CLAIMS

1. A method for developing an assay for identification of a human race from a sample comprising the steps of:

(a.) ~~shortlisting a plurality of genetic variations representative of at least four races types;~~shortlisting ten SNPs representative of at least four race types via analyzing SNP allele frequencies and corresponding ethnicities via at least one correspondence database, the ten SNPs comprise loci rs12913832 (Region: HERC2 gene), rs1426654 (Region: SLC24A5 gene), rs28777 (Region: SLC45A2 gene), rs3827760 (Region: EDAR gene), rs1015869 (Region: intergenic region of Chr 6), rs1800414 (Region: OCA2 gene), rs3935223 (Region: intergenic region of Chr 2), rs6569733 (Region: AKAP7 gene), rs6429644 (Region: SLC6A9 gene), and rs3176383 (Region: MPG gene);

(b.) configuring, via the use of a microarray, probes and primers associated with each of the ~~plurality of~~ten SNPs, the configuration comprises a step of introducing mismatches to the microarray in order to strengthen or reduce binding to specific DNA strands corresponding to the shortlisted SNPs;

(c.) detecting whether a plurality of probe signals are present and if present, sending the detected probe signals to a first ML/AI engine; and

(d.) distinguishing between probe signals by the first ML/AI engine to provide at least one SNP call; wherein the first ML/AI engine generates at least one SNP combination having a predetermined number of characters~~.~~; and

~~2. The method of claim 1, wherein the plurality of genetic variations includes single-nucleotide polymorphisms (SNP), and wherein each of the at least one SNP combination comprises ten (10) characters.~~

~~3. The method of claim 1 or 2, the method further comprises the step of~~(e.) sending the at least one SNP combination to a second ML/AI engine for a prediction of human race~~.~~

~~4. The method of claim 3,~~; wherein the prediction of human race may include

a step of training the second ML/AI engine, the step of training the second ML/AI engine includes a step of calculating model parameters. based on a Mahalanobis distance calculation method.

5. 2. The method of claim 41, wherein the calculationidentification of model parameters is based on a Mahalanobis distance calculation method.

6. The methodhuman race requires the combination of any oneall of the preceding claims, wherein the step of shortlisting a plurality of genetic variations includes shortlisting ten 10 SNPs via analyzing SNP allele frequencies and corresponding ethnicities via at least one correspondence databasesequences.

73. The method of claim 61, wherein the SNP allele frequencies for each human race were first arranged according to a highest frequency to a lowest frequency based on predetermined threshold.

84. The method of claim 73, wherein the predetermined threshold may include a higher allele frequency of 0.9 and a lower allele frequency of 0.1.

95. The method of claim 84, wherein the SNPs with the highest and lowest frequencies were selected and compared across the different human races.

10. A method for developing an assay for identification of a plurality of phenotypic traits from a sample comprising the steps of analysing if the sample belongs to a human being; if determined to be a human being;

(a.) analysing if the human being is a male or a female;

(b.) determining the blood type of the human being; wherein the step of determining the blood type of the human being includes performing at least one SNP allele discrimination for ABO gene.

11. The method of claim 10, wherein the SNP allele discrimination for ABO gene includes sending the at least one SNP allele to a ML/AI engine for prediction of blood group.

12. The method of claim 10, further comprises a step of training the ML/AI engine,

~~wherein the step of training includes a step of generating microarray signal data using known samples and using a support vector machine algorithm of the ML/AI engine to calculate the model parameters.~~

~~13. The method of claim 12, wherein after the model parameters are derived, the model parameters are input to an algorithm to predict/classify the right SNP allele judgement when presented with the microarray signals from an unknown sample and subsequently, a blood type judgement of the sample.~~

~~14. The method of claim 13, wherein the development of primer and probe sequence(s) for identification of ABO blood type is designed based on an introduction of artificial base-substitutions.~~

~~15. The method of claim 14, wherein the introduction of artificial base-substitutions is followed by an in-silico (performed by a computer processor/chip) calculation and verification.~~

~~16~~6. A system for developing an assay for identification of a human race from a sample comprising:

a LOC device configured to receive the sample, the LOC device comprises at least one microarray;

a processor configured to: (a.) shortlist ~~a plurality of genetic variations~~ten SNPs representative of a plurality of ~~races~~race types~~; (b.)~~ by analyzing SNP allele frequencies and corresponding ethnicities via at least one correspondence database that comprises of loci rs12913832 (Region: HERC2 gene), rs1426654 (Region: SLC24A5 gene), rs28777 (Region: SLC45A2 gene), rs3827760 (Region: EDAR gene), rs1015869 (Region: intergenic region of Chr 6), rs1800414 (Region: OCA2 gene), rs3935223 (Region: intergenic region of Chr 2), rs6569733 (Region: AKAP7 gene), rs6429644 (Region: SLC6A9 gene), and rs3176383 (Region: MPG gene); (b.) configure, via the use of the microarray, probes and primers associated with each of the ~~plurality of genetic variations~~ten SNPs, the configuration comprises a step of introducing mismatches to the microarray in order to strengthen or reduce binding to specific DNA strands corresponding to the shortlisted SNPs; (c.) detect whether a

plurality of probe signals are present; ~~and~~

a first ML/AI engine to receive the plurality of probe signals and if present, send the detected probe signals to a first ML/AI engine to distinguish between probe signals to provide at least one SNP call; wherein the first ML/AI engine generates at least one SNP combination having a predetermined number of characters~~.~~; and

~~17. The system of claim 16, further comprises~~ a second ML/AI engine to receive the at least one SNP combination to determine or predict a human race type associated with the at least one SNP combination, the second ML/AI engine implements a Mahalanobis distance calculation method.

~~18. A system for developing an assay for identification of a plurality of phenotypic traits from a sample comprising:~~

~~a LOC device configured to receive the sample, the LOC device comprises at least one microarray;~~

~~a processor configured to analysing if the sample belongs to a human being, and if determined to be a human being, the processor is configured to (a.) analyse if the human being is a male or a female; (b.) determine the blood type of the human being; wherein the step of determining the blood type of the human being includes performing at least one SNP allele discrimination for ABO gene.~~

~~19~~7. A non-transitory computer readable medium having stored thereon software instructions that, when executed by a processor, cause the processor to execute the steps of claims 1 to ~~9, and/or claims 10 to 15~~5.