

Correction

Developing a Risk-scoring Model for Ankylosing Spondylitis Based on a Combination of HLA-B27, Single-nucleotide Polymorphism, and Copy Number Variant Markers

Jung SH, Cho SM, Yim SH, Kim SH, Park HC, Cho ML, et al. Developing a risk-scoring model for ankylosing spondylitis based on a combination of HLA-B27, single-nucleotide polymorphism, and copy number variant markers. *J Rheumatol* 2016;43:2136–41. In the print version of Table 1, the headings on some of the columns are misplaced. The corrected table is below.

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Table 1. The association of each genetic variant with the AS risk.

Location	AS Risk Variant Type	Gene	Model Construction Set		Independent Validation Set	
			OR (95% CI)	p	OR (95% CI)	p
CNV						
1q32.2	Copy number loss	<i>HHAT</i>	4.04 (2.91–5.62)	1.68×10^{-17}	1.72 (1.37–2.15)	2.51×10^{-6}
2q31.2	Copy number loss	<i>PRKRA</i>	3.02 (2.19–4.17)	1.30×10^{-11}		
13q13.1	Copy number loss	<i>EEF1DP3</i>	4.06 (2.90–5.67)	5.16×10^{-17}	2.08 (1.66–2.61)	2.74×10^{-10}
16p13.3	Copy number loss	—	3.13 (1.73–5.68)	1.04×10^{-4}	2.05 (1.30–3.24)	0.002
SNP						
2p15	rs10865331 (A)	—	3.50 (2.48–4.96)	4.12×10^{-13}	1.74 (1.37–2.20)	4.46×10^{-6}
5q15	rs27044 (G)	<i>ERAP1</i>	1.20 (0.85–1.68)	0.304		
5q15	rs27434 (A)	<i>ERAP1</i>	1.10 (0.78–1.55)	0.599		
5q15	rs27037 (T)	<i>ERAP1</i>	0.59 (0.43–0.81)	0.001		
5q15	rs30187 (T)	<i>ERAP1</i>	1.09 (0.77–1.53)	0.660		
5q15	rs17482078 (C)	<i>ERAP1</i>	0.68 (0.24–1.90)	0.600		
5q15	rs10050860 (C)	<i>ERAP1</i>	1.00 (0.99–1.00)	1.000		
HLA-B27						
6p21.33	Positive	<i>HLA-B27</i>	321.34 (157.82–654.29)	2.50×10^{-135}	145.40 (95.62–221.09)	1.9×10^{-230}

AS: ankylosing spondylitis; CNV: copy number variants; SNP: single-nucleotide polymorphism.