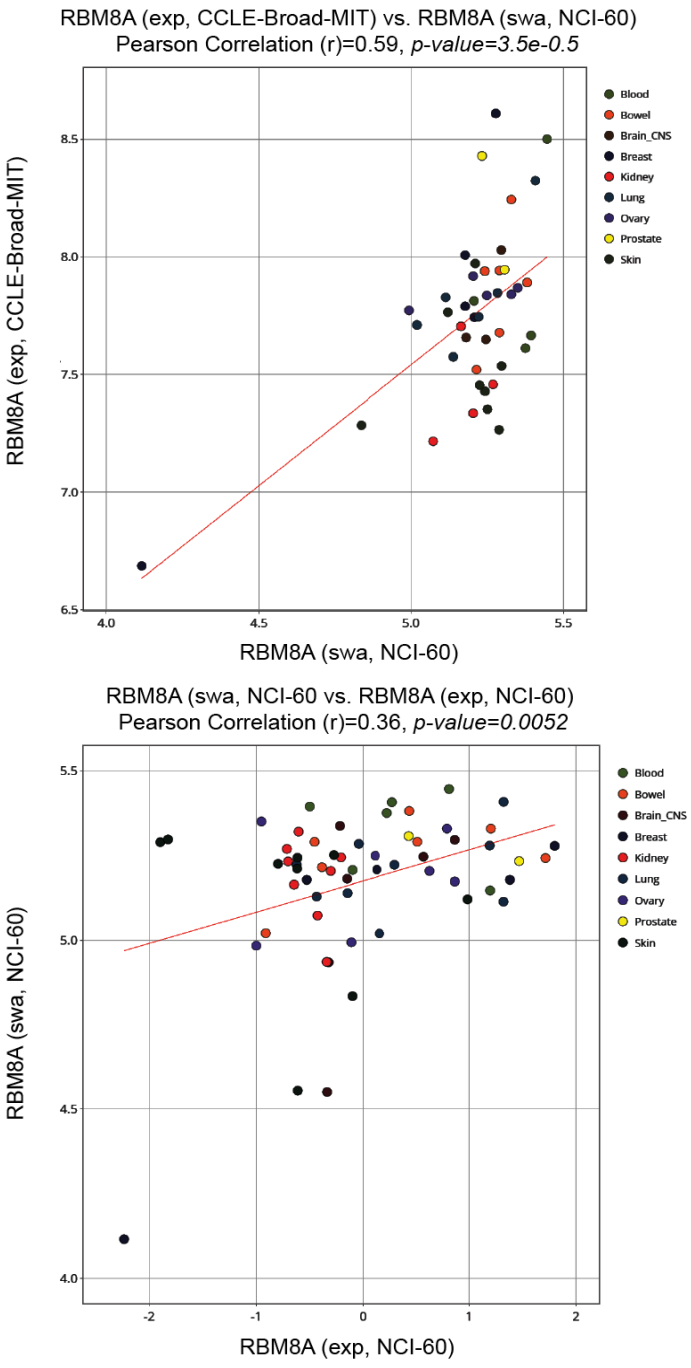
A


RBM8A (exp, CCLE-Broad-MIT) vs. RBM8A (swa, NCI-60)
Pearson Correlation (r)=0.59, p-value=3.5e-0.5
RBM8A (exp, CCLE-Broad-MIT)
RBM8A (swa, NCI-60)
Blood
Bowel
Brain_CNS
Breast
Kidney
Lung
Ovary
Prostate
Skin
RBM8A (swa, NCI-60 vs. RBM8A (exp, NCI-60)
Pearson Correlation (r)=0.36, p-value=0.0052
RBM8A (swa, NCI-60)
RBM8A (exp, NCI-60)

B

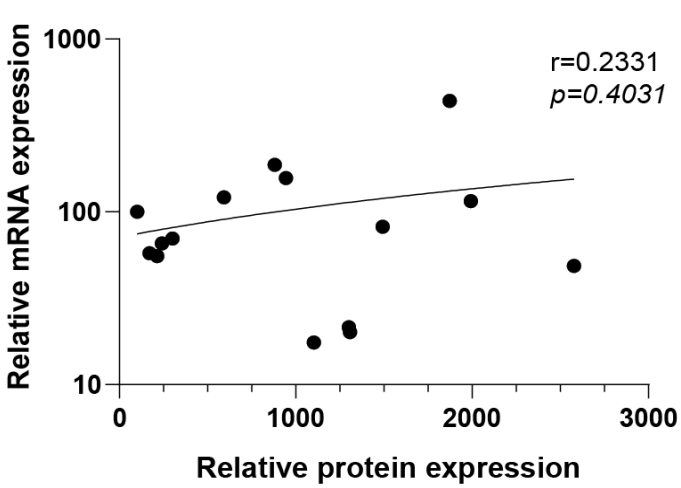

r=0.2331
p=0.4031
Relative mRNA expression
Relative protein expression

Figure S1. Correlation of RBM8A protein and RNA expression in different human cell lines. (**A)**. Data were obtained using CellMinerCDB (https://discover.nci.nih.gov/rsconnect/cellminercdb/, accessed on 28 April 2020). Upper graph: RBM8A protein expression (NCI-60 dataset) on x-axis and mRNA expression (CCLE-Broad-MIT dataset) on y-axis. Lower graph: RNA expression on x-Axis (NCI-60 dataset) and protein expression on y-axis (NCI-60 dataset). (**B)** Correlation of RBM8A protein and RNA expression in mesothelioma cell lines.

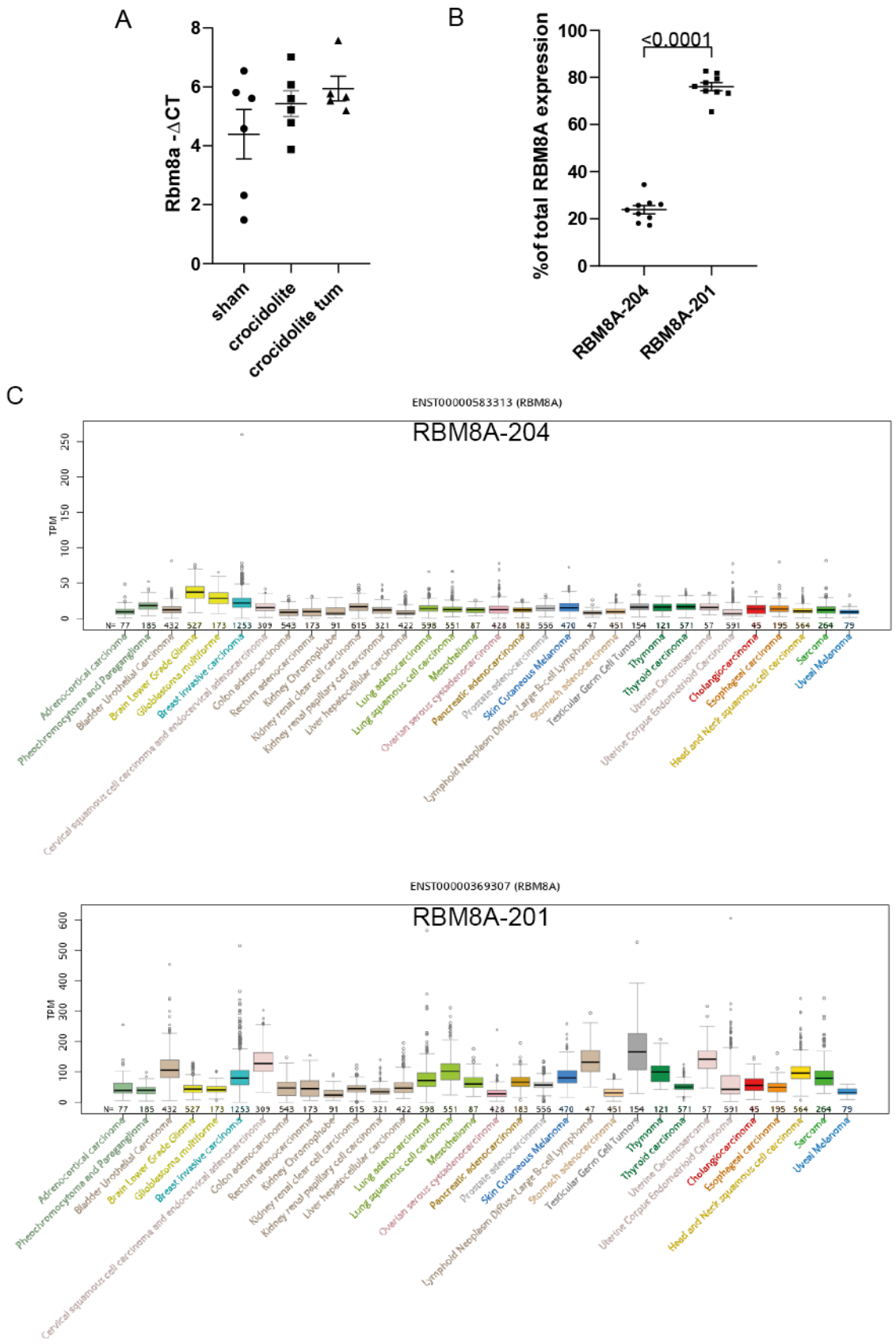


Figure S2. *Rbm8a* mRNA expression in crocidolite (blue asbestos) exposed mice and abundance of *RBM8A* transcripts in mesothelial cells or various cancers. (**A**). *Rbm8a* expression levels do not vary significantly upon crocidolite exposure. (**B**)

RBM8A-204 levels are significantly lower compared to *RBM8A-201* levels in in mesothelial cells. C. Expression profile of *RBM8A-204* (upper panel) and RBM8A -201 (lower panel) in different cancer types. TPM=Transcripts per Million.

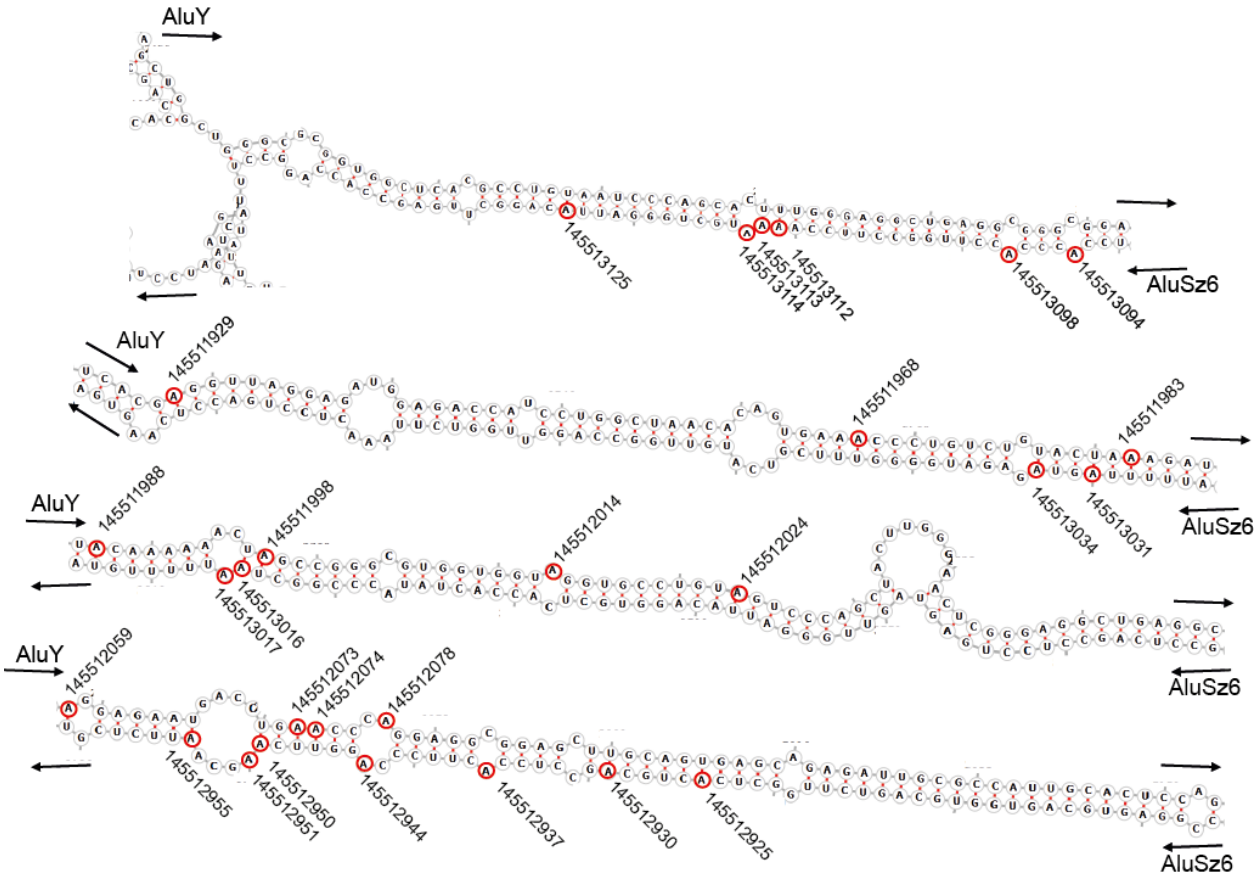


Figure S3. dsRNA stretch of RBM8A 3'UTR formed by AluY and AluSz6 elements. Red circles indicate A-I editing sites and the number refers to nucleotide positions on chromosome 1, hg19. Structure is predicted by RNAfold webserver (http://rna.tbi.univie.ac.at//cgi-bin/RNAWebSuite/RNAfold.cgi, accessed on 27 April 2021).

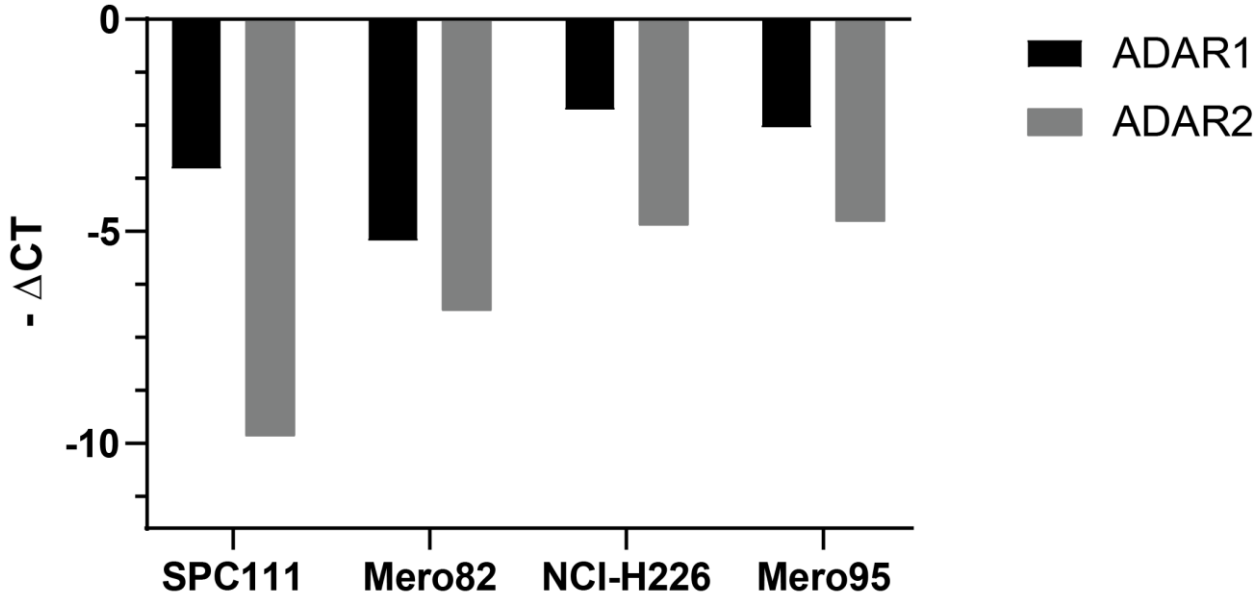


Figure S4. ADAR1/2 mRNA heterogeneous expression in four MPM cell lines. *ADAR1* (black) and *ADAR2* (gray) mRNA levels in SPC111, Mero82, NCI-H226 and Mero95 MPM cell lines.

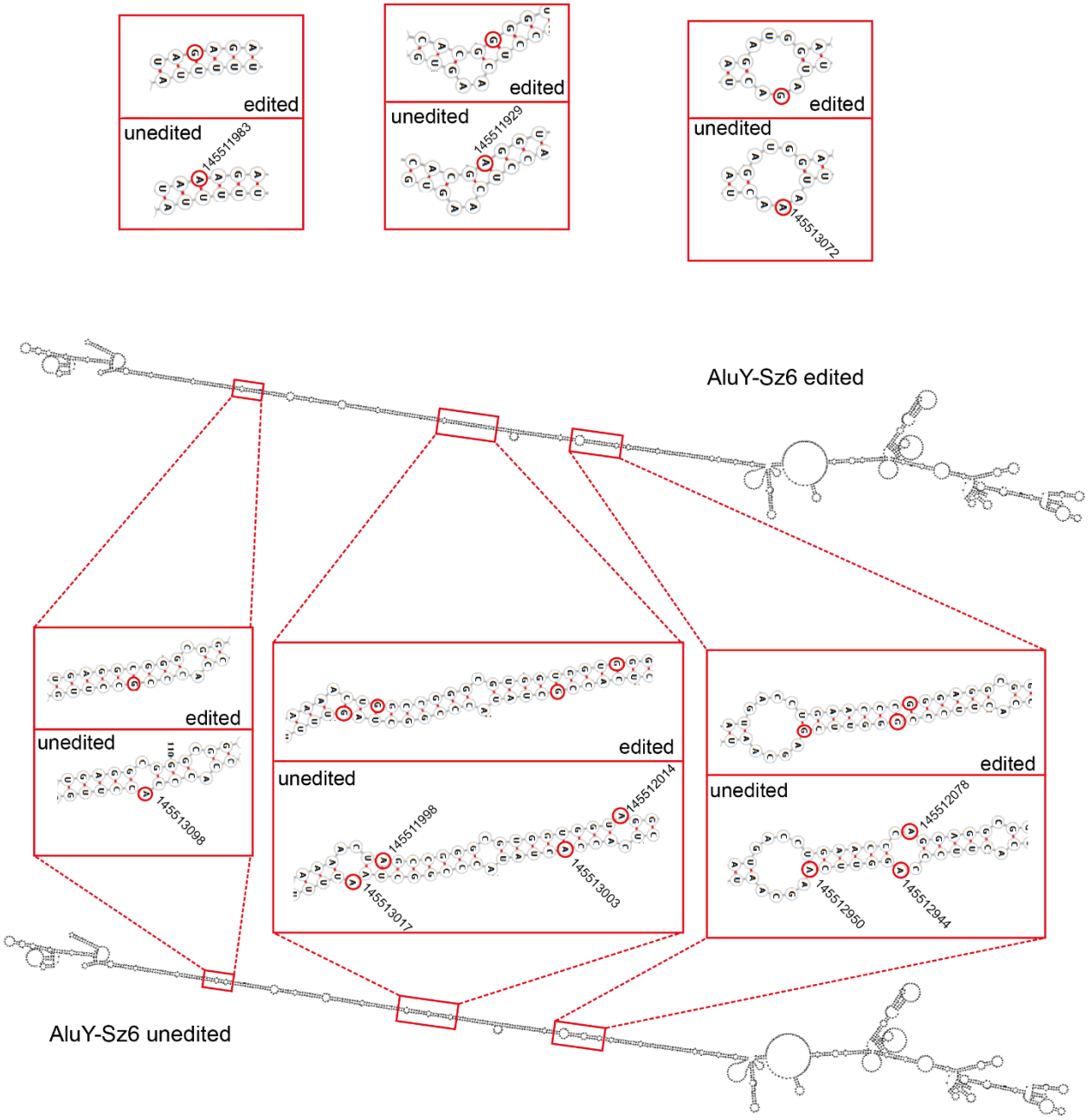


Figure S5. Editing of *RBM8A* 3′UTR AluY-AluSz6 entails structural changes. Red squares in lower part magnify sections with structure change upon editing. Red circles indicate editing sites and numbers of the nucleotide position in chromosome 1, hg19. In the upper part are shown some edited sites leading to no structural change. Structures are predicted by RNAfold webserver (http://rna.tbi.univie.ac.at//cgi-bin/RNAWebSuite/RNAfold.cgi, accessed on 27 April 2021).

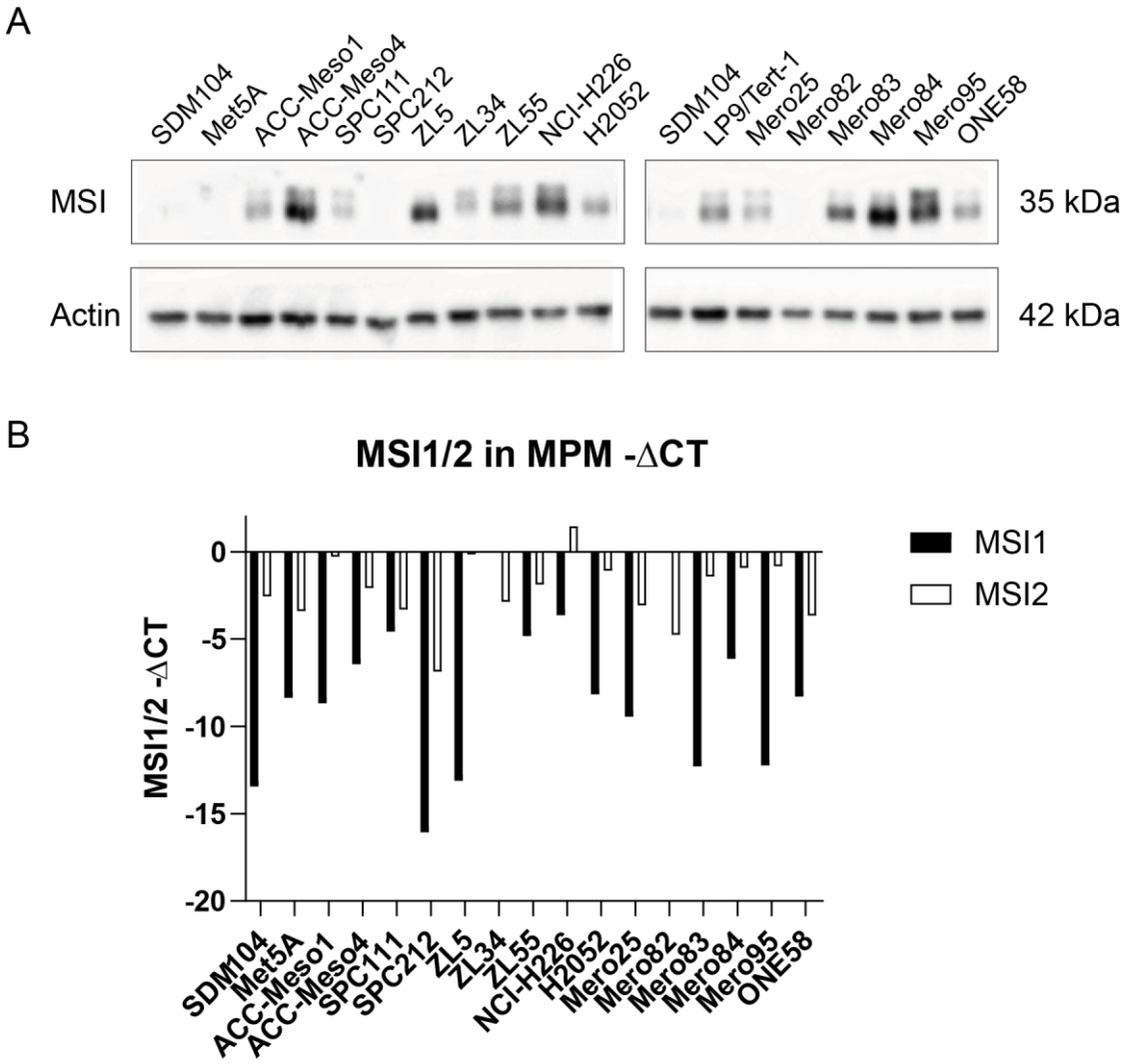


Figure S6. MSI2 expression is higher compared to MSI1 in MPM. (**A**). Western Blot analysis of MSI protein expression in 16 MPM cell lines and mesothelial cells. Actin is used as loading control. (**B)** Relative mRNA levels for *MSI1* (black) and *MSI2* (white).

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Bonobo          ggctgggcgcggtggctcacgcctgtaatcccagcactttgggaggctgaggcgggcgga 60
Human           ggctgggcgcggtggctcacgcctgtaatcccagcactttgggaggctgaggcgggcgga 60
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AluY

AluSz

Figure S7. AluY-AluSz6 sequence is highly conserved between humans and primates**.** *RBM8A* 3'UTR sequence containing AluY and AluSz6 elements compared between human, bonobo, orangutan and gibbon using Clustal Omega alignment tool (https://www.ebi.ac.uk/Tools/msa/clustalo/, accessed on 23 September 2021). AluY is highlighted in yellow, AluSz6 in green. Stars indicate identical nucleotide in all species.

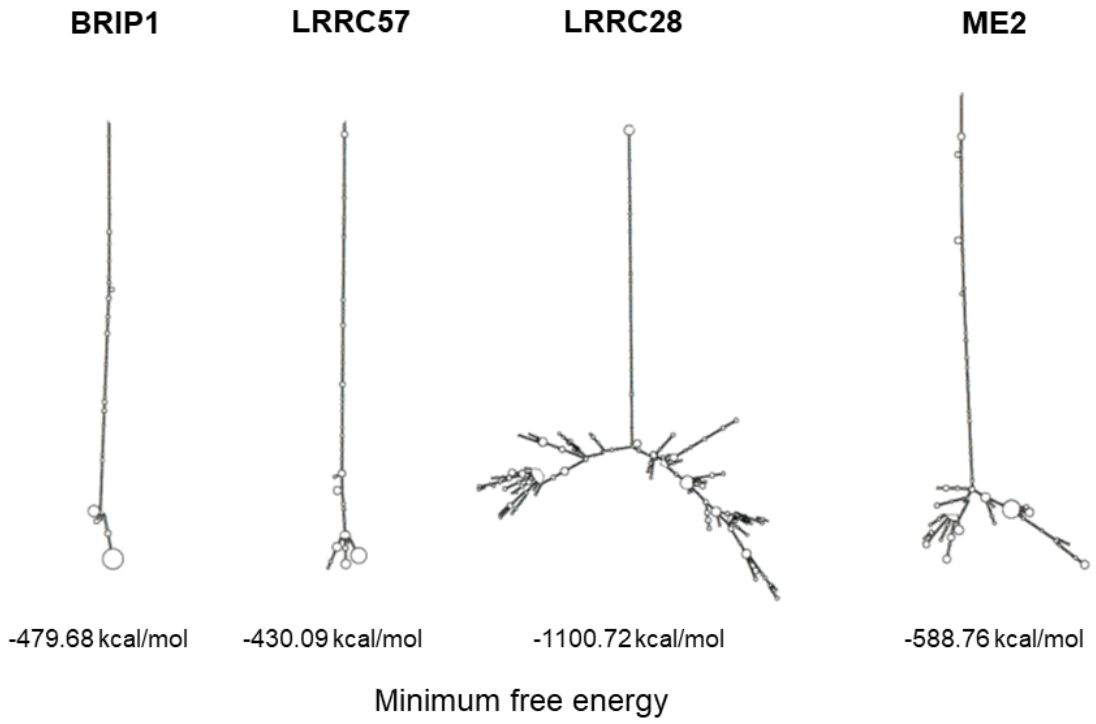

Figure S8. AluY-AluSz6 dsRNA structure is conserved in other transcripts enriched in the MPM translatome. Performing BLASTN using *RBM8A* 3'UTR sequence containing AluY and AluSz6 elements retrieved transcripts known to be edited by ADARs, to interact with MSI2 and to be present in the MPM translatome. They bear a similar dsRNA structure as RBM8A 3'UTR. BRIP1: BRCA1 interacting helicase 1, LRRC57: leucine rich repeat containing 57, LRRC28: leucine rich repeat containing 28, ME2: malic enzyme 2. Structures are predicted by RNAfold webserver (http://rna.tbi.univie.ac.at//cgi-bin/RNAWebSuite/RNAfold.cgi, accessed on 1 November 2021).