Corrigendum

Expanded functionality, increased accuracy, and enhanced speed in the de novo genotyping-by-sequencing pipeline GBS-SNP-CROP

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In the original article, there was an error in the formatting of Table 1.

This has been corrected and the corrected table appears below.

Table 1. Comparative summary of GBS-SNP-CROP v.4.0 performance, based on a set of simulated data from GBS-Pacecar

| Pipeline | MR geno | Time (min) | Variants called | Type I error | Type II error | Accuracy |
|----------|---------|------------|-----------------|--------------|--------------|----------|
| UNEAK    | NA      | 8.5        | 2642            | 0.9%         | 92.5%        | 7.5%     |
| GSC v.1.0| 1       | 370.8      | 23 395          | 1.3%         | 34.1%        | 65.4%    |
| GSC v.4.0| 1       | 121.7      | 29 738          | 0.6%         | 15.6%        | 84.0%    |
|          | 5       | 156.9      | 26 885          | 0.6%         | 23.6%        | 76.0%    |
|          | 10      | 171.5      | 26 854          | 0.5%         | 23.7%        | 76.1%    |
|          | 15      | 179.1      | 26 897          | 0.5%         | 23.6%        | 76.1%    |
|          | 20      | 183.0      | 26 892          | 0.5%         | 23.6%        | 76.1%    |
|          | 25      | 163.2      | 26 901          | 0.5%         | 23.5%        | 76.2%    |

Note: In total, 25 000 SNPs and 10 000 indels were simulated across a genomic space of 100 000 GBS fragments. A total of 60 002 165 single-end reads were simulated for a population of 25 individuals (average of 2.4 million reads per genotype), with a sequencing error rate of 1.1%. See Supplementary Table S1 for more details.

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