Corrigendum

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

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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	–	–

^ACryptic 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.