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In the article, 'Genomewide meta-analysis identifies loci associated with IGF-I and IGFBP-3 levels with impact on age-related traits', the published Table 1 was incorrect, due to an error. The correct version of the table is shown below:

Table 1 Loci associated with IGF-I and IGFBP-3 concentrations in men and women combined samples at genomewide significance ($P < 5 \times 10^{-8}$) after final stage

Trait	SNP	A1	A2	F1	P	I ²	Chr	Position	Nearest Gene	Gene Distance	Direction effect	
											IGF-I	IGFBP-3
IGF-I*	rs700753	C	G	0.35	1.60E-23	4.2	7	46 720 209	<i>TNS3</i>	561 067	–	–
IGF-I	rs780093	T	C	0.41	2.19E-13	24.5	2	27 596 107	<i>GCKR</i>	0	–	+
IGF-I	rs978458	T	C	0.26	1.56E-10	0.0	12	101 326 369	<i>IGF1</i>	0	+	–
IGF-I	rs2153960	A	G	0.69	5.16E-09	22.5	6	109 082 339	<i>FOXO3</i>	0	+	+
IGF-I	rs934073	C	G	0.71	6.48E-09	21.8	2	25 790 669	<i>ASXL2</i>	25 087	–	–
IGF-I	rs1065656	C	G	0.31	1.17E-08	47.9	16	1 778 837	<i>NUBP2</i>	0	–	–
IGF-I	rs509035	A	G	0.31	2.09E-08	0.0	3	173 646 143	<i>GHSR</i>	0	+	+
IGFBP-3*	rs11977526	A	G	0.41	4.16E-161	51.5	7	45 974 635	<i>IGFBP3</i>	47 239	–	+
IGFBP-3*	rs700753	C	G	0.35	1.11E-46	26.7	7	46 720 209	<i>TNS3</i>	56 1067	–	–
IGFBP-3*	rs1065656	C	G	0.31	8.55E-23	24.1	16	1 778 837	<i>NUBP2</i>	0	–	–
IGFBP-3*	rs4234798	T	G	0.39	8.86E-19	0.0	4	7 270 834	<i>SORCS2</i>	0	–	–
Bivariate analysis	rs646776	T	C	0.78	6.87E-9	26.1/43.1	1	109 620 053	<i>CELSR2</i>	152	–	+

*Known association; '-', coding allele associated with lower IGF-1 and IGFBP-3 levels (indicated by bold italicized text were genomewide significant); "+", coding allele associated with higher IGF-1 and IGFBP-3 levels (indicated by bold italicized text were genomewide significant); Chr, chromosome; A1, coding allele; A2, other allele; F1, frequency of coding allele.

We apologize for the inconvenience caused.