SUPPLEMENTARY MATERIAL

Supplementary Table S1: The intraclass correlation coefficient (ICC), standard error of measurement (SEM) as well as the minimum detectable change at 90% confidence (MDC90) of genu recurvatum (passive and active) and anterior-posterior laxity (133 N anterior and posterior translation compliance index, active and maximum displacement) measurements in the non-dominant leg.

	ICC(2,1)	SEM	MDC90	N
Genu Recurvatum				
▪ **Passive** (°)	0.79	2.08	4.86	30
▪ **Active** (°)	0.79	2.12	4.95	30
Anterior-posterior laxity				
▪ **133 N Anterior Translation** (mm)	0.80	1.05	2.46	27
▪ **133 N Posterior Translation** (mm)	0.61	0.68	1.59	27
▪ **Compliance Index** (mm)	0.78	0.84	1.95	28
▪ **Active Displacement** (mm)	0.83	0.96	2.24	27
▪ **Maximum Displacement** (mm)	0.87	0.87	2.04	27

The intra-rater reliability of the knee laxity measurements was determined in a subset of 30 (15 male and 15 female) of the recruited participants.

The average age, height, body mass and BMI of the sub-set of the participants were 28.0 ± 5.7 years, 173.8 ± 9.4 cm, 72.3 ± 12.2 kg and 23.8 ± 2.3 kg/m^2, respectively. Twenty-three (76.7%) of the participants were right leg dominant

Anterior-posterior laxity was measured using the measured using the KT-1000 arthrometer

ICC values <0.5 indicate poor reliability, between 0.5 and 0.75 moderate reliability, between 0.75 and 0.9 good reliability, and >0.9 excellent reliability

Supplementary Table S2: Descriptive data for the five trials of the reliability study for of genu recurvatum (passive and active) and anterior-posterior laxity (133 N anterior (Ant) and posterior (Post) translation (Trans), compliance index, active and maximum (Max) displacement) measurements in the non-dominant leg.

	Trial 1	**Trial 2**	**Trial 3**	**Trial 4**	**Trial 5**	**N**
Genu Recurvatum						
▪ **Passive** (°)	176.6 ± 4.0	177.2 ± 4.6	177.9 ± 4.0	177.2 ± 5.2	176.9 ± 5.0	30
▪ **Active** (°)	174.9 ± 4.0	175.0 ± 4.9	175.5 ± 4.2	175.1 ± 4.6	175.4 ± 5.1	30
Anterior-posterior laxity						
▪ **133 N Ant Trans** (mm)	6.5 ± 2.3	6.6 ± 2.3	6.7 ± 2.4	6.9 ± 2.3	6.9 ± 2.3	27
▪ **133 N Post Trans** (mm)	3.7 ± 1.1	3.6 ± 1.1	3.6 ± 1.0	3.7 ± 0.9	3.9 ± 1.4	27
▪ **Compliance Index** (mm)	4.2 ± 2.0	4.1 ± 1.9	4.3 ± 2.1	4.3 ± 2.0	4.3 ± 2.1	28
▪ **Active Displacement** (mm)	4.6 ± 2.5	4.4 ± 2.1	4.5 ± 2.4	4.4 ± 2.2	4.9 ± 2.4	27
▪ **Max Displacement** (mm)	7.2 ± 2.0	7.2 ± 2.5	7.1 ± 2.6	7.3 ± 2.5	7.3 ± 2.4	27

Variables are reported as average ± standard deviation

Anterior-posterior laxity was measured using the measured using the KT-1000 arthrometer

Supplementary Table S3: The *COL5A1* rs12722 (T/C) genotype effects on the general characteristics, Beighton score and sit and reach measurements of participants with a history of an uninjured non-dominant leg.

	***COL5A1* rs12722**		
	CC	**CT + TT [a]**	**P-value**
	n = 15	n = 89	
Sex (% male)	66.7	53.9	0.411
Age (years)	26.0 (24.0; 30.0)	26.0 (24.0; 30.0)	0.967
Height (cm)	176.5 ± 11.6	174.3 ± 9.7	0.439
Body mass (kg)	75.0 (61.2; 88.0)	71.7 (61.1; 80.7)	0.541
BMI (kg/m^2)	23.9 (22.2; 25.7)	23.7 (21.1; 25.5)	0.627
Flexibility Training (% Yes)	53.3	55.1	1.000
Beighton Score	1.0 (0.0; 2.0)	2.0 (0.0; 4.0)	0.077
Sit and Reach (cm)	41.0 (38.4; 47.5)	42.9 (36.0; 50.8) [b]	0.901

Sex and flexibility training are reported as relative percentages. The remaining continuous variables are reported as average ± standard deviation or median (IQR)

Unable to genotype 2 participants for rs12722

BMI, body mass index

[a] The TT (n = 28) and CT (n = 61) genotypes of rs12722 were combined for the analysis because of the previous association of the CC genotype with range of motion (Brown et al. 2011; Lim et al. 2015)

[b] n = 85

Supplementary Table S4: The *COL11A1* rs3753841 (T/C), rs1676486 (C/T) and *COL11A2* rs1799907 (A/T) genotype effects on the general characteristics, Beighton score and sit and reach measurements of participants with a history of an uninjured non-dominant leg.

	***COL11A1* rs3753841**			***COL11A1* rs1676486**			***COL11A2* rs1799907**		
	CC	**TC + TT [a]**	**P-value**	**TT**	**CT + CC [b]**	**P-value**	**AA**	**AT + TT [c]**	**P-value**
	n = 17	n = 89		n = 5	n = 101		n = 49	n = 55	
Sex (% male)	58.8	53.9	0.794	80.0	53.5	0.374	53.1	56.4	0.844
Age (years)	25.0 (23.0; 27.0)	26.0 (24.0; 30.0)	0.202	25.0 (23.5; 28.0)	26.0 (24.0; 30.0)	0.549	26.0 (23.0; 30.0)	26.0 (24.0; 30.0)	0.559
Height (cm)	173.7 ± 11.3	174.9 ± 9.6	0.656	173.5 ± 10.0	174.7 ± 9.9	0.788	173.7 ± 9.1	175.9 ± 10.6	0.253
Body mass (kg)	67.0 (60.7; 79.5)	73.3 (61.0; 81.1)	0.532	75.2 (63.1; 79.5)	71.7 (60.8; 81.1)	0.837	67.7 (60.6; 78.8)	75.0 (61.2; 82.0)	0.202
BMI (kg/m^2)	23.7 (21.0; 24.3)	23.7 (21.3; 25.6)	0.595	24.3 (22.2; 25.6)	23.7 (21.1; 25.5)	0.551	23.3 (21.1; 25.5)	23.7 (21.6; 25.5)	0.594
Flexibility training (% Yes)	70.6	52.8	0.111	60.0	55.4	1.000	51.0	58.2	0.555
Beighton Score	1.0 (0.0; 4.0)	2.0 (0.0; 4.0)	0.588	3.0 (0.0; 4.0)	2.0 (0.0; 4.0)	0.983	2.0 (0.0; 4.0)	1.0 (0.0; 4.0)	0.591
Sit and Reach (cm)	46.4 ± 9.7 [d]	42.5 ± 10.6 [e]	0.172	43.3 ± 10.0	43.1 ± 10.6 [f]	0.973	42.2 ± 10.1 [g]	44.1 ± 11.1 [h]	0.378

Sex and flexibility training are reported as relative percentages. The remaining continuous variables are reported as average ± standard deviation or median (IQR)

Unable to genotype 2 participants for rs1799907

BMI, body mass index

Similar to the *COL5A1* analysis, the *COL11A1* and *COL11A2* genotypes containing the allele associated with increased risk of musculoskeletal soft tissue injury were combined and compared to the protective CC, TT and AA genotypes for rs3753841, rs1676486 and rs1799907 respectively (Hay et al. 2013)

[a] *COL11A1* rs3753841: TC = 49 and TT = 40; [b] *COL11A1* rs1676486: CT = 28 and CC = 73 [c] *COL11A2* rs1799907: AT = 43 and TT =12

[d] n = 16, [e] n = 87, [f] n = 98, [g] n = 48, [h] n = 53

Supplementary Table S5: The *COL5A1* rs12722 (T/C) genotype effects on the general characteristics, Beighton score and sit and reach measurements for the subset of participants with a history of an uninjured non-dominant leg measured on the Robotic Knee Testing (RKT) device.

	***COL5A1* rs12722**		
	CC	**CT + TT [a]**	**P-value**
	n = 11	n = 65	
Sex (% male)	72.7	58.5	0.511
Age (years)	26.0 (22.0; 33.0)	26.0 (24.0; 30.0)	0.988
Height (cm)	180.1 ± 10.5	174.4 ± 9.5	0.061
Body mass (kg)	77.6 ± 13.0	73.6 ± 12.8	0.341
BMI (kg/m^2)	24.0 (22.2; 25.7)	23.8 (22.4; 26.0)	0.912
Flexibility Training (% Yes)	54.5	56.9	1.000
Beighton Score	1.0 (0.0; 3.0)	2.0 (0.0; 4.0)	0.176
Sit and Reach (cm)	44.8 ± 10.1	43.4 ± 10.4 [b]	0.690

Sex and flexibility training are reported as relative percentages. The remaining continuous variables are reported as average ± standard deviation or median (IQR)

Unable to genotype 2 participants for rs12722

BMI, body mass index

[a] The TT (n = 17) and CT (n = 48) genotypes of rs12722 were combined for the analysis because of the previous association of the CC genotype with range of motion (Brown et al. 2011; Lim et al. 2015)

[b] n = 62

Supplementary Table S6: The *COL11A1* rs3753841 (T/C) and *COL11A2* rs1799907 (A/T) genotype effects on the general characteristics, Beighton score and sit and reach measurements for the subset of participants with a history of an uninjured non-dominant leg measured on the Robotic Knee Testing (RKT) device.

	***COL11A1* rs3753841**			***COL11A2* rs1799907**		
	CC	**TC + TT [a]**	**P-value**	**AA**	**AT + TT [b]**	**P-value**
	n = 11	n = 66		n = 35	n = 42	
Sex (% male)	54.5	60.6	0.748	57.1	61.9	0.816
Age (years)	25.0 (23.0; 28.0)	26.5 (24.0; 31.3)	0.260	26.0 (24.0; 31.0)	26.5 (23.8; 30.0)	0.805
Height (cm)	174.7 ± 13.1	175.0 ± 9.3	0.915	174.0 ± 9.2	175.8 ± 10.2	0.433
Body mass (kg)	70.2 ± 12.5	74.6 ± 12.9	0.289	71.9 ± 11.4	75.7 ± 13.8	0.199
BMI (kg/m^2)	23.7 (21.0; 24.3)	24.0 (22.4; 26.0)	0.122	23.8 (21.2; 25.6)	23.9 (22.6; 26.0)	0.631
Flexibility training (% Yes)	63.6	56.1	0.749	57.1	57.1	1.000
Beighton Score	1.0 (0.0; 3.0)	2.0 (0.0; 4.0)	0.317	2.0 (0.0; 4.0)	1.0 (0.0; 4.0)	0.522
Sit and Reach (cm)	46.2 ± 10.6 [c]	43.3 ± 10.2 [d]	0.404	42.4 ± 10.7 [e]	44.9 ± 9.9 [f]	0.299

Sex and flexibility training are reported as relative percentages. The remaining continuous variables are reported as average ± standard deviation or median (IQR)

Unable to genotype 2 participants for rs1799907

BMI, body mass index

The COL11A1 rs1676486 polymorphisms was not included because there were only 3 particiopants with a TT genotype (15 and 59 participants had TC and CC genotypes respectively)

Similar to the *COL5A1* analysis, the *COL11A1* and *COL11A2* genotypes containing the allele associated with increased risk of musculoskeletal soft tissue injury were combined and compared to the protective CC and AA genotypes for rs3753841 and rs1799907 respectively. (Hay et al. 2013)

[a] *COL11A1* rs3753841: TC = 36 and TT = 30; [b] *COL11A2* rs1799907: AT = 32 and TT =10

[c] n = 10, [d] n = 64, [e] n = 34, [f] n = 40

Supplementary Table S7: The *COL5A1* rs12722 (T/C) genotype effects on the (i) passive and active genu recurvatum measurements, (ii) anterior (Ant) and posterior (Post) tibial translation, active and maximum (Max) displacement as well as compliance index measured using the KT-1000 arthrometer, and (iii) internal and external rotation, as well as slack measured using the Robotic Knee Testing (RKT) device of participants with a history of an uninjured non-dominant leg.

	***COL5A1* rs12722**		
	CC	**CT + TT**	**P-value**
Genu Recurvatum [a]	n = 15	n = 89	
▪ **Passive** (°)	178.4 ± 6.8	176.6 ± 5.6	0.280
▪ **Active** (°)	176.4 ± 6.2	174.5 ± 5.6	0.225
Anterior-Posterior Tibial Translation	n = 15	n = 89	
▪ **133 N Ant Translation** (mm)	6.4 ± 2.1	7.4 ± 2.7	0.189
▪ **133 N Post Translation** (mm)	4.5 (3.0; 5.5)	4.0 (3.0; 5.3) [b]	0.569
▪ **Compliance Index** (mm)	4.2 ± 1.5	4.9 ± 2.1	0.198
▪ **Active Displacement** (mm)	5.2 ± 3.3	4.9 ± 2.6 [b]	0.765
▪ **Max Displacement** (mm)	7.0 (6.0; 9.0)	7.5 (5.5; 10.0)	0.534
External-Internal Rotation	n = 11	n = 65	
▪ **External Rotation** (°)	4.6 ± 1.5	5.6 ± 1.1	**0.017**
▪ **Internal Rotation** (°)	5.3 (4.8; 6.2)	5.7 (5.2; 6.4)	0.130
▪ **Slack** (°)	15.9 ± 3.5	17.8 ± 3.2	0.081

Values are expressed as either average ± standard deviation or median (IQR)

Unable to genotype 2 participants for rs12722

Compliance index = 133 N - 67 N Anterior Translation

The TT and CT genotypes of rs12722 were combined for the analysis because of the previous association of the CC genotype and T allele with range of motion (Brown et al. 2011; Lim et al. 2015)

[a] Lower degree values for genu recurvatum indicates a greater amount of knee hyperextension

[b] n = 88

Supplementary Table S8: The *COL11A1* rs3753841 (T/C), rs1676486 (C/T) and *COL11A2* rs1799907 (A/T) genotype effects on the (i) passive and active genu recurvatum measurements, (ii) anterior (Ant) and posterior (Post) tibial translation, active and maximum (Max) displacement as well as compliance index measured using the KT-1000 arthrometer, and (iii) internal and external rotation, as well as slack measured using the Robotic Knee Testing (RKT) device of participants with a history of an uninjured non-dominant leg.

	***COL11A1* rs3753841**			***COL11A1* rs1676486**			***COL11A2* rs1799907**		
	CC	**TC + TT**	**P-value**	**TT**	**CT + CC**	**P-value**	**AA**	**AT + TT**	**P-value**
Genu Recurvatum [a]	n = 17	n = 89		n = 5	n = 101		n = 49	n = 55	
▪ **Passive** (°)	177.9 ± 4.3	176.7 ± 6.9	0.448	176.4 ± 5.3	176.9 ± 5.8	0.842	178.0 ± 6.2	176.0 ± 5.3	0.080
▪ **Active** (°)	175.6 ± 4.5	174.6 ± 5.8	0.490	173.7 ± 5.3	174.8 ± 5.7	0.674	175.6 ± 6.1	174.0 ± 5.2	0.144
Ant-Post Translation	n = 17	n = 89		n = 5	n = 101		n = 49	n = 55	
▪ **133 N Ant Translation** (mm)	6.5 (5.8; 8.0)	7.0 (5.8; 9.0)	0.600	8.1 ± 2.1	7.2 ± 2.6	0.441	7.0 ± 2.3	7.5 ± 2.9	0.372
▪ **133 N Post Translation** (mm)	4.0 (2.6; 5.8)	4.0 (3.0; 5.3)	0.991	5.0 (3.5; 6.0)	4.0 (3.0; 5.0) [c]	0.301	4.0 (3.0; 6.0)	4.0 (3.0; 5.0) [e]	0.782
▪ **Compliance Index** (mm)	5.0 ± 2.4	4.7 ± 2.0	0.580	6.0 (5.0; 7.3)	4.5 (3.0; 6.3)	0.071	4.6 ± 1.9	5.0 ± 2.2	0.337
▪ **Active Displacement** (mm)	5.0 (2.8; 7.0)	5.0 (3.0; 7.0) [b]	0.864	6.0 (3.8; 7.0)	5.0 (3.0; 7.0) [c]	0.558	4.7 ± 2.6 [d]	5.2 ± 2.8	0.352
▪ **Max Displacement** (mm)	7.0 (4.5; 8.8)	7.0 (5.8; 10.0)	0.388	8.5 (7.0; 11.0)	7.0 (5.3; 10.0)	0.260	7.0 (5.3; 10.0)	7.5 (6.0; 10.5)	0.442
External-internal Rotation	n = 11	n = 66		n = 3	n = 74		n = 35	n = 42	
▪ **External Rotation** (°)	5.8 ± 1.4	5.4 ± 1.2	0.252	n.d.	n.d.	n.d.	5.2 (4.6; 6.5)	5.4 (4.6; 6.3)	0.827
▪ **Internal Rotation** (°)	6.2 (5.3; 7.0)	5.5 (5.0; 6.3)	0.140	n.d	n.d	n.d	5.5 (5.0; 6.3)	5.8 (5.2; 6.4)	0.417
▪ **Slack** (°)	18.4 ± 3.4	17.4 ± 3.2	0.342	n.d	n.d	n.d	16.7 (15.5; 18.7)	17.9 (15.2; 20.1)	0.780

Values are expressed as either average ± standard deviation or median (IQR)
Unable to genotype 2 participants for rs1799907;
n.d., not determined because only 3 particiopants had a COL11A1 rs1676486 TT genotype
Compliance index = 133 N - 67 N Anterior Translation
Similar to the *COL5A1* analysis, the *COL11A1* and *COL11A2* genotypes containing the allele associated with increased risk of musculoskeletal soft tissue injury were combined and compared to the protective CC, TT and AA genotypes for rs3753841, rs1676486 and rs1799907 respectively (Hay et al. 2013)
[a] Lower degree values for genu recurvatum indicates a greater amount of hyperextension
[b] n = 88, [c] n = 100, [d] n = 48, [e] n = 54

Supplementary Table S9: The *COL5A1* rs12722 (T/C) genotype effects on the general characteristics, Beighton score and sit and reach measurements of participants with a history of an uninjured non-dominant leg, as well as those with a history of non-dominant lower limb injury and/or treatment.

	***COL5A1* rs12722**		
	CC	**CT + TT** [a]	**P-value**
	n = 19	n = 113	
Sex (% male)	68.4	57.5	0.455
Age (years)	26.0 (24.0; 30.0)	27.0 (24.0; 32.5)	0.511
Height (cm)	176.3 ± 10.7	174.1 ± 9.6	0.364
Body mass (kg)	75.0 (61.9; 86.7)	73.5 (61.1; 81.4)	0.583
BMI (kg/m^2)	24.0 (22.8; 25.6)	23.7 (21.5; 26.0)	0.637
Flexibility Training (% Yes)	57.9	55.8	1.000
Beighton Score	0.0 (0.0; 2.0)	2.0 (0.0; 4.0)	0.088
Sit and Reach (cm)	43.1 ± 11.2	42.5 ± 10.8 [b]	0.814

Sex and flexibility training are reported as relative percentages. The remaining continuous variables are reported as average ± standard deviation or median (IQR)

Unable to genotype 2 participants for rs12722

BMI, body mass index

[a] The TT (n = 32) and CT (n = 81) genotypes of rs12722 were combined for the analysis because of the previous association of the CC genotype with range of motion (Brown et al. 2011; Lim et al. 2015)

[b] n = 109

Supplementary Table S10: The *COL5A1* rs12722 (T/C) genotype effects on the (i) passive and active genu recurvatum measurements, and (ii) anterior (Ant) and posterior (Post) tibial translation, active and maximum (Max) displacement as well as compliance index measured using the KT-1000 arthrometer of participants with a history of an uninjured non-dominant leg, as well as those with a history of non-dominant lower limb injury and/or treatment.

	***COL5A1* rs12722**		
	CC	**CT + TT [a]**	**P-value**
Genu Recurvatum [b]	n = 19	n = 113	
▪ **Passive** (°)	179.2 ± 6.5	176.7 ± 5.4	0.075
▪ **Active** (°)	176.9 ± 5.8	174.5 ± 5.3	0.070
Anterior-Posterior Tibial Translation	n = 19	n = 113	
▪ **133 N Ant Translation** (mm)	6.7 ± 2.1	7.5 ± 2.7	0.255
▪ **133 N Post Translation** (mm)	4.0 (3.0; 5.0)	4.0 (3.0; 5.5) [c]	0.908
▪ **Compliance Index** (mm)	4.5 (4.0; 6.0)	4.5 (3.5; 7.0)	0.394
▪ **Active Displacement** (mm)	5.5 (2.5; 7.0)	5.0 (3.0; 7.0) [c]	0.939
▪ **Max Displacement** (mm)	7.0 (6.0; 9.0)	8.0 (5.5; 10.5)	0.815

Values are expressed as either average ± standard deviation or median (IQR)

Unable to genotype 2 participants for rs12722

Compliance index = 133 N - 67 N Anterior Translation

Internal and external rotation, as well as slack were not measured in the participants with a history of non-domiant lower limb injury and/or treatment using the Robotic Knee Testing (RKT) device

[a] The TT (n = 32) and CT (n = 81) genotypes of rs12722 were combined for the analysis because of the previous association of the CC genotype and T allele with range of motion (Brown et al. 2011; Lim et al. 2015)

[b] Lower degree values for genu recurvatum indicates a greater amount of hyperextension

[c] n = 112

Supplementary Table S11: The *COL11A1* rs3753841 (T/C), rs1676486 (C/T) and *COL11A2* rs1799907 (A/T) genotype effects on the general characteristics, Beighton score and sit and reach measurements of participants with a history of an uninjured non-dominant leg, as well as those with a history of non-dominant lower limb injury and/or treatment.

	***COL11A1* rs3753841**			***COL11A1* rs1676486**			***COL11A2* rs1799907**		
	CC	**TC + TT [a]**	**P-value**	**TT**	**CT + CC [b]**	**P-value**	**AA**	**AT + TT [c]**	**P-value**
	n = 19	n = 114		n = 7	n = 126		n = 61	n = 71	
Sex (% male)	63.2	57.0	0.803	85.7	56.3	0.238	55.7	60.6	0.194
Age (years)	25.0 (23.0; 28.0)	27.0 (24.0; 33.0)	0.073	26.0 (24.0; 28.0)	27.0 (24.0; 33.0)	0.420	26.0 (23.5; 33.0)	27.0 (24.0; 30.0)	0.930
Height (cm)	174.5 ± 11.0	174.6 ± 9.5	0.990	175.8 ± 9.1	174.5 ± 9.8	0.728	173.7 ± 9.3	175.4 ± 10.1	0.316
Body mass (kg)	71.0 (61.4; 79.5)	73.7 (61.1; 82.1)	0.652	75.6 (64.9; 79.5)	73.4 (61.1; 81.6)	0.562	71.0 (60.6; 80.8)	75.0 (62.3; 82.4)	0.284
BMI (kg/m^2)	23.3 ± 2.1	24.0 ± 3.2	0.401	24.3 (23.6; 25.6)	23.7 (21.6; 25.7)	0.568	23.5 (21.1; 25.7)	23.8 (22.0; 25.6)	0.598
Flexibility training (% Yes)	63.2	56.1	0.625	42.9	57.9	0.461	50.8	60.6	0.294
Beighton Score	1.0 (0.0; 4.0)	1.5 (0.0; 4.0)	0.387	0.0 (0.0; 4.0)	1.0 (0.0; 4.0)	0.421	2.0 (0.0; 4.0)	1.0 (0.0; 4.0)	0.456
Sit and Reach (cm)	44.6 ± 11.4 [d]	42.5 ± 10.7 [e]	0.444	39.3 ± 12.5	42.9 ± 10.7 [f]	0.392	41.5 ± 10.1 [g]	43.3 ± 11.5 [h]	0.532

Sex and flexibility training are reported as relative percentages. The remaining continuous variables are reported as average ± standard deviation or median (IQR)
Unable to genotype 1 participant for rs3753841, 1 participant for rs1676486 and 2 participants for rs1799907
BMI, body mass index
Similar to the *COL5A1* analysis, the *COL11A1* and *COL11A2* genotypes containing the allele associated with increased risk of musculoskeletal soft tissue injury were combined and compared to the protective CC, TT and AA genotypes for rs3753841, rs1676486 and rs1799907 respectively (Hay et al. 2013)
[a] *COL11A1* rs3753841: TC = 62 and TT = 52; [b] *COL11A1* rs1676486: CT = 33 and CC = 93 [c] *COL11A2* rs1799907: AT = 56 and TT =15
[d] n = 18, [e] n = 111, [f] n = 122, [g] n = 60, [h] n = 68

Supplementary Table S12: The *COL11A1* rs3753841 (T/C), rs1676486 (C/T) and *COL11A2* rs1799907 (A/T) genotype effects on the (i) passive and active genu recurvatum measurements, and (ii) anterior (Ant) and posterior (Post) tibial translation, active and maximum (Max) displacement as well as compliance index measured using the KT-1000 arthrometer of participants with a history of an uninjured non-dominant leg, as well as those with a history of non-dominant lower limb injury and/or treatment.

	***COL11A1* rs3753841**			***COL11A1* rs1676486**			***COL11A2* rs1799907**		
	CC	**TC + TT**	**P-value**	**TT**	**CT + CC**	**P-value**	**AA**	**AT + TT**	**P-value**
Genu Recurvatum [a]	n = 19	n = 114		n = 7	n = 126		n = 61	n = 71	
▪ **Passive** (°)	177.8 ± 4.1	176.8 ± 5.8	0.473	176.9 ± 4.7	177.0 ± 5.7	0.951	177.8 ± 6.2	176.4 ± 5.1	0.154
▪ **Active** (°)	175.7 ± 4.3	174.7 ± 5.5	0.470	174.4 ± 4.9	174.8 ± 5.4	0.841	175.5 ± 6.0	174.4 ± 4.9	0.252
Ant-Post Translation	n = 19	n = 114		n = 7	n = 126		n = 61	n = 71	
▪ **133 N Ant Translation** (mm)	7.0 (6.0; 8.0)	7.0 (5.5; 9.0)	0.920	8.0 (7.0; 10.0)	7.0 (5.5; 9.0)	0.207	7.0 (6.0; 9.0)	7.0 (5.5; 9.5)	0.749
▪ **133 N Post Translation** (mm)	4.0 (2.9; 5.1) [b]	4.0 (3.0; 5.5)	0.803	5.0 (3.0; 6.0)	4.0 (3.0; 5.5) [d]	0.359	4.0 (3.0; 5.8)	4.0 (3.0; 5.1) [f]	0.878
▪ **Compliance Index** (mm)	5.0 (4.0; 6.5)	4.9 ± 2.2	0.714	6.0 (5.0; 7.0)	4.5 (3.4; 6.5)	0.099	4.5 (3.5; 6.0)	5.0 (3.0; 6.5)	0.636
▪ **Active Displacement** (mm)	4.6 ± 2.1	5.0 (3.0; 7.0) [c]	0.442	6.0 (2.5; 7.0)	5.0 (3.0; 7.0) [d]	0.934	4.8 ± 2.7 [e]	5.0 ± 2.4	0.463
▪ **Max Displacement** (mm)	8.0 (5.0; 9.0)	7.5 (6.0; 10.0)	0.568	9.0 (8.0; 11.0)	7.3 (5.5; 10.0)	0.135	7.0 (5.8; 10.0)	8.0 (6.0; 10.5)	0.496

Values are expressed as either average ± standard deviation or median (IQR)
Unable to genotype 1 participant for rs3753841, 1 participant for rs1676486 and 2 participants for rs1799907
Compliance index = 133 N - 67 N Anterior Translation
Internal and external rotation, as well as slack were not measured in the participants with a history of non-domiant lower limb injury and/or treatment using the Robotic Knee Testing (RKT) device
Similar to the *COL5A1* analysis, the *COL11A1* and *COL11A2* genotypes containing the allele associated with increased risk of musculoskeletal soft tissue injury were combined and compared to the protective CC, TT and AA genotypes for rs3753841, rs1676486 and rs1799907 respectively (Hay et al. 2013)
[a] Lower degree values for genu recurvatum indicates a greater amount of hyperextension
[b] n = 18, [c] n = 113, [d] n = 125, [e] n = 60, [f] n = 70

Supplementary Table S13: The *COL5A1* rs12722 (T/C), *COL11A1* rs3753841 (T/C), *COL11A1* rs1676486 (T/C) and *COL11A2* rs1799907 (A/T) genotype score effects on the general participant characteristics, Beighton score and sit and reach measurements.

	Genotype Score			
	0	**2**	**4 or 6**	**P-value**
	n = 41	n = 44	n = 17	
Sex (% male)	53.7	56.8	58.8	0.924
Age (years)	26.0 (24.0; 30.0)	26.0 (23.0; 30.0)	25.0 (23.5; 30.0)	0.779
Height (cm)	175.5 ± 10.8	173.4 ± 8.7	176.4 ± 11.2	0.734
Body mass (kg)	76.9 (61.3; 82.7)	69.4 (61.0; 80.7)	67.1 (60.7; 79.5)	0.486
BMI (kg/m^2)	23.8 (21.5; 26.0)	23.3 (21.8; 25.5)	23.4 (21.0; 24.3)	0.535
Flexibility Training (% Yes)	58.5	50.0	52.9	0.730
Beighton Score	2.0 (0.0; 4.0)	1.0 (0.0; 4.0)	2.0 (0.0; 3.5)	0.668
Sit and Reach (cm)	43.2 ± 12.1 [a]	43.2 ± 9.8 [b]	42.6 ± 10.0	0.979

Sex and flexibility training are reported as percentages, while the the remaining continuous variables are reported as average ± standard deviation or median (IQR)

Participants received a genotype score of 2 for each *COL5A1* rs12722 CC, *COL11A1* rs3753841 CC, *COL11A1* rs1676486 TT and *COL12A1* rs1799907 AA genotypes and 0 for all other genotypes, so that the genotype scores ranged from 0 to 8

None of the participants had a genotype score of 8 and the genotype scores of 4 (n = 13) and 6 (n = 4) combined for the analysis

BMI, body mass index

[a] n = 40; [b] n = 42

Supplementary Table S14: The *COL5A1* rs12722 (T/C), *COL11A1* rs3753841 (T/C), *COL11A1* rs1676486 (T/C) and *COL11A2* rs1799907 (A/T) genotype score effects on the general participant characteristics, Beighton score and sit and reach measurements for the subset group of participants measured on the Robotic Knee Testing (RKT) device.

	Genotype Score			
	0	**2**	**4 or 6**	**P-value**
	n = 31	n = 33	n = 12	
Sex (% male)	61.3	57.8	66.7	0.855
Age (years)	26.0 (24.0; 33.0)	26.0 (23.0; 30.0)	25.5 (24.0; 32.3)	0.887
Height (cm)	175.4 ± 10.0	173.2 ± 9.2	178.8 ± 11.0	0.235
Body mass (kg)	77.1 ± 13.7	71.6 ± 12.0	74.0 ± 11.8	0.225
BMI (kg/m^2)	24.0 (21.0; 25.3)	23.7 (22.3; 25.5)	23.9 (21.0; 25.3)	0.247
Flexibility Training (% Yes)	61.3	51.5	58.3	0.726
Beighton Score	2.0 (0.0; 4.0)	2.0 (0.0; 4.0)	1.5 (0.0; 3.0)	0.559
Sit and Reach (cm)	44.5 ± 10.5 [a]	43.1 ± 10.3 [b]	42.7 ± 10.3	0.817

Sex and flexibility training are reported as percentages, while the the remaining continuous variables are reported as average ± standard deviation or median (IQR)

Participants received a genotype score of 2 for each *COL5A1* rs12722 CC, *COL11A1* rs3753841 CC, *COL11A1* rs1676486 TT and *COL12A1* rs1799907 AA genotypes and 0 for all other genotypes, so that the genotype scores ranged from 0 to 8

None of the participants had a genotype score of 8 and the genotype scores of 4 (n = 10) and 6 (n = 2) combined for the analysis

BMI, body mass index

[a] n = 30; [b] n = 31

Supplementary Table S15: The *COL5A1* rs12722 (T/C), *COL11A1* rs3753841 (T/C), *COL11A1* rs1676486 (T/C) and *COL11A2* rs1799907 (A/T) genotype score effects on the (i) anterior (Ant) and posterior (Post) tibial translation, active and maximum (Max) displacement as well as compliance index measured using the KT-1000 arthrometer, and (ii) internal and external rotation, as well as slack measured using the Robotic Knee Testing (RKT) device of the participants' non-dominant leg.

	Genotype Score			Global P-value	Mutiple Comparisons P-value
	0	2	4 or 6		
Anterior-Posterior Tibial Translation	n = 41	n = 44	n = 17		
▪ **133 N Ant Translation** (mm)	7.6 ± 2.7	7.2 ± 2.7	6.8 ± 2.0	0.540	0.269 [a]
▪ **133 N Post Translation** (mm)	4.0 (3.0; 5.0)	4.0 (3.0; 6.0) [c]	4.0 (2.8; 5.0)	0.788	1.000 [b]
▪ **Compliance Index** (mm)	5.0 ± 2.1	4.7 ± 2.1	4.5 ± 1.8	0.678	0.385 [a]
▪ **Active Displacement** (mm)	5.1 ± 2.6	4.9 ± 3.1 [c]	4.8 ± 2.4	0.885	0.623 [a]
▪ **Max Displacement** (mm)	7.5 (5.0; 10.5)	8.0 (5.6; 10.0)	7.0 (4.5; 9.0)	0.533	0.584 [b]
External-Internal Rotation	n=31	n = 33	n = 12		
▪ **External Rotation** (°)	5.3 ± 0.9	5.5 ± 1.4	5.4 ± 1.3	0.787	0.682 [a]
▪ **Internal Rotation** (°)	5.8 (5.2; 6.2)	5.5 (5.0; 6.6)	5.4 (5.2; 6.6)	0.959	1.000 [b]
▪ **Slack** (°)	17.5 ± 3.0	17.6 ± 3.6	17.2 ± 3.3	0.943	0.855 [a]

Variables are reported as average ± standard deviation or median (IQR)

Participants received a genotype score of 2 for each *COL5A1* rs12722 CC, *COL11A1* rs3753841 CC, *COL11A1* rs1676486 TT and *COL12A1* rs1799907 AA genotypes and 0 for all other genotypes, so that the genotype scores ranged from 0 to 8

None of the participants had a genotype score of 8 and the genotype scores of 4 and 6 combined for the analysis

Compliance index = 133 N - 67 N Anterior Translation

[a] Test for linear trend

[b] Dunn's multiple comparisons test respectively of the 0 versus 4 or 6 genotype scores

[c] n = 43

Supplementary Table S16: The *COL5A1* rs12722 (T/C), *COL11A1* rs3753841 (T/C), *COL11A1* rs1676486 (T/C) and *COL11A2* rs1799907 (A/T) genotype score effects on the general characteristics, Beighton score and sit and reach measurements of participants with a history of an uninjured non-dominant leg, as well as those with a history of non-dominant lower limb injury and/or treatment.

	Genotype Score			
	0	**2**	**4 or 6**	**P-value**
	n = 51	n = 58	n = 20	
Sex (% male)	58.8	56.9	65.0	0.817
Age (years)	27.0 (25.0; 32.0)	28.0 (23.8; 33.0)	25.0 (23.3; 29.5)	0.296
Height (cm)	175.4 ± 10.3	173.1 ± 9.0	177.1 ± 10.4	0.221
Body mass (kg)	74.8 ± 13.4	71.8 ± 13.5	72.5 ± 11.3	0.497
BMI (kg/m^2)	23.8 (21.6; 26.0)	23.7 (21.9; 25.7)	23.7 (21.1; 24.3)	0.539
Flexibility Training (% Yes)	62.7	51.7	50.0	0.436
Beighton Score	2.0 (0.0; 4.0)	1.0 (0.0; 5.0)	1.0 (0.0; 3.0)	0.140
Sit and Reach (cm)	42.4 ± 11.8 [a]	43.5 ± 10.2 [b]	41.0 ± 10.7	0.478

Sex and flexibility training are reported as percentages, while the the remaining continuous variables are reported as average ± standard deviation or median (IQR)

Participants received a genotype score of 2 for each *COL5A1* rs12722 CC, *COL11A1* rs3753841 CC, *COL11A1* rs1676486 TT and *COL12A1* rs1799907 AA genotypes and 0 for all other genotypes, so that the genotype scores ranged from 0 to 8

None of the participants had a genotype score of 8 and the genotype scores of 4 (n = 15) and 6 (n = 5) combined for the analysis

Internal and external rotation, as well as slack were not measured in the participants with a history of non-domiant lower limb injury and/or treatment using the Robotic Knee Testing (RKT) device

BMI, body mass index

[a] n = 49; [b] n = 56

Supplementary Table S17: The *COL5A1* rs12722 (T/C), *COL11A1* rs3753841 (T/C), *COL11A1* rs1676486 (T/C) and *COL11A2* rs1799907 (A/T) genotype score effects on the (i) passive and active genu recurvatum measurements, and (ii) anterior (Ant) and posterior (Post) tibial translation, active and maximum (Max) displacement as well as compliance index measured using the KT-1000 arthrometer of participants with a history of an uninjured non-dominant leg, as well as those with a history of non-dominant lower limb injury and/or treatment.

	Genotype Score			Global P-value	Mutiple Comparisons P-value
	0	2	4 or 6		
Genu Recurvatum [a]	n = 51	n = 58	n = 20		
Passive (°)	176.0 (173.0; 179.0)	177.0 (173.0; 182.0)	179.0 (176.3; 181.0)	0.057	0.036 [b]
Active (°)	173.8 ± 4.8	175.0 ± 6.0	176.9 ± 5.3	0.093	0.032 [c]
Anterior-Posterior Tibial Translation	n = 51	n = 58	n = 20		
▪ **133 N Ant Translation** (mm)	7.0 (5.0; 9.5)	7.5 (6.0; 9.0)	7.0 (6.0; 8.0)	0.750	1.000 [b]
▪ **133 N Post Translation** (mm)	4.0 (3.0; 5.5)	4.0 (3.0; 5.8) [d]	3.5 (2.7; 5.0)	0.460	0.614 [b]
▪ **Compliance Index** (mm)	4.5 (3.0; 6.9)	4.5 (3.5; 6.6)	4.5 (4.0; 6.0)	0.895	1.000 [b]
▪ **Active Displacement** (mm)	5.2 ± 2.6	5.1 ± 2.9 [c]	4.6 ± 2.4	0.705	0.477 [c]
▪ **Max Displacement** (mm)	7.5 (5.0; 10.5)	8.0 (6.0; 10.1)	7.5 (5.3; 9.0)	0.749	1.000 [b]

Variables are reported as average ± standard deviation or median (IQR)

Participants received a genotype score of 2 for each *COL5A1* rs12722 CC, *COL11A1* rs3753841 CC, *COL11A1* rs1676486 TT and *COL12A1* rs1799907 AA genotypes and 0 for all other genotypes, so that the genotype scores ranged from 0 to 8

None of the participants had a genotype score of 8 and the genotype scores of 4 (n = 15) and 6 (n = 5) combined for the analysis

Internal and external rotation, as well as slack were not measured in the participants with a history of non-domiant lower limb injury and/or treatment using the Robotic Knee Testing (RKT) device

Compliance index = 133 N - 67 N Anterior Translation

[a] Lower degree values for genu recurvatum indicates a greater amount of hyperextension

[b] Dunn's multiple comparisons test respectively of the 0 versus 4 or 6 genotype scores

[c] Test for linear trend

[d] n = 57

Supplementary Table S18: Summary of multiple linear regression model for active genu recurvatum of participants with a history of an uninjured non-dominant leg.

Passive Genu Recurvatum	**Unstandardised coefficient (β)**	**95% CI for β**	**SE β**	**P-Value**
Constant	174.7	166.2 to 183.1	4.27	<0.001
Sex (male)	4.48	1.77 to 7.19	1.37	0.001
Age (years)	0.20	-0.01 to 0.40	0.10	0.060
Body Mass (kg)	-0.12	-0.23 to -0.02	0.05	0.026
Genotype Score (2)	1.51	-0.84 to 3.87	1.19	0.206
Genotype Score (4 or 6)	2.94	-0.17 to 6.03	1.56	0.063
$R^2 = 0.18$ and Adjusted $R^2 = 0.14$				

CI = confidence interval; SE β = standard error of the coefficient; R^2 = coefficient of determination
Units are shown in parentheses
COL5A1, *COL11A1*, *COL11A2* genotyping score coding: 0, 2 and 4 or 6

Supplementary Table S19: Summary of multiple linear regression model for passive genu recurvatum of participants with a history of an uninjured non-dominant leg, as well as those with a history of non-dominant lower limb injury and/or treatment.

Passive Genu Recurvatum	**Unstandardised coefficient (β)**	**95% CI for β**	**SE β**	**P-Value**
Constant	177.9	170.9 to 184.8	3.52	<0.001
Sex (male)	4.94	2.55 to 7.34	1.21	<0.001
Age (years)	0.15	-0.01 to 0.30	0.08	0.063
Body Mass (kg)	-0.12	-0.21 to -0.03	0.05	0.009
Genotype Score (2)	1.03	-0.98 to 3.04	1.03	0.311
Genotype Score (4 or 6)	3.40	0.63 to 6.17	1.40	0.017
$R^2 = 0.18$ and Adjusted $R^2 = 0.15$				

CI = confidence interval; SE β = standard error of the coefficient; R^2 = coefficient of determination
Units are shown in parentheses
COL5A1, *COL11A1*, *COL11A2* genotyping score coding: 0, 2 and 4 or 6

Supplementary Table S20: The *COL5A1* rs12722 (T/C), *COL11A1* rs3753841 (T/C), *COL11A1* rs1676486 (T/C) and *COL11A2* rs1799907 (A/T) genotype score effects on the absolute change in the length of the anterior bundle of the ACL (aACL), posterior bundle of the ACL (pACL), anterior bundle of the PCL (aPCL), posterior bundle of the PCL (pPCL), anterior bundle of the superficial layer of the MCL (aMCL), inferior bundle of the superficial layer of the MCL (iMCL), anterior bundle of the deep layer of the MCL (aDMCL), posterior bundle of the deep layer of the MCL (pDMCL), posterior bundle of the superficial layer of the MCL (pMCL) and the LCL of the non-dominant leg.

	Genotype Score			
	0	**2**	**4 or 6**	**P-Value**
	n = 31	n = 33	n = 12	
aACL (mm)	1.2 (0.8; 1.6)	1.3 (0.9; 1.5)	1.0 (0.7; 1.6)	0.655
pACL (mm)	2.7 ± 1.4	3.0 ± 1.2	3.0 ± 1.4	0.925
aPCL (mm)	2.2 (1.3; 2.9)	1.5 (0.9; 3.1)	1.5 (1.3; 3.2)	0.480
pPCL (mm)	1.4 (0.7; 2.9)	1.3 (1.0; 2.1)	1.4 (0.6; 2.5)	0.929
aMCL (mm)	3.8 (3.0; 5.0)	3.5 (3.0; 4.8)	3.7 (2.2; 4.6)	0.900
iMCL (mm)	3.3 (2.8; 4.2)	3.1 (2.7; 4.4)	3.2 (2.0; 4.3)	0.838
aDMCL (mm)	6.1 (4.6; 7.6)	5.4 (4.9; 7.5)	5.5 (4.7; 7.5)	0.875
pDMCL (mm)	6.8 (5.3; 7.9)	6.1 (5.2; 8.3)	6.0 (5.5; 8.1)	0.995
pMCL (mm)	4.1 ± 1.6	4.1 ± 1.4	3.9 ± 1.3	0.845
LCL (mm)	1.1 (0.9; 1.8)	1.3 (0.8; 1.7)	1.1 (0.7; 2.0)	0.919

Values are expressed as either average ± standard deviation or median (IQR)

Participants received a genotype score of 2 for each *COL5A1* rs12722 CC, *COL11A1* rs3753841 CC, *COL11A1* rs1676486 TT and *COL12A1* rs1799907 AA genotypes and 0 for all other genotypes, so that the genotype scores ranged from 0 to 8

None of the participants had a genotype score of 8 and the genotype scores of 4 (n = 10) and 6 (n = 2) combined for the analysis

Supplementary Material References

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