Table S1. Patients' clinical information (n=56)

Variables	Reference	SP	UP	P value*
HbA1C		5.607 ± 0.1893, n=29	6.295 ± 0.2267, n=26	0.0227
CHOL	mmol/L	4.534 ± 0.1286, n=29	4.863 ± 0.2511, n=27	0.2395
TG	mmol/L	1.417 ± 0.1159, n=29	1.793 ± 0.1644, n=27	0.0639
LDL-C	mmol/L	2.632 ± 0.1011, n=29	3.1 ± 0.1749, n=27	0.0221
HDL-C	mmol/L	1.173 ± 0.0457, n=29	1.041 ± 0.04506, n=27	0.0455

Table S2. Primers used for quantitative real-time PCR

GAPDH	
Forward Primer	TGTGGGCATCAATGGATTTGG
Reverse Primer	ACACCATGTATTCCGGGTCAAT
MYOCD	
Forward Primer	ACGGATGCTTTTGCCTTTGAA
Reverse Primer	AACCTGTCGAAGGGGTATCTG
CD68	
Forward Primer	CTTCTCTCATTCCCCTATGGACA
Reverse Primer	GAAGGACACATTGTACTCCACC
ACTA2	
Forward Primer	GTGTTGCCCCTGAAGAGCAT
Reverse Primer	GCTGGGACATTGAAAGTCTCA
Circ ENC1	
Forward Primer	GCTATGACTACATTTTGAGGTTTTG
Reverse Primer	TGGCCTCTCCGAAGTAGAAA
ENC1	
Forward Primer	CTTAGACCTCACCTACGTGACG
Reverse Primer	TTGTCCCGGTGCTTGGATTG
U6	
Forward Primer	CTCGCTTCGGCAGCACA
Reverse Primer	AACGCTTCACGAATTTGCGT
miR-513a-5p	
Forward Primer	GCGCGTTCACAGGGAGG
Reverse Primer	AGTGCAGGGTCCGAGGTATT

MYH9	
Forward Primer	ATCCTGGAGGACCAGAACTGCA
Reverse Primer	GGCGAGGCTCTTAGATTTCTCC

Table S3. Antibodies used for western blotting

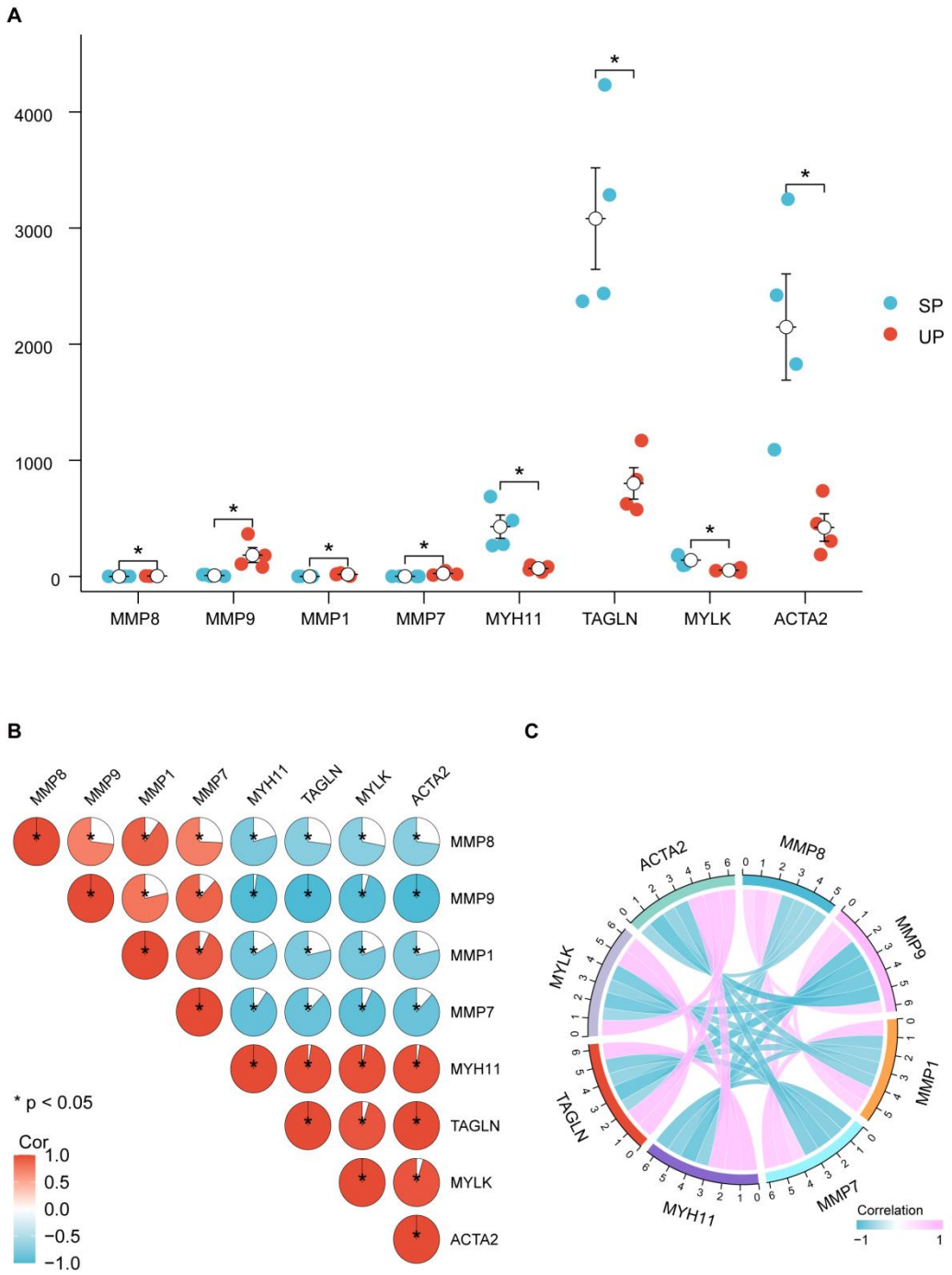
name	Vendor or Source	Catalog #
ACTA2	Cell Signaling Technology	19245
CD68	Cell Signaling Technology	97778
MYH9	Abcam	ab138498
SM22α	Proteintech	15502-1- AP
MYOCD	Sigma	SAB4200539
β-actin	Bioss	bs-0061R

Table S4. Antibodies used for immunofluorescence staining

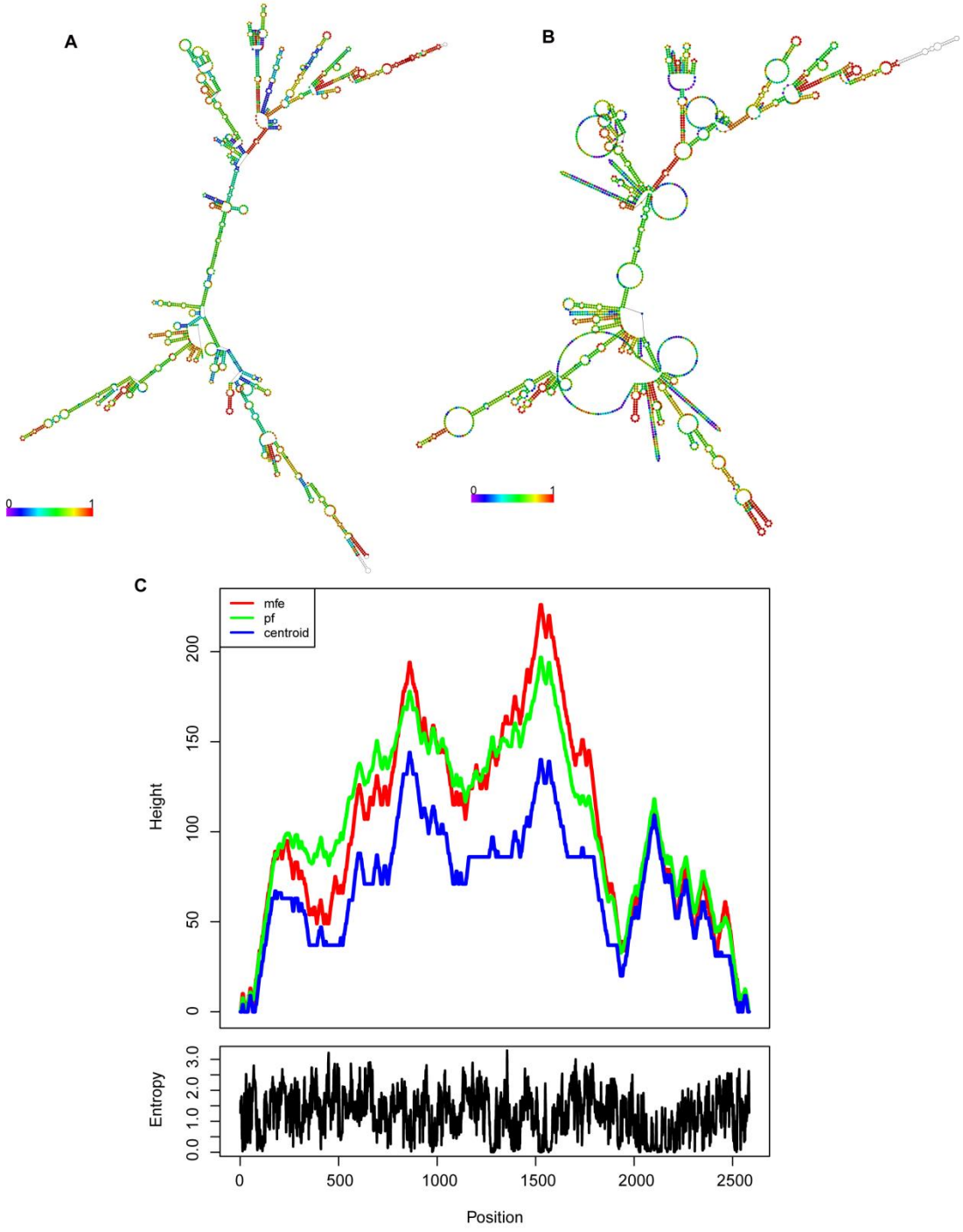
name	Vendor or Source	Catalog #
ACTA2	Cell Signaling Technology	19245
CD68	Cell Signaling Technology	97778
MYH9	Abcam	ab138498
MYH9	Cell Signaling Technology	3403

Table S5. Antibodies for immunohistochemistry analysis

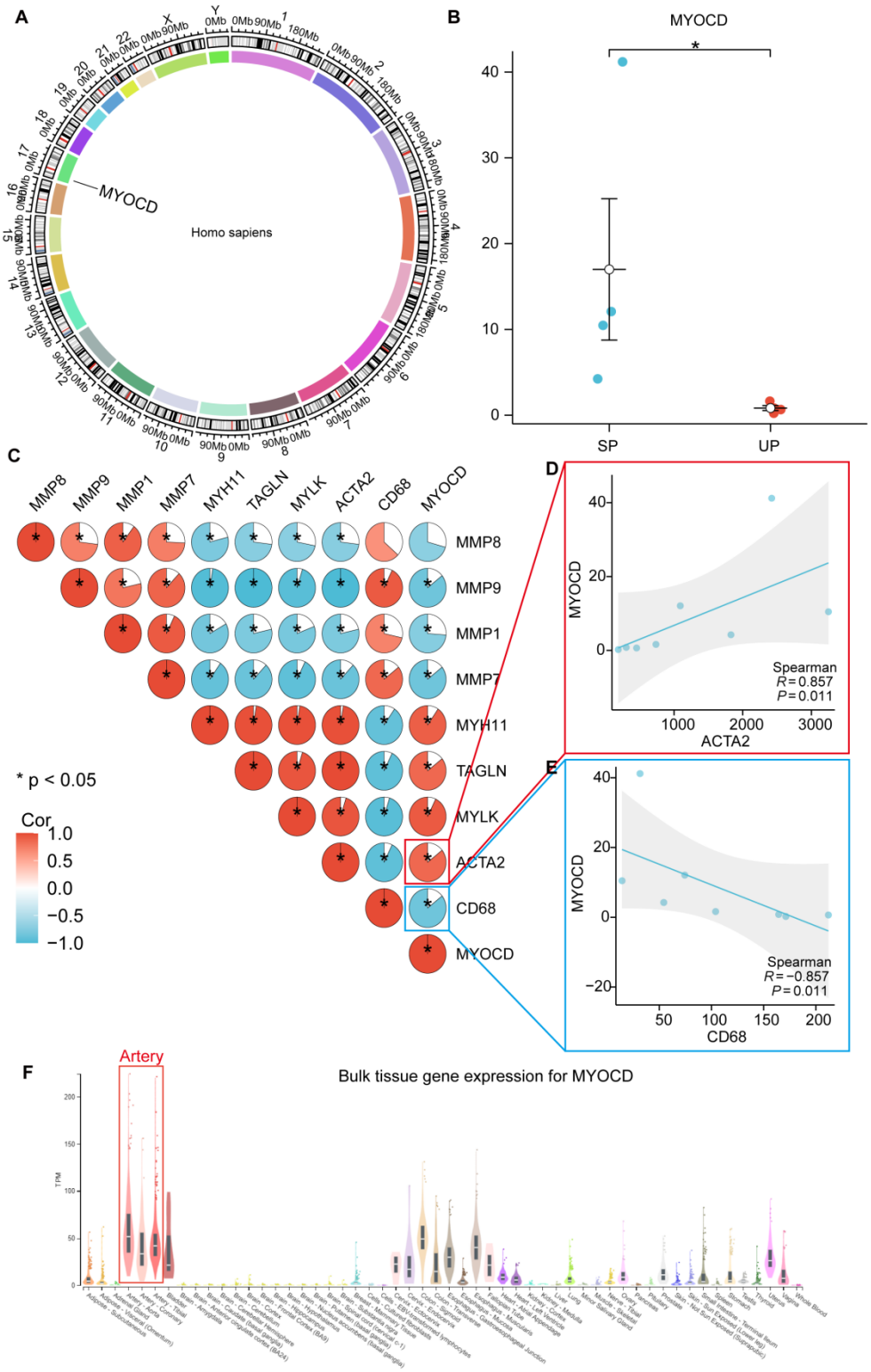
name	Vendor or Source	Catalog #
ACTA2	Cell Signaling Technology	19245
SM22α	Proteintech	15502-1- AP
CD68	Cell Signaling Technology	97778
MYOCD	Sigma	SAB4200539
MYH9	Abcam	ab238131



Supplemental Figure 1 (A). Expression difference map of the phenotypic switching-related mRNAs in GSE120521 dataset. **(B-C).** Correlation analysis of phenotypic switching-related mRNAs in GSE120521 dataset.

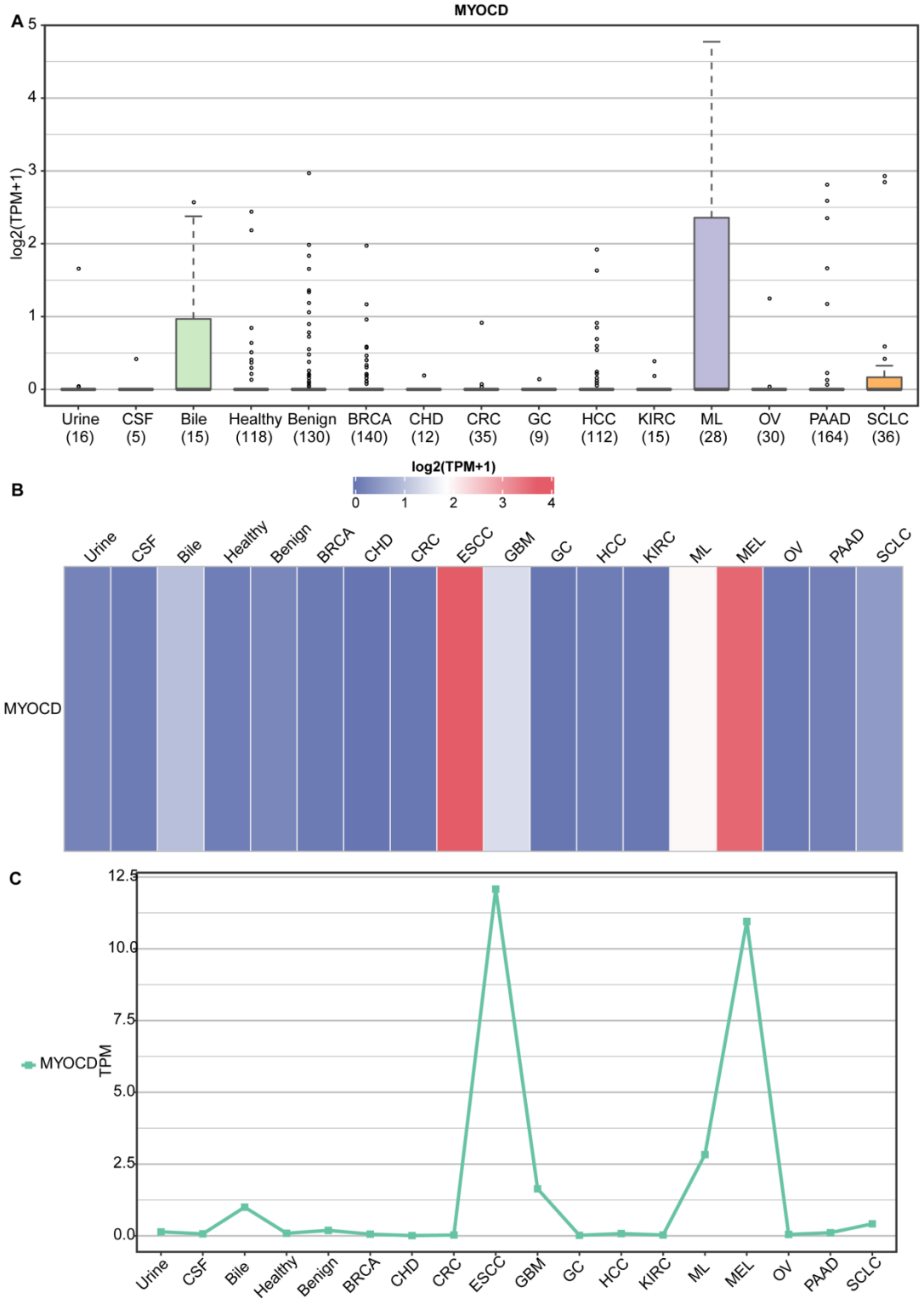


Supplemental Figure 2 (A-C). The secondary structure of TPRG1-AS1 that predicted by RNAfold server.



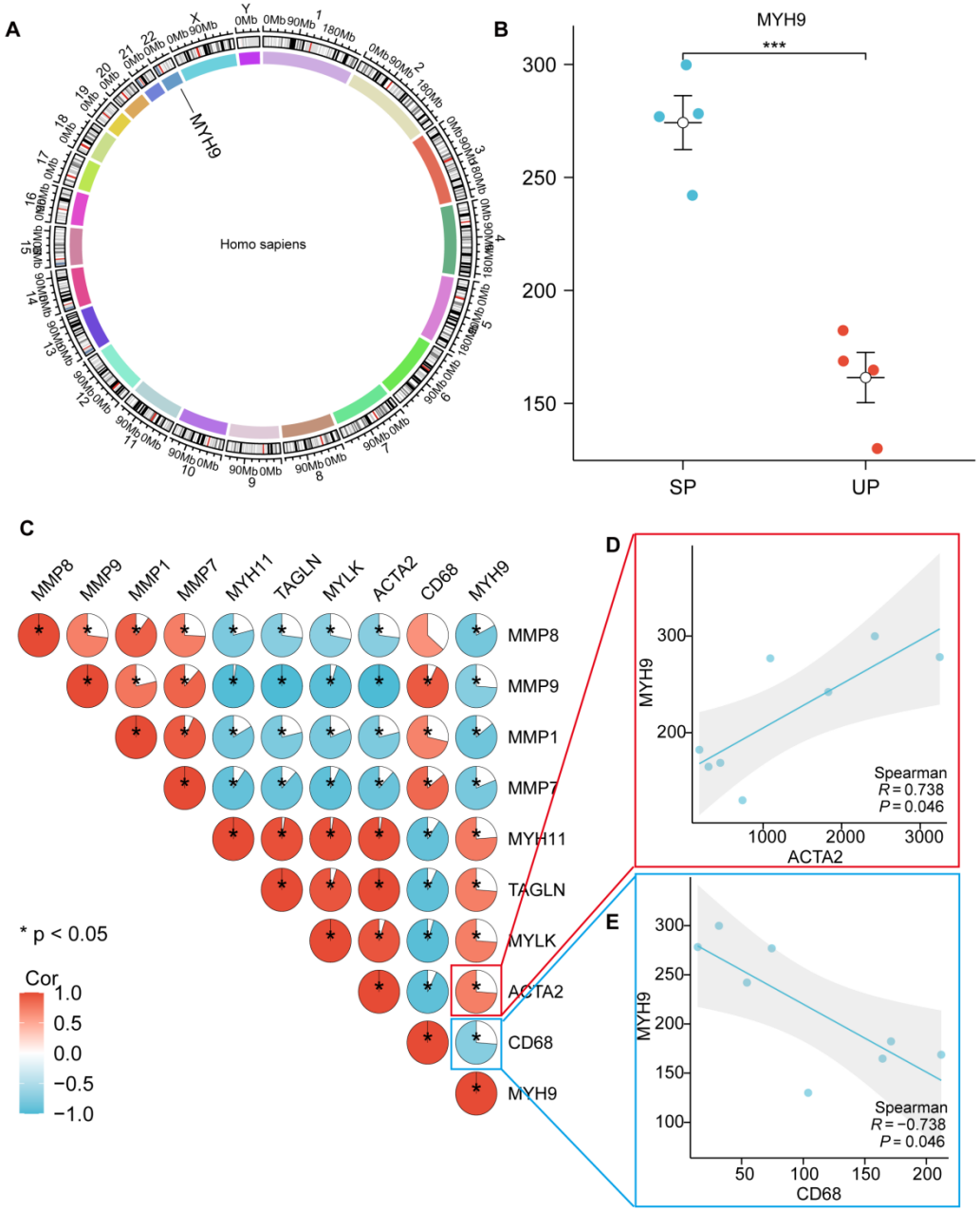
Supplemental Figure 3 (A). Chromosomal map of the MYOCD. **(B).** Expression difference map of the MYOCD in GSE120521 dataset. **(C).** Correlation analysis of phenotypic switching-related mRNAs in GSE120521 dataset. **(D).** Correlation analysis of MYOCD and ACTA2 in GSE120521 dataset. **(E).** Correlation analysis of MYOCD

and CD68 in GSE120521 dataset. **(F).** Prediction of the expression of MYOCD in different tissues via the Genotype-Tissue Expression Project.



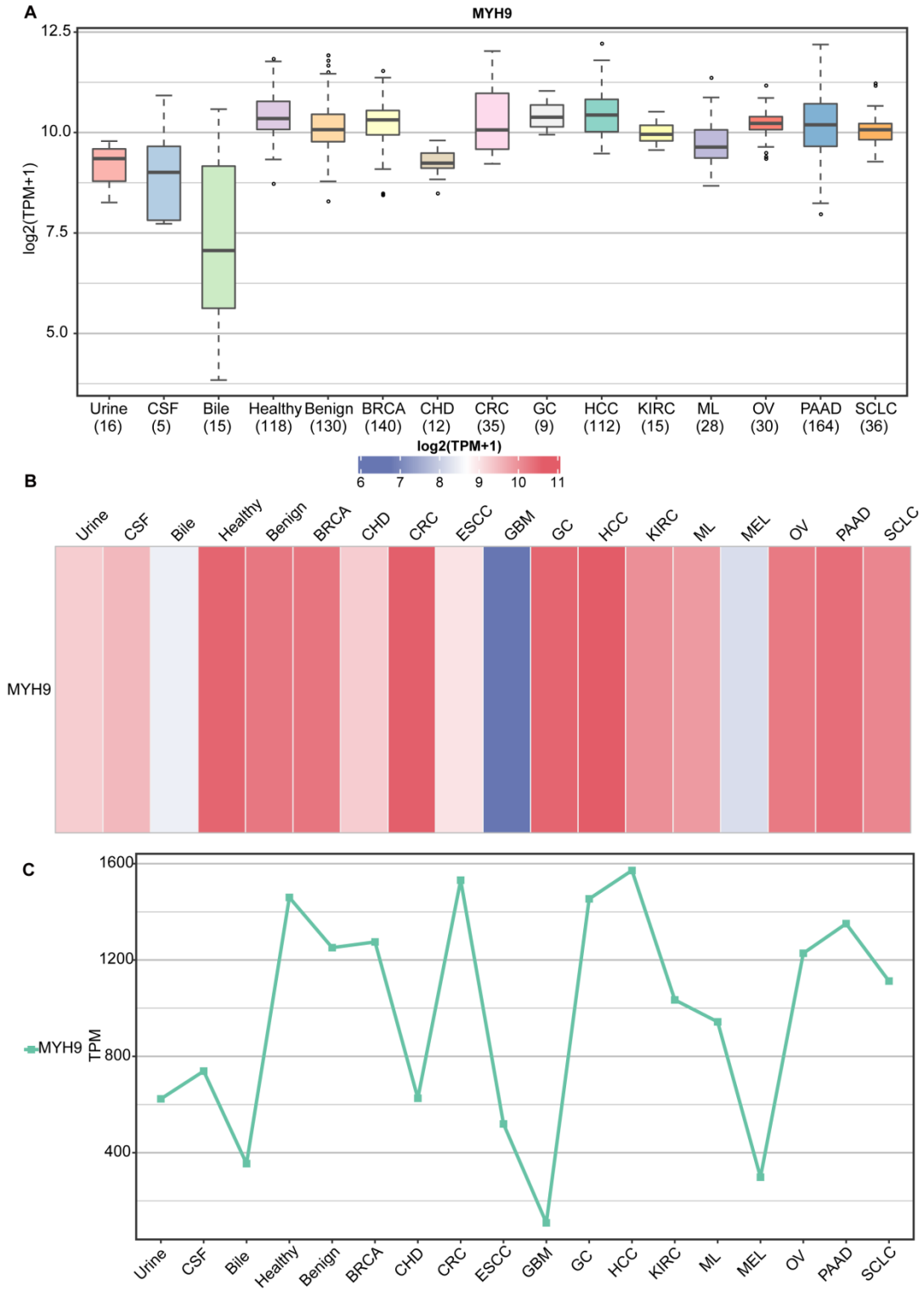
Supplemental Figure 4 (A-C). Predicted levels of MYOCD in urine, healthy patients,

and blood exosomes from different diseases in exobase.



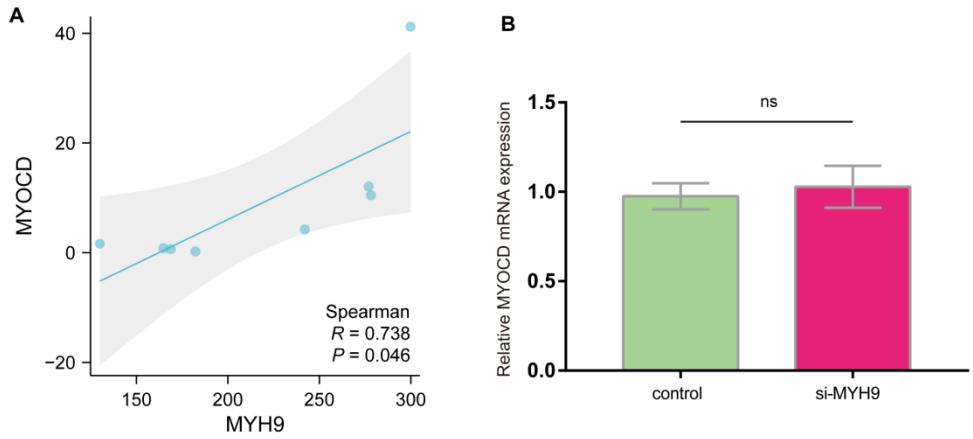
Supplemental Figure 5 (A). Chromosomal map of the MYH9. **(B).** Expression difference map of the MYH9 in GSE120521 dataset. **(C).** Correlation analysis of

phenotypic switching-related mRNAs in GSE120521 dataset. **(D).** Correlation analysis of MYH9 and ACTA2 in GSE120521 dataset. **(E).** Correlation analysis of MYH9 and CD68 in GSE120521 dataset.



Supplemental Figure 6 (A-C). Predicted levels of MYH9 in urine, healthy patients,

and blood exosomes from different diseases in exobase.



Supplemental Figure 7 (A). Correlation analysis of MYOCD and MYH9 in GSE120521 dataset. **(B).** QRT–PCR was performed to evaluate the levels of MYOCD in control and MYH9 knockdown group.