

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

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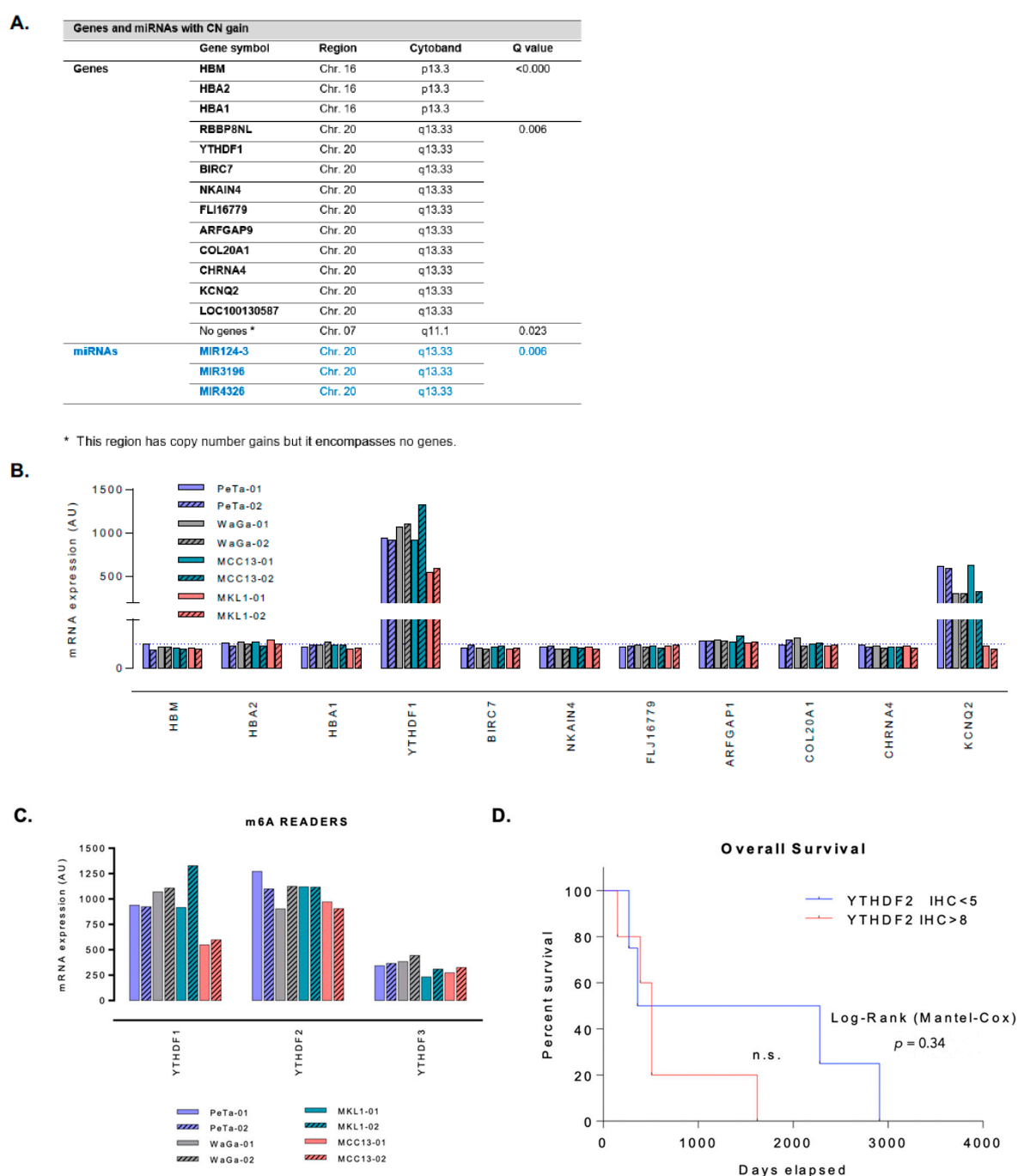


Figure S1. (A) Genes and miRNAs with copy number gain across all MCC cell lines (FDR < 0.05). (B) mRNA expression levels in genes with high copy number gains in MCC cell lines. Y axis has the arbitrary units (AU) of the fluorescence intensity. (C) mRNA expression in members of YTHDF gene family, YTHDF1,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

| Site # | m ⁶ A | Position | Sequence context | Score (binary) | Score (knn) | Score (spectrum) | Score (combined) | Probability |
|--------|------------------|----------|--|----------------|-------------|------------------|------------------|-------------|
| 1 | 1 | 410 | AAUAAUCCACAAGCUC AGAAGUGACUUCUCU AUGUUUGAUGAGGUC | 0.555 | 0.644 | 0.688 | 0.604 | High |
| | 2 | 463 | AUUUCCUUGGGAAGA AUUUGGAACUUAUA GGAUUAUAUGCAAAG | 0.658 | 0.476 | 0.370 | 0.533 | Low |
| 2 | 3 | 885 | UGACGAGGCCCCUUAU AUUUGGACACUAA AUUCAAGAAUGGUG | 0.530 | 0.384 | 0.605 | 0.553 | Low |
| | 4 | 966 | AUAUUGGCCCAUCC ACACGGGACCAACUC AAGAUCAGAAAGCC | 0.559 | 0.727 | 0.660 | 0.608 | High |
| 3 | 5 | 1090 | UUCUCAGCGUCCAG GCUUCAGACUCCAG UCCAGAGGACCCGAU | 0.493 | 0.542 | 0.633 | 0.551 | Low |
| | 6 | 1106 | CUUCAGACUCCAGU CCAGAGGCCCGAUA UACCUCCGACACCC | 0.514 | 0.536 | 0.643 | 0.567 | Moderate |
| 4 | 7 | 2023 | AUUAUCUUGCCCAU UAUCUAGACUUGCA AAACCAUUCUUGC | 0.611 | 0.575 | 0.520 | 0.573 | Moderate |
| | 8 | 2211 | AGAGAUCCUGGAAU GACCAGGACAGAAU GCUAUGUAAGAGU | 0.645 | 0.652 | 0.478 | 0.579 | Moderate |
| 5 | 9 | 2920 | UGCUCACAAGAGAA AUUAAAAACUGGAAG CAAAUUUACAGAGU | 0.532 | 0.338 | 0.710 | 0.593 | Moderate |
| | 10 | 2998 | GAAAAUGUAGAGCU GGUCAGGACCCUCUG CUCAAUAUUCUUAU | 0.528 | 0.632 | 0.555 | 0.544 | Low |
| 6 | 11 | 3631 | CACUCCAUUCUUAUC UAAAAGGACAGUAGU UAGAGUAUUAUAAA | 0.685 | 0.635 | 0.391 | 0.565 | Moderate |
| | 12 | 3982 | AAUACCAGCACCUA AUCAUGAACUCUUU CAUGUCCCAAUAUG | 0.720 | 0.745 | 0.348 | 0.572 | Moderate |
| 8 | 13 | 4920 | GCCACUAAUAGAGAA UUUGAAAACUGUUA GCUGUGAACCAAGU | 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 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.

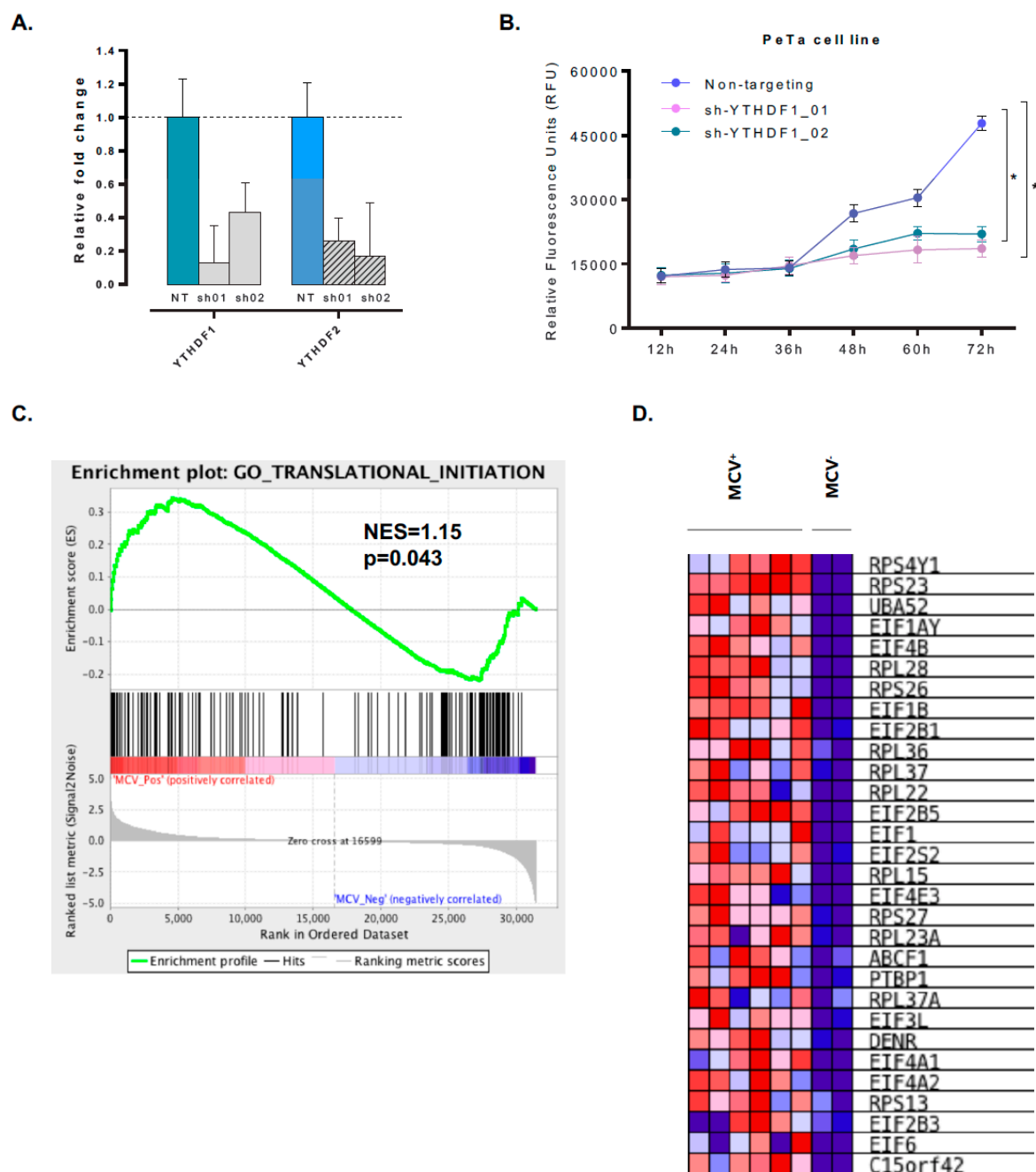


Figure S3. (A) qPCR indicating knock down efficiency in PeTa cell line. Non-targeting shRNA is used as control. (B) Cell proliferation rate is reduced upon YTHDF1 knockdown in PeTa cells. Asterisks indicates $p < 0.05$. (C) GSEA plot shows enrichment of GO term: Translational_Initiation in MCV^{positive} 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

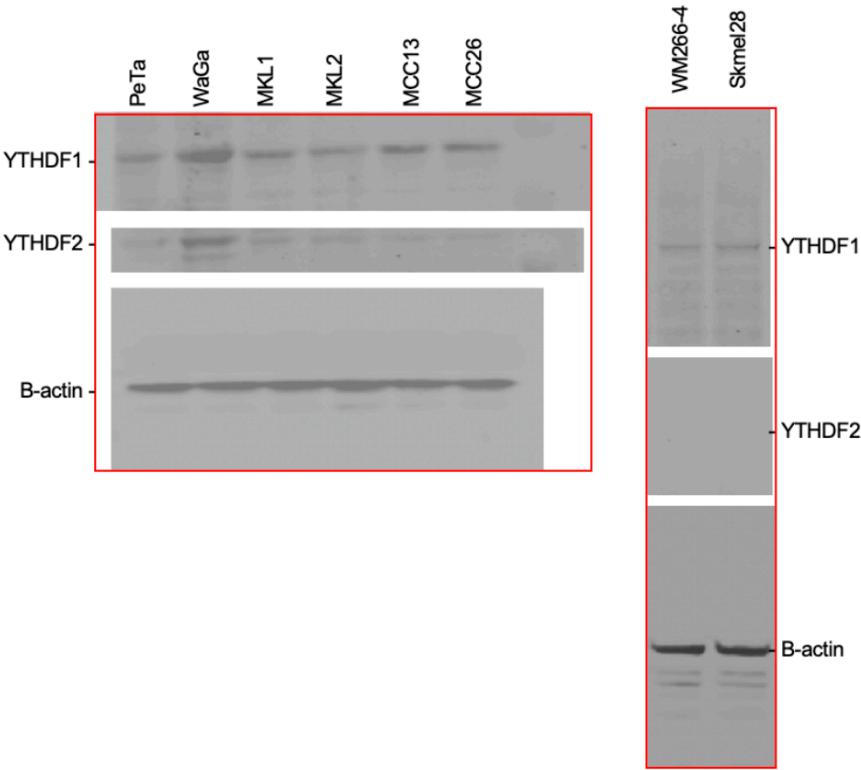


Figure 4B

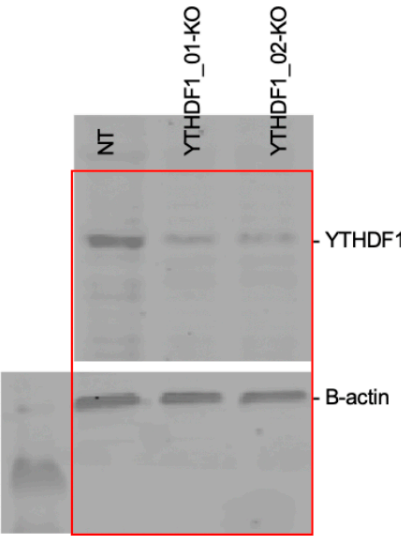


Figure 4D

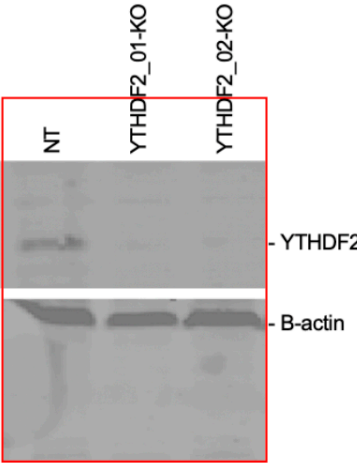


Figure S4. Whole blot for Figure 1 and Figure 4.

