

## Appendix A. Supplementary data

An epigenome-wide association study based on cell type-specific whole-genome bisulfite sequencing: Screening for DNA methylation signatures associated with bone mass

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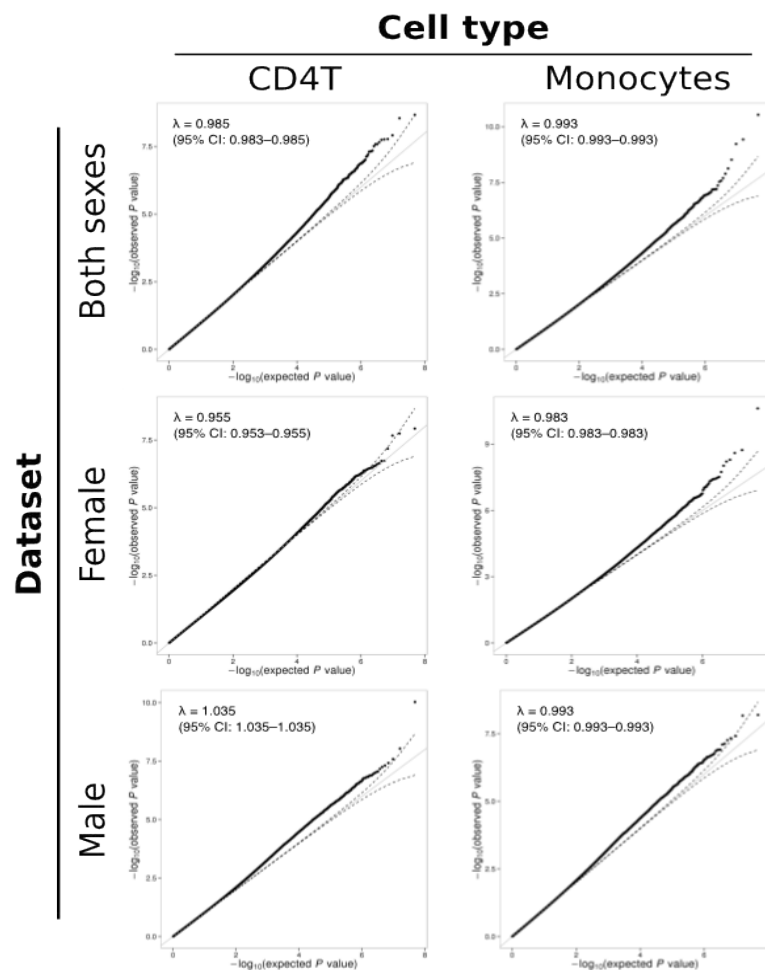
**Table S1.** Associations between previously reported DNA methylation signatures<sup>1</sup> and bone mass obtained in this study

Cell type	Chr	Position	Both sexes				Female			Male		
			DNAm (mean ± sd)	Coefficient (95% CI)	P value	R <sup>2</sup> *2	Coefficient (95% CI)	P value	R <sup>2</sup> *2	Coefficient (95% CI)	P value	R <sup>2</sup> *2
CD4T	5	131562848	80.54 ± 7.38	-0.16 (-0.51 – 0.18)	0.35	0.09	-0.35 (-0.90 – 0.20)	0.20	0.15	-0.35 (-0.90 – 0.20)	0.35	0.07
	6	32627784	70.91 ± 27.55	-0.64 (-1.97 – 0.68)	0.34	0.04	-1.04 (-2.92 – 0.85)	0.27	0.06	-1.04 (-2.92 – 0.85)	0.57	0.05
	10	30722660	0.46 ± 1.31	-0.04 (-0.10 – 0.02)	0.20	0.03	0.02 (-0.08 – 0.11)	0.69	0.05	0.02 (-0.08 – 0.11)	0.13	0.09
	14	59295237	97.72 ± 3.04	-0.03 (-0.18 – 0.12)	0.67	0.02	-0.02 (-0.25 – 0.22)	0.88	0.02	-0.02 (-0.25 – 0.22)	0.81	0.03
	16	55866997	68.76 ± 18.71	0.00 (-0.99 – 0.99)	1.00	0.01	0.45 (-0.91 – 1.81)	0.51	0.03	0.45 (-0.91 – 1.81)	0.94	0.04
Monocytes	19	3834745	92.33 ± 4.86	-0.12 (-0.35 – 0.11)	0.30	0.05	-0.03 (-0.34 – 0.27)	0.83	0.02	-0.03 (-0.34 – 0.27)	0.66	0.09
	5	131562848	60.93 ± 10.73	0.33 (-0.20 – 0.85)	0.22	0.03	0.05 (-0.68 – 0.78)	0.89	0.08	0.60 (-0.29 – 1.48)	0.18	0.06
	6	32627784	76.19 ± 21.61	-0.04 (-1.09 – 1.01)	0.94	0.05	0.17 (-1.36 – 1.69)	0.83	0.05	-0.08 (-1.85 – 1.69)	0.93	0.06
	10	30722660	0.47 ± 1.44	0.02 (-0.05 – 0.09)	0.64	0.01	-0.02 (-0.14 – 0.11)	0.80	0.01	0.06 (-0.03 – 0.15)	0.17	0.04
	14	59295237	97.82 ± 3.68	-0.09 (-0.28 – 0.09)	0.31	0.02	-0.18 (-0.45 – 0.09)	0.20	0.04	-0.08 (-0.39 – 0.23)	0.60	0.01
	16	55866997	33.52 ± 20.17	0.07 (-0.90 – 1.04)	0.89	0.05	0.66 (-0.59 – 1.92)	0.29	0.07	0.13 (-1.61 – 1.86)	0.88	0.05
	19	3834745	93.69 ± 6.00	-0.07 (-0.36 – 0.22)	0.65	0.04	0.08 (-0.26 – 0.42)	0.63	0.11	-0.04 (-0.60 – 0.52)	0.88	0.05

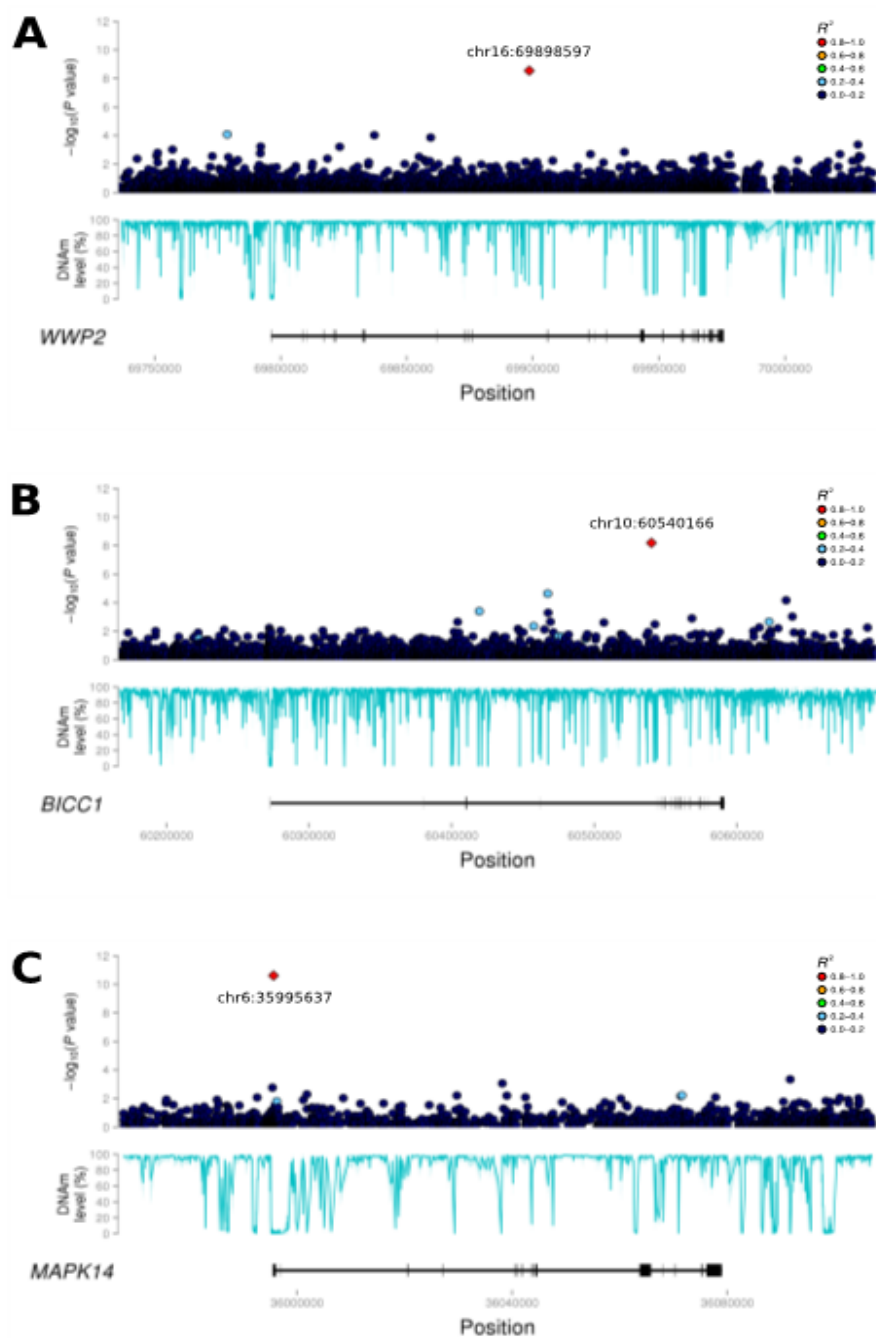
<sup>1</sup>J.A. Morris, P.-C. Tsai, R. Joehanes, J. Zheng, K. Trajanoska, M. Soerensen, V. Forgetta, J.E. Castillo-Fernandez, M. Frost, T.D. Spector, K. Christensen, L. Christiansen, F. Rivadeneira, J.H. Tobias, D.M. Evans, D.P. Kiel, Y.-H. Hsu, J.B. Richards, J.T. Bell, Epigenome-wide association of DNA methylation in whole blood with bone mineral density, *J. Bone Miner. Res.* xx (2017) 1–7. doi:10.1002/jbmr.3148.

\*2 Coefficient of determination.

Chr: chromosome, CD4T: CD3<sup>+</sup>/CD4<sup>+</sup> T cells, sd: standard deviation, CI: confidence interval.



**Figure S1.** Quantile-Quantile plots of *P* values from association analyses based on different cell types and datasets. Inflation factors ( $\lambda$ ) are also presented for each analysis. CD4T: CD3<sup>+</sup>/CD4<sup>+</sup> T cells, CI: confidence interval.



**Figure S2.** Regional association plots around DNA methylation signatures [(A) chr16:69898597 of CD4T of both sexes, (B) chr10:60540166 of monocytes of male, (C) chr6:35995637 of monocytes of female] identified in this study. Mean DNA methylation level of each CpG site and structure of neighboring genes are also presented. Colors indicate the correlation ( $R^2$ ) of the DNAm levels with the DNAm signatures (presented by diamonds). DNAm: DNA methylation.

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