Oncogenic Role of an Epigenetic Reader of m⁶A RNA Modification, YTHDF1 in Merkel Cell Carcinoma

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	Gene symbol	Region	Cytoband	Q value
Genes	HBM	Chr. 16	p13.3	<0.000
	HBA2	Chr. 16	p13.3	
	HBA1	Chr. 16	p13.3	
	RBBP8NL	Chr. 20	q13.33	0.006
	YTHDF1	Chr. 20	q13.33	
	BIRC7	Chr. 20	q13.33	
	NKAIN4	Chr. 20	q13.33	
	FLI16779	Chr. 20	q13.33	
	ARFGAP9	Chr. 20	q13.33	
	COL20A1	Chr. 20	q13.33	
	CHRNA4	Chr. 20	q13.33	
	KCNQ2	Chr. 20	q13.33	
	LOC100130587	Chr. 20	q13.33	
	No genes *	Chr. 07	q11.1	0.023
miRNAs	MIR124-3	Chr. 20	q13.33	0.006
	MIR3196	Chr. 20	q13.33	
	MIR4326	Chr. 20	q13.33	

* This region has copy number gains but it encompasses no genes.

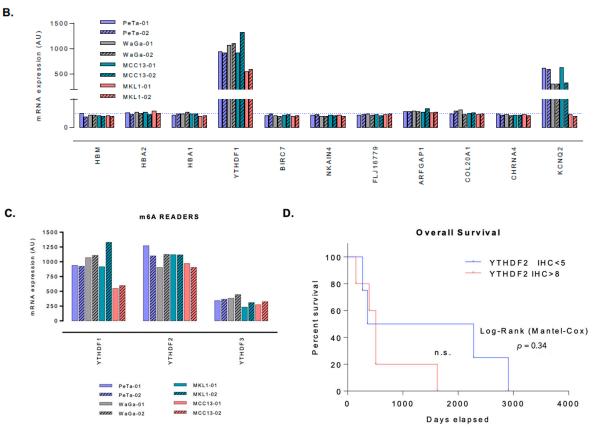


Figure S1. (**A**) Genes and miRNAs with copy number gain across all MCC cell lines (FDR < 0.05). (**B**) mRNA expression levels in genes with high copy number gains in MCC cell lines. Y axis has the arbitrary units (AU) of the fluorescence intensity. (**C**) mRNA expression in members of YTHDF gene family, YTHDF1, YTHDF2 and YTHDF3 across MCC cell lines. (**D**) Overall survival data in YTHDF2^{high} (IHC > 8) versus YTHDF2^{low} (IHC < 5) in MCC cohort (Log-Rank *p* value = 0.34).

Site #	m⁰A	Position	Sequence context	Score (binary)	Score (knn)	Score (spectrum)	Score (combined)	Probability
1 1	1	410	AAUAAUCCACAAGCUC	0.555	0.644	0.666	0.604	High
			AGAAGUGACUUCUCU					-
			AUGUUUGAUGAGGUC					
	2	463	AUUUCCUUGGGAAGA	0.656	0.476	0.370	0.533	Low
			AUAUG <u>GAACU</u> UUAAA					
		GGAUUAUAUGCAAAG						
2 3	3	885	UGACGAGGCCCCUAU	0.530	0.384	0.605	0.553	Low
			AUAUG <u>GGACC</u> ACUAA					
			AUUCAAAGAAUGGUG					
	4	966	AUAUGGGCCCAAUCC	0.559	0.727	0.660	0.608	High
			ACACG <u>GGACC</u> AACUC					
			AAGAUCCAGAAAGCC					
3 5	5	1090	UUCUCAGCGUCCCAG	0.493	0.542	0.633	0.551	Low
			GCUUCAGACUCCCAG					
	-	1100	UCCAGAGGACCCGAU	0.544	0.500	0.040	0.507	
	6	1106	CUUCAGACUCCCAGU	0.514	0.536	0.643	0.567	Moderate
			CCAGA <u>GGACC</u> CGAUA					
4 7	7	2023	UACCUCCCGAACACC AUUAUCUUAGCCCAU	0.611	0.575	0.520	0.573	Moderate
4	/	2023	UAUCUAGACUUUGCA	0.011	0.575	0.520	0.573	moderate
8			AAACCAUUUCCUUGC					
	0	2211	AGAGAUGCUGGAAAU	0.645	0.652	0.478	0.579	Moderate
	0	2211	GACCAGGACAGAAAU	0.045	0.052	0.470	0.579	moderate
			GCUAUGUAAGAAGUU					
5 9 	Q	2920	UGCUUACAAGAAGAA	0.532	0.338	0.710	0.593	Moderate
	9	2020	AUUAAAAACUGGAAG	0.002	0.000	0.710	0.000	Moderate
			CAAAUUUUACAGAGU					
	10	2998	GAAAAUGUAGAAGCU	0.528	0.632	0.555	0.544	Low
	10	2000	GGUCAGGACCCUCUG	0.020	0.002	0.000	0.011	2011
			CUCAAUAUUCUUAUU					
6 11	11	3631	CACUCCAUUCUCAUC	0.685	0.635	0.391	0.565	Moderate
			UAAAAGGACAGUAGU					
			UAGAGUAUUACUAAA					
7	12	3982	AAUACCAGCACCAUA	0.720	0.745	0.348	0.572	Moderate
			AUCAU <u>GAACU</u> CUUUU					
			CAUGUCCCAAUAAUG					
8 13	13	4920	GCCACUAAUGAGAAA	0.535	0.503	0.583	0.553	Low
			UUUGA <u>AAACU</u> GUUCA					
			GCUGUGAACCCAAGU					

Figure S2. This table shows the output of SRAMP algorithm performed on MCV sequence of WaGa cell lines to predict m⁶A sites. Position of each of the m⁶A sites in MCV genome as well as binary, KNN (K-nearest neighbors), spectrum and combined score are shown.

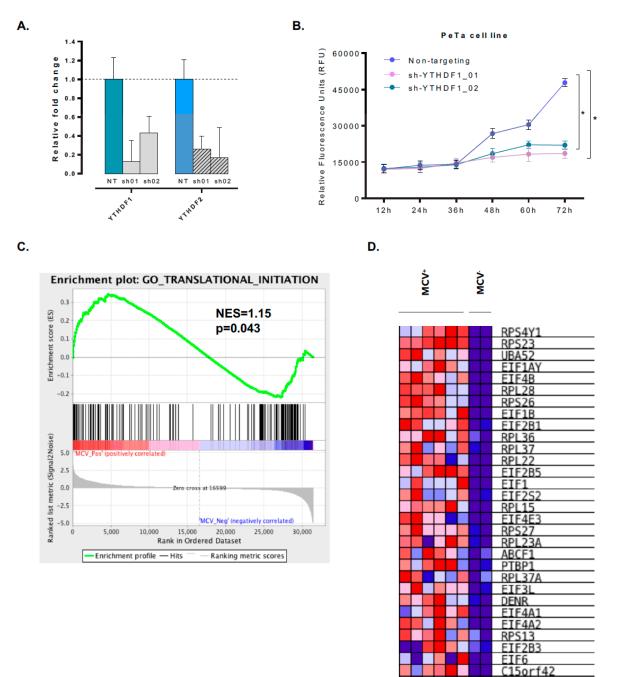


Figure S3. (**A**) qPCR indicating knock down efficiency in PeTa cell line. Non-targeting shRNA is used as control. (**B**) Cell proliferation rate is reduced upon YTHDF1 knockdown in PeTa cells. Asterisks indicates p < 0.05. (**C**) GSEA plot shows enrichment of GO term: Translational_Initiation in MCV^{positive} cells versus MCV^{negative} cells (NES = 1.15, p = 0.043). (**D**) Heatmap shows gene set of translation initiation factors and their expression in MCV^{positive} and MCV^{negative} MCC samples.

Figure 1G

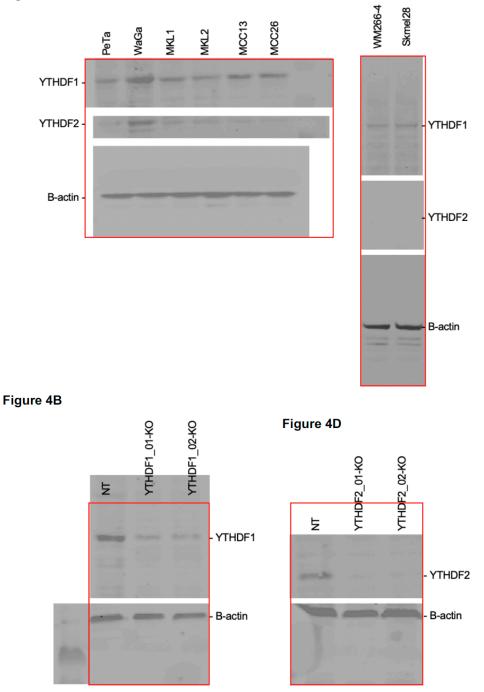


Figure S4. Whole blot for Figure 1 and Figure 4.



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