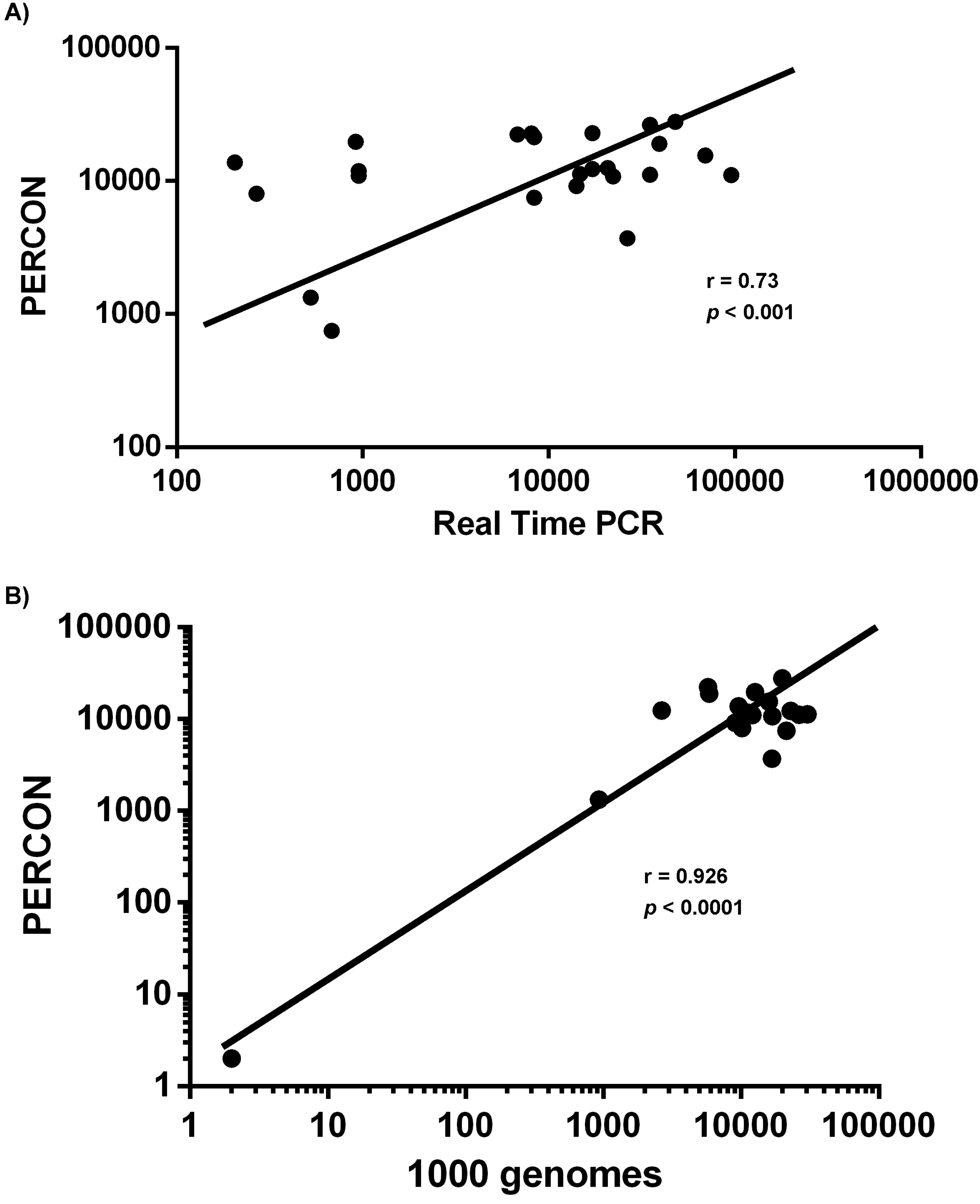
A)
PERCON
100000
10000
1000
100
100
1000
10000
100000
1000000
Real Time PCR
r = 0.73
$p < 0.001$
B)
PERCON
100000
10000
1000
100
10
1
1
10
100
1000
10000
100000
1000 genomes
r = 0.926
$p < 0.0001$

Figure S8. **Positive correlation of copy number in each centromeric array as determined by qPCR assays, *in silico* analysis of the 1000 Genomes Project, and the PERCON Analysis on hg38**. A) Correlation of α-repeat copy number in each array determined by qPCR and PERCON bioinformatics analysis. The average values are shown in Table 1. The Spearman's correlation coefficient and the *p* value are shown. A statistically significant positive correlation was found between the two detection methodologies. A discordant correlation was found in the arrays D7Z1, D13Z1/D21Z1, D20Z2, D4Z1, D12Z3, D15Z3 and D17Z1. B) Correlation of the copy number of α-repeats in each array determined by our bioinformatics analysis in the 1000 Genomes Project and the PERCON Analysis of hg38. The average values are shown in Table 1. The Spearman's correlation coefficient and the *p* value are shown. A statistically significant positive correlation was found using the two bioinformatics methodologies.