CORRECTION

Correction to: The application of deep learning for the classification of correct and incorrect SNP genotypes from whole-genome DNA sequencing pipelines

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The original version on this paper contained an error. Figure 5 was published with the same image of figure 4. The correct figure 5 is presented here. The original article has been corrected.

The online version of the original article can be found at https://doi.org/10.1007/s13353-020-00586-0
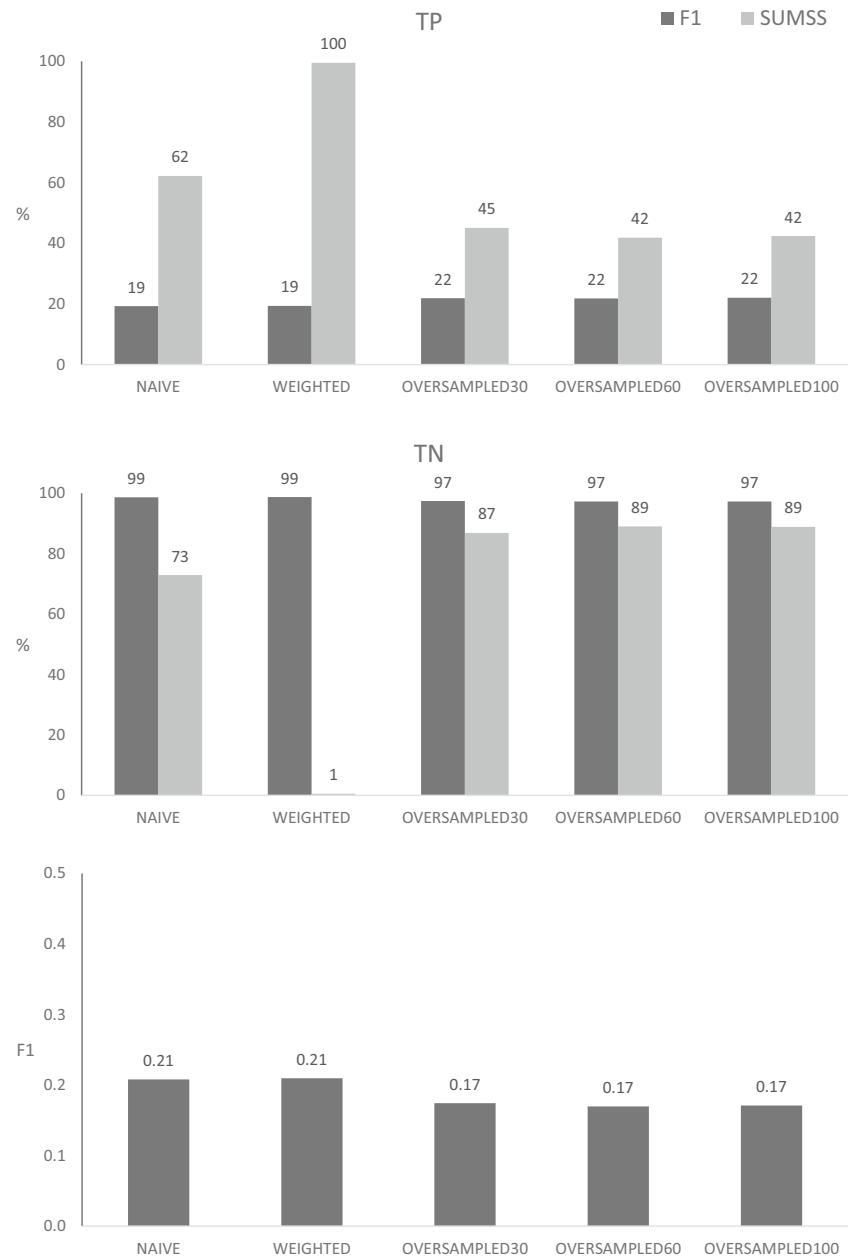
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Fig. 5 Classification of validation data by the different algorithms, based on the probability cutoff thresholds estimated for the F1 or SUMSS metrics. The numbers above columns represent TP—percentages of true positive results, TN—percentages of true negative results, F1—values of the F1 metric