Figure S1. (A) A representative image of immunohistochemical staining of pancreatic cancer with Ki-67 (magnification, x40; scale bar, 50 μm). (B) Correlation between Ki-67 and the nuclear staining rate.

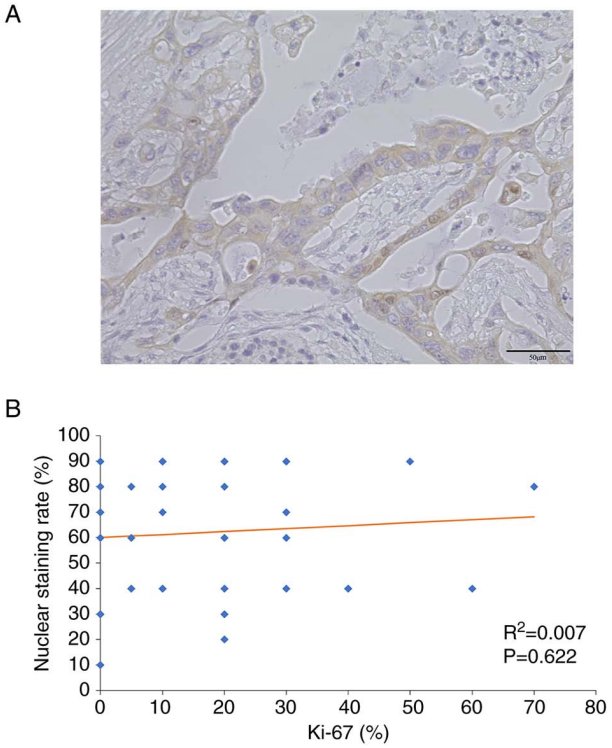

Figure S2. Representative images of signal recognition particle 9 and nuclei immunocytochemically stained in the four media groups. The fluorescence results for (A) MTN(+), (B) M(-), (C) TN(-) and (D) MTN(-) (magnification, x40; scale bar, 100 μm). MTN(+), consisting of L-amino acids, niacin and tryptophan; M(-), methionine-free medium; TN(-), tryptophan- and niacin-free medium; MTN(-), methionine-, tryptophan- and niacin-free medium.

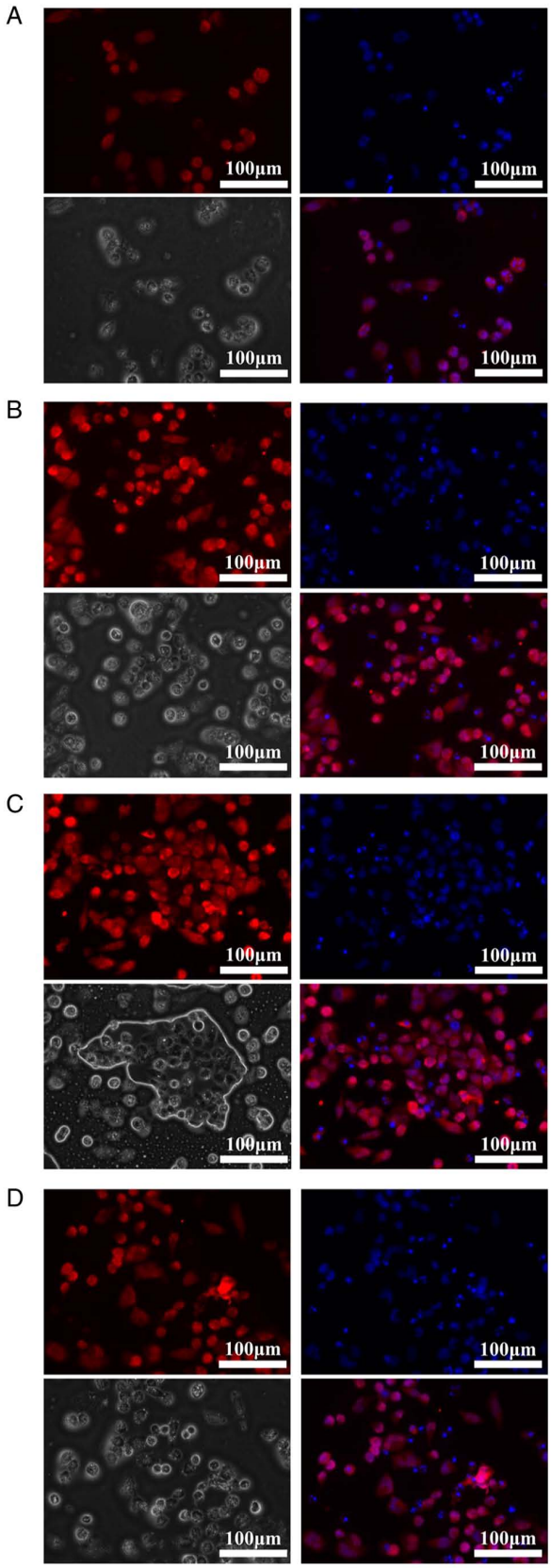

Figure S3. Evaluation of signal recognition particle 9 variants under different nutrient conditions. (A) The v1 and v2 bands were confirmed by PCR following a 24-h incubation in M(-), TN(-), MTN (-) and MTN(+). (B) The ratios of v1 and v2 densities in the four groups were compared. (C) The housekeeping gene, GAPDH, was confirmed amplified by electrophoresis. v1, variant 1; v2, variant 2; MTN(+), consisting of L-amino acids, niacin and tryptophan; M(-), methionine-free medium; TN(-), tryptophan- and niacin-free medium; MTN(-), methionine-, tryptophan- and niacin-free medium.

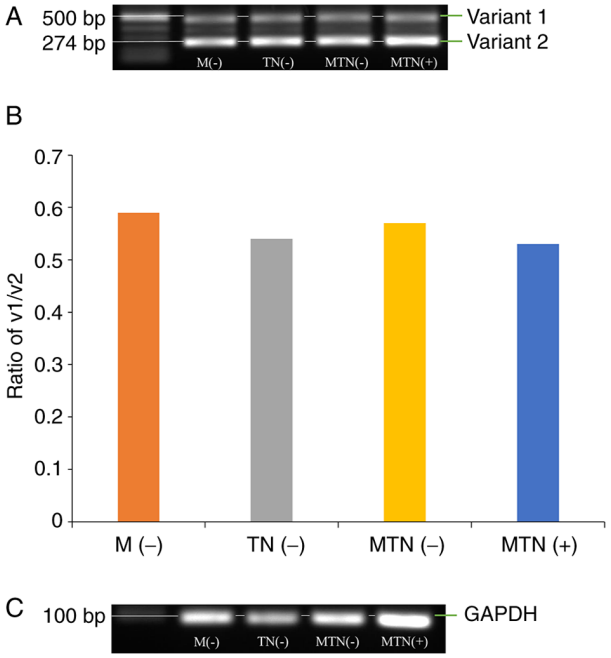

Figure S4. *In vitro* tumor viability under amino acid depletion. (A) MTT formazan products were measured, and tumor viability was examined. In the methionine-depleted state, tumor viability was significantly inhibited in (B) Panc10.05, (C) Caski, and (D) 293T cells compared with the control [n=4 for both the control and M(-) groups]. *P<0.05 by Mann-Whitney U test. Error bars represent the standard deviation. M(-), methionine-free medium.

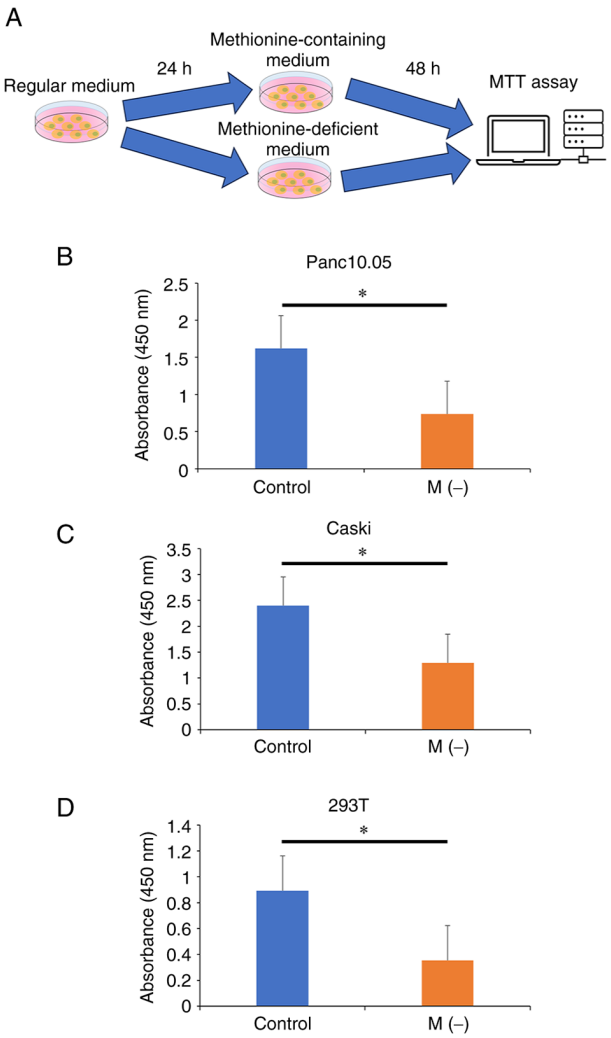

Figure S5. RNA sequencing of tumors in HT-29-implanted mice fed a diet without methionine/tryptophan/niacin. (A) Mice subcutaneously implanted with HT-29 cells were maintained for 2 weeks on a diet without methionine/tryptophan/niacin. When the tumor diameter was >75 mm^3, the mice were sacrificed, the tumors were removed and RNA sequencing were performed. (B) A marked increase in the expression of a non-coding RNA, RN7SL1, was observed. (C) In a subsequent repeat experiment, RNA sequencing of MTN(+) (n=1), M(-) (n=2), TN(-) (n=1) and MTN(-) (n=1) mice was performed to compare the TPM of RN7SL1. TPM, Transcripts Per Million; MTN(+), mice raised on a normal diet containing methionine, tryptophan and niacin; M(-), mice raised on a methionine-free diet; TN(-), mice raised on a tryptophan- and niacin-free diet; MTN(-), mice raised on a methionine-, tryptophan- and niacin-free diet.

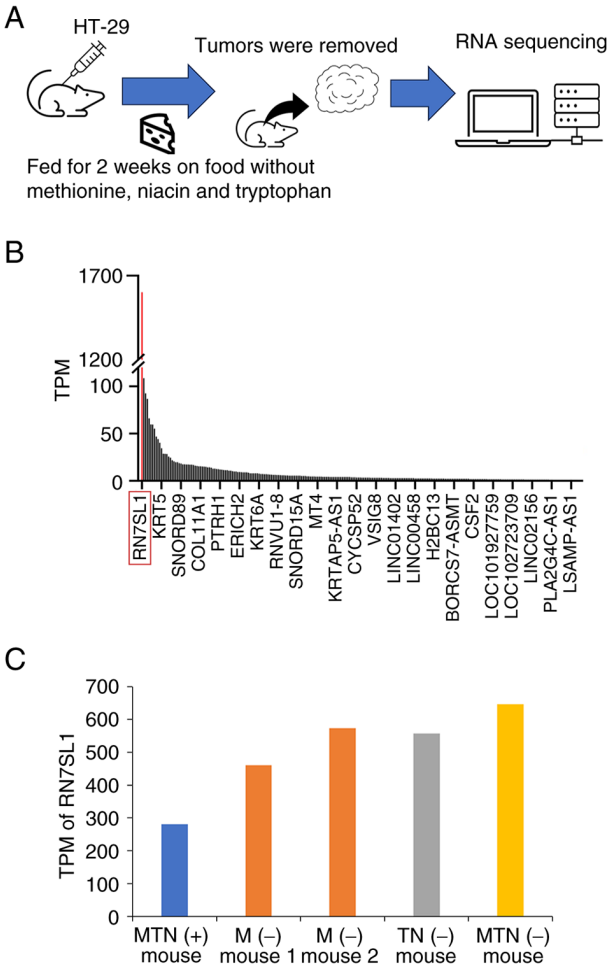

Figure S6. Mutated SRSF2 in MDS compared with healthy controls in terms of the percentage of exon 3. Comprehensive analysis for SRSF2 was performed to determine the effect of these commonly mutated splicing factors on pre-mRNA splicing in splicing factor mutant MDS stem/progenitor cells and erythroid/myeloma progenitor cells. In the database (https://www.ncbi.nlm.nih.gov/geo/), 15 samples of healthy subjects and 15 samples of patients with MDS (SRSF2 mutation) were obtained, data (fastq files) were downloaded, the fastq files were mapped using Hisat2 and a sorted bam file (mapping result file) was created. (A) A magnified view of exon 3 of SRP9 and (B) an example of counting the number of mappings. (C) The sorted bam file was checked for SRP9 expression using IGV (mapping result visualization software), and the percentage of exon 3 was compared between the healthy group and the SRSF2-mutant group. **P<0.01 by Mann-Whitney U test. Error bars represent the standard deviation. MDS, myelodysplastic syndrome; SRSF2, serine and arginine rich splicing factor 2; SRP9, signal recognition particle 9.

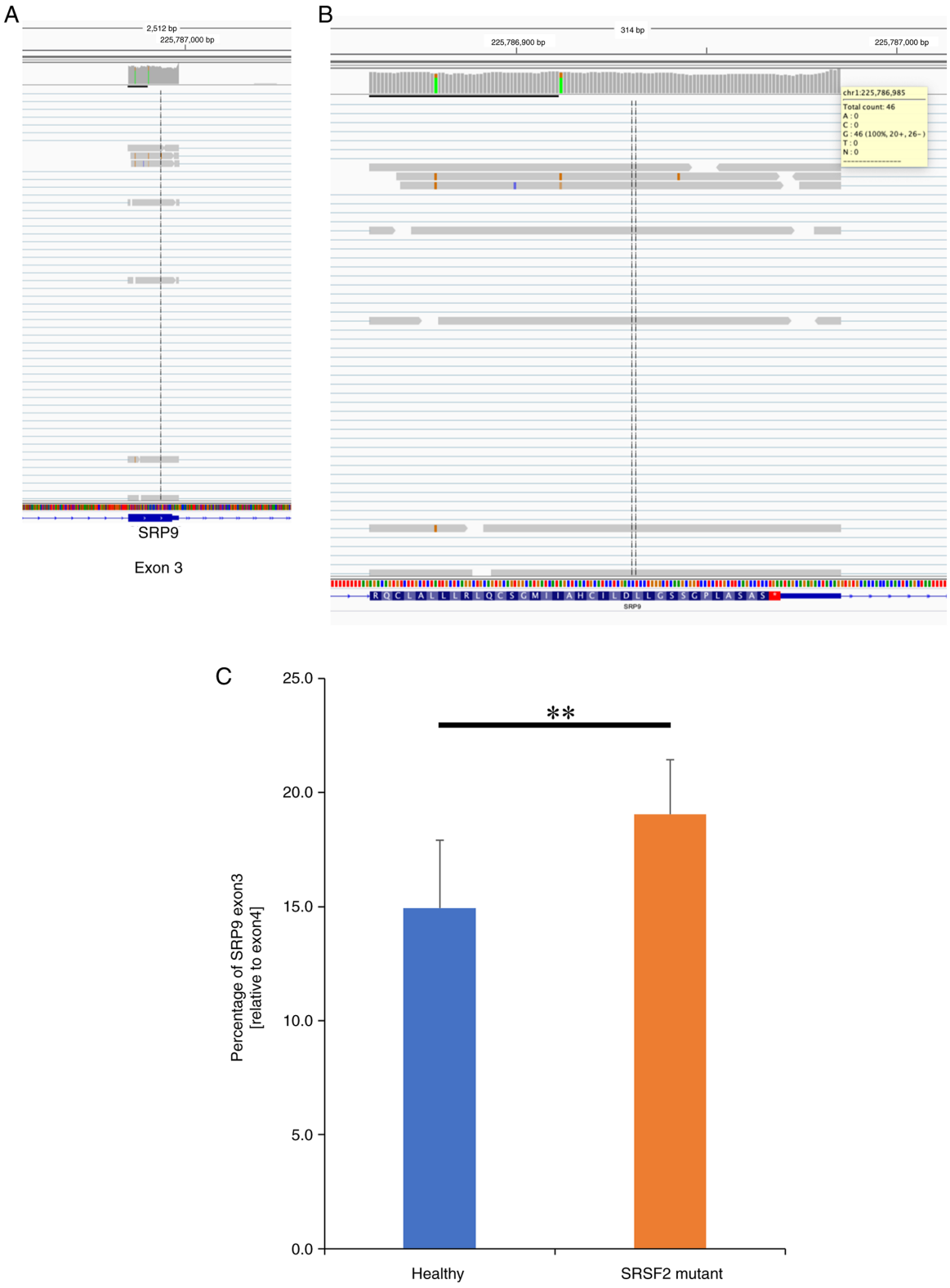

Figure S7. Comparison of the patient PNI in two signal recognition particle 9 expression groups. No significant difference in PNI was observed between the two groups [nuclear staining ≤50% vs. nuclear staining >50%, 46.9 (37.8-54.0) vs. 44.1 (38.0-54.9), median (range); P=0.096]. PNI, prognostic nutritional index; n.s., not significant.