Erratum to: Receptor for advanced glycation end-products (RAGE) provides a link between genetic susceptibility and environmental factors in type 1 diabetes

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Two corrections need to be made to this paper:
J. M. Forbes and J. Söderlund contributed equally to this article.
In Table 2 the superscript ^a should have appeared in place of the double dagger (‡), for rs204993, and should not have been attached to the ‘Minor allele’ heading. The corrected table is shown overleaf.

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Table 2 SNP associations between *AGER* and type 1 diabetes: analysis of genomic DNA from patients with T1D from the FinnDiane cohort and from newborn infants with the highest risk HLA genotype (*DR3*)-*DQA1**05-*DQB1**02/*DRB1**0401-*DQB1**0302 obtained as part of the Finnish Type 1 DIPP

Position NCBI35 Chr 6 (bp)	SNP (alleles)	Minor allele	SNP location	The FinnDiane cohort		HLA- <i>DR3/DR4</i> matched		OR (95% CI) ^b
				MAF controls/patients	<i>p</i> value	MAF controls/patients	<i>p</i> value	
Sample size (<i>n</i>)				703/2,921	3,624	373/546	924	924
32,269,408	rs204990 (G/T)	T	5'	0.148/0.231	1.82×10^{-11} ^c	0.468/0.45	0.465	0.932 (0.773–1.125)
32,269,374	rs3132940 (C/A)	A	5'	0.143/0.043	1.45×10^{-39} ^c	0.011/0.015	0.436	1.404 (0.598–3.298)
32,269,302	rs12663103 (T/C)	C	5'	0.025/0.005	6.30×10^{-10} ^c	0/0.002	n/a	n/a
32,263,559	rs204993 (T/C)	C	5	0.18/0.318 ^a	1.27×10^{-23} ^c	0.445/0.425	0.380	1.088 (0.901–1.314)
32,262,976	rs204994 (G/A)	A	5'	0.148/0.220	2.82×10^{-9} ^c	0.464/0.446	0.499	0.937 (0.777–1.131)
32,260,420	rs1800625 (T/C)	C	Promoter	0.146/0.218	2.76×10^{-9} ^c	0.463/0.444	0.474	0.933 (0.772–1.128)
32,260,365	rs1800624 (T/A)	A	Promoter	0.291/0.348	5.89×10^{-5} ^c	0.270/0.239	0.109	0.839 (0.677–1.040)
32,259,421	rs2070600 (G/A)	A	G82S	0.074/0.118	2.71×10^{-6} ^c	0.091/0.127	0.017	1.452 (1.068–1.973)
32,259,200	rs1035798 (C/T)	T	Intronic	0.295/0.348	1.53×10^{-4} ^c	0.268/0.239	0.132	0.848 (0.685–1.051)
32,254,635	rs9469089 (G/C)	C	3'	0.234/0.142	3.03×10^{-16} ^c	0.084/0.037	3.65×10^{-5}	0.423 (0.282–0.637)
32,253,685	rs2269423 (G/T)	T	3'	0.440/0.280	1.36×10^{-30} ^c	0.150/0.143	0.785	0.964 (0.741–1.254)
32,253,377	rs17493811 (C/G)	G	3'	0.026/0.048	6.34×10^{-4} ^c	0.056/0.082	0.031	1.518 (1.038–2.220)
32,253,183	rs3134947 (G/A)	A	3'	0.150/0.219	1.23×10^{-8} ^c	0.465/0.444	0.423	0.926 (0.767–1.118)

In the FinnDiane cohort, the *p* values are from logistic regression analyses, adjusted for sex, and reflect the joint effect of *AGER* and HLA. The DIPP HLA *DR3/DR4* matched set show the effect of *AGER* conditional for HLA haplotype

^a The minor allele is the opposite in the *DR3/DR4* matched data

^b The allelic ORs with 95% CIs are modelled for the respective minor allele

^c SNPs in the FinnDiane cohort that survive the stringent Bonferroni correction for multiple testing nucleotide polymorphism
MAF, minor allele frequency

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