Figure S1. Normalized mRNA expression (ΔΔCq) of *TET* genes in multiple myeloma cell lines after treatment with demethylating agents. The ΔΔCq value was normalized to DMSO control with (A) KMS 12-BM, (B) KMS12-PE, (C) U266/B1, (D) RPMI and (E) OPM2 myeloma cell lines, using β2-microglobulin as the reference gene. Cells were co-treated with 5-azacytidine (0.2 and 0.5 μmol/l) and 5-aza-2'-deoxycytidine (0.2 and 0.5 μmol/l) for 48 h, with retreatment after 24 h (n=3 independent biological experiments). Each biological experiment was measured in technical triplicate and mean values were used for analysis. Data are presented as the mean ± SD. The significance was assessed using the non-parametric Kruskal-Wallis test with Bonferroni correction for pairwise comparisons. A statistically significant change was observed between *TET1*, *TET2* and *TET3* expression only in the KMS12-PE cell line (***P<0.001). TET, ten-eleven translocation.

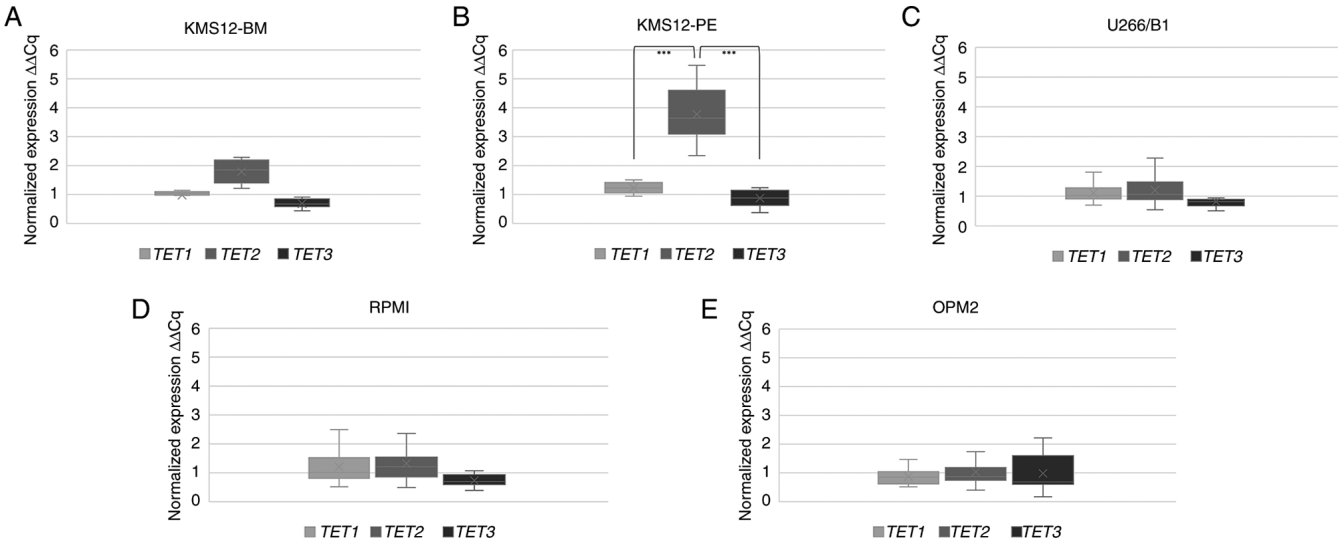


Figure S2. Representative biological replicate of *TET1* and *TET2* protein expression analysis. Western blotting analysis represents an independent biological replicate of the experiments shown in Fig. 3. Protein expression levels of (A) *TET1* (~235 kDa), (B) *TET2* (~130 kDa) and (C) GAPDH (~37 kDa) were evaluated in KMS12-PE and KMS12-BM cell lines following treatment with AZA and DAC at concentrations of 0.2 and 0.5 μmol/l. GAPDH served as the internal loading control. Proteins were transferred to the same membrane, which was subsequently cut according to molecular weight and probed with the indicated antibodies. These data confirm the reproducibility of the protein expression trends observed in the primary study. TET, ten-eleven translocation; AZA, 5-azacytidine; DAC, 5-aza-2'-deoxycytidine.

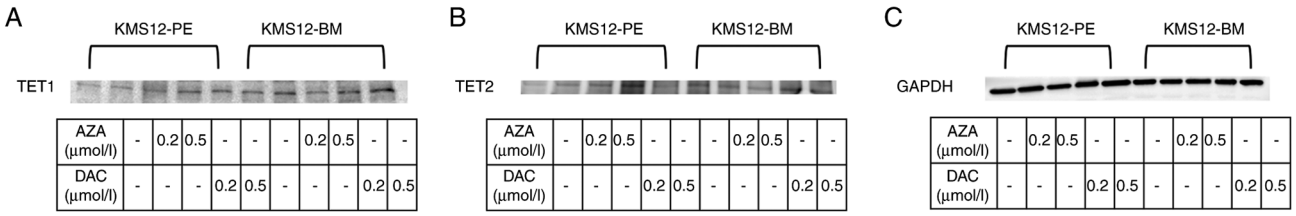
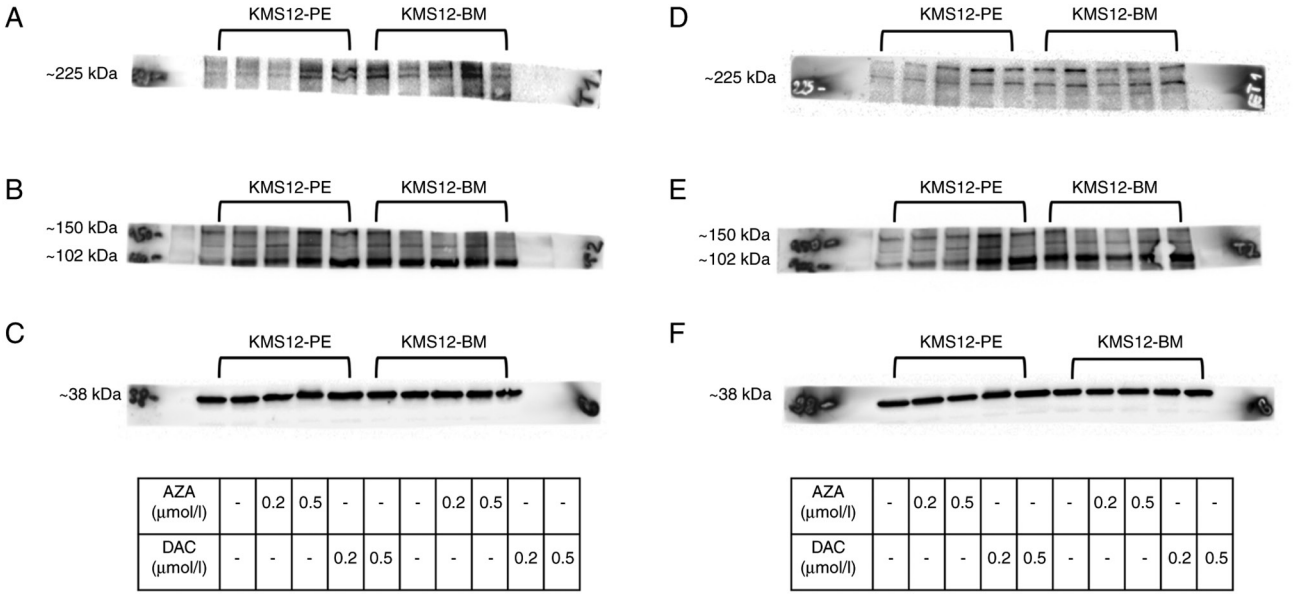


Figure S3. Full-length western blotting membranes with molecular weight markers. Uncropped representative western blotting images showing protein expression of (A) TET1 (-235 kDa), (B) TET2 (C) and GAPDH (~37 kDa) in KMS12-PE and KMS12-BM cell lines after AZA and DAC treatment. Panels (D-F) represent independent biological duplicates confirming the observed trends. (D) TET1 (-235 kDa), (E) TET2 (~130 kDa) and (F) GAPDH (~37 kDa) expression in KMS-PE and KMS12-BM cells after AZA and DAC (both 0.2 and 0.5 μmol/l) treatment. Full-length membranes with visible molecular weight markers are provided to verify antibody specificity and protein size. Cells were treated with AZA and DAC at concentrations of 0.2 and 0.5 μmol/l. GAPDH served as the internal loading control. Proteins were transferred to the same membrane, which was subsequently cut according to molecular weight and probed with the indicated antibodies. TET, ten-eleven translocation; AZA, 5-azacytidine; DAC, 5-aza-2'-deoxycytidine.



AZA (µmol/l)	-	0.2	0.5	-	-	-	0.2	0.5	-	-
DAC (µmol/l)	-	-	-	0.2	0.5	-	-	-	0.2	0.5

AZA (µmol/l)	-	0.2	0.5	-	-	-	0.2	0.5	-	-
DAC (µmol/l)	-	-	-	0.2	0.5	-	-	-	0.2	0.5