Table 1. Aberrant expression of RNA modifiers and RNA modifications linked to cancer. Ψ, pseudouridine; A-to-I, Adenosine-to-Inosine edition; AML, Acute Myeloid Leukaemia; CDS, coding regions, CML, Chronic Myeloid Leukaemia; CRC, Colorectal cancer; EMT, Epithelial-Mesenchymal-Transition; ESCC, Oesophageal squamous cell carcinoma; GBM, glioblastoma multiforme; HCC, Hepatocellular carcinoma; HNSCC, Head and Neck Squamous Carcinoma; m1A, N1-methyladenosine; m5C, 5-methyl cytidine; m6A, N6-methyladenosine.

Gene symbol	Activity	Consequences on cancer	Type of cancer	References
Writers				
METTL3	m6A	Overexpression is associated with increased translation of oncogenic transcripts (e.g. MYC, BCL2 or PTEN)	AML	(Vu et al., 2017)
METTL3	m6A	Depletion in immunodeficient mice increases differentiation of leukemic cells and decreased anti-tumoral effect	AML	(Barbieri et al., 2017)
METTL3	m6A	Upregulation is a prognosis factor for adverse overall survival. It regulates the m^6A levels at the CDS of the EMT gene SNAIL causing polysome-mediated translation of Snail mRNA.	Liver cancer	(Lin et al., 2019)
METTL3	m6A	Overexpression is associated with increased expression of EMT effectors (e.g. MMP2 and N-cadherin)	Melanoma	(Dahal et al., 2019).
METTL3	m6A	Overexpression promotes the maturation of pri-miR221/222 resulting in decreased expression of the tumour suppressor gene PTEN	Bladder cancer	(Han et al., 2019b)
METTL3	m6A	Overexpression promotes the maturation of pri-miRNA126 leading to decreased metastatic potential in hepatocellular carcinoma	HCC	(Ma et al., 2017)
METTL3	m6A	Downregulation results in activation of p-p38 and p-ERK tumour suppressor pathway.	CRC	(Deng et al., 2019)
METTL14	m6A	Overexpression is associated with increased expression of oncogenic mRNA targets (e.g. MYB and MYC)	AML	(Weng et al., 2018)

METTL14	m6A	Hotspots genetic mutations lead to decreased expression of the negative AKT regulator PHLPP2 and increased expression of the positive AKT regulator mTORC2	Endometrial cancer	(Liu et al., 2018)
ALKBH3	m1A	Mediates increased mRNA abundance of CSF1 promoting cell invasion without affecting cell proliferation or migration	Ovarian and breast cancer	(Woo and Chambers, 2019)
ALKBH3	m1A	Loss mediates abundance of collagen mRNAs conferring poor prognosis	Hodgkin lymphoma	(Esteve-Puig et al., 2020)
NSUN2	m5C	Overexpression is associated with low IGF-II expression leading to higher overall and disease progression-free survival	Ovarian cancer	(Yang et al., 2017a)
NSUN2	m5C	Overexpression is associated with shorter overall survival and a higher mortality risk. Its expression has been proposed as a biomarker for the prediction of response to immunotherapy through a mechanism involving T-cell activation	HNSCC	(Lu et al., 2020)
NSUN2	m5C	Stabilizes the oncogenic LINC01672 which binds to chromatin regulator BPTF, resulting in increased expression of MMP3 and MMP10 by ERK1/2 activation	ESCC	(Li et al., 2018a)
NSUN5	m5C	Epigenetically silencing is associated with unmethylation at the C3782 position of 28S rRNA resulting in depletion of protein synthesis and affecting the stress adaptive translational program	Glioblastoma	(Janin et al., 2019)
DKC1	ψ	Overexpression is associated with tumour progression and poor overall survival by the stabilization of the telomerase RNA component TERC	Lung cancer	(Penzo et al., 2015)
DKC1	ψ	Downregulation by siRNA- caused a decrease of p53 mRNA translation and p53 protein inactivation	Breast cancer	(Montanaro et al., 2010)
PUS10	ψ	Forms a complex with the ncRNA SRA1 to bind retinoic acid receptor-γ and establishing the transcriptional pre-initiation complex	Melanoma and breast cancer	(Zhao et al., 2004)
PUS10	ψ	Participates in TRAIL-induced apoptosis by regulating caspase-3 activity	Prostate cancer	(Jana et al., 2017)
PUS10	ψ	Depletion results in reduced expression of a large number of mature miRNAs and concomitant accumulation of unprocessed primary microRNAs (pri-miRNAs)	Multiple human cell lines	(Song et al., 2020)
ADAR1	A-to-I	Overexpression is associated with increased substitution of serine to glycine	HCC	(Chen et al.,

		at residue 367 and prevention of the degradation of the ornithine decarboxylase ODC and cyclin D1 oncoproteins		2013)
ADAR1	A-to-I	Overexpression is associated with hyperediting of FLNB and COPA	HCC, ESCC	(Chan et al., 2014) (Qin et al., 2014)
ADAR1	A-to-I	Overexpression is associated with the induced activation of the JAK/STAT pathway by type I interferon	ESC	(Zhang et al., 2017b)
ADAR1	A-to-I	Overexpression is associated with expression of PU.1 (myeloid transcription factor) inducing a malignant reprogramming of embryonic stem cells	CML with BCR-ABL fusion gene	(Jiang et al., 2013a)
ADAR1	A-to-I	Overexpression is associated with enhanced editing frequencies of target transcripts such as NEIL1and the oncogenic miR-381	HNSCC	(Anadón et al., 2016a)
ADAR1	A-to-I	Mediates editing of miRNAs (e.g., miR-455-5p) by a mechanism involving the inhibition of the tumour suppressor gene CPEB1	Melanoma	(Shoshan et al., 2015)
ADAR1	A-to-I	Influences the phosphorylation level of crucial players of mTOR signalling pathway enhancing oncogenesis	Gastric cancer	(Dou et al., 2016)
ADAR2	A-to-I	Mediates editing of the tumour suppressor the PODXL	Gastric cancer	(Chan et al., 2016)
ADAR2	A-to-I	Mediates editing and stabilization of IGFBP leading to cell apoptosis and inhibition of tumour growth	ESCC	(Chen et al., 2017)
ADAR2	A-to-I	Overexpression is associated with regulation of cell cycle proteins (e.g., Skp2, p21 and p27), and inhibition of the cellular growth	High-grade astrocytoma and GBM	(Galeano et al., 2013)
ADAR2	A-to-I	Overexpression is associated with regulation of both oncogenic and tumour suppressor (e.g. miRNAs miR221, miR222 and miR-21)	GBM	(Tomaselli et al., 2015)
ADAR3	A-to-I	Overexpression is associated with compromised RNA editing at the Q/R site of the transcript *GRIA2*	High-grade astrocytoma and GBM	(Oakes et al., 2017b)
Erasers				
FTO	m6A	Decreases m6A levels and increases the stability of pro-tumourigenic genes (e.g., PDCD1, CXCR4, and SOX10). It is also associated with resistance to	Melanoma	(Yang et al., 2019)

		immunotherapy		
FTO	m6A	Decreases m6A levels in ASB2 and RARA mRNA transcripts leading to inhibition of all-trans-retinoic acid (ATRA)-induced AML cell differentiation and promotion of leukemogenesis	AML	(Li et al., 2017b)
FTO	m6A	It is inhibited by an oncometabolite produced in IDH1/2-mutant tumours leading to increased m6A content on specific targets	AML	(Elkashef et al., 2017)
ALKBH5	m6A	Overexpression is correlated with poor prognosis. It is implicated on the stabilization of the FOXM1 mRNA transcript involved for the maintenance of glioblastoma stem-cells properties and self-renewal	Glioblastoma	(Zhang et al., 2017c)
ALKBH5	m6A	Overexpression (stimulated by hypoxia-inducible factors) results in gain of NANOG stability favouring a stem cell phenotype	Breast cancer	(Zhang et al., 2016)
Readers				
YTHDF1	m6A	Together with METTL3, it regulates the m^6A levels at the CDS of the EMT gene SNAIL causing polysome-mediated translation of Snail mRNA	Liver cancer	(Lin et al., 2019)
YTHDF1	m6A	Depletion favours the therapeutic efficacy of PD-L1 checkpoint blockade mediated by its role on the antigen presentation in dendritic cells and neoantigen-specific immunity	CCR and melanoma	(Han et al., 2019a)
YTHDF2	m6A	Overexpression is correlated with gain of expression of the metastasis-related gene HIF-1α	CCR	(Tanabe et al., 2016)
YTHDF2	m6A	Together with FTO, it decreases m6A levels and increases the stability of pro-tumourigenic genes (e.g., PDCD1, CXCR4, and SOX10). It is also associated with resistance to immunotherapy	Melanoma	(Yang et al., 2019)
YTHDF2	m6A	Overexpression is associated with diminished half-life of TNFRSF2 transcript avoiding apoptosis in leukaemia stem cells and promoting tumour expansion	AML	(Paris et al., 2019)
YBX1	m5C	Overexpression is correlated with increased m5C levels at the PI3K–AKT35 and ERK–MAPK36 oncogenic pathways.	Bladder cancer	(Chen et al., 2019)