACGCTATTATCAATTACC
	R107A-rev	GGTAATTGATAATTGCGTAAGTTAGAGTGT
	H113A-for	TTATCAATTACCCAGCTGATATGAAGCCAT
	H113A-rev	ATGGCTTCATATCTGCTGGGTAATTGATAA
	K116A-for	TTACCCACATGATATGGCGCCATCCGCAGT
	K116A-rev	CGCCATATCATGTGGGTAATTGATAATCCT
	K121A-for	GAAGCCATCCGCAGTGGCAGACAGTATTGG
	K121A-rev	TGCCACTGCGGATGGCTTCATATCATGTGG
Mut-MMP-7	MMP-7-for	TCAGATCTCGAGCTCAATGCGACTCACCGTGCTGT
	MMP-7(92)-rev	GGAGGTGTCGGAAACATCTGGCACTCCACATC
	MMP-7(129)-for	GCAGTGAAAGACAGTGTGTCAAAGGCTTTAAACATGTG
	MMP-7-rev	CCGGGCCCGCGGTACTTTCTTTCTTGAATTACTTCGTTT
	MMP-26(88)-for	GGAGTGCCAGATGTTTCCGACACCTCCATCTCGC
	MMP-26(123)-rev	TAAAGCCTTTGACACACTGTCTTTCACTGCG