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Yonghe Ding, … , Timothy M. Olson, Xiaolei Xu

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Corrigendum

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A modifier screen identifies *DNAJB6* as a cardiomyopathy susceptibility gene

Yonghe Ding, Pamela A. Long, J. Martijn Bos, Yu-Huan Shih, Xiao Ma, Rhianna S. Sundsbak, Jianhua Chen, Yiwen Jiang, Liqun Zhao, Xinyang Hu, Jianan Wang, Yongyong Shi, Michael J. Ackerman, Xueying Lin, Stephen C. Ekker, Margaret M. Redfield, Timothy M. Olson, and Xiaolei Xu

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In Table 2, the nucleotide change resulting in the p.F93F variant of *DNAJB6* was incorrectly noted. The correct table is below.

The authors regret the error.

Table 2. Summary of DNAJB6 variants identified in human cardiomyopathy patients (*n* = 325)

Nucleotide Change (Protein Change)	Genotype Frequency	ExAC MAF Frequency (%)	Clinical Phenotype	SIFT Prediction	PolyPhen2 Prediction
c.886G > A (p.A296T) and c.887C > G (p.A296G) Together p.A296R	A296T, A296G, and A296R 0/6500 (EVS) 0/5489 (ExAC) 1/214 (DCM)	0.00	Atypical DCM with features of HCM, LVNC, and congenital heart block	Tolerated (0.12) Damaging (0.05) Damaging (0.05)	Benign (0.001) Benign (0.028) –
c.947C > G (p.S316W)	0/6500 (EVS) 0/59650 (ExAC) 1/214 (DCM)	0.00	DCM	Damaging (0.03)	Possibly damaging (0.466)
c.573A > G (p.I191M)	0/60700 (ExAC) 1/17 (DCM)	0.00	DCM	Tolerated (0.06)	Benign (0.347)
c.962C > T (p.S321L)	7/6496 (EVS) 72/114074 (ExAC) 1/86 (HCM)	0.06	HCM	Damaging (0.03)	Benign (0.002)
[A]c.279 C>T (p.F93F)	27/6474 (EVS) 167/121408 (ExAC) 1/86 (HCM)	0.14	HCM	–	–

[A]Cryptic splice-site variant. DCM, dilated cardiomyopathy; EVS, exome variant server; ExAC, exome aggregation consortium; HCM, hypertrophic cardiomyopathy. MAF, minor allele frequency; SIFT, sorting intolerant from tolerant; LVNC, left ventricular noncompaction.