

Table SI. Similarities and differences among MTA1, MTA2 and MTA3.

Comparison item	MTA1	MTA2	MTA3	(Refs.)
Chromosomal localization	14q32.3	11q12–q13.1	2p21	(10)
Molecular weight, kDa	~80	~70	~65	(9)
Conserved domains	Contains BAH, ELM2 and SANT domains	Contains BAH, ELM2, SANT and an atypical GATA zinc finger domain	Highly homologous structure to MTA1/2, with distinct C-terminal sequences	(10,11,21)
Normal tissue expression	Broad expression in most tissues	High expression in testis, brain, heart, lung, liver and kidney	-	(39-41)
Physiological functions	-	Maintains intestinal lineage stability, sperm maturation, B-cell development and stem cell pluripotency	Cooperates with MTA2 to maintain stem cell pluripotency and repress mesodermal differentiation	(10,14)
Expression in cancer	Frequently overexpressed in most tumors	Predominantly amplified (rarely mutated), with overexpression in most solid tumors	Expression often decreases with tumor progression	(13,18-20)
Family cross-regulation	Overexpression reduces MTA2/MTA3 protein levels without affecting mRNA	Degraded by MTA1 in breast cancer; forms an antagonistic pair with MTA1	Downregulated by MTA1 overexpression	(17-19)
Core oncogenic functions	Promotes tumor progression; context-dependent anti-metastatic effects reported	A master driver of metastasis, EMT, drug resistance and epigenetic silencing	Regulates epithelial cell state via Snail-related pathways; context-dependent EMT regulation	(13-16)

BAH, bromo-adjacent homology; ELM2, Egl-27 and MTA1 homology 2; EMT, epithelial-mesenchymal transition; MTA, metastasis-associated; SANT, Swi3/Ada2/N Cor/TFIIIB domain.