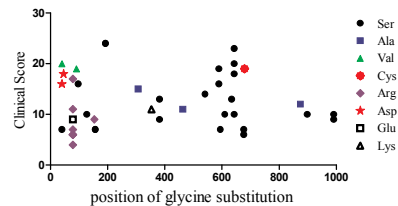
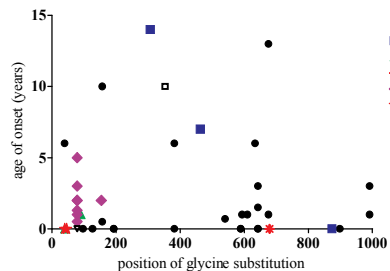


Supplement Figure 1. Correlation of serum ALP levels and clinical score of OI. After adjusted for age and gender, the serum ALP level was negatively correlated to clinical score of OI. $Y = -0.013x + 14.0$ ($P < 0.001$)

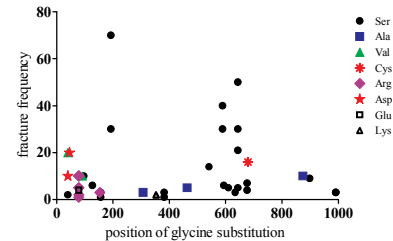
A



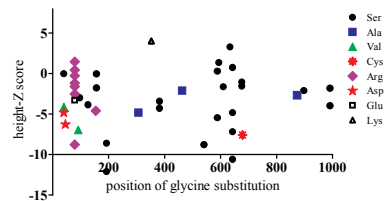
B



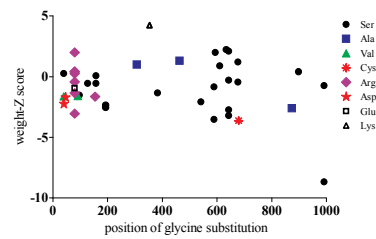
C



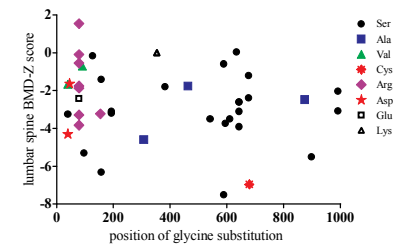
D



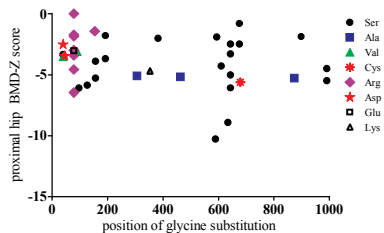
E



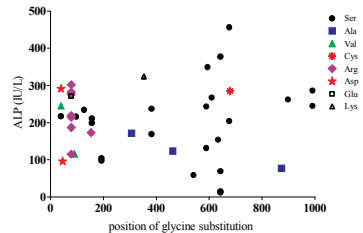
F



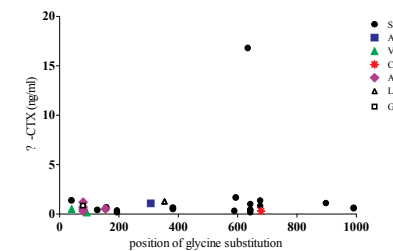
G



H



I



Supplement Figure 2. Relationships between the positions of glycine substitutions in collagen type I α 1 chains and phenotype.

A. Relationship between the positions of glycine substitutions in collagen type I α 1 chains and clinical score.

B. Relationship between the positions of glycine substitutions in collagen type I α 1 chains and age of onset.

C. Relationship between the positions of glycine substitutions in collagen type I α 1 chains and fracture frequency.

D. Relationship between the positions of glycine substitutions in collagen type I α 1 chains and height-Z score.

E. Relationship between the positions of glycine substitutions in collagen type I α 1 chains and weight-Z score.

F. Relationship between the positions of glycine substitutions in collagen type I α 1 chains and lumbar spine BMD-Z score.

G. Relationship between the positions of glycine substitutions in collagen type I α 1 chains and proximal hip BMD-Z score.

H. Relationship between the positions of glycine substitutions in collagen type I α 1 chains and ALP levels.

I. Relationship between the positions of glycine substitutions in collagen type I α 1 chains and β -CTX levels.

-Supplemental Table 1. List of primers for PCR amplification of exons of *COL1A1*

Exon	Primer sequence (5' → 3')	Length (bp)	Annealing Tm (°C)
E1	Forward: CCTGCTCTCCATCAGGACA Reverse: GGATCATCCACGTCTCGTTT	365	60
E2-3	Forward: GGGGAAAGGTGGTTAAGCTG Reverse: GGGGGAGAAGAAACAAGAGG	550	60.5
E4-5	Forward: GGAGCAGCATTAGCAAACCT Reverse: CACAAACTGTGAAGGGTATGT	567	60
E6	Forward: CACCAGGAAGTGCATGATGT Reverse: CTTCTGTCATCCATGCTCCC	202	60
E7-8	Forward: AGTCCAGAAAGGATGCAGGA Reverse: CAGGCCTGGGAGTTCTTCTA	444	59.5
E9	Forward: CCTGGGGTCTTCCTTACCTC Reverse: GTTCCCAAATGTGGTGGAGT	234	60
E10	Forward: AACCTGACCTGCAACAATCC Reverse: GGACTTGGGGAGCTTAAATG	368	60
E11	Forward: TGGGTCCACAGTGATGTGTT Reverse: GGAAGAGGTTGGGACTGGAT	181	60
E12	Forward: AGGTGGATGTCAAGGCTGTT Reverse: TCATTCATGGTGGGACTCTG	178	59.5
E13-15	Forward: AGGTGGATGTCAAGGCTGTT Reverse: TCATTCATGGTGGGACTCTG	551	60
E16	Forward: AACCCAGGACTTCCTCTGT Reverse: GGGAACAGGGAGACATGAAC	204	59.5

E17	Forward: CTGTCCCTGTCTCCCCTTC Reverse: CAGGCAAGGACTCTGAGGTT	248	59.5
E18	Forward: GTCCCCGACTCAGTGTCC Reverse: CCTGCTCCCCAGATGAGAG	400	60
E19	Forward: CCCTTTCCCTCTGCTCCTA Reverse: GTCTTCCTGCTCCCCAGAT	225	59
E20	Forward: ATCTGGGGAGCAGGAAGAC Reverse: AGTGA ACTCCGCGACACAC	528	60
E21	Forward: AGGAACCCCTGACACTGGAG Reverse: AGTGA ACTCCGCGACACAC	281	61
E22-24	Forward: CTCATTGCCTGGCTGGTG Reverse: AAAGCAGCAGTGAGGACAGC	627	61
E25	Forward: AAGTATCACTCCCCCTGAACC Reverse: AGCCCAGGACTCCTTCAAGT	255	59.5
E26-29	Forward: GGGCCAAACAGTCTTTTGAA Reverse: CTCTGGATTCCCTGCATCTC	745	60
E30	Forward: CGTGCTTTCCAGCAGAGTG Reverse: GCACCTTGACGGATGCAG	150	60
E31-32	Forward: CGTACTTGGCCCTATCTCCA Reverse: GATTCAAAGCAGGCAGAGATG	622	60
E33	Forward: CCTCTCAGGAAACCCAGACA Reverse: CCTGCTGAGGAGGCTATGTG	248	60.5
E34-35	Forward: GCTCTCCTGGGGTCATCTACT Reverse: CTGACGCCTTTGTCCTCATT	425	60
E36-38	Forward: TTCCTGCCTCCATTACTGCT Reverse: ATGAGGATAGGAGGGGCTGT	651	60
E39-40	Forward: GACTGAGGACCCAATGATGC	543	60

	Reverse: GAGTCCGCTGGAGTCATCTC		
	Forward: TGACTCCAGCGGACTCAAG		
E41-42	Reverse: GGAGAGCAGGGGAATATGG	432	60
	Forward: GCAACACTCCATGACCACAG		
E43	Reverse: TTAAGGCCCTGACATCTTGC	342	60
	Forward: GCCTGACAGTTTGTCCCTTTC		
E44-45	Reverse: GCTTGGGGCTCAGGAAG	571	60
	Forward: GCCCTCAGGCTACATTTGAC		
E46-47	Reverse: CCTGCACAGAGAGGGAAGAG	676	60
	Forward: CCTGTTGTATGTAGCCCCTCA		
E48	Reverse: GAGTCAGGGAAAGGGAGCA	490	60
	Forward: CTCCCTCCCTCCTACTCCTG		
E49	Reverse: GGCTAGCCCATCTCCTAACA	349	59.5
	Forward: CTCCCTCCCTCCTACTCCTG		
E50	Reverse: TGTCCATCACCCCTTAGCAGA	406	60
	Forward: AGGCCATAGTGCCCTCTCTC		
E51(1)	Reverse: CAGATTTGGGAAGGAGTGGA	631	60.5
	Forward: ACTTGCTTGAAGACCCATGC		
E51(2)	Reverse: CCCAACTCCAAAGAAGGAAA	1161	60
	Forward: CCTCTCTCCATCACTCCCAC		
E52	Reverse: TCAGTTTGGGTTGCTTGTCTG	287	60

Supplemental Table 2. Relationship between phenotypes and types of glycine substitutions in type I collagen

	Serine (n=24)	Othersubstitution (n=18)	Statistical values	P
Male	19 (79.2)	12 (66.2)	0.83*	0.362
Age of onset (years)	0.9 (0.0, 3.0)	1.2 (0.0, 3.5)	191.0	0.512
Age of visit (years)	10.0 (6.9, 18.5)	10.9 (5.0, 17.0)	211.0	0.899
OI types (I/II/III)	7/11/6	7/8/3	0.63*	0.730
Blue sclera	21 (87.5)	17 (94.4)	0.58*	0.448
DI	9 (39.1)	5 (27.83)	0.58*	0.447
Hearing loss	0 (0.0)	1 (5.6)	1.37*	0.243
Ligament relaxation	14 (63.6)	12 (66.7)	0.40*	0.842
Height Z score	-3.35 ± 3.87	-3.10 ± 3.30	-0.23	0.821
Weight Z score	-0.96 ± 2.36	-0.61 ± 1.97	-0.50	0.619
lumbar spine BMD Z score	-3.03 ± 1.87	-2.20 ± 1.99	-1.34	0.176
proximal hip BMD Z score	-4.26 ± 2.38	-3.55 ± 1.69	-1.06	0.297
Number of fractures	6 (3, 28)	8 (3, 10)	199.5	0.673
Frequency of fractures (per year)	1.2 (0.6, 2.2)	0.8 (0.5, 2.0)	172.5	0.269
Deformity of bone	14 (58.3)	8 (44.4)	0.80*	0.372
Wormian bones	19 (79.2)	12 (75.0)	0.10*	0.757
VCF	14 (77.8)	12 (70.6)	0.24*	0.627
Scoliosis	8 (38.1)	5 (29.4)	0.32*	0.575
Limited movement	9 (39.1)	6 (33.3)	0.15*	0.702
Clinical score	12.9 ± 5.8	12.0 ± 5.2	0.50	0.636
Ca (mmol/L)	2.48 ± 0.11	2.44 ± 0.10	1.28	0.266
P (mmol/L)	1.57 ± 0.29	1.56 ± 0.26	0.09	0.772
ALP (U/L)	213 (110, 257)	216 (121, 283)	192.5	0.550
β-CTX (ng/ml)	0.600 (0.400, 1.075)	0.500 (0.300, 1.050)	100.0	0.679
25OHD (ng/ml)	18.8 ± 8.6	17.2 ± 9.1	<0.001	0.991
PTH (pg/ml)	22.7 (14.8, 34.2)	17.6 (11.8, 29.0)	98.0	0.328
ALT (U/L)	14 (11, 20)	15 (11, 24)	193.0	0.771
Cr (μmol/L)	40 ± 16	40 ± 13	0.10	0.750

The data were shown as mean ± SD, median (Q1, Q3), or n (%).

*χ²-value, †T value, or otherwise U value.

OI: Osteogenesis imperfecta, DI: dentinogenesis imperfecta; BMD: bone mineral density; VCF: vertebral compressive fractures; Ca: Serum calcium; P: Serum phosphate; ALP: alkaline phosphatase; β-CTX: β-isomerized carboxy-telopeptide of type I collagen; 25OHD: 25 hydroxy-vitamin D; PTH: parathyroid hormone; ALT: alanine aminotransferase; Cr: creatinine.