Table S1. TAAD-related Gene list

TAAD-related Genes									
ACTA2	GATA5	PTPN22	TGFBR1	ARFGEF2	COL1A1	ERMARD	HGD	MED12	POR
FBN1	LOX	SLC2A10	TGFBR2	B3GAT3	COL5A1	FBLN5	HLA-B	MYH3	PRDM16
COL3A1	MFAP5	SMAD3	BGN	BCR	COL5A2	FBN2	IFIH1	MYPN	PTEN
ELN	MYH11	SMAD4	PLOD1	C12orf57	CYP11B1	FLNA	IL12B	NEDD4L	RERE
ENG	MYLK	SMAD6	ADAR	CHD7	CYP17A1	FLNB	KANSL1	NOD2	RIN2
PRKG1	NKX2-5	TGFB2	ALDH18A1	CHRNG	DNMT3A	FMR1	KCNH1	NSMCE2	RNASEH2A
FOX3	NOTCH1	TGFB3	ARF1	CHST3	EFEMP2	GABRD	LMNA	PIGN	RNASEH2B
RNASEH2C	TAB2	SMAD2	HCN4	TNXB	SLC25A24	ZMPSTE24	EMILIN1	CBS	MAT2A
ROBO4	TMTC3	TPM3	SEMA3E	ADAMTS-2	TIMP3	ARIH1	LTBP1	NOTCH2	MSTN
SAMHD1	TPM2	TREX1	SKI	COL4A5	TIMP1	COL1A2	LTBP3	NOTCH3	*
BAV-related Genes									
JAG1	COLLAGEN3	AXIN1	MSX1	GLI1	ELASTIN	PDIA2	NOS1	VEGFC	WNT4
SNAI3	MCTP2	SOX9	TBX5	SLC35B2	NFATC1	VEGFB	TEX26	APC	AXIN2
ZNF236	GATA4	PAX6	FLT1	PIGF	NOS3	KCNJ2	PTCH2	PPP3CA	EGFR

*Genetic analysis of both LAMA4 and SOS2 genes were performed only in patient TAAD0077.

Table S2. Multiple gene mutations identified in Sporadic TAAD

ID	Sex	Age	Disease	Hypertension	Gene	variant	Type	classification	Syndrome
TAAD0001	M	37	AD	N	COL1A2	c.3338A>T, p. Asp1113Val	Missense	VUS	N
					SMAD3	c.245G>A, p. Gly82Glu	Missense	VUS	
TAAD0004	M	41	AD	Y	GATA4	c.487C>T, p. Pro163Ser	Missense	VUS	N
					COL5A1	c.1970C>T, p. Pro657Leu	Missense	VUS	
TAAD0006	M	37	AD	Y	FBN2	c.6665C>T, p. Pro2222Leu	Missense	VUS	N
					NOS3	c.2984+4A>G	Splicing	VUS	
TAAD0009	M	46	AD	Y	COL3A1	c.3490G>T, p. Gly1164Trp	Missense	VUS	N
					FLNB	c.2183C>T, p. Pro728Leu	Missense	VUS	
TAAD0010	M	53	AD	Y	SMAD6	c.919A>C, p. Asn307His	Missense	VUS	N
					MED12	c.2665C>G, p. Leu889Val	Missense	VUS	
TAAD0017	F	74	AD	N	MYH11	c.5838_5839del, p. Arg1946SerfsX2	Frameshift	LP	N
					JAG1	c.3286C>T, p. Arg1096Trp	Missense	VUS	
TAAD0030	M	56	AD	Y	COL5A2	c.3884C>A, p. Thr1295Lys	Missense	VUS	N
					HCN4	c.995G>A, p. Arg332Gln	Missense	VUS	
TAAD0035	M	43	TAA+BAV	N	COL1A1	c.1072C>G, p. Gln358Glu	Missense	VUS	N
					GATA4	c.221C>A, p. Ala74Asp	Missense	VUS	

TAAD0036	M	48	AD	Y	COL5A1	c.5045T>G, p. Phe1682Cys	Missense	VUS	N
					MYH11	c.4786A>G, p. Arg1596Gly	Missense	VUS	
					PTCH2	c.2483G>C, p. Gly828Ala	Missense	VUS	
TAAD0037	M	38	TAA+BAV	N	FBN2	c.577C>T, p. Pro193Ser	Missense	VUS	N
					FBN1	c.7559C>T, p. Thr2520Met	Missense	VUS	
TAAD0044	M	55	AD	Y	FLNA	c.1484T>C, p. Val495Ala	Missense	VUS	N
					MCTP2	c.694_695del, p. Lys232SerfsX3	Frameshift	VUS	
TAAD0048	M	38	AD	Y	LOX	c.433C>T, p. Gln145Ter	Nonsense	LP	N
					NOS3	c.1399T>A, p. Tyr467Asn	Missense	VUS	
TAAD0050	M	58	AD	N	FLNB	c.6028C>T, p. Arg2010Cys	Missense	VUS	N
					COL1A2	c.1976A>G, p. Glu659Gly	Missense	VUS	
TAAD0077	M	70	AD	Y	LAMA4	c.307C>G, p. Arg103Gly	Missense	VUS	N
					NOTCH2	c.4666G>A, p. Glu1556Lys	Missense	VUS	
					PRDM16	c.3623T>C, p. Val1208Ala	Missense	VUS	
					SOS2	c.3027C>G, p. Asn1009Lys	Missense	VUS	
TAAD0083	M	50	AD	N	NOTCH3	c.709G>A, p.Val237Met	Missense	VUS	N
					FBN1	c.2860C>T, p.Arg954Cys	Missense	P	
TAAD0097	M	2 months	TAA	N	B3GAT3	c.47C>A, p.Ser16Ter	Nonsense	LP	Y
					B3GAT3	c.752T>C, p.Val251Ala	Missense	VUS	
TAAD0046	M	52	AD	N	TGFBR2	c.1483C>T, p. Arg495Ter	Nonsense	P	Y
					APC	c.1865A>G, p. Tyr622Cys	Missense	VUS	
					TEX26	c.31C>T, p. Gln11Ter	Nonsense	VUS	

F: female; M: male; AD: aortic dissection; TAA: thoracic aortic aneurysm; BAV: bicuspid aortic valve; VUS: variant of uncertain significance; P: pathogenic; LP: likely pathogenic.

Table S3. Multiple mutations of different genes in Familial TAAD

ID	Sex	Age	Disease	Hypertension	Gene	Variant	Type	Classification	Syndrome
TAAD0047	M	27	AD	Y	FBN1	c.1838-2A>G	Splicing	LP	Y
					MSX1	c.458C>A, p. Pro153Gln	Missense	VUS	
TAAD0075	M	40	AD	N	FBN1	c.5797G>A, p. Glu1933Lys	Missense	VUS	Y
					BAG3	c.317G>A, p. Arg106Gln	Missense	VUS	
TAAD0076	F	42	AD	Y	FBN1	c.5797G>A, p. Glu1933Lys	Missense	VUS	Y
					BAG3	c.317G>A, p. Arg106Gln	Missense	VUS	
TAAD0081	M	31	/	N	FBN1	c.7113G>A, p. Trp2371Ter	Nonsense	LP	Y
					COL5A1	c.526A>C, p. Asn176His	Missense	VUS	
					MYH11	c.33G>T, p. Glu11Asp	Missense	VUS	
TAAD0082	M	27	TAA	N	FBN1	c.7113G>A, p. Trp2371Ter	Nonsense	LP	Y
					COL5A1	c.526A>C, p. Asn176His	Missense	VUS	
					MYH11	c.33G>T, p. Glu11Asp	Missense	VUS	
TAAD0087	F	43	AD	N	FBN1	c.6575G>T, p. Cys2192phe	Missense	LP	Y
					LOX	c.218G>A, p. Gly73Asp	Missense	VUS	
TAAD0088	F	41	TAA	N	FBN1	c.6575G>T, p. Cys2192Phe	Missense	LP	Y
					ELN	c.1876G>A, p. Ala626Thr	Missense	VUS	

M: male; F: female; AD: aortic dissection; TAA: thoracic aortic aneurysm; LP: likely pathogenic; VUS: variant of uncertain significance. Three pairs of siblings from three unrelated families were underlined.