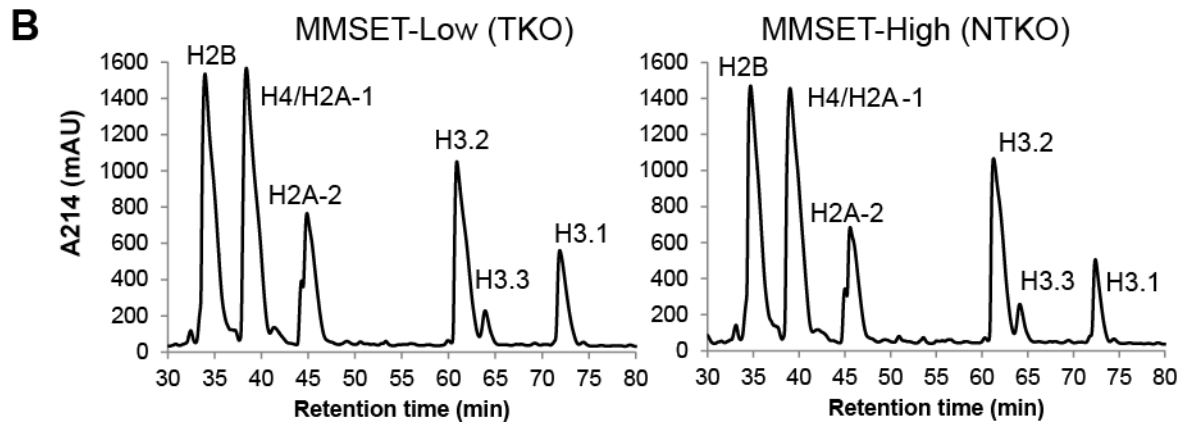


**A**

H3.1	ART	KQTARKS	TGGKAPRKQL	ATKAARKSAP	ATGGVKKPHR	YRPGT	VALRE
H3.3	ART	KQTARKS	TGGKAPRKQL	ATKAARKSAP	STGGVKKPHR	YRPGT	VALRE
		4	9		27		36
H3.1	IRRYQKSTEL LIRKLPFQRL VREIAQDFKT DLRFQSSAVM ALQEACEAYL						
H3.3	IRRYQKSTEL LIRKLPFQRL VREIAQDFKT DLRFQSA AIG ALQEASEAYL						
					79		
H3.1	VGLFEDTNLC AIHAKRVTIM PKDIQLARRI RGERA						135
H3.3	VGLFEDTNLC AIHAKRVTIM PKDIQLARRI RGERA						135



**Fig S1.** (A). The alignment of H3.1 and H3.3 variants. The different residues are labeled as red and the globular domain is indicated within a box. (B) UV trace of reverse phase HPLC separation of acid extracted total histones from MMSET-Low and MMSET-High cells.