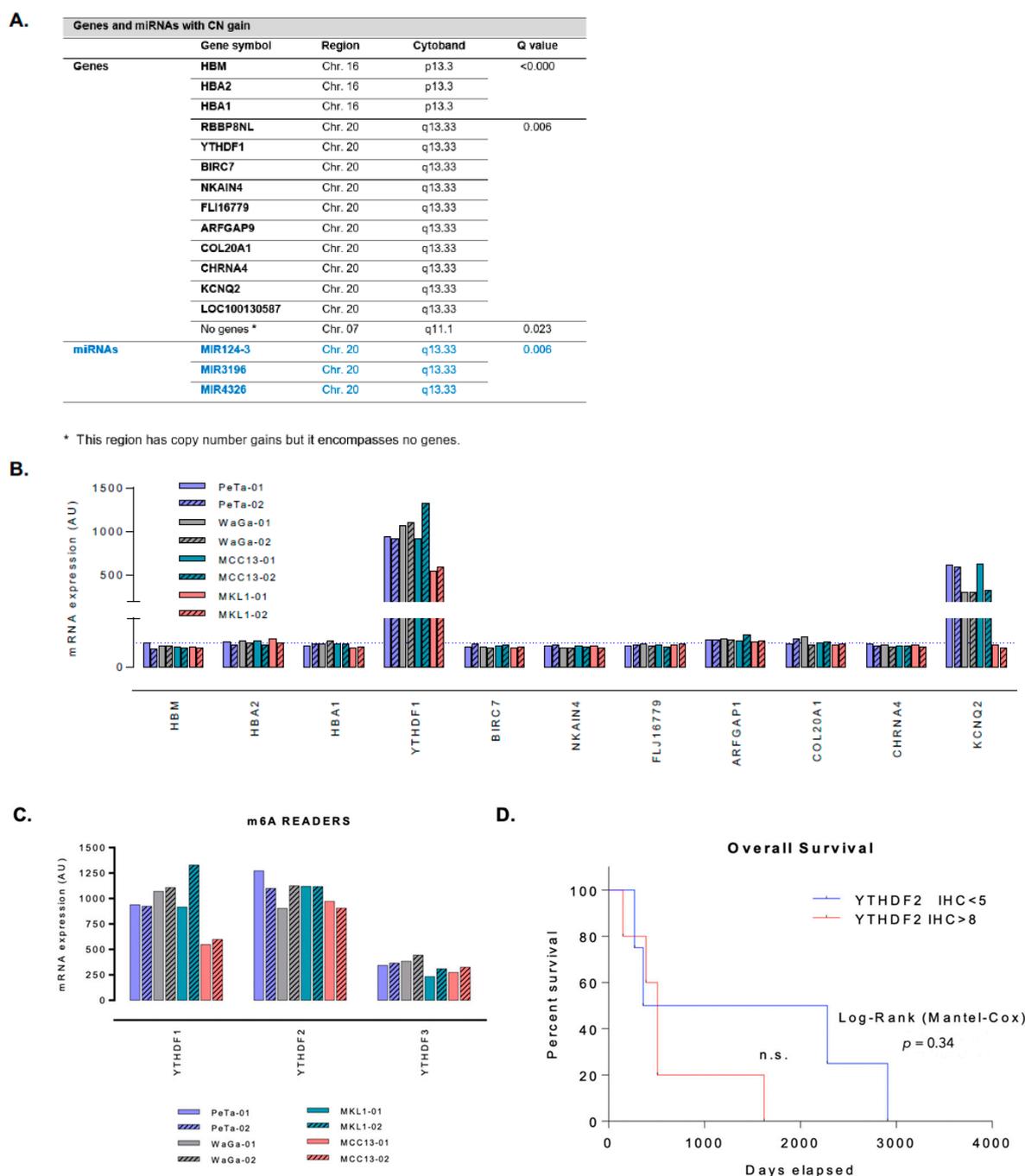


# Oncogenic Role of an Epigenetic Reader of m<sup>6</sup>A RNA Modification, YTHDF1 in Merkel Cell Carcinoma

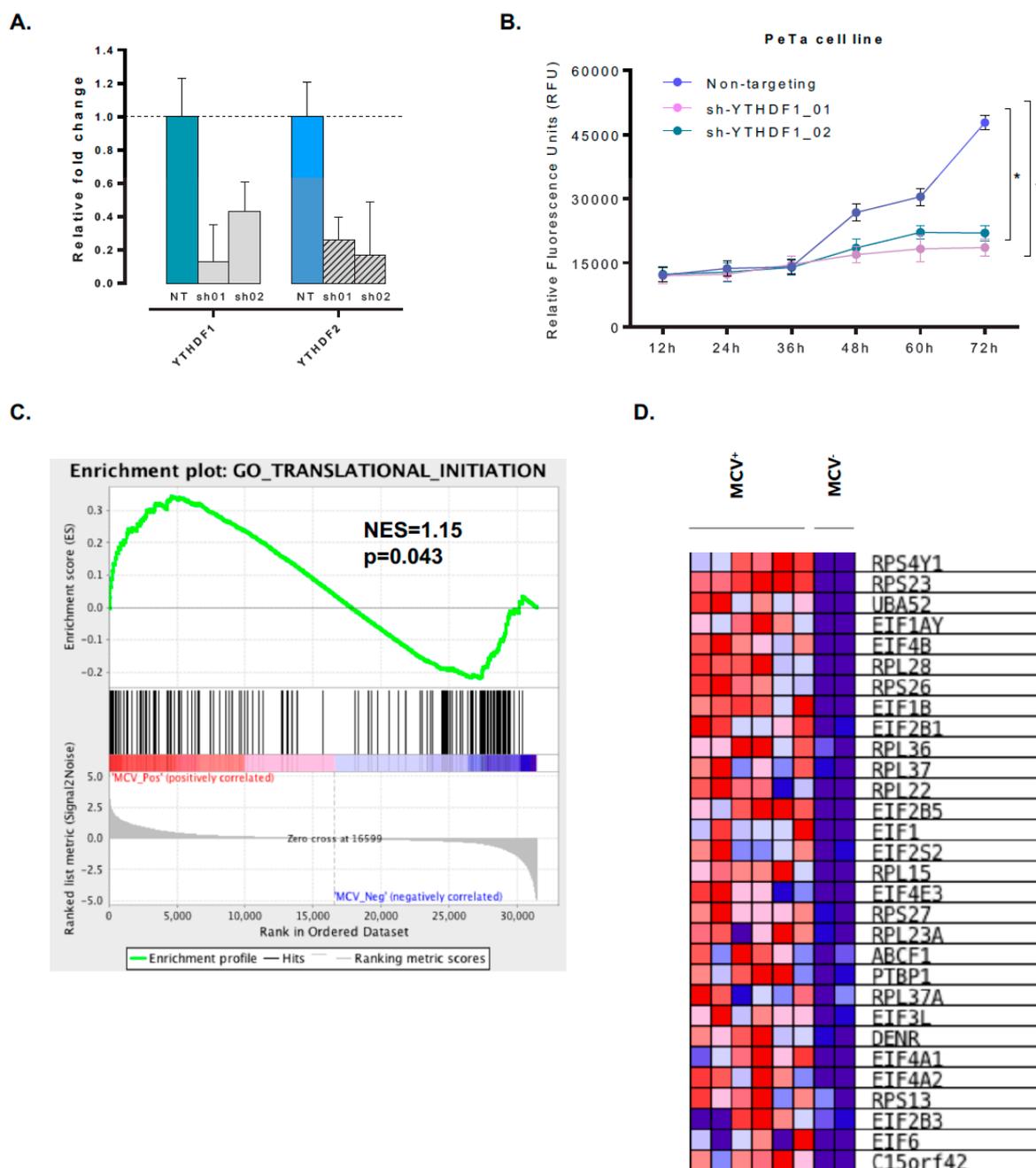
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**Figure S1.** (A) Genes and miRNAs with copy number gain across all MCC cell lines (FDR < 0.05). (B) mRNA expression levels in genes with high copy number gains in MCC cell lines. Y axis has the arbitrary units (AU) of the fluorescence intensity.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

Site #	m <sup>6</sup> A	Position	Sequence context	Score (binary)	Score (knn)	Score (spectrum)	Score (combined)	Probability
1	1	410	AAUAAUCCACAAGCUC AGAAGUGACUUCUCU AUGUUUGAUGAGGUC	0.555	0.644	0.686	0.604	High
		2	463	AUUUCCUUGGGAAGA AUUUGGAACUUIAAA GGAUUUAUGCAAAG	0.656	0.476	0.370	0.533
2	3	885	UGACGAGGCCCCUUAU AUUUGGACCCACUAA AUUCAAGAAUUGGUG	0.530	0.384	0.605	0.553	Low
		4	966	AUUUGGGCCAAUCC ACACGGGACCAACUC AAGAUCCAGAAAGCC	0.559	0.727	0.660	0.608
3	5	1090	UUCUCAGCGUCCAG GCUUCAGACUCCAG UCCAGAGGACCCGAU	0.493	0.542	0.633	0.551	Low
		6	1106	CUUCAGACUCCAGU CCAGAGGCCCGAUA UACCUCCGAAACCC	0.514	0.536	0.643	0.567
4	7	2023	AUUUAUCUUGCCCAU UAUCUAGACUUGCA AAACCAUUUCUUGC	0.611	0.575	0.520	0.573	Moderate
		8	2211	AGAGAUCCUUGAAA GACCAAGGACAGAAA GCUAUGUAAGAGLU	0.645	0.652	0.470	0.579
5	9	2920	UGC UUACAAGAAGAA AUUAAAAACUGGAAG CAAAUUUUAACAGAU	0.532	0.338	0.710	0.593	Moderate
		10	2998	GAAAUUGUAGAAGCU GGUCAGGACCCUCUG CUCAAUAUUCUUAUU	0.528	0.632	0.555	0.544
6	11	3631	CACUCCAUUCUCAUC UAAAAGGACAGUAGU UAGAGUAUUACUAAA	0.685	0.635	0.391	0.565	Moderate
		7	12	3982	AAUACCAGCACC AUA AUCAUGAACUCUUUU CAUGUCCCAAUAUUG	0.720	0.745	0.348
8	13	4920	GCCACUAUUGAGAAA UUUGAAAACUGUUCA GCUGUGAACCCAAGU	0.535	0.503	0.583	0.553	Low

**Figure S2.** This table shows the output of SRAMP algorithm performed on MCV sequence of WaGa cell lines to predict m<sup>6</sup>A sites. Position of each of the m<sup>6</sup>A 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<sup>positive</sup> cells versus MCV<sup>negative</sup> cells (NES = 1.15,  $p = 0.043$ ). (D) Heatmap shows gene set of translation initiation factors and their expression in MCV<sup>positive</sup> and MCV<sup>negative</sup> MCC samples.

Figure 1G

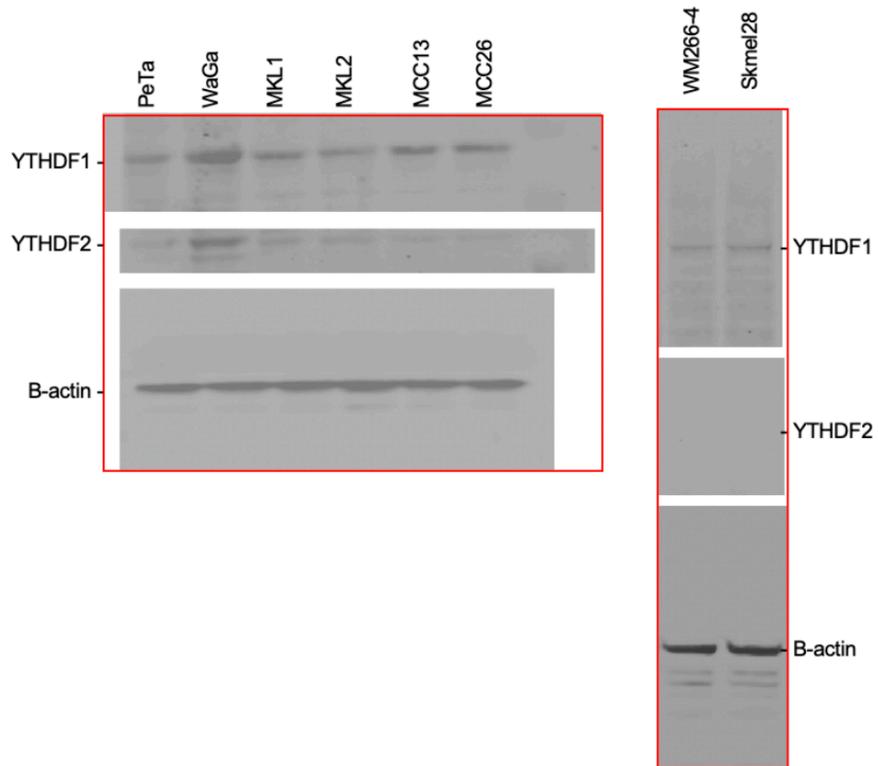


Figure 4B

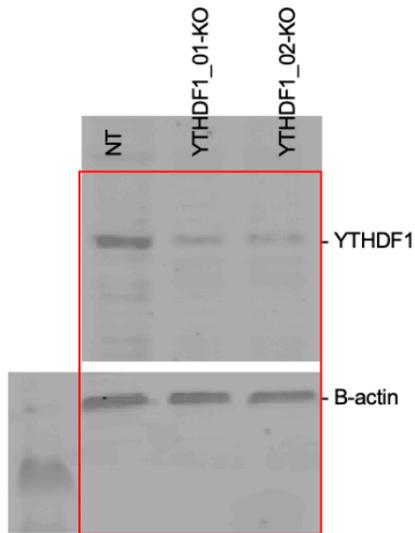


Figure 4D

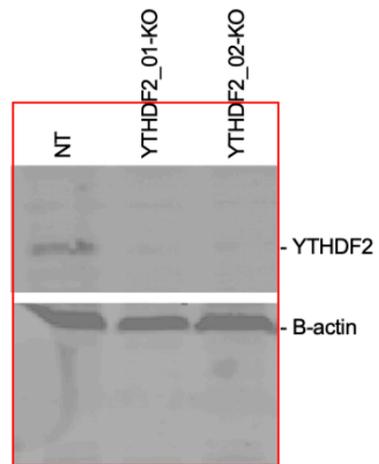


Figure S4. Whole blot for Figure 1 and Figure 4.

