

Correction



Correction: Xingchen Zhou, et al. Whole Exome Sequencing in Psoriasis Patients Contributes to Studies of Acitretin Treatment Difference. *Int. J. Mol. Sci.* 2017, *18*, 295

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We would like to submit the following correction to the published paper [1], the reason for this action is that the data in Table 3 were reanalyzed by one more accurate statistic method: On page 12, the sentence of paragraph three "OR and 95% CI were calculated by limited backward-LR (likelihood ratio) logistic regression analysis with adjustment by clinical variables" should be corrected into "OR and 95% CI were calculated by limited by limited by limited by limited by limited by limited enter logistic regression analysis with adjustment by clinical variables". The corrections resulted some changes in Table 3 and related data in text, while the significance and the conclusions remained unchanged. Furthermore, in order to make the reader easy to understand the data in Table 3, we revised the table title and added notes for Table 3 (page 7).

Table 3 should be replaced:

Table 3. Multivariate logistic regression analysis of four positive SNPs.

Gene	SNPs	Genotypes/	PASI < 75	PASI≥75	Adjusted OR 1	<i>p</i> Value
		Alleles	<i>n</i> = 100	n = 66	[95% CI]	
CRB2	rs1105223	TT, n (%)	40 (42.6)	23 (37.1)	1.00	
		CT, n (%)	31 (33)	33 (53.2)	2.012 [0.710-5.706]	0.188
		CC, n (%)	23 (24.4)	6 (9.7)	4.098 [1.461–11.493]	0.007
		CT/CC, n (%)	54 (57.4)	39 (62.9)	1.363 [0.679–2.735]	0.383
		TT/CT, n (%)	71 (75.5)	56 (90.3)	0.588 [0.363-0.955]	0.032
		T, n (%)	111 (59)	79 (63.7)	1.00	
		C, n (%)	77 (41)	45 (36.3)	1.118 [0.687–1.820]	0.652
ANKLE1	rs11086065	AA, n (%)	33 (33.7)	36 (56.3)	1.00	
		AG, n (%)	50 (51)	22 (34.3)	2.552 [0.876–7.439]	0.086
		GG, n (%)	15 (15.3)	6 (9.4)	0.905 [0.303–2.700]	0.858
		AG/GG, n (%)	65 (66.3)	28 (43.8)	2.756 [1.415-5.368]	0.003
		AA/AG, n (%)	83 (84.7)	58 (90.6)	0.815 [0.485–1.369]	0.439
		A, n (%)	116 (59.2)	94 (73.4)	1.00	
		G, n (%)	80 (40.8)	34 (26.6)	1.939 [1.171–3.210]	0.010

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ARHGEF3	rs3821414	TT, n (%)	51 (51)	18 (27.3)	1.00	
		CT, n (%)	39 (39)	34 (51.5)	0.253 [0.095–0.675]	0.006
		CC, n (%)	10 (10)	14 (21.2)	0.568 [0.222-1.451]	0.237
		CT/CC, n (%)	49 (49)	48 (72.7)	0.386 [0.194–0.765]	0.006
		TT/CT, n (%)	90 (90)	52 (78.8)	1.593 [1.024–2.479]	0.039
		T, n (%)	141 (70.5)	70 (53)	1.00	
		C, n (%)	59 (29.5)	62 (47)	0.487 [0.305–0.779]	0.003
SFRP4	rs1802073	GG, n (%)	14 (14)	7 (10.6)	1.00	
		GT, n (%)	60 (60)	28 (42.4)	0.483 [0.167–1.394]	0.178
		TT, n (%)	26 (26)	31 (47)	0.402 [0.199–0.812]	0.011
		GT/TT, n (%)	86 (86)	59 (89.4)	0.797 [0.296–2.149]	0.797
		GG/GT, n (%)	74 (74)	35 (53)	2.400 [1.226-4.696]	0.011
		G, n (%)	88 (44)	42 (31.8)	1.00	
		T, n (%)	112 (56)	90 (68.2)	0.612 [0.380-0.984]	0.043

¹ adjusted for age, gender and BMI. Bold and italics in *p* value mean the significant result.

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Table 3. Association of four positive SNPs with response to acitretin via logistic regression analysis.

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Gene	SNPs	Genotypes/	PASI < 75	$PASI \ge 75$	Adjusted OR ¹	<i>p</i> Value
		Alleles	<i>n</i> = 100	<i>n</i> = 66	[95% CI]	
CRB2	rs1105223ª	TT, n (%)	40 (42.6)	23 (37.1)	1.00	
		CT, n (%)	31 (33)	33 (53.2)	0.498 [0.234-1.062]	0.071
		CC, <i>n</i> (%)	23 (24.4)	6 (9.7)	1.852 [0.640-5.359]	0.256
		CT/CC, n (%)	54 (57.4)	39 (62.9)	0.734 [0.366–1.472]	0.383
		TT/CT, n (%)	71 (75.5)	56 (90.3)	0.371 [0.139–1.085]2	0.048
		T, n (%)	111 (59)	79 (63.7)	1.00	
		C, n (%)	77 (41)	45 (36.3)	1.118 [0.687–1.820]	0.652
ANKLE1	rs11086065 ^b	AA, n (%)	33 (33.7)	36 (56.3)	1.00	
		AG, n (%)	50 (51)	22 (34.3)	2.922 [1.413-6.041]	0.004
		GG, n (%)	15 (15.3)	6 (9.4)	2.553 [0.851–7.652]	0.094
		AG/GG, n (%)	65 (66.3)	28 (43.8)	2.835 [1.436-5.600]	0.003
		AA/AG, n (%)	83 (84.7)	58 (90.6)	0.664 [0.235–1.875] 3	0.439
		A, n (%)	116 (59.2)	94 (73.4)	1.00	
		G, n (%)	80 (40.8)	34 (26.6)	1.966 [1.181–3.271]	0.009
ARHGEF3	rs3821414	TT, n (%)	51 (51)	18 (27.3)	1.00	
		CT, n (%)	39 (39)	34 (51.5)	0.464 [0.222-0.968]	0.041
		CC, n (%)	10 (10)	14 (21.2)	0.256 [0.098-0.713]	0.009
		CT/CC, n (%)	49 (49)	48 (72.7)	0.402 [0.201-0.805]	0.01
		TT/CT, n (%)	90 (90)	52 (78.8)	2.465 [1.011-6.013] 4	0.047
		T, n (%)	141 (70.5)	70 (53)	1.00	
		C, n (%)	59 (29.5)	62 (47)	0.497 [0.310-0.797]	0.004
SFRP4	rs1802073	GG, n (%)	14 (14)	7 (10.6)	1.00	
		GT, n (%)	60 (60)	28 (42.4)	1.196 [0.421–3.396]	0.737
		TT, n (%)	26 (26)	31 (47)	0.449 [0.153–1.321]	0.146
		GT/TT, n (%)	86 (86)	59 (89.4)	0.797 [0.296–2.149]	0.655
		GG/GT, n (%)	74 (74)	35 (53)	2.570 [1.294-5.107] 5	0.007
		G, n (%)	88 (44)	42 (31.8)	1.00	
		T, n (%)	112 (56)	90 (68.2)	0.603 [0.374–0.971]	0.037

¹ adjusted for age, gender and BMI, OR < 1 means response to acitretin, OR > 1 means non-response to acitretin; ² compared to the CC genotype; ³ compared to the GG genotype; ⁴ compared to the CC genotype; ⁵ compared to the TT genotype; ^a total of 156 samples were detected; ^b total of 162 samples were detected; Bold and italics in *p* value mean the significant result.

In addition, there were some writing errors: "rs1802073T>G" should be corrected into "rs1802073G>T" (in Abstract, and page 10, paragraph 1 and page 11, paragraph 5). According to the contribution, the affiliation order was corrected: "Department of Clinical Pharmacology, Xiangya Hospital, Central South University" was corrected into the first affiliation.

These changes have no material impact on the conclusions of our paper. The manuscript will be updated and the original will remain online on the article webpage. We apologize for any inconvenience caused to our readers.

Conflicts of Interest: The authors declare no conflict of interest.

References

 Zhou, X.; He, Y.; Kuang, Y.; Li, J.; Zhang, J.; Chen, M.; Chen, W.; Su, J.; Zhao, S.; Liu, P.; et al. Whole Exome Sequencing in Psoriasis Patients Contributes to Studies of Acitretin Treatment Difference. *Int. J. Mol. Sci.* 2017, *18*, 295; doi:10.3390/1ijms18020295.



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