Population Genomics in Sardinia: a novel approach to hunt for genomic combinations underlying complex traits and diseases

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The wrong figure was used for the paper. The correct Fig. 1 follows:

Fig. 1. Minimum sampling gives a reliable estimate of five microsatellite polymorphisms in a well-defined Mendelian breeding unit. When derived from a good representative sampling of a breeding unit, estimates of the individual allelic frequencies remain essentially the same when calculated on progressively smaller sample aliquots of the total number of observations. Chi-square analysis showed that even the largest deviation observed in the smallest group (about 20% of the total) is not significant at the 5% confidence level.