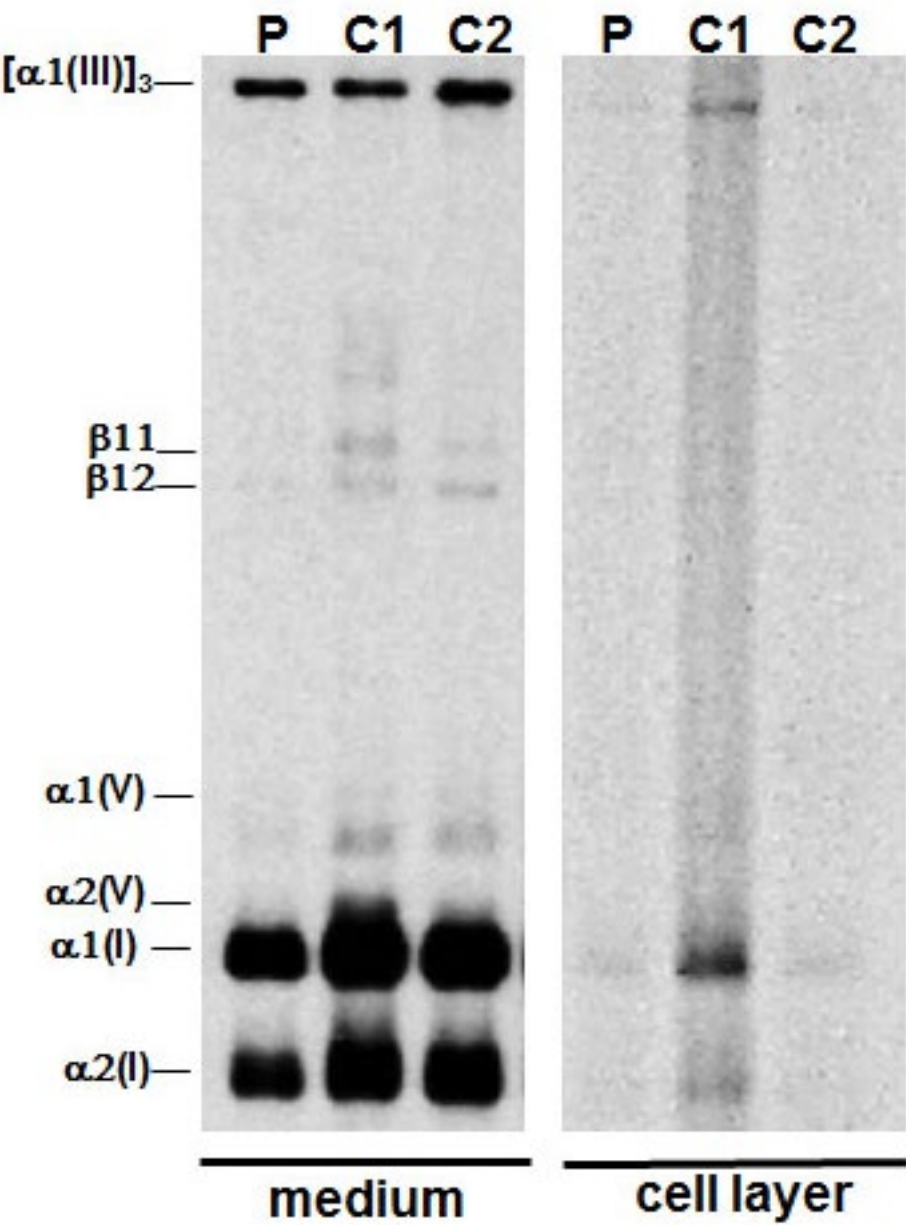


Supplementary data

Supplementary Figure S1: Steady-state analysis of collagen in the medium and the cell layer



**Supplementary Table S1:** NGS panel for connective tissue disorders

<i>ABCC6</i>	NM_001171	<i>DSE</i>	NM_013352	<i>PPIB</i>	NM_000942
<i>ACTA2</i>	NM_001613	<i>DSPP</i>	NM_014208	<i>PRDM5</i>	NM_016599
<i>ACVRL1</i>	NM_000020	<i>EFEMP2</i>	NM_016938	<i>PRKG1</i>	NM_006258
<i>ADAMTS2</i>	NM_014244	<i>ELN</i>	NM_000501	<i>PYCR1</i>	NM_006907
<i>ADAMTS4</i>	NM_019032	<i>ENG</i>	NM_000118	<i>RIN2</i>	NM_001242581
<i>ALDH18A1</i>	NM_002860	<i>FBLN5</i>	NM_006329	<i>RUNX2</i>	NM_001024630
<i>ALPL</i>	NM_000478	<i>FBN1</i>	NM_000138	<i>RYR1</i>	NM_000540
<i>ANO5</i>	NM_213599	<i>FBN2</i>	NM_001999	<i>SEC24D</i>	NM_014822
<i>ATP6V0A2</i>	NM_012463	<i>FGFR2</i>	NM_000141	<i>SEPN1</i>	NM_020451
<i>ATP7A</i>	NM_000052	<i>FGFR3</i>	NM_001163213	<i>SERPINF1</i>	NM_002615
<i>B3GALT6</i>	NM_080605	<i>FKBP10</i>	NM_0213939	<i>SERPINH1</i>	NM_001235
<i>B4GALT7</i>	NM_007255	<i>FKBP14</i>	NM_017946	<i>SKI</i>	NM_003036
<i>BMP1</i>	NM_006129	<i>FLCN</i>	NM_144997	<i>SLC25A2</i>	NM_000112
<i>CASR</i>	NM_001178065	<i>FLNA</i>	NM_001456	<i>SLC2A10</i>	NM_030777
<i>CBS</i>	NM_000071	<i>GLA</i>	NM_000169	<i>SLC39A13</i>	NM_001128225
<i>CHRD1</i>	NM_001143981	<i>GORAB</i>	NM_152281	<i>SMAD3</i>	NM_005902
<i>CHST14</i>	NM_130468	<i>IFITM5</i>	NM_001025295	<i>SMAD4</i>	NM_005359
<i>COL11A1</i>	NM_001854	<i>LEPRE1</i>	NM_001243246	<i>SOX9</i>	NM_000346
<i>(COL11A2)</i>	NM_080680	<i>LRP5</i>	NM_002335	<i>SP7</i>	NM_001173467
<i>COL12A1</i>	NM_004370	<i>LTBP2</i>	NM_000428	<i>SPARC</i>	NM_003118
<i>COL1A1</i>	NM_000088	<i>LTBP4</i>	NM_0035732	<i>STAT1</i>	NM_007315
<i>COL1A2</i>	NM_000069	<i>MAT2A</i>	NM_005911	<i>STAT3</i>	NM_139278
<i>COL2A1</i>	NM_001844	<i>MED12</i>	NM_005120	<i>TGFB1</i>	NM_000660
<i>COL3A1</i>	NM_000090	<i>MFAP5</i>	NM_003480	<i>TGFB2</i>	NM_001135599
<i>COL5A1</i>	NM_000093	<i>MMP2</i>	NM_004530	<i>TGFB3</i>	NM_003239
<i>COL5A2</i>	NM_000393	<i>MYH11</i>	NM_002474	<i>TGFBR1</i>	NM_004612
<i>COL6A1</i>	NM_001846	<i>MYLK</i>	NM_053025	<i>TGFBR2</i>	NM_001024847
<i>COL6A2</i>	NM_001849	<i>NOTCH1</i>	NM_017617	<i>TMEM38B</i>	NM_018112
<i>COL6A3</i>	NM_004369	<i>NOTCH3</i>	NM_000435	<i>TRIP11</i>	NM_004239
<i>COL9A1</i>	NM_001851	<i>P4HB</i>	NM_000918	<i>WNT1</i>	NM_005430
<i>COL9A2</i>	NM_001852	<i>PLOD1</i>	NM_000302	<i>XYLT1</i>	NM_022166
<i>CREB3L1</i>	NM_052854	<i>PLOD2</i>	NM_182943	<i>XYLT2</i>	NM_022167
<i>CRTAP</i>	NM_006371	<i>PLOD3</i>	NM_001084	<i>ZDHHC9</i>	NM_018032
<i>DCHS1</i>	NM_003737	<i>PLS3</i>	NM_005032	<i>ZNF469</i>	NM_001127464

Supplementary Table S2

Primers and PCR conditions for <i>TNXB</i> (NM_0019105.7) Sanger sequencing		
Exons 2-31 PCR: 95 °C, 3'; 95 °C, 30"; 58 °C, 20"; 72 °C, 45"; 72 °C, 7'; 10 °C, ∞; 32 cycles		
Exon 2	TNxBex2aF TNxBex2aR	GATTACTTGTGGGTGGTGGG TACCTCTGAAGCAAGGACTGG
	TNxBex2bF TNxBex2bR	AAGCCCTCTTCTCAGCTTT GGCTCAGATCAAAACACACCA
Exon 3	TNxBex3aF TNxBex3aR	GAGCAGACATGGCCTTATGA CTCATGCCACAGTCGTCAC
	TNxBex3bF TNxBex3bR	AATGATCAGGGTCGCTGTG CGCAATCGGTTCCAGTGTA
	TNxBex3cF TNxBex3cR	GGCGAGGACTGTGGTACG CCTGAGTAGCCTGCGTCAC
	TNxBex3dF TNxBex3dR	GAGAACGGCGTGTGTGTTT ACAGGCACACTCCTTGAC
	TNxBex3eF TNxBex3eR	GCAGGCTACTCAGGGGAAG TCCACTCTTCCTCAGGCTCA
	TNxBex3fF TNxBex3fR	GGGAGATTCTGTGCTCCTGA GCCATCTGGACTCAACCAAT
Exon 4	TNxBex4F TNxBex4R	GGGAGATTCTGTGCTCCTGA GCCATCTGGACTCAACCAAT
Exon 5	TNxBex5F TNxBex5R	GGACCTGTTTCGTAGGGTTG ACTCAGGTGGGTGTCTGGTT
Exon 6	TNxBex6F TNxBex6R	GCTCTTGGGAAGGAAAGATGATG ACAGGACTCCAGGCATCTGA
Exon 7	TNxBex7F TNxBex7R	CAGGTGAGGGAACCAGAAAGT GCTGAACCTGCAATTCCTTT
Exon 8	TNxBex8F TNxBex8R	GACCTGAAACCCCCGAAAGAT ATGCCCTGTTCTCCAGCCAGAG
Exon 9	TNxBex9F TNxBex9R	CAGTCCCTCTGTACTCCCTCA ACTTCTGGGAAGCCTGACAC
Exon 10	TNxBex10F TNxBex10R	CCCAGAAAGTTTAGCACTCGAA TGGCAAAATGAGCTGAGAAG
Exon 11	TNxBex11F TNxBex11R	GCTGTCTCAGCCTTCTCCAT CAGCCTCAAGGTTCCACTG
Exon 12	TNxBex12F TNxBex12R	TTTACTAACAGCCCCCTACCA GTCAGGGAACAGAAAGACTGG
Exon 13	TNxBex13F TNxBex13R	AACTATTCCCCATCTCAGTTCAC TCAAATGAGACAGAGCAGGTG
Exon 14	TNxBex14F TNxBex14R	GGAAATATTTGGGGAAGCAC CTGGGGCCAAATAATGGTAAT
Exon 15	TNxBex15F TNxBex15R	GCTGCCATTACCATTATTGG GGATGATCGAAAGCAGACAGT
Exon 16	TNxBex16F TNxBex16R	CTGGTCTTTCGATTGCTGACT TGGAAGAGAGGACTGAGGTG
Exon 17	TNxBex17F TNxBex17R	TTCAGTGATGGGAAGCATGT AGTGGTCAACCTCACAGGAAG
Exon 18	TNxBex18F TNxBex18R	GGCCTCTCTGAAGTACCTC CTGGATTGCTCTCTGTCC
Exon 19	TNxBex19F TNxBex19R	TTGAGGGACCATAAGGAAGC CTGGGGCAATACCAAAGTCT
Exon 20	TNxBex20F TNxBex20R	AGAGAATCCCAGAGTCCCTTG AGTTCAGAGAGGCCATTCTT
Exon 21	TNxBex21F TNxBex21R	GGCCTCTCTGAAGTACCTC GTGAAAGGGCACAGCAGTAA
Exon 22	TNxBex22F TNxBex22R	GGATACCTCACCAGGCTCTTA TCTCCATGACATGTCTTTCCA
Exon 23	TNxBex23aF	CAATCCAGCAAATGAAGCAA

	TNXBex23R	CAGTCATCACCAAAGAGCAAG
Exon 24	TNXBex24F TNXBex24R	AGCTGACCCTGGAACCTTGTC TCTTAGCAAGATCCCCAAGC
Exon 25	TNXBex25F TNXBex25R	CTCTTGGGCACTTTGTGTTTT CACCCAGGAAGATCTGTCAGT
Exon 26	TNXBex26F TNXBex26R	CCTCAGAGCTTGTCATGTGTG AAGCCTGCTGAATCCAAATC
Exon 27	TNXBex27F TNXBex27R	CAGGGTGAGGGATAGGAAAG ACCAAAGAGCAAGAGGTGG
Exon 28	TNXBex28F TNXBex28R	CCCAAGAATGGACTTCTCTGA TGAGGCAGGATCATTAGCAA
Exon 29	TNXBex29F TNXBex29R	TCATATGTTGTGCGAGGGTTA CAATAAATCAGTGGGTGCTGAG
Exon 30	TNXBex30F TNXBex30R	AGGGGACACTTGCTTTCTTG ACACAGAGGGACTCACTTTCCG
Exon 31	TNXBex31F TNXBex31R	GTTCTCCCTCATTCCTGTGG CCTGCTCTGGACTCCTTGAT
Exons 32-44	<i>Long-range PCR (5440 bp) as template for nested-PCR</i> 95 °C, 4'; 95 °C, 30"; 60 °C, 30"; 72 °C, 5'; 72 °C, 10'; 10 °C, ∞; 30 cycles	
	Intr30F	GTGGCCTTGTCAGATAGC
	3'UTR-R	ACAGCCCGGGCCAGAG
<i>Nested-PCR: 95 °C, 3'; 95 °C, 30"; 58 °C, 20"; 72 °C, 45"; 72 °C, 7'; 10 °C, ∞; 32 cycles</i>		
Exon 32	TNXBex32F TNXBex32R	GACTGGGCCTGGACCTATAA AGCCCATCCATCCTCTCTC
Exon 33	TNXBex33F TNXBex33R	TGCAAGTCCCTGGTTACAGA AAGTCGCTCTGCAGATTCTT
Exons 34-37	TNXBex33F TNXBex37R	CTGACACTGTATGGGCTGCG CACAGACCCTACCTGTGGTG
Exons 37-38	TNXBex37F TNXBex38R	TTGTCCTCCACCAACTACA ATCTCCTGTGGGACAGACAAG
Exons 39-41	TNXBex38F TNXBex41R	TACCTGCTCAGCTTCCACAC TCACAGCCTCTGCTTACCTG
Exon 42	TNXBex42F TNXBex42R	GCATGGATGGACAGACAGAC GCGTAGTGGCAGTTCTGTGA
Exon 43	TNXBex43F TNXBex43R	CTCGGCTGCGGAGTACTACC ACACTGTGGGGCTGAAACCT
Exon 44	TNXBex44F TNXBex44R	GAGGGAGCTGGAGTTGATTTA ACTGCAGTGTATCCTCAAGA

**Supplementary Table S3:** Published *TNXB* pathogenic variants

Patient	Family	Sex	Age (years)	Cons.	Status	Allele 1	Type	Allele 2	Type	References
P1	I	F	43	+	Homozygous	Exon 15: c.5362del, p.(Thr1788Profs*100)	Frameshift-PTC	Exon 15: c.5362del, p.(Thr1788Profs*100)	Frameshift-PTC	This report
P2	II	F	69	-	Homozygous	Exon 8: c.3290_3291del, p.(Lys1097Argfs*48)	Frameshift-PTC	Exon 8: c.3290_3291del, p.(Lys1097Argfs*48)	Frameshift-PTC	Schalkwijk <i>et al.</i> , 2001
P3		F	59							
P4	III	F	60	-	Compound heterozygous	TNXA conversion <sup>a</sup>	Frameshift-PTC	TNXA conversion <sup>a</sup>	Frameshift-PTC	
P5		F	55							
P6		M	59							
P7	IV	M	57 <sup>+</sup>	-	Homozygous	Exon 3: c.2117_2118insGT p.(Glu707*)	Frameshift-PTC	Exon 3: c.2117_2118insGT p.(Glu707*)	Frameshift-PTC	
P8	V	F	49 <sup>+</sup>	-	Homozygous	Exon 8: c.3290_3291del, p.(Lys1097Argfs*48)	Frameshift-PTC	Exon 8: c.3290_3291del, p.(Lys1097Argfs*48)	Frameshift-PTC	
P9	VI	M	36	-	Compound heterozygous	TNXB/TNXA fusion <sup>b</sup>	Frameshift-PTC	TNXA conversion <sup>b</sup>	Frameshift-PTC	
P10	VII	F	32	-	Compound heterozygous	Exon 3: c.903del, p.(Tyr301*)	Nonsense	Exon 42: c.12464-1G>A	Splicing	
P11		F	31							
P12	VIII	M	29	+	Homozygous	Exon 8: c.3290_3291del, p.(Lys1097Argfs*48)	Frameshift-PTC	Exon 8: c.3290_3291del, p.(Lys1097Argfs*48)	Frameshift-PTC	
P13	IX	F	27	-	Compound heterozygous	Exon 8: c.3290_3291del, p.(Lys1097Argfs*48)	Frameshift-PTC	TNXB/TNXA fusion <sup>c</sup>	Frameshift-PTC	Hendriks <i>et al.</i> , 2012
P14	X	F	12	-	Compound heterozygous	TNXB/TNXA fusion <sup>d</sup>	Frameshift-PTC	TNXA conversion <sup>d</sup>	Frameshift-PTC	
P15	XI	M	42	-	Compound heterozygous	TNXB/TNXA fusion <sup>e</sup>	Frameshift-PTC	Exon 41: c.12214C>T, p.(Arg4072Cys)	Missense	Pénisson-Besnier <i>et al.</i> , 2013
P16	XII	F	45	-	Compound heterozygous	Exon 6: c.2539C>T, p.(Arg847*)	Nonsense	Exon 9: c.3574C>T, p.(Gln1192*)	Nonsense	Sakiyama <i>et al.</i> , 2015
P17	XIII	M	13	-	Compound heterozygous	Exon 9 : c.3637G>A, p.(Val1213Ile)	Missense	Exon 22: c.7774G>A, p.(Gly2592Ser)	Missense	Mackenroth <i>et al.</i> , 2016
P18	XIV	F	48	-	Compound heterozygous	Exon 43: c.12553C>T, p.(Arg4185*)	Nonsense	Exon 6: c.2590C>T, p.(Gln864*)	Nonsense	Demirdas <i>et al.</i> , 2017
P19	XV	F	23	-	Compound heterozygous	Exon 6: c.2590C>T, p.(Gln864*)	Nonsense	TNXB/TNXA fusion <sup>f</sup>	Frameshift-PTC	

<b>P20</b>	XVI	M	16	-	Compound	Exon 5: c.2461C>T,	Nonsense	<i>TNXA</i> conversion <sup>§</sup>	Frameshift-PTC
<b>P21</b>		M	14	-	heterozygous	p.(Arg821)*			
<b>P22</b>	XVII	F	12	-	Compound	Exon 2: c.107_108delinsA,	Frameshift-PTC	Exon 22: c.7826-1G>C	Splicing
<b>P23</b>		M	6	-	heterozygous	p.(Ala36Aspfs*68)			

Note: Exons and mutations numbering are based on transcript NM\_019105.6; NP\_061978.6; cons. Consanguinity; † patient died. PTC: Premature termination codon.

<sup>a</sup> Patients 4, 5, and 6 were compound heterozygous for the 120 bp deletion [c.11435\_11524+30del, p.(Gly3812Phefs\*11)] and the “*TNXA*-derived” missense variant [c.12174C>G, p.(Cys4058Trp)], probably due to gene conversion in both alleles;

<sup>b</sup> Patient 9 was compound heterozygous for a *TNXB/TNXA* fusion gene in one allele, characterized by the *TNXA*-derived variations: 120bp deletion [c.11435\_11524+30del, p.(Gly3812Phefs\*11)] and [c.12174C>G, p.(Cys4058Trp)], and a gene conversion in the other allele, characterized by the 120 bp deletion [c.11435\_11524+30del, p.(Gly3812Phefs\*11)];

<sup>c</sup> Patient 13 was compound heterozygous for a recurrent frameshift deletion in exon 8 in one allele, and a *TNXB/TNXA* fusion gene characterized by the *TNXA*-derived variations: 120 bp deletion [c.11435\_11524+30del, p.(Gly3812Phefs\*11)] and missense variant [c.12174C>G, p.(Cys4058Trp)];

<sup>d</sup> Patient 14 was compound heterozygous for a gene conversion in one allele and a *TNXB/TNXA* fusion gene in other allele, characterized both by the “*TNXA*-derived” missense variant [c.12174C>G, p.(Cys4058Trp)];

<sup>e</sup> Patient 15 was compound heterozygous for a *TNXB/TNXA* fusion gene in one allele characterized by the 120 bp deletion [c.11435\_11524+30del, p.(Gly3812Phefs\*11)], and a missense variant in the other allele;

<sup>f</sup> Patient 18 was compound heterozygous for a nonsense variant and a *TNXB/TNXA* fusion gene characterized by the *TNXA*-derived variations: 120 bp deletion [c.11435\_11524+30del, p.(Gly3812Phefs\*11)], and missense variant [c.12174C>G, p.(Cys4058Trp)];

<sup>§</sup> Patients 19 and 20 were compound heterozygous for a nonsense variant in one allele and a gene conversion in the other allele, characterized by the 120 bp deletion [c.11435\_11524+30del, p.(Gly3812Phefs\*11)].