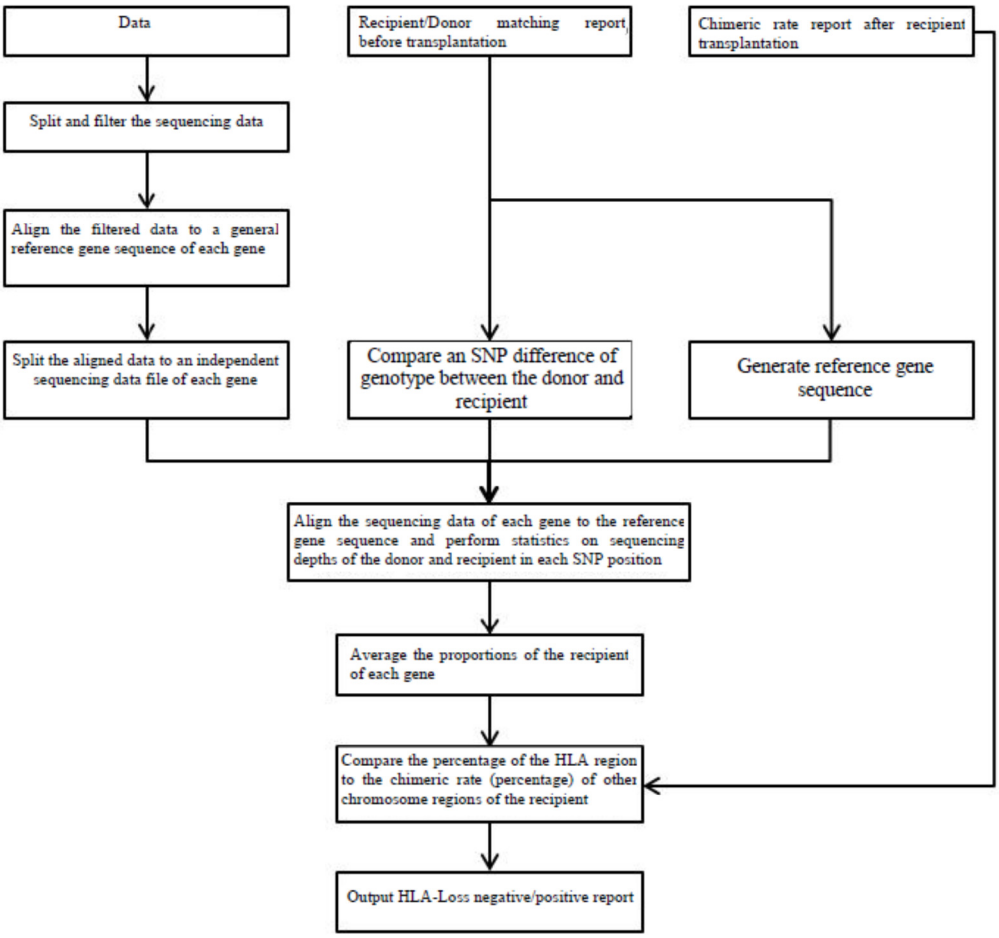
Data
Recipient/Donor matching report before transplantation
Chimeric rate report after recipient transplantation
Split and filter the sequencing data
Align the filtered data to a general reference gene sequence of each gene
Split the aligned data to an independent sequencing data file of each gene
Compare an SNP difference of genotype between the donor and recipient
Generate reference gene sequence
Align the sequencing data of each gene to the reference gene sequence and perform statistics on sequencing depths of the donor and recipient in each SNP position
Average the proportions of the recipient of each gene
Compare the percentage of the HLA region to the chimeric rate (percentage) of other chromosome regions of the recipient
Output HLA-Loss negative/positive report

FIG. 1

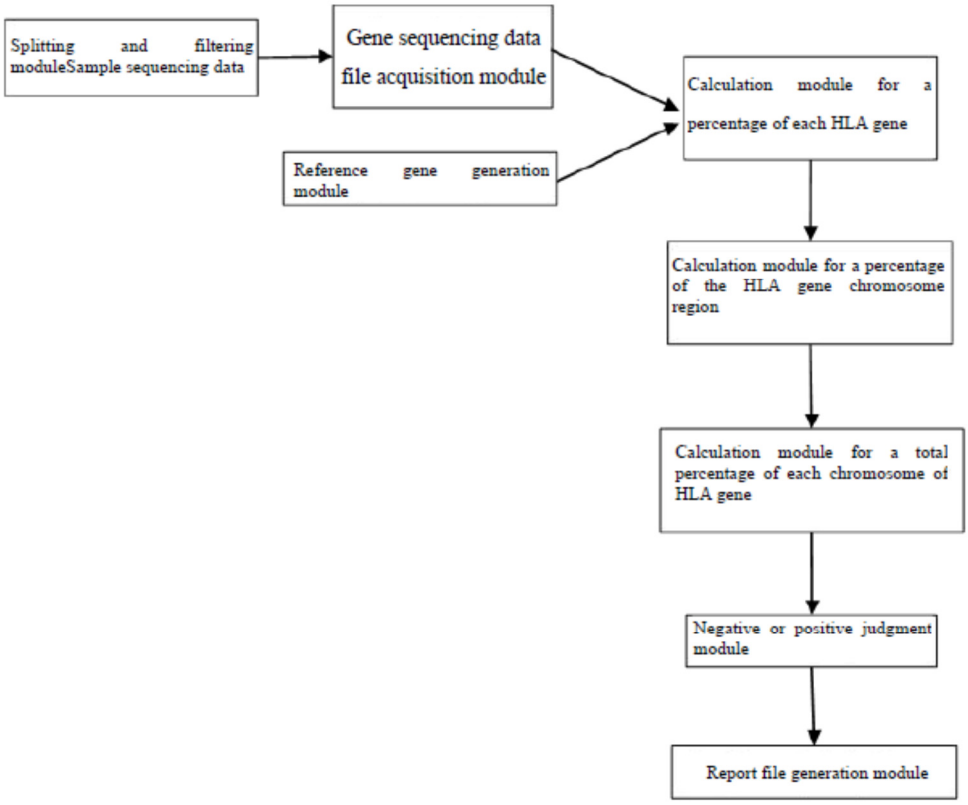
Splitting and filtering moduleSample sequencing data
Gene sequencing data file acquisition module
Reference gene generation module
Calculation module for a percentage of each HLA gene
Calculation module for a percentage of the HLA gene chromosome region
Calculation module for a total percentage of each chromosome of HLA gene
Negative or positive judgment module
Report file generation module

FIG. 2

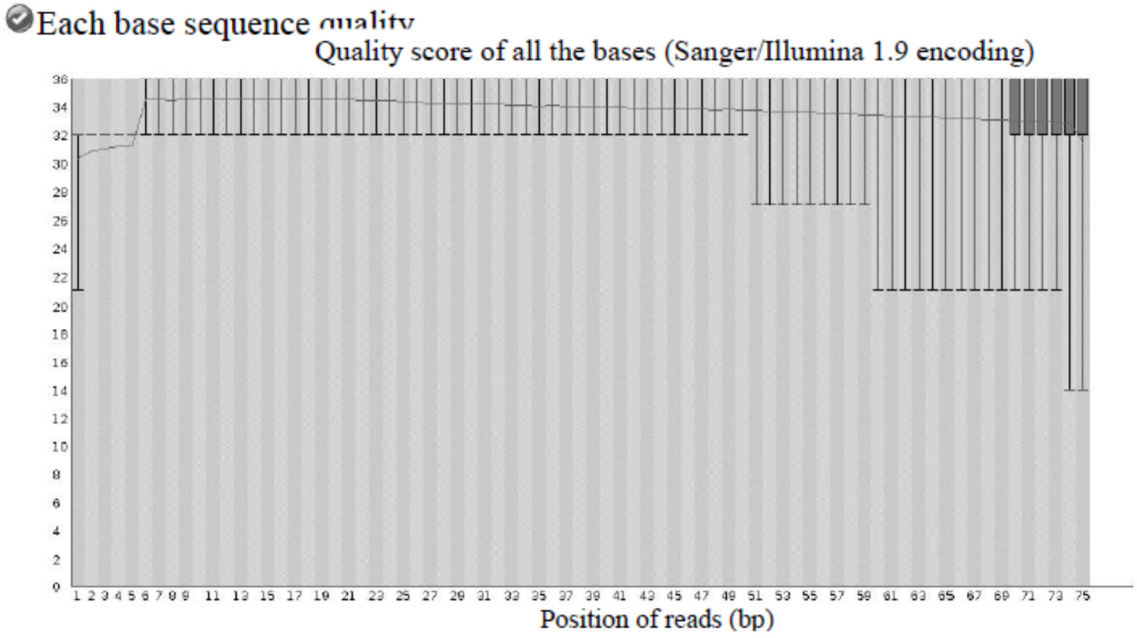
Each base sequence quality
Quality score of all the bases (Sanger/Illumina 1.9 encoding)
Position of reads (bp)

FIG. 3

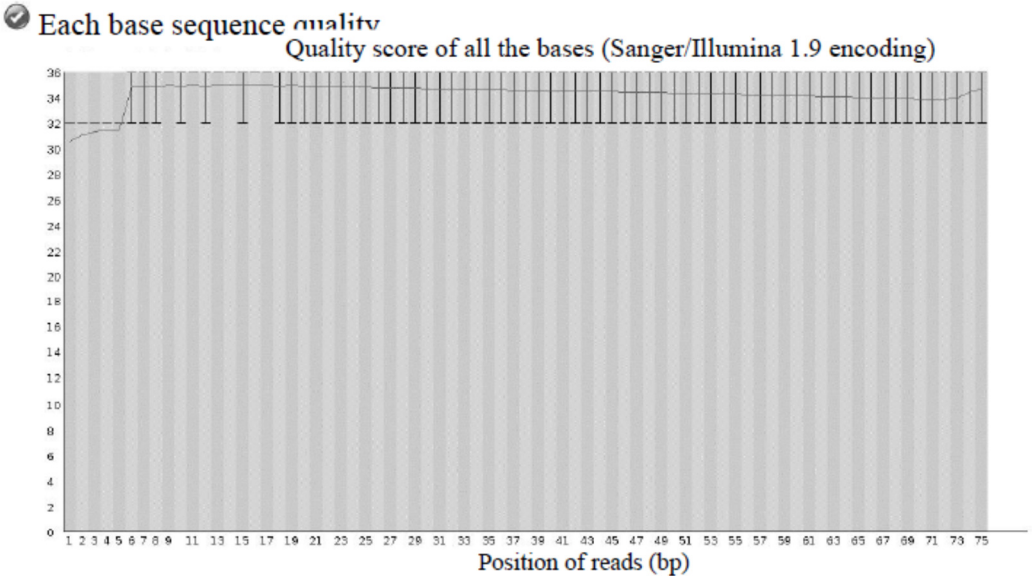
Each base sequence quality
Quality score of all the bases (Sanger/Illumina 1.9 encoding)
Position of reads (bp)

FIG. 4

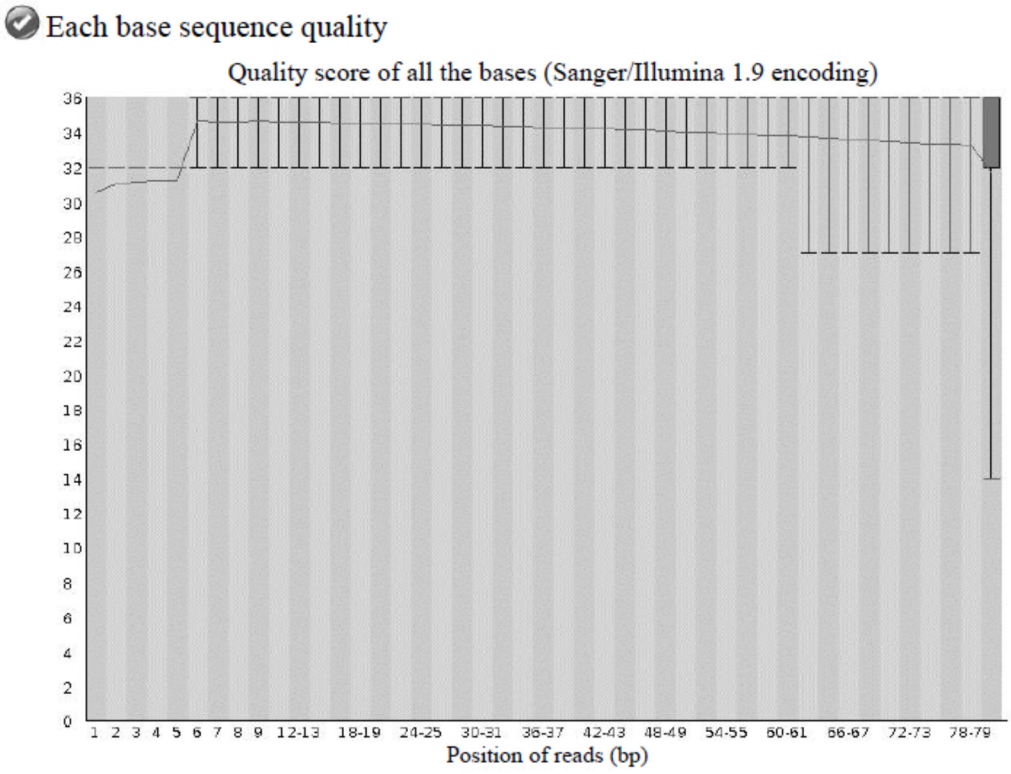
Each base sequence quality
Quality score of all the bases (Sanger/Illumina 1.9 encoding)
Position of reads (bp)

FIG. 5

Each base sequence quality

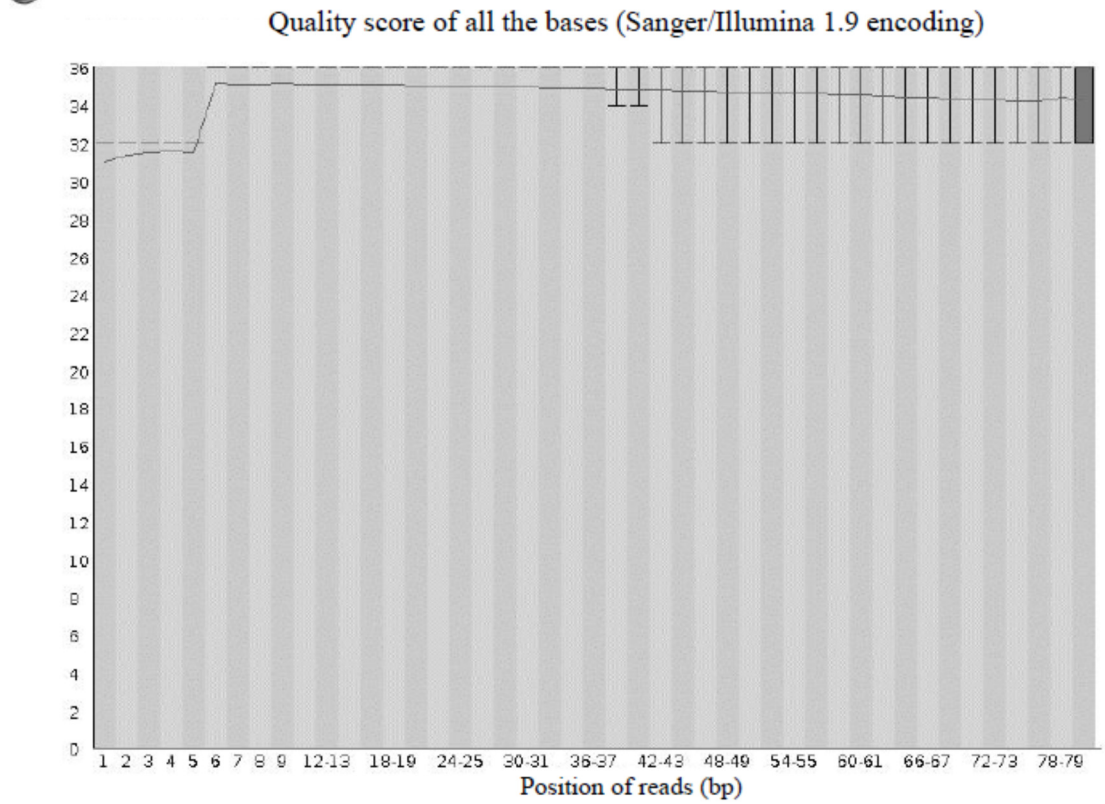

FIG. 6

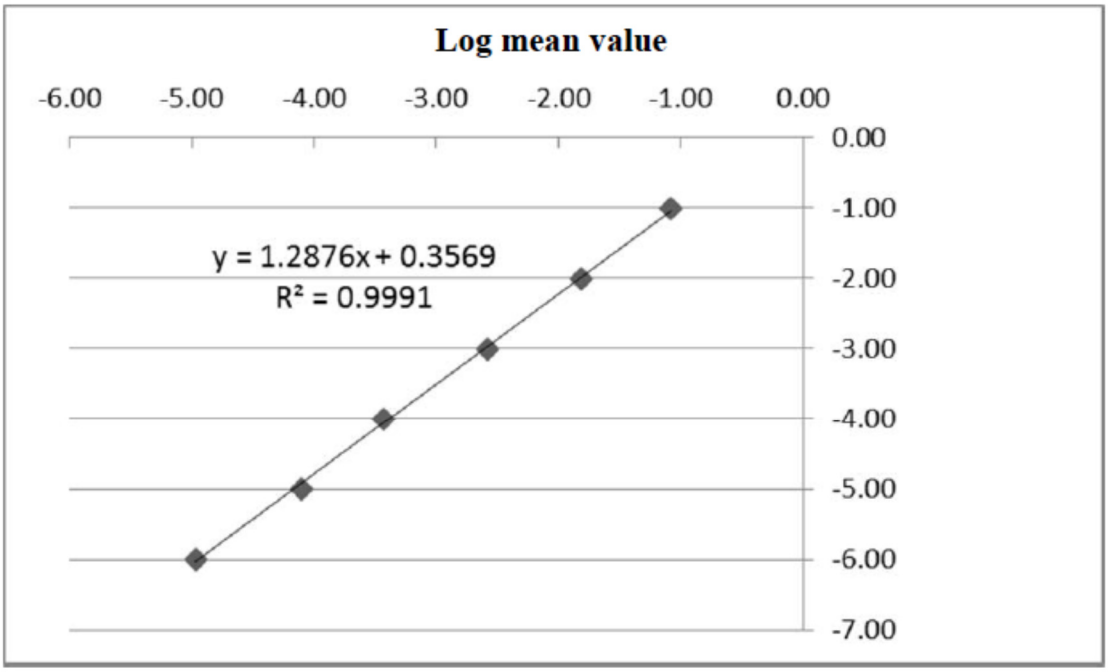

FIG. 7