

CORRECTION

# Correction: Genome-Wide Association Study on Male Genital Shape and Size in *Drosophila melanogaster*

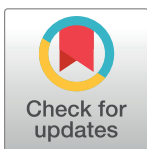
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There are errors in Table 1. The SNP coordinates used in the genome-wide association analysis are based on Release 5 of the *D. melanogaster* reference genome. However, the candidate gene search was performed on the FlyBase in which the coordinates of the genes are based on Release 6 of the *D. melanogaster* reference genome. Because the genome sequences used for each release are different, the SNP coordinates needed to be converted to the coordinates of the Release 6 reference genome. Please see the corrected Table 1 here.

**Table 1. Candidate genes from this study for PC1 and PC2 and QTL identified in McNeil et al. (2011).**

Trait	Chromosome	Candidate gene	McNeil et al. (2011)	
			<b>QTL</b>	
PC1	2L	<i>Pde1c</i>		
		<i>beat-IIIb</i>		
		CG44406		
		CR44408		
	2R	<i>Rx</i>		
		<i>Rgk3</i>		
	3L	CG7255		
		<i>GluRIB</i>	Q2	
	3R	CG4770		
		<i>Sec13</i>		
<i>RpS3</i>				
<i>RunxB</i>				
PC2		2L	<i>Hel25E</i>	
		2R	<i>Obp58d</i>	
<i>Obp58c</i>				
CR43735				
CD30275				
CG42260				
<i>twi</i>				
3L	CG42741			
	CG13197			
	<i>unc-13-4A</i>			
	3R	CG5404		
<i>Osi17</i>		Q3		
X	<i>hang</i>			
	Size	2L	CG31933	
		CG31664		
2R		<i>HLH54F</i>		
	3L	CG43693	Q2	

(Continued)



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**Table 1.** (Continued)

Trait	Chromosome	Candidate gene	McNeil et al. (2011)
			QTL
		<i>Nrx-IV</i>	Q2
		<i>CAH2</i>	Q2
		<i>bru-3</i>	
		<i>CG17145</i>	Q3
		<i>cdi</i>	

<https://doi.org/10.1371/journal.pone.0205301.t001>

## Reference

1. Takahara B, Takahashi KH (2015) Genome-Wide Association Study on Male Genital Shape and Size in *Drosophila melanogaster*. PLoS ONE 10(7): e0132846. <https://doi.org/10.1371/journal.pone.0132846> PMID: 26182199