CORRIGENDUM

Correction to: A haplotype-resolved, de novo genome assembly for the wood tiger moth (*Arctia plantaginis*) through trio binning

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In the original version of the article "A haplotype-resolved, de novo genome assembly for the wood tiger moth (*Arctia plantaginis*) through trio binning" by Eugenie C. Yen et al. [1] there were a number of mis-reported statistics in Table 1.

In the bottom section, the result is incorrect as this is the number of element types identified rather than the number of elements identified in the genome as these types may occur multiple times. Therefore, the correct number of elements that should be reported are as below:

The numbers have been corrected in the published manuscript, and the authors apologize for the error.

References

1. Yen EC, McCarthy SA, Galarza JA et al. A haplotype-resolved, de novo genome assembly for the wood tiger moth (*Arctia plantaginis*) through trio binning. GigaScience 2020;**9**(8):1–12. https://doi.org/10.1093/gigascience/giaa088.

Table 1.

Genome annotation statistics		iArcPla.TrioW (paternal)	iArcPla.TrioY (maternal)
Total Genome size (bp)		584 621 344	577 993 050
Repetitive sequences (bp)		239 949 688	247 356 128
Masked repeats (%)		41.04	42.8
Mapped RNA-seq reads (n)		599 065 138	590 780 528
Mapped RNA-seq reads (%)		95.45	94.13
Protein-coding genes (n)		19 899	18 894
Mean gene length (bp)		5 966	5 951
BUSCO Completeness (%; n:1658)		98	95.9
Repeat Elements (n)	Total	1 220 592	1 232 654
	DNA Transposons	366 732	372 834
	LTR	127 169	139 770
	LINES	425 833	433 388
	SINES	43 022	71 790
	Unclassified	257 836	214 872