

Table S1: Clinical features overview LOX patients

	Family 1 p.(Leu18Profs*111)							Family 2 p.(Arg118Glyfs*119)			Family 3 p.(Gly149*)				Family 4 p.(Met298Arg)	Family 5 p.(Leu306Pro)
Individual	II:2	II:3	III:4	III:6	III:10	IV:1	IV:7	III:1	II:1	I:1	II:4	II:5	III:1	II:1	II:1	III:1
Gender	M	M	M	M	M	M	F	M	M	M	M	M	F	M	F	M
Age (years)	60	50	43	45	43	25	16	40	53	66	56	53	28	59	50	21
Arterial anomalies	Bental surgery age 60 after dissection, died 73 due to myocardial infarction	Sudden death (age 50)	Type A dissection (53mm)	Aortic dissection (age 45-84mm) and Bentall surgery	Aortic sinus diameter (43mm - age 43)	Normal diameter	Normal diameter	Type A dissection at age of 19 (underwent composite graft surgery)	Discrete mitral and aortic valve insufficiency		Borderline aortic sinus (41mm)	Mild valve regurgitation			Left carotid dissection (age 46)	Dilatation of aorta sinus and ascendens (age 6)
															Coronary artery dissection (age 44)	Elective replacement of the ascending aorta (age 14)
Connective tissue anomalies								Splenic rupture	Inguinal hernia surgery	Varicose veins	Inguinal hernia surgery (age 3)	Tall stature	Joint hypermobility	Bilateral inguinal hernia	Increased skin elasticity	Tall stature
								Spontaneous pneumo-thorax		Cataract	Rupture of supraspinatus ligament (age 41)	Narrow palate	Arachno-dactyly	Tall stature	Beighton score of 4/9	
								Varicose veins		Ischemic heart disease	Tibialis posterior neuralgia (age 42)	Pes planus	Pes planus	Joint hypermobility	Enlarged armspan	
										Contra-lateral and incarcerated hernia		Inguinal hernia surgery (age 40)	Shoulder dislocations and ankle distortions		Recurrent joint dislocation	

Table S2: ACMG classification and pathogenicity predictions of *LOX* variants

	Gnomad	CADD	REVEL	MetaLR	PolyPhen2	Mutation-Taster	ACMG classification
p.(Leu18Profs*111)	Absent	-	-	-	-	Disease causing	Pathogenic (PVS1; PM2; PS3; PP4)
p.(Arg118Glyfs*119)	Absent	-	-	-	-	Disease causing	Pathogenic (PVS1, PS3, PM2)
p.(Gly149*)	Absent	34	-	-	-	Disease causing	Pathogenic (PVS1, PS3, PM2)
p.(Met298Arg)	Absent	32	0,736	0,313	Probably damaging	Disease causing	Pathogenic (PP3; PM1; PM2; PS1; PS3)
p.(Leu306Pro)	Absent	31	0,811	0,358	Probably damaging	Disease causing	VUS (PM1; PM2; PP3)

Table S4: Genes included in TAAD gene panel

Gene	Reference transcript (Ensembl)	Alternative exon	Reference transcript for alternative exon (Ensembl)
<i>ABL1</i>	ENST00000372348		
<i>ACTA2</i>	ENST00000458208		
<i>ARIH1</i>	ENST00000379887		
<i>BGN</i>	ENST00000331595		
<i>COL3A1</i>	ENST00000304636		
<i>EFEMP2/FBLN4</i>	ENST00000307998		
<i>ELN</i>	ENST00000358929		
<i>EMILIN1</i>	ENST00000380320		
<i>FBN1</i>	ENST00000316623		
<i>FBN2</i>	ENST00000262464		
<i>FLNA</i>	ENST00000369850		
<i>FOXE3^a</i>	ENST00000335071		
<i>HCN4</i>	ENST00000261917		
<i>LMOD1</i>	ENST00000367288		
<i>LOX</i>	ENST00000231004		
<i>LTBP3</i>	ENST00000301873		
<i>MAT2A</i>	ENST00000306434		
<i>MFAP5</i>	ENST00000359478		
<i>MYH11</i>	ENST00000452625	Exon 42B	ENST00000396324
<i>MYLK</i>	ENST00000360304		
<i>NOTCH1</i>	ENST00000277541		
<i>PLOD1</i>	ENST00000196061	Exon 2A	ENST00000449038
<i>PMEPA1/TMEPAI</i>	ENST00000341744		
<i>PRKG1^b</i>	ENST00000401604		
<i>SKI</i>	ENST00000378536		
<i>SLC2A10</i>	ENST00000359271		
<i>SMAD2</i>	ENST00000402690		
<i>SMAD3</i>	ENST00000327367	Exon 1A	ENST00000439724
<i>SMAD4</i>	ENST00000342988		
<i>SMAD6</i>	ENST00000288840		
<i>TGFB2</i>	ENST00000366929		
<i>TGFB3</i>	ENST00000238682		
<i>TGFBR1</i>	ENST00000374994		
<i>TGFBR2</i>	ENST00000359013		

^aOnly Forkhead domein

^bOnly exon 3