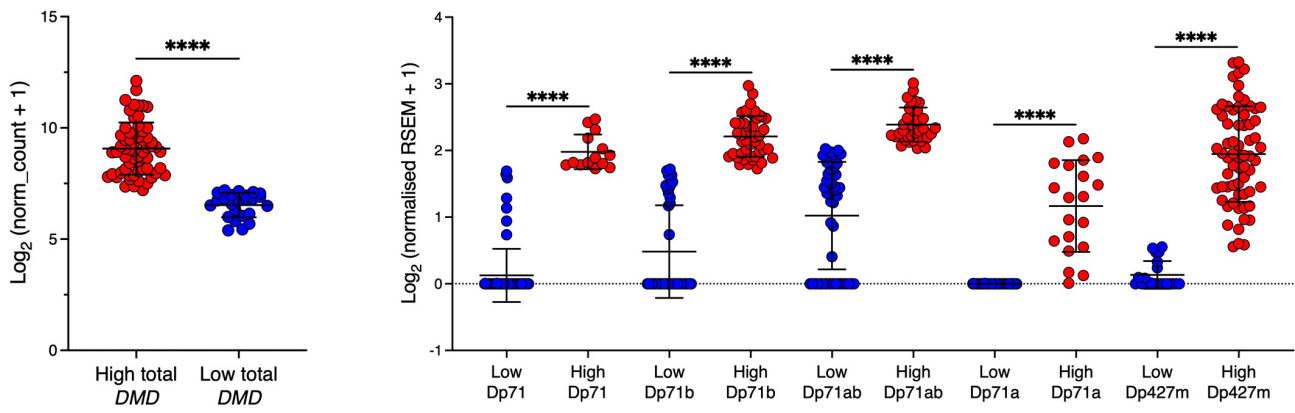
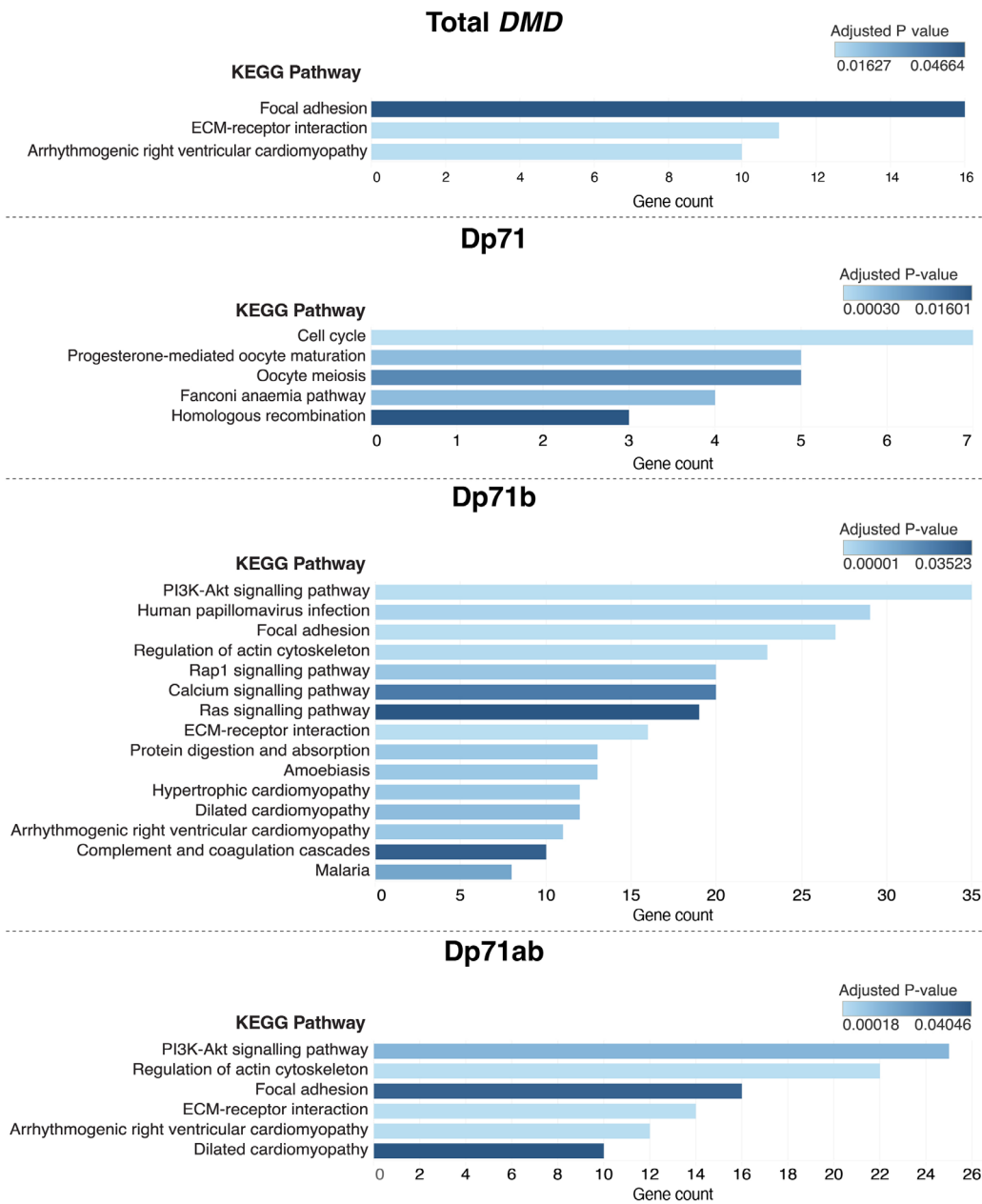


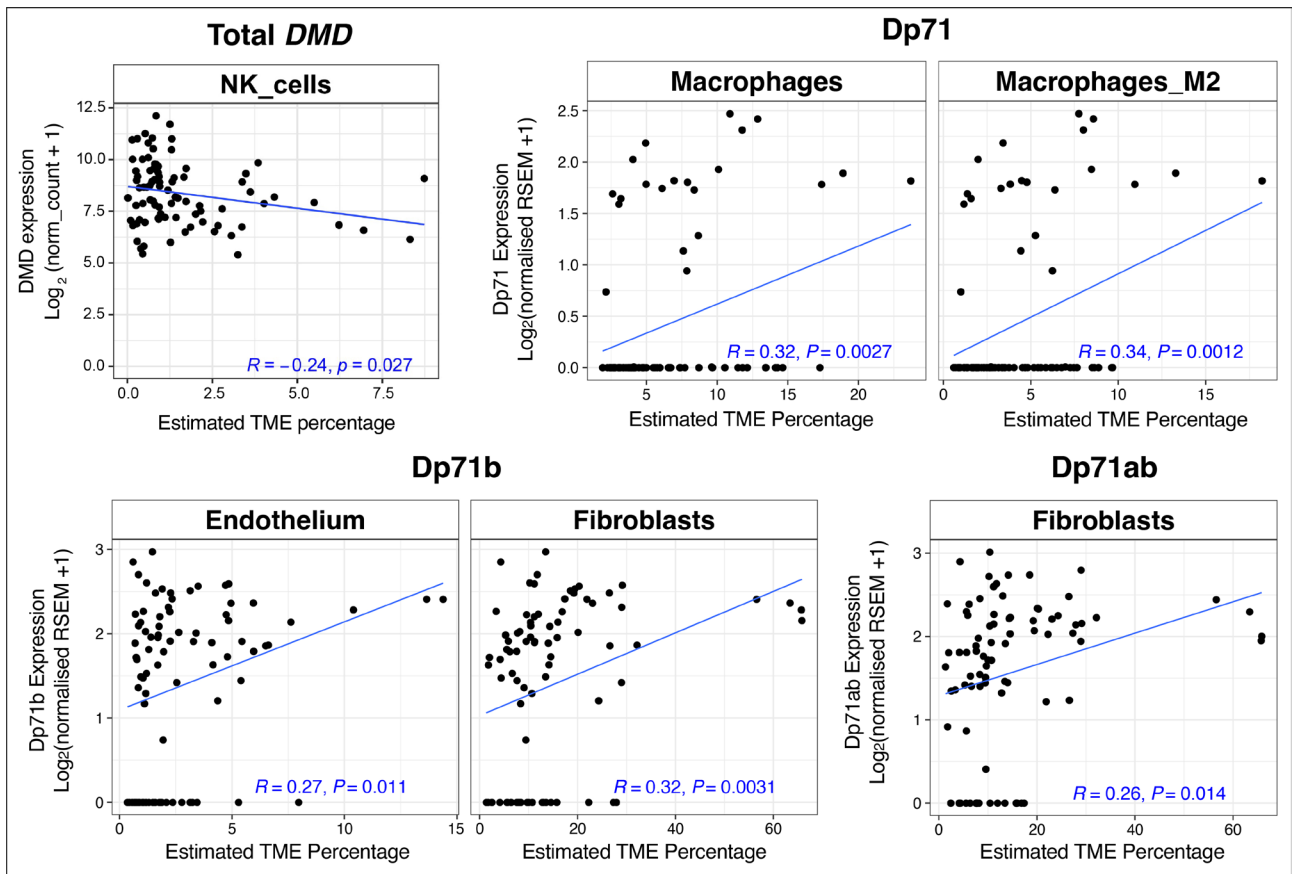
Supplementary



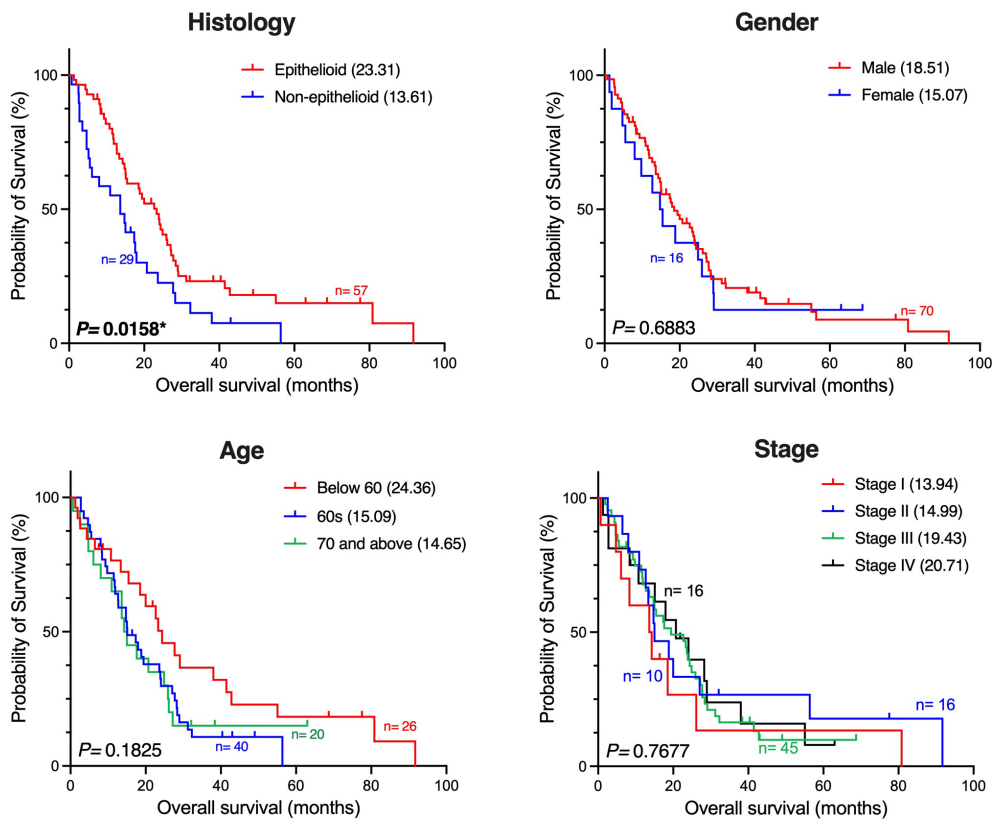
**Figure S1** The difference in *DMD* gene/transcript expression between the high and low expression groups used in the survival analyses. Data are presented as mean  $\pm$  SD (\*\*\*\*,  $P < 0.0001$ ).



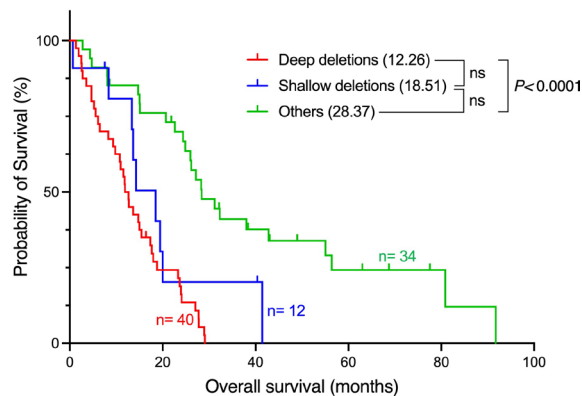
**Figure S2** The KEGG pathways enriched in the DEGs in the high versus low expression groups of *DMD* gene/transcripts (adjusted P value <0.05).



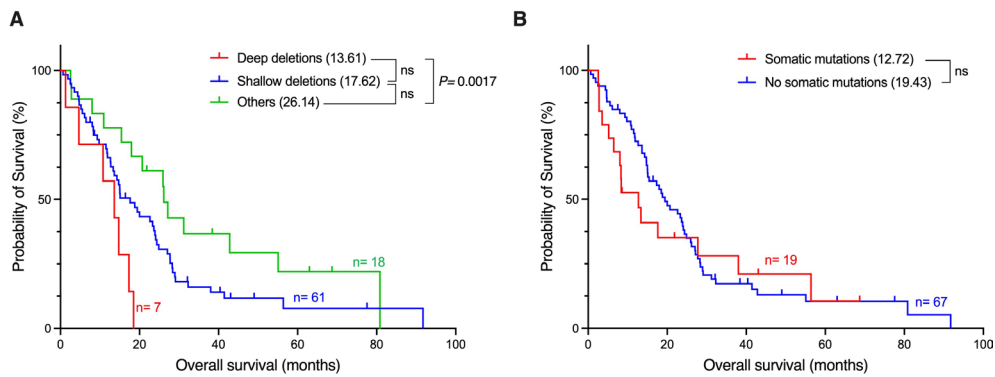
**Figure S3** Correlation between the expression of *DMD* gene/transcripts and the inferred percentages of immune and stromal cells within the TME in mesothelioma samples. The Pearson correlation coefficient R and P value are displayed in the figure.



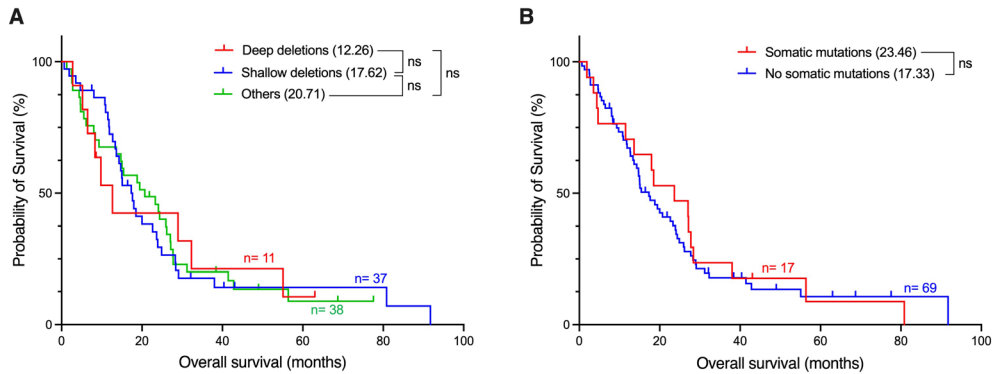
**Figure S4** The association between four clinical pathological parameters (histology, gender, age at diagnosis, and tumour stage) and survival of patients in the TCGA MESO cohort. Kaplan-Meier curves were generated in GraphPad Prism and analysed using the Log-rank test. Numbers in brackets are median survival times in months. Numbers of patients in each group and P values for the log-rank test are displayed in the figure. \*,  $P < 0.05$ .



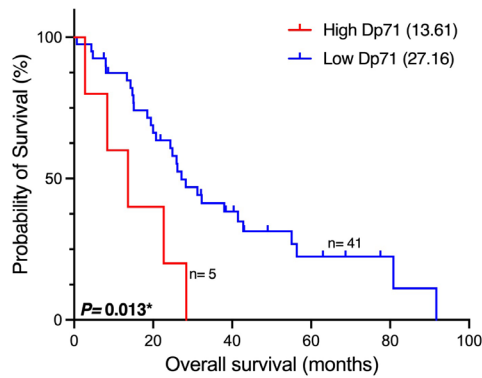
**Figure S5** Kaplan-Meier curve of OS for mesothelioma patients with deep deletions, shallow deletions, and no deletions in the *CDKN2A* gene. Numbers in brackets are median survival times in months. Numbers of patients in each group and P values for the log-rank test are displayed in the figure. The alpha value was adjusted to 0.017 to correct for multiple testing. ns, not significant.



**Figure S6** Association between genomic *NF2* gene alterations and mesothelioma survival. Kaplan-Meier curve of overall survival for mesothelioma patients with (A) deep deletions, shallow deletions, and no deletions in the *NF2* gene and (B) patients with and without somatic mutations in the *NF2* gene. Numbers in brackets are median survival times in months. Numbers of patients in each group and P values for the log-rank test are displayed in the figure. The alpha value was adjusted to 0.017 to correct for multiple testing. ns, not significant.



**Figure S7** Association between genomic *BAP1* gene alterations and mesothelioma survival. Kaplan-Meier curve of overall survival for mesothelioma patients with (A) deep deletions, shallow deletions, and no deletions in the *BAP1* gene and (B) patients with and without somatic mutations in the *BAP1* gene. Numbers in brackets are median survival times in months. Numbers of patients in each group and P values for the log-rank test are displayed in the figure. The alpha value was adjusted to 0.017 to correct for multiple testing. ns, not significant.



**Figure S8** Kaplan-Meier curve of overall survival for the high (red) versus low (blue) Dp71 expression groups of mesothelioma patients with no deep deletions in the *CDKN2A* gene. Numbers in brackets are median survival times in months. Numbers of patients in each group and P values for the log-rank test are displayed in the figure. \*,  $P < 0.05$ .

**Table S1** KEGG pathways enriched in the DEGs between the high versus low *DMD* expression groups

Pathway	Adjusted P value	Genes
ECM-receptor interaction	0.016	<i>COL1A2, ITGB3, ITGA2, TNC, FN1, ITGAV, ITGB6, ITGA5, THBS2, THBS1, THBS3</i>
Arrhythmogenic right ventricular cardiomyopathy	0.016	<i>GJA1, CDH2, ITGB3, ITGA2, ITGAV, DSG2, DMD, ITGB6, ITGA5, DSC2</i>
Focal adhesion	0.047	<i>SHC3, ITGB3, ITGA2, FN1, TNC, VEGFC, THBS2, THBS1, MYLK, IGF1R, THBS3, COL1A2, FLNB, ITGAV, ITGB6, ITGA5</i>

**Table S2** KEGG pathways enriched in the DEGs between the high versus low Dp71 expression groups

Pathway	Adjusted P value	Genes
Cell cycle	$3.01 \times 10^{-4}$	<i>CCNA2, CCNB1, ESPL1, BUB1B, TTK, BUB1, MAD2L1</i>
Fanconi anaemia pathway	0.004	<i>RAD51, FANCM, FANCD2, BRCA1</i>
Progesterone-mediated oocyte maturation	0.004	<i>CCNA2, CCNB1, BUB1, AURKA, MAD2L1</i>
Oocyte meiosis	0.010	<i>CCNB1, ESPL1, BUB1, AURKA, MAD2L1</i>
Homologous recombination	0.016	<i>RAD51, RAD54L, BRCA1</i>

**Table S3** KEGG pathways enriched in the DEGs between the high versus low Dp71b expression groups

Pathway	Adjusted P value	Genes
Focal adhesion	5.94×10 <sup>-6</sup>	<i>MYLK2, FLT1, ITGB3, TNC, THBS2, THBS1, MYLK, IGF1R, PAK6, FLNB, ITGAV, PAK3, PDGFRB, ACTN1, HGF, CAV1, ITGA2, ITGA1, FN1, LAMB1, COL1A2, COL4A2, COL4A1, ITGA10, ITGA11, ITGA8, VCL</i>
ECM-receptor interaction	3.53×10 <sup>-5</sup>	<i>ITGB3, ITGA2, ITGA1, TNC, FN1, LAMB1, THBS2, THBS1, COL1A2, COL4A2, SV2B, COL4A1, ITGA10, ITGA11, ITGA8, ITGAV</i>
PI3K-Akt signalling pathway	4.50×10 <sup>-5</sup>	<i>FLT1, IRS1, ITGB3, TNC, THBS2, THBS1, IGF1R, FGF5, GHR, FGF7, ERBB3, CREB3L1, MYB, ITGAV, PDGFRB, ANGPT2, BDNF, HGF, ITGA2, F2R, ITGA1, FN1, LAMB1, NGF, COL1A2, CDK6, CCNE2, COL4A2, COL4A1, ITGA10, DDIT4, ITGA11, ITGA8, TEK, CREB5</i>
Regulation of actin cytoskeleton	0.001	<i>PDGFRB, MYLK2, ACTN1, ITGB3, ITGA2, F2R, ITGA1, FN1, IQGAP3, MYLK, ENAH, FGF5, ACTR3C, FGF7, ITGA10, SPATA13, ITGA11, ITGA8, PAK6, ITGAV, PAK3, MYH10, VCL</i>
Human papillomavirus infection	0.002	<i>NOTCH2, NOTCH3, NOTCH1, ITGB3, TNC, THBS2, THBS1, PARD6B, PARD6A, CREB3L1, ITGAV, PDGFRB, FZD2, ITGA2, ITGA1, MX1, FN1, LAMB1, COL1A2, CDK6, RBL1, CCNE2, COL4A2, COL4A1, ITGA10, ITGA11, ITGA8, CRB3, CREB5</i>
Amoebiasis	0.006	<i>TGFB2, NOS2, ACTN1, FN1, CXCL1, LAMB1, COL3A1, COL1A2, PLCB4, COL4A2, COL4A1, IL12A, VCL</i>
Protein digestion and absorption	0.006	<i>CPA3, KCNK5, COL27A1, CPB1, COL24A1, MME, COL11A1, COL3A1, COL1A2, COL4A2, COL5A1, COL4A1, COL5A2</i>
Arrhythmogenic right ventricular cardiomyopathy	0.006	<i>CDH2, ITGB3, CACNA2D1, ITGA2, ITGA10, ITGA1, ITGA11, ITGA8, ITGAV, DMD, CACNA1C</i>
Hypertrophic cardiomyopathy	0.006	<i>TGFB2, ITGB3, CACNA2D1, ITGA2, ITGA10, ITGA1, TPM1, ITGA11, ITGA8, ITGAV, DMD, CACNA1C</i>
Rap1 signalling pathway	0.006	<i>PDGFRB, FLT1, ANGPT2, HGF, ITGB3, F2R, ARAP3, NGF, THBS1, IGF1R, ENAH, FGF5, FGF7, PARD6B, PLCB4, PARD6A, P2RY1, TEK, RAPGEF6, F2RL3</i>
Dilated cardiomyopathy	0.009	<i>TGFB2, ITGB3, CACNA2D1, ITGA2, ITGA10, ITGA1, TPM1, ITGA11, ITGA8, ITGAV, DMD, CACNA1C</i>
Malaria	0.015	<i>TGFB2, KLRB1, HGF, SDC2, IL18, IL12A, THBS2, THBS1</i>
Calcium signalling pathway	0.025	<i>PDGFRB, MYLK2, FLT1, NOS2, HGF, F2R, CAMK2A, ADRA1D, MST1R, CACNA1C, NGF, RYR3, MYLK, FGF5, FGF7, HTR7, PLCB4, ERBB3, SLC25A4, PLCD1</i>
Complement and coagulation cascades	0.033	<i>C3, PROCR, F2R, SERPING1, C4BPA, PLAT, CLU, CFB, F2RL2, F2RL3</i>
Ras signalling pathway	0.035	<i>PDGFRB, FLT1, ANGPT2, BDNF, HGF, RASGRF2, PLA2G2A, RASAL2, NGF, ETS1, RASGRP4, IGF1R, FGF5, FGF7, HTR7, RASA2, PAK6, TEK, PAK3</i>

**Table S4** KEGG pathways enriched in the DEGs between the high versus low Dp71ab expression groups

Pathway	Adjusted P value	Genes
ECM-receptor interaction	1.78×10 <sup>-4</sup>	<i>ITGB4, ITGB3, ITGA2, ITGA1, TNC, FN1, HMMR, THBS1, VTN, FRAS1, COL4A1, ITGA11, ITGAV, ITGA5</i>
Regulation of actin cytoskeleton	2.52×10 <sup>-4</sup>	<i>ITGB4, ITGB3, ITGA2, F2R, ITGA1, FN1, BAIAP2, IQGAP3, MYLK, ENAH, FGF5, TIAM1, FGF7, FGF18, ITGA11, ARHGEF4, PAK6, BDKRB1, ITGAV, ITGA5, MYH10, VCL</i>
Arrhythmogenic right ventricular cardiomyopathy	4.59×10 <sup>-4</sup>	<i>GJA1, CDH2, ITGB4, ITGB3, CACNA2D1, ITGA2, ITGA1, ITGA11, ITGAV, DMD, ITGA5, DSC2</i>
PI3K-Akt signalling pathway	0.012	<i>PHLPP2, IRS1, ITGB4, ITGB3, TNC, BRCA1, THBS1, FGF5, GHR, VTN, FGF7, NTF3, ITGAV, ANGPT1, ITGA2, F2R, ITGA1, FN1, NGF, CCNE2, COL4A1, FGF18, ITGA11, ITGA5, CREB5</i>
Focal adhesion	0.037	<i>SHC3, ITGB4, ITGB3, ITGA2, ITGA1, FN1, TNC, THBS1, MYLK, VTN, COL4A1, ITGA11, PAK6, ITGAV, ITGA5, VCL</i>
Dilated cardiomyopathy	0.040	<i>ITGB4, ITGB3, CACNA2D1, ITGA2, ITGA1, ITGA11, ADCY3, ITGAV, DMD, ITGA5</i>

**Table S5** SPSS output for the multivariate Cox regression analysis of the association between the combined D71 and Dp71b transcripts expression and mesothelioma survival

D71 and Dp71b across mesothelial patients	P value	HR	95% CI for HR	
			Lower	Upper
Dp71 + Dp71b (high high; low low)	0.037*	2.229	1.049	4.736
<i>CDKN2A</i> deletion status (deep deletions; no deep deletions)	0.001*	3.525	1.634	7.602
Histology (non-epithelioid; epithelioid)	0.028*	2.240	1.089	4.608
<i>NF2</i> deletion status (deep deletions; no deep deletions)	0.636	1.361	0.380	4.873

\*, statistically significant P values. HR, hazard ratio; CI, confidence interval.