BMC Genomics

CORRECTION

Correction to: small RNA discovery in the interaction between barley and the powdery mildew pathogen

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Correction to: BMC Genomics
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Following the publication of the original article [1], the authors noted several typesetting errors which are noted in this Correction article.

In the section "PhasiRNA analysis" there was an error in the first equation in the PDF version of the article. A fraction bar was erroneously introduced between (20 m and n-x), (m and x), and (21 m and n).

The incorrect version was:

$$\text{p--value} = \sum_{x=k}^{m} \frac{\left(\frac{20m}{n-x}\right)\left(\frac{m}{n}\right)}{\left(\frac{21m}{n}\right)}$$

The correct version is:

$$\text{p--value} = \sum_{x=k}^{m} \frac{\left(\begin{array}{c}20m \\ n-x\end{array}\right)\left(\begin{array}{c}m \\ x\end{array}\right)}{\left(\begin{array}{c}21m \\ n\end{array}\right)}$$

Furthermore, due to the formatting of Table 3 there was an error in the formatting of the alignment bars. The correct Table 3 is provided in this Correction article.

The publisher would like to apologize to the authors and readers for any inconvenience caused. The original article has been corrected.

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Reference
1. Hunt, et al. BMC Genomics. 2019;20:610 https://doi.org/10.1186/s12864-019-5947-z.

Table 3 Differentially expressed predicted miRNAs and barley mapped reads with homology to miRBase miRNAs

Predicted miRNA or read	Sequence	miRBase match	Number of predicted barley copies	DE time points (and log$_2$ fold changes)	miRBase blastn overlap		Mismatches
DE barley mapped read	TCGGACCAGGCTTCATGCCCC	miR165	NA	bln1 16 HAI (-2.55), bln1 20 HAI (-2.39), mla6 20 HAI (-1.77), rar3 20 HAI (-2.14), bln1 24 HAI (-2.47), mla6 24 HAI (-2.02), bln1 48 HAI (-2.41), mla6 48 HAI (-1.78)	UserSeq 1 / bdi-miR166d-3p 1	ucggaccaggcuucaugcccc 21 ||||||||||||| ||| ucggaccaggcuucauuuccc 21	1
DE barley mapped read	TTCGGACCAGGCTTCCTTCCC	miR166	NA	mla6 48 HAI (1.92)	UserSeq 2 / gma-miR166i-3p 1	ucggaccaggcuucuuuccc 21 |||||||||||| ||||| ucggaccaggcuucauuccc 20	2
DE barley mapped read	TGGGACCAGGCTTCATTCCCC	miR166	NA	bln1 20 HAI (-2.24), rar3 20 HAI (-1.71)	UserSeq 1 / tcc-miR166a 1	ugggaccaggcuucauuccc 21 |||||||||||||||||||| ucggaccaggcuucauuccc 21	1
DE barley mapped read	TCGGACCAGGGTTCATTCCCC	miR166	NA	bln1 48 HAI (-2.31), mla6 48 HAI (-1.80)	UserSeq 1 / hvu-miR166b 1	ucggaccaggguucauuccc 21 ||||||||||| ||||||||| ucggaccaggcuucauuccc 21	1
DE barley mapped read	TTCGGACCAGGCTTCAGTCCC	miR166	NA	rar3 48 HAI (-2.10)	UserSeq 2 / gma-miR166j-3p 1	ucggaccaggcuucagucc 21 |||||||||||| |||| ucggaccaggcuucauuccc 20	2
DE predicted miRNA	ACACAAACCGGGACTAAAG	miR2120	9	mla6 20 HAI (1.59)	UserSeq 1 / osa-miR2120b-5p 1	acacaaaccgggacuaaag 19 |||| ||||| ||||||| acaccaaccgcgacuaaag 19	2
DE predicted miRNA	GTGTTCTCAGGTCGCCCCGC	miR398	2	mla6 32 HAI (2.03)	UserSeq 1 / zma-miR398a-3p 2	guguucucaggucgcccccgc 20 |||||||||||||||||||| guguucucaggucgcccccg 21	1
DE predicted miRNA	AGAACAGAGAATGGCGATAGACTC	miR398	1	mla6 0 HAI (1.63), mla6 20 HAI (1.72), mla6 24 HAI (1.66), mla6 48 HAI (1.93)	UserSeq 1 / csi-miR398a-5p 1	agaacagagaauggcgauag 20 ||||||||| ||||| || agaacagaggguggcguugg 20	4
DE barley mapped read	TGTGTTCTCAGGTCGCCCCCG	miR398	NA	mla6 24 HAI (1.71), mla6 32 HAI (2.57)	UserSeq 1 / zma-miR398a-3p 1	uguguucucaggucgcccccg 21 ||||||||||||||||||||| uguguucucaggucgcccccg 21	0
DE predicted miRNA	TCCTGTGCCTGCCTCTTCCAT	miR528	1	mla6 20 HAI (1.97), mla6 24 HAI (2.27), mla6 32 HAI (2.18)	UserSeq 2 / zma-miR528a-3p 1	ccugugccugccucuuccau 21 ||||||||||||||||||| ccugugccugccucuuccau 21	1
DE barley mapped read	TCCTGTGCCTGCCTCTTCCAT	miR528	NA	mla6 24 HAI (2.07), mla6 32 HAI (2.19)	UserSeq 2 / zma-miR528a-3p 1	ccugugccugccucuuccau 21 ||||||||||||||||||| ccugugccugccucuuccau 20	1
DE barley mapped read	TGGAAGGGGCATGCAGAGGA	miR528	NA	mla6 32 HAI (1.86)	UserSeq 1 / osa-miR528-5p 1	uggaagggcaugcagagga 20 ||||||||||||||||||| uggaagggcaugcagagga 20	0

Table 3 Differentially expressed predicted miRNAs and barley mapped reads with homology to miRBase miRNAs (Continued)

Predicted miRNA or read	Sequence	miRBase match	Number of predicted barley copies	DE time points (and log$_2$ fold changes)	miRBase blastn overlap	Mismatches
DE barley mapped read	TGGAAGGGGCATGCAGAGGAG	miR528	NA	mla6 16 HAI (2.20), mla6 20 HAI (2.40), mla6 24 HAI (2.21), mla6 32 HAI (2.09)	UserSeq 1 uggaagggggcaugcagaggag 21 / ||||||||||||||||||||| / osa-miR528-5p 1 uggaagggggcaugcagaggag 21	0
DE barley mapped read	CCTGTGCCTGCCTCTTCCATT	miR528	NA	mla6 0 HAI (1.99)	UserSeq 1 ccugugccugccucuuccauu 21 / ||||||||||||||||||||| / zma-miR528a-3p 1 ccugugccugccucuuccauu 21	0
DE predicted miRNA	ATTTTGCTTCGTATGTAGACT	none	17	mla6 0 HAI (1.97)	none	NA
DE predicted miRNA	TATTAGTTGACAGAGGGAGTA	none	5	mla6 48 HAI (-1.77), mla6-bln1 48 HAI (-2.44), bln1 48 HAI (-2.40)	none	NA
DE predicted miRNA	AACTAGTACTACTCTAATGTGCCT	none	3	mla6 0 HAI (-1.07)	none	NA
DE predicted miRNA	GCTTTCATAGCTCAGTTGGTTA GAGCACCCG	none	1	bln1 32 HAI (1.64)	none	NA
DE predicted miRNA	AATTTGAACTGTGAAACT	none	1	mla6 0 HAI (1.46), mla6 20 HAI (1.76), mla6 24 HAI (1.56)	none	NA