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Corrigendum: Genome-wide association study identifies variants at 16p13 associated with survival in multiple myeloma patients

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In this Article, members of the UCSF cohort who had been alive for longer than two years were inadvertently included in the data presented in Table 3. USCF/old treatments should have 109 patients with a hazard ratio of 3.35 and a *P* value of 0.00028 instead of the 124 patients with a hazard ratio of 3.37 and a *P* value of 0.00026. The USCF/new patients should have 187 patients with a hazard ratio of 3.57 and a *P* value of 0.0007 instead of the 208 patients with a hazard ratio of 3.62 and a *P* value of 0.0006. Finally, in the table legend, the first line should read ‘All models are adjusted for age, gender and principal components 1–3’. The exclusion of these individuals does not change the conclusions of the study. The correct version of Table 3 appears below.

Table 3
Effect of SNP by initial treatment among patients in the UCSF cohort

	HR*	95% CI	P value†
Mayo Clinic			
Old treatments‡		*N* = 136, 102 deaths	
RS72773978	1.90	0.98–3.83	0.057
New treatments§		*N* = 93, 64 deaths	
RS72773978	2.71	1.56–4.70	0.00045
Entire sample adjusted for treatment		*N* = 229, 166 deaths	
RS72773978	2.18	1.43–3.32	0.00028
UCSF			
Old treatments‡		*N* = 109 60 deaths	
RS72773978	3.35	1.74–6.44	0.00028
New treatments§		*N* = 187, 30 deaths	
RS72773978	3.57	1.71–7.43	0.0007
Entire sample adjusted for treatment		*N* = 296, 90 deaths	
RS72773978	3.35	2.07–5.41	8.2×10^{-7}

*All models are adjusted for age, gender and principal components 1-3.

†*P* values are calculated from proportional hazards models.

§Treatments containing at least one of the following agents: thalidomide, botezomib or lenalidomide.

‡Regimens including vincristine/adriamycin/dexamethasone or melphalan/prednisone.