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CORRECTION

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

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Correction to: BMC Genomics

<https://doi.org/10.1186/s12864-019-5947-z>

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:

$$\text{p-value} = \sum_{x=k}^m \frac{\binom{20m}{n-x} \binom{m}{n}}{\binom{21m}{n}}$$

The correct version is:

$$\text{p-value} = \sum_{x=k}^m \frac{\binom{20m}{n-x} \binom{m}{x}}{\binom{21m}{n}}$$

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

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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	TCGGACCAAGGCTTCATGCCCC	miR165	NA	<i>bin1</i> 16 HAI (-2.55), <i>bin1</i> 20 HAI (-2.39), <i>mla6</i> 20 HAI (-1.77), <i>rar3</i> 20 HAI (-2.14), <i>bin1</i> 24 HAI (-2.47), <i>mla6</i> 24 HAI (-2.02), <i>bin1</i> 48 HAI (-2.41), <i>mla6</i> 48 HAI (-1.78)	UserSeq 1 ucggaccaggcuucaugcccc bdi-miR166d-3p 1 ucggaccaggcuucauuccc	21 1 21
DE barley mapped read	TTCGACCAAGGCTTCCTTCCC	miR166	NA	<i>mla6</i> 48 HAI (1.92)	UserSeq 2 ucggaccaggcuucauuccc gma-miR166i-3p 1 ucggaccaggcuucauuccc	21 2 20
DE barley mapped read	TGGACCAAGGCTTCATTCCCC	miR166	NA	<i>bin1</i> 20 HAI (-2.24), <i>rar3</i> 20 HAI (-1.71)	UserSeq 1 ugggaccaggcuucauuccc tcc-miR166a 1 ucggaccaggcuucauuccc	21 1 21
DE barley mapped read	TCGGACCAAGGTTTCATTCCCC	miR166	NA	<i>bin1</i> 48 HAI (-2.31), <i>mla6</i> 48 HAI (-1.80)	UserSeq 1 ucggaccaggcuucauuccc hvu-miR166b 1 ucggaccaggcuucauuccc	21 1 21
DE barley mapped read	TTCGACCAAGGCTTCAGTCCC	miR166	NA	<i>rar3</i> 48 HAI (-2.10)	UserSeq 2 ucggaccaggcuucauuccc gma-miR166j-3p 1 ucggaccaggcuucauuccc	21 2 20
DE predicted miRNA	ACACAAACCGGGACTAAAG	miR2120	9	<i>mla6</i> 20 HAI (1.59)	UserSeq 1 acacaacccgggacuaaag osa-miR2120b-5p 1 acaccaaccggacuaaag	19 1 19
DE predicted miRNA	GTGTTCTCAGTGC GCCCCGCG	miR398	2	<i>mla6</i> 32 HAI (2.03)	UserSeq 1 guguuucucaggucgcccccg zma-miR398a-3p 2 guguuucucaggucgcccccg	20 1 21
DE predicted miRNA	AGAACACAGAATGGCGATAG ACTC	miR398	1	<i>mla6</i> 0 HAI (1.63), <i>mla6</i> 20 HAI (1.72), <i>mla6</i> 24 HAI (1.66), <i>mla6</i> 48 HAI (1.93)	UserSeq 1 agaacaagagaugggcgauag csi-miR398a-5p 1 agaacagaggugggcgauag	20 1 20
DE barley mapped read	TGTGTTCTCAGTGC GCCCCCGG	miR398	NA	<i>mla6</i> 24 HAI (1.71), <i>mla6</i> 32 HAI (2.57)	UserSeq 1 uguuuucucaggucgcccccg zma-miR398a-3p 1 uguuuucucaggucgcccccg	21 1 21
DE predicted miRNA	TCCTGTGCTGCCTCTTCCAT	miR528	1	<i>mla6</i> 20 HAI (1.97), <i>mla6</i> 24 HAI (2.27), <i>mla6</i> 32 HAI (2.18)	UserSeq 2 ccugugcugccucuccau zma-miR528a-3p 1 ccugugcugccucuccau	21 2 20
DE barley mapped read	TCCTGTGCTGCCTCTTCCAT	miR528	NA	<i>mla6</i> 24 HAI (2.07), <i>mla6</i> 32 HAI (2.19)	UserSeq 2 ccugugcugccucuccau zma-miR528a-3p 1 ccugugcugccucuccau	21 2 20
DE barley mapped read	TGAAGGGGCATGCAGAGGA	miR528	NA	<i>mla6</i> 32 HAI (1.86)	UserSeq 1 uggaaggggcaugcagagga osa-miR528-5p 1 uggaaggggcaugcagagga	20 1 20

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	TGGAAGGGCATGCAGAGGAG	miR528	NA	<i>mla6</i> 16 HAI (2.20), <i>mla6</i> 20 HAI (2.40), <i>mla6</i> 24 HAI (2.21), <i>mla6</i> 32 HAI (2.09)	UserSeq 1 osa-miR528-5p 1 UserSeq 1 zma-miR528a-3p 1 none	21 21 21 21 NA
DE barley mapped read	CCTGTGCTGCCTCTTCCATT	miR528	NA	<i>mla6</i> 0 HAI (1.99)	21 21 21 21 21	0
DE predicted miRNA	ATTTTGCTTCGTATGTAGACT	none	17	<i>mla6</i> 0 HAI (1.97)	NA	NA
DE predicted miRNA	TATTAGTTGACAGAGGGAGTA	none	5	<i>mla6</i> 48 HAI (-1.77), <i>mla6</i> - <i>bin1</i> 48 HAI (-2.44), <i>bin1</i> 48 HAI (-2.40)	NA	NA
DE predicted miRNA	AACTAGTACTACTCTAATGTGCCT	none	3	<i>mla6</i> 0 HAI (-1.07)	NA	NA
DE predicted miRNA	GCTTTCATAGCTCAGTTGGTTA GAGCACCCG	none	1	<i>bin1</i> 32 HAI (1.64)	NA	NA
DE predicted miRNA	AATTTGAACGTGTGAAACT	none	1	<i>mla6</i> 0 HAI (1.46), <i>mla6</i> 20 HAI (1.76), <i>mla6</i> 24 HAI (1.56)	NA	NA