

CORRECTION

Correction: A Genome-Wide Association Study for Diabetic Retinopathy in a Japanese Population: Potential Association with a Long Intergenic Non-Coding RNA

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There are errors in Tables [2](#) and [S2](#). Please see the corrected tables below.



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Citation: Awata T, Yamashita H, Kurihara S, Morita-Ohkubo T, Miyashita Y, Katayama S, et al. (2015) Correction: A Genome-Wide Association Study for Diabetic Retinopathy in a Japanese Population: Potential Association with a Long Intergenic Non-Coding RNA. PLoS ONE 10(4): e0126789. doi:10.1371/journal.pone.0126789

Published: April 24, 2015

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Table 2. SNPs showing associations with diabetic retinopathy (DR) in combined stages 1 and 2 samples with $P < 10^{-3}$ using the allele model.

SNP	Chr./Position	RefSeq genes										ENCODE/GENECODE genes										Stage 1			Stage 2			Overall analysis			Meta-analysis			Stage 3			Overall analysis			Meta-analysis			Stage 1 + 2 + 3		
		Gene	Left gene	Right gene	Gene	Left gene	Right gene	Allele (Risk/Other)	OR	P	OR	P	OR	P	OR	P	OR	P	OR	P	Risk:allele frequency/DR(+)/DR (-)	OR	P	P_{meta}	OR	P	P_{meta}	OR	P	P_{meta}	OR	P	P_{meta}												
		Gene	Left gene	Right gene	Gene	Left gene	Right gene	Allele (Risk/Other)	OR	P	OR	P	OR	P	OR	P	OR	P	OR	P	Risk:allele frequency/DR(+)/DR (-)	OR	P	P_{meta}	OR	P	P_{meta}	OR	P	P_{meta}	OR	P	P_{meta}												
rs115623936	1/4909707	NA	AJAP1	MIR4417	NA	AJAP1	C/A	1.71	1.5×10^{-4}	1.25	6.6×10^{-2}	1.43	8.4×10^{-5}	1.43	8.8×10^{-5}	1.43	8.8×10^{-5}	1.43	8.8×10^{-5}	0.399/0.351	1.23	1.9×10^{-3}	1.3×10^{-3}	1.24	1.3×10^{-3}	1.3×10^{-3}	1.24	1.3×10^{-3}	1.3×10^{-3}	1.24	1.3×10^{-3}	1.3×10^{-3}													
rs1719215	1/54178200	GLIS1	DMRTB1	NDCl	GLIS1	DMRTB1	A/G	1.56	1.0×10^{-3}	1.41	1.7×10^{-2}	1.46	4.3×10^{-4}	1.47	3.9×10^{-4}	1.47	3.9×10^{-4}	1.47	3.9×10^{-4}	0.811/0.770	1.28	2.4×10^{-3}	2.2×10^{-3}	1.28	2.4×10^{-3}	2.2×10^{-3}	1.28	2.4×10^{-3}	2.2×10^{-3}	1.28	2.4×10^{-3}	2.2×10^{-3}													
rs4580644	4/15785201	CD38	BST1	FGFBP1	CD38	BST1	T/C	1.62	2.2×10^{-3}	1.41	1.1×10^{-2}	1.51	5.7×10^{-5}	1.50	7.4×10^{-5}	1.50	7.4×10^{-5}	1.50	7.4×10^{-5}	0.263/0.226	1.22	6.9×10^{-3}	1.8×10^{-3}	1.20	1.8×10^{-3}	1.8×10^{-3}	1.20	6.9×10^{-3}	1.8×10^{-3}	1.20	6.9×10^{-3}	1.8×10^{-3}													
rs12641981	4/4579883	NA	GNPDA2	GABRG1	NA	RP1F-362T1.1	T/C	1.52	3.2×10^{-3}	1.58	9.3×10^{-3}	1.42	2.2×10^{-4}	1.45	8.1×10^{-5}	1.45	8.1×10^{-5}	1.45	8.1×10^{-5}	0.347/0.305	1.21	5.3×10^{-3}	3.3×10^{-3}	1.23	3.3×10^{-3}	3.3×10^{-3}	1.23	3.3×10^{-3}	3.3×10^{-3}	1.23	3.3×10^{-3}	3.3×10^{-3}													
rs1156082	6/77501140	NA	IMP1	HTR1B	NA	RP1F-35J1.1	C/T	1.69	1.4×10^{-1}	1.29	3.2×10^{-2}	1.45	3.4×10^{-5}	1.44	3.8×10^{-5}	1.44	3.8×10^{-5}	1.44	3.8×10^{-5}	0.602/0.552	1.21	4.0×10^{-3}	3.7×10^{-3}	1.21	4.0×10^{-3}	3.7×10^{-3}	1.21	4.0×10^{-3}	3.7×10^{-3}	1.21	4.0×10^{-3}	3.7×10^{-3}													
rs862354	6/8578268	NA	CEP162	TBX18	RP1-90L14.1	KIAA1009	T/C	1.84	4.1×10^{-3}	1.52	7.1×10^{-4}	1.67	4.4×10^{-4}	1.64	1.4×10^{-4}	1.64	1.4×10^{-4}	1.64	1.4×10^{-4}	0.365/0.291	1.40	1.1×10^{-3}	1.7×10^{-3}	1.36	1.7×10^{-3}	1.7×10^{-3}	1.36	1.7×10^{-3}	1.7×10^{-3}	1.36	1.7×10^{-3}	1.7×10^{-3}													
rs7083364	10/27196099	NA	ABI1	LINC00202-1	NA	snoU13	T/G	2.36	3.5×10^{-5}	1.52	2.8×10^{-2}	1.83	1.0×10^{-5}	1.83	1.4×10^{-5}	1.83	1.4×10^{-5}	1.83	1.4×10^{-5}	0.867/0.846	1.19	7.3×10^{-2}	8.8×10^{-5}	1.18	7.3×10^{-2}	8.8×10^{-5}	1.18	7.3×10^{-2}	8.8×10^{-5}	1.18	7.3×10^{-2}	8.8×10^{-5}													
rs10894267	11/133714861	NA	C11orf44	SNX19	RP1F-890B15.2	C11orf44	T/C	1.78	2.8×10^{-3}	1.32	1.8×10^{-2}	1.49	5.5×10^{-4}	1.49	5.8×10^{-4}	1.49	5.8×10^{-4}	1.49	5.8×10^{-4}	0.564/0.518	1.20	4.4×10^{-3}	2.2×10^{-3}	1.22	4.4×10^{-3}	2.2×10^{-3}	1.22	4.4×10^{-3}	2.2×10^{-3}	1.22	4.4×10^{-3}	2.2×10^{-3}													

doi:10.1371/journal.pone.0126789.t001

Supporting Information

S2 Table. Stage 1 SNPs showing associations with diabetic retinopathy with $P < 10^{-5}$ using the best model.

(DOCX)

Reference

1. Awata T, Yamashita H, Kurihara S, Morita-Ohkubo T, Miyashita Y, Katayama S, et al. (2014) A Genome-Wide Association Study for Diabetic Retinopathy in a Japanese Population: Potential Association with a Long Intergenic Non-Coding RNA. PLoS ONE 9(11): e111715. doi:[10.1371/journal.pone.0111715](https://doi.org/10.1371/journal.pone.0111715) PMID: [25364816](https://pubmed.ncbi.nlm.nih.gov/25364816/)