CORRECTION

Correction: Development of a High-Throughput Resequencing Array for the Detection of Pathogenic Mutations in Osteogenesis Imperfecta

Yao Wang, Yazhou Cui, Xiaoyan Zhou, Jinxiang Han

There are a number of errors in the published article.

Reference sequences for genes with identified variants were inadvertently omitted from the published pdf. The GenBank reference sequence records are:

COL1A1 gene: NG_007400.1, *COL1A1* mRNA: NM_000088.3

COL1A2 gene: NG_007405.1, *COL1A2* mRNA: NM_000089.3

The variant in patient 2, reported as c.2191G>C in [Table 2](#) should be c.2192G>C, which yields the stated amino acid change p.Gly731Ala. Please see the correct [Table 2](#) here.

OPEN ACCESS

Citation: Wang Y, Cui Y, Zhou X, Han J (2015)

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Table 2. Mutations identified in OI patients.

Sample	Gene	Exon/Intron	Mutation (cDNA)	Mutation (Protein)	Mutation Type	Zygosity of mutation
1	<i>COL1A1</i>	Intron 1	c.104-1 G>A	NA	Splicing	Heterozygous
2	<i>COL1A1</i>	Exon 32	c.2192 G>C*	p.Gly731Ala	Missense	Heterozygous
3	<i>COL1A1</i>	Exon 38	c.2569 G>T	p.Gly857Cys	Missense	Heterozygous
4	<i>COL1A2</i>	Exon 24	c.1135 G>A	p.Gly379Arg	Missense	Heterozygous
5	<i>COL1A1</i>	Intron 17	c.1155+1 G>A	NA	Splicing	Heterozygous
6	<i>COL1A1</i>	Intron 17	c.1155+1 G>A	NA	Splicing	Heterozygous
7	<i>COL1A2</i>	Intron 19	c.937-3 C>T	NA	Splicing	Heterozygous
8	<i>COL1A2</i>	Exon 23	c.1310_1312dupGAT	p.Asp437dup	Insertion	
9	<i>COL1A1</i>	Exon 15	c.967 G>A	p.Gly323Arg	Missense	Heterozygous
10	<i>COL1A2</i>	Exon 38	c.2332 G>A	p.Gly778Ser	Missense	Heterozygous
11	<i>COL1A2</i>	Exon 40	c.2467 G>A	p. Gly823Ser	Missense	Heterozygous
12	<i>COL1A1</i>	Exon 48	c.3433 G>T	p.Gly1145Cys	Missense	Heterozygous
13	<i>COL1A2</i>	Exon 52	c.4048 G>A	p.Gly1350Ser	Missense	Heterozygous

* new mutation found in the present study

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The variant in patient 4, c.1135G>A, p.Gly379Arg in *COL1A2*, reported to be in exon 24 actually lies in exon 21.

The variant in patient 7, c.937-3C>T in *COL1A2*, reported to be in intron 19 actually lies in intron 18.

Sources for the sequence files in S3 Supplementary data information can be found online in the Ensembl database: <http://www.ensembl.org/index.html> as well as the Osteogenesis Imperfecta Variant Database: <https://oi.gene.le.ac.uk/home.php>

Reference

1. Wang Y, Cui Y, Zhou X, Han J (2015) Development of a High-Throughput Resequencing Array for the Detection of Pathogenic Mutations in Osteogenesis Imperfecta. PLoS ONE 10(3): e0119553. doi:10.1371/journal.pone.0119553 PMID: 25742658