



NIH Public Access

Author Manuscript

Osteoporos Int. Author manuscript; available in PMC 2010 November 16.

Published in final edited form as:

Osteoporos Int. 2010 October 4; 21: 1455. doi:10.1007/s00198-010-1232-3.

Erratum to: Genome-wide copy number variation association study suggested *VPS13B* gene for osteoporosis in Caucasians

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Erratum to: *Osteoporos Int* (2010) 21:579–587

Table 3 unfortunately contained errors. The correct version is given here.

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Table 3
Association between CNV_084 and bone phenotypes in the sample

Phenotype	Phenotypic value		P value		
	CNV state=1	CNV state=2	Total	Female	Male
SPN BMD	1.18 (0.22) [16]	1.03 (0.16) [965]	0.0001	0.0559	0.0003
Hip BMD	1.09 (0.20) [16]	0.97 (0.15) [963]	0.0002	0.0096	0.0071
FN BMD	0.92 (0.20) [16]	0.81 (0.14) [952]	0.0001	0.0032	0.0103
CT	0.18 (0.04) [16]	0.15 (0.03) [958]	0.0001	0.0029	0.0042
CSA	3.13 (0.77) [16]	2.83 (0.64) [958]	0.0030	0.0150	0.0510
BR	10.71 (2.92) [16]	12.04 (2.73) [958]	0.0170	0.1140	0.0710

Presented are mean (SD) [observation number]. In the total sample, age and gender were adjusted. In the gender-stratified analyses, age was adjusted as a covariate. Marked in *bold* are data that remained significant after Bonferroni correction