Supplementary Table 1. Calculation of the proportion using locus-DNA containng probability ©

C= 0.044

No. amplicons detedted by one PCR run	$_4C_n$	P	4Cn*P	Correction by the same alleles						Corrected Proportion	Observation		
				Duplica	Triplic	Quadrupli	Dup	Dupl	Two D		Observed number	Observed proportion	Residual sum of squares
0	1	0.8353	0.835279							0.83527901	427	0.8388998	1.31101E-05
1	4	0.0384	0.153775	0.0018	2E-05	5.86E-08				0.15555992	80	0.15717092	2.59532E-06
2	6	0.0018	0.010616	-0.002			0	0		0.00886293	2	0.00392927	2.4341E-05
3	4	8E-05	0.000326		-2E-05		-0		0	0.00029485	0	0	8.69387E-08
4	1	4E-06	3.75E-06			5.86E-08		-0	-0	3.3967E-06	0	0	1.15377E-11
Sum			1							1.00000	509		4.01334E-05

Supplementary Table 2. Simulation of the proportion

	Locus-DNA containing probability (C				
No. ampl. Detedted	0.01	0.05	0.1	0.2	0.3
0	0.961	0.8145	0.6561	0.4096	0.2401
1	0.039	0.1738	0.29987	0.4364	0.4594
2	5E-04	0.0113	0.040689	0.1295	0.2257
3	4E-06	0.0004	0.003253	0.0231	0.0678
4	9E-09	6E-06	9.06E-05	0.0015	0.0073
Residual sum o	0.029	0.0009	0.055141	0.2786	0.5037

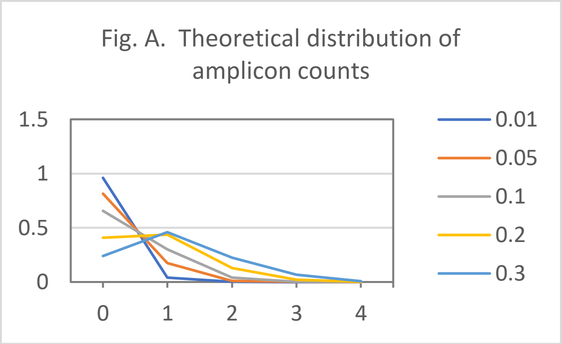

Fig. A. Theoretical distribution of amplicon counts

Supplementary Table 3. Comparison between observed and simulated distributions

No. ampl. Detedted	0.044	Observed	Residural square
0	0.835	0.8389	1.31E-05
1	0.156	0.1572	2.6E-06
2	0.009	0.0039	2.43E-05
3	3E-04	0	8.69E-08
4	3E-06	0	1.15E-11
Residual sum of squares			4.01E-05

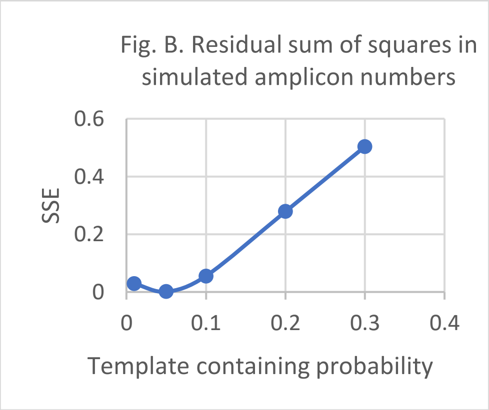

Fig. B. Residual sum of squares in simulated amplicon numbers

Supplementary File. Calculation of probability

Let **p** be the probability that any allele is detected by PCR (i.e., the locus-DNA containing probability, **C**). Then, the probability of each amplicon count (**n**, ranging from 0 to 4)—representing the number of alleles detected in a PCR run—is given by:

$_4C_n \times (1-p)(1-n) \times (p)n$.

If the amplicon count is 2 or more, the detected alleles may include two or more that are identical in size. In such cases, the apparent amplicon count may be lower than the actual number. This probability can be calculated using the same approach as the main formula—by multiplying the number of events by their respective probabilities. To correct for this, the calculated probability of size-identical alleles is subtracted from the probability of the original amplicon count and added to the probability of the corresponding lower amplicon count.