Supplementary Figure S1.

STEP1
Marker mining

MTV RNA-Seq
└ **Differentially expressed gene (DEG) analysis**

Upregulated genes   **Downregulated genes**

DEGs   →   Functional annotation

STEP2
Evaluation
using a large dataset

TCGA dataset
└ PAAD ─ DEG analysis

MUGs
MDGs   → **Patient survival**

MAGs

Genetic alteration → **Patient survival**

Correlation with existing markers
(**unfavorable** and **favorable** genes)

STEP3
Correlation
with clinical outcomes

Correlation of the MAGs with clinical outcomes

→ **Clinical information**
├ **Tumor grade**
├ **Treatment response**
├ **Post-treatment outcome**
└ **Patient mortality**

STEP4
Potential
miRNA therapeutics

MAG-coupled miRNAs

→ **Inversely correlated miRNAs** → **Patient survival**

STEP5
Validation
in protein levels

MAG expression validation in patient tissues

→ IHC analysis → **Transcriptome analysis-based**
(Protein Atlas)   **Pattern matching**