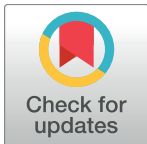


CORRECTION

# Correction: Whole-Genome Saliva and Blood DNA Methylation Profiling in Individuals with a Respiratory Allergy

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There is a typographical error in [Table 2](#). [Table 2](#) reports averaged values of multiple CpG sites in the reported gene regions instead of the average of the single CpG site corresponding to the validated cg-probes. For instance, for cg19754622 in the STK32C gene region ([S1 Dataset](#)), the authors reported the average of the 6 CpG sites that were analyzed along with the CpG-site of interest (cg19754622 = CpG1). A similar switch of data for the other two gene regions is also present.



**OPEN ACCESS**

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**Table 2. Comparison of methylation differences between RA cases and controls in PBMC and saliva as assessed by Illumina 450K bead chips and bisulfite pyrosequencing.**

Assay	cg-probe	gene	Blood PBMC			Saliva		
			Mean $\beta$ (%) $\pm$ SD		$\Delta\beta$ (%)	Mean $\beta$ (%) $\pm$ SD		$\Delta\beta$ (%)
			RA cases	Controls		RA cases	Controls	
450K <sup>1</sup>	cg19754622	STK32C	52.39 $\pm$ 5.3	72.17 $\pm$ 21.0	-19.78*	30.62 $\pm$ 13.0	64.82 $\pm$ 28.5	-34.21*
	cg08899523	FGFR2	45.15 $\pm$ 10.5	58.47 $\pm$ 9.5	-13.32*	39.52 $\pm$ 15.2	59.81 $\pm$ 9.5	-20.30*
	cg11965913	PM20D1	55.24 $\pm$ 36.6	18.65 $\pm$ 17.6	36.58*	62.63 $\pm$ 33.7	21.69 $\pm$ 20.4	40.94*
pyroseq. <sup>2</sup>	cg19754622	STK32C	52.00 $\pm$ 9.8	72.00 $\pm$ 18.6	-20.00	25.20 $\pm$ 14.6	61.20 $\pm$ 27.8	-36.00*
	cg08899523	FGFR2	39.80 $\pm$ 9.0	53.27 $\pm$ 11.4	-13.47	31.20 $\pm$ 14.9	51.60 $\pm$ 13.2	-20.40 <sup>^</sup>
	cg11965913	PM20D1	59.00 $\pm$ 32.6	25.20 $\pm$ 24.3	33.80	64.70 $\pm$ 33.9	24.80 $\pm$ 21.5	39.90*

Statistics were performed: <sup>1</sup>using M-values with Limma package, or <sup>2</sup>Mann-Witney U test to study differences between RA cases and controls (\*P $\leq$ 0.05; <sup>^</sup>P<0.1).

<https://doi.org/10.1371/journal.pone.0183088.t001>

The statistical analyses were performed with the correct values, so this error does not affect the results or conclusions of this study. Please see the corrected [Table 2](#) here.

## Supporting information

**S1 Dataset. Pyrosequencing Data.**  
(XLSX)

## Reference

- Langie SAS, Szarc vel Szic K, Declerck K, Traen S, Koppen G, Van Camp G, et al. (2016) Whole-Genome Saliva and Blood DNA Methylation Profiling in Individuals with a Respiratory Allergy. PLoS ONE 11(3): e0151109. doi:[10.1371/journal.pone.0151109](https://doi.org/10.1371/journal.pone.0151109) PMID: [26999364](https://pubmed.ncbi.nlm.nih.gov/26999364/)