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

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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>.



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	<i>bin1</i> 16 HAI (-2.55), <i>bin1</i> 20 HAI (-2.39), <i>mi66</i> 20 HAI (-1.77), <i>rar3</i> 20 HAI (-2.14), <i>bin1</i> 24 HAI (-2.47), <i>mi66</i> 24 HAI (-2.02), <i>bin1</i> 48 HAI (-2.41), <i>mi66</i> 48 HAI (-1.78)	UserSeq 1 ucggaccaggcuucaugcccc bdi-miR166d-3p 1 ucggaccaggcuucauuccc	21 1
DE barley mapped read	TTCGGACCAGGCTTCCTTCCC	miR166	NA	<i>mi66</i> 48 HAI (1.92)	UserSeq 2 ucggaccaggcuucauuccc gma-miR166i-3p 1 ucggaccaggcuucauuccc	21 20
DE barley mapped read	TGGACCAGGCTTCATGCCCC	miR166	NA	<i>bin1</i> 20 HAI (-2.24), <i>rar3</i> 20 HAI (-1.71)	UserSeq 1 uggaccaggcuucauuccc tcc-miR166a 1 ucggaccaggcuucauuccc	21 21
DE barley mapped read	TCGGACCAGGTTTCATGCCCC	miR166	NA	<i>bin1</i> 48 HAI (-2.31), <i>mi66</i> 48 HAI (-1.80)	UserSeq 1 ucggaccaggcuucauuccc hvu-miR166b 1 ucggaccaggcuucauuccc	21 21
DE barley mapped read	TTCGGACCAGGCTTCAGTCCC	miR166	NA	<i>rar3</i> 48 HAI (-2.10)	UserSeq 2 ucggaccaggcuucauuccc gma-miR166j-3p 1 ucggaccaggcuucauuccc	21 20
DE predicted miRNA	ACACAAACCGGACTAAAG	miR2120	9	<i>mi66</i> 20 HAI (1.59)	UserSeq 1 acacaaacgggacuaaag osa-miR2120b-5p 1 acacaaacgggacuaaag	19 19
DE predicted miRNA	GTGTTCTCAGGTCGCCCCCGC	miR398	2	<i>mi66</i> 32 HAI (2.03)	UserSeq 1 guguucucaggucgccccg zma-miR398a-3p 2 guguucucaggucgccccg	20 21
DE predicted miRNA	AGAACAGAGAATGGCGATAG ACTC	miR398	1	<i>mi66</i> 0 HAI (1.63), <i>mi66</i> 20 HAI (1.72), <i>mi66</i> 24 HAI (1.66), <i>mi66</i> 48 HAI (1.93)	UserSeq 1 agaacagagaauaggauag csi-miR398a-5p 1 agaacagaggugcgguugg	20 20
DE barley mapped read	TGTGTTCTCAGGTCGCCCCCGC	miR398	NA	<i>mi66</i> 24 HAI (1.71), <i>mi66</i> 32 HAI (2.57)	UserSeq 1 uguguucucaggucgccccg zma-miR398a-3p 1 uguguucucaggucgccccg	21 21
DE predicted miRNA	TCCTGTGCCTGCCTCTTCCAT	miR528	1	<i>mi66</i> 20 HAI (1.97), <i>mi66</i> 24 HAI (2.27), <i>mi66</i> 32 HAI (2.18)	UserSeq 2 ccugugccugccuuccau zma-miR528a-3p 1 ccugugccugccuuccau	21 20
DE barley mapped read	TCCTGTGCCTGCCTCTTCCAT	miR528	NA	<i>mi66</i> 24 HAI (2.07), <i>mi66</i> 32 HAI (2.19)	UserSeq 2 ccugugccugccuuccau zma-miR528a-3p 1 ccugugccugccuuccau	21 20
DE barley mapped read	TGGAAGGGGATGCAGAGGA	miR528	NA	<i>mi66</i> 32 HAI (1.86)	UserSeq 1 uggaaggggcaugcagagga osa-miR528-5p 1 uggaaggggcaugcagagga	20 20

