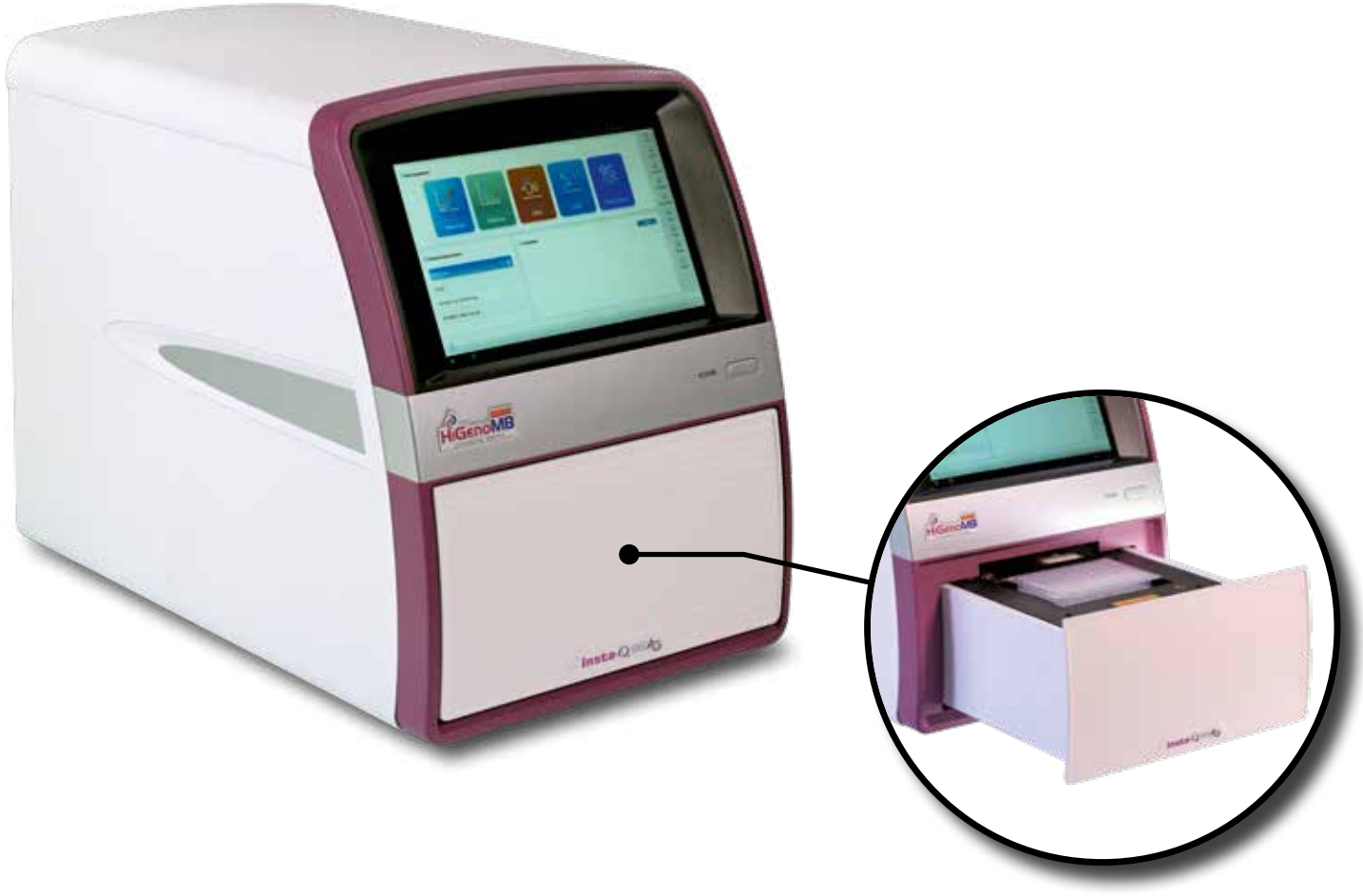
Touchscreen Real Time PCR

Insta-Q 96 AG



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Unzipping Genes

Product Description

Insta-Q96® AG is Inbuilt touch screen RTPCR system based on the excellent quality of the Insta-Q96® family, using the thermoelectric refrigeration technology, a light source and optical circuit design. The unique constant current power supply and 6-zone independent temperature control method ensure that the product is fast, accurate and stable in fluorescence quantitative analysis. The product adopts modular design, with a variety of configuration options, at the same time, the addition of temperature gradient, sample 4°C cryopreservation, automatic dehumidification and other functions, fully meet the scientific research and clinical medical needs.

Features

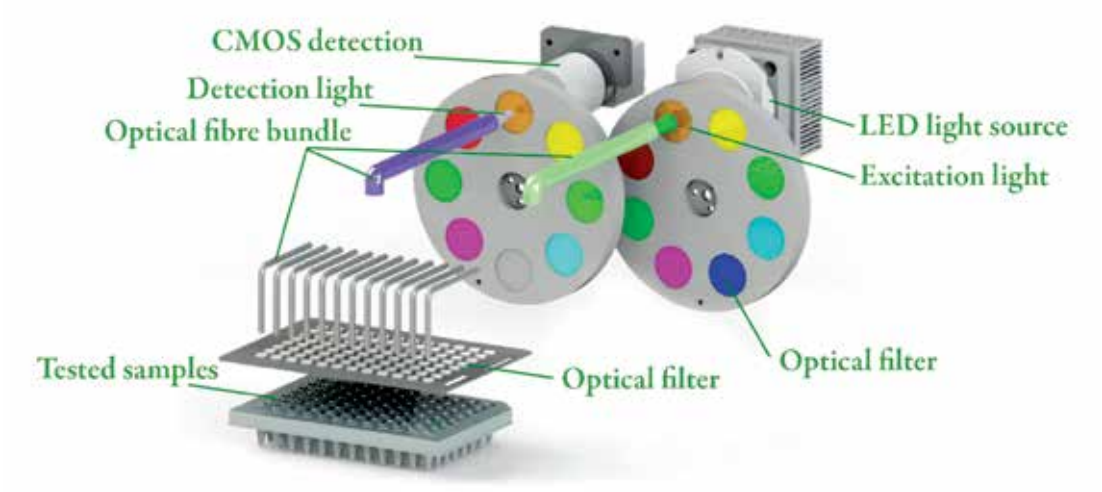
- 10” Inbuilt touchscreen for ease operation with 100 GB Inbuilt memory
- Top imaging CMOS detection
- 6 Segment thermal cycling module
- Automatic pop-up sample bin
- Intelligent adjustable hot cover
- Easy to operate software system
- Truely open system

Dye Library

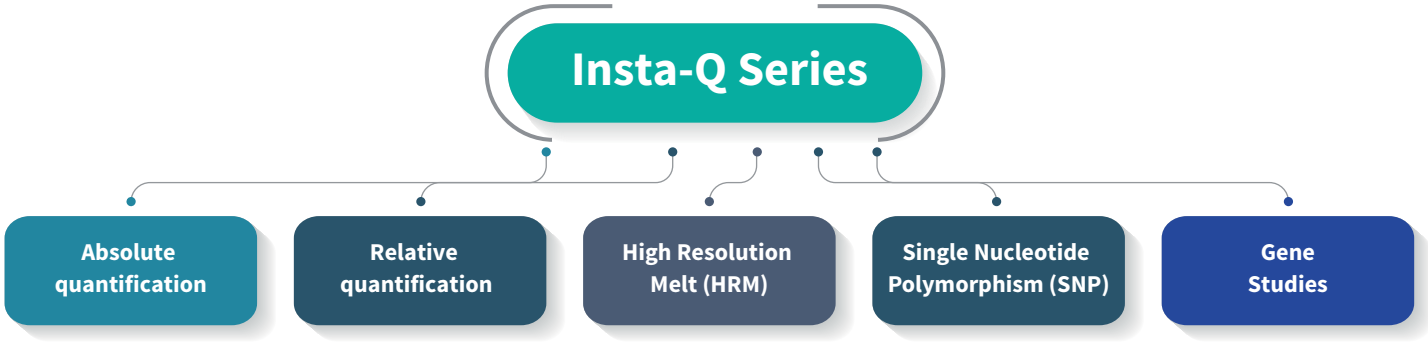
Channel Wavelength	Dyes
470nm – 525nm	FAM, SYBR, EvaGreen®
523nm – 564nm	HEX, JOE, TET, VIC, Cal Fluor® Gold 540 / Yakima Yellow
571nm – 612nm	ROX, TexRed, Cal Fluor® Red 610 / JUN
628nm – 692nm	CY5, Mustang Purple / Quasar 670 / Pulsar 650
678nm – 718nm	Cy5.5, Quasar 705
550nm – 585nm	TAMRA, NED, Cy3, ABY

Working Principle of the Machine

- Peltier technology used for thermal cycling during PCR assay.
- LED based excitation source with advanced fibre optic transmission technology for Sensitive and Reliable photoelectric detection system.
- CMOS technology detects fluorescent emission.
- Scanning time period: 3 seconds for one channel. System scan all channels regardless of plate setup.



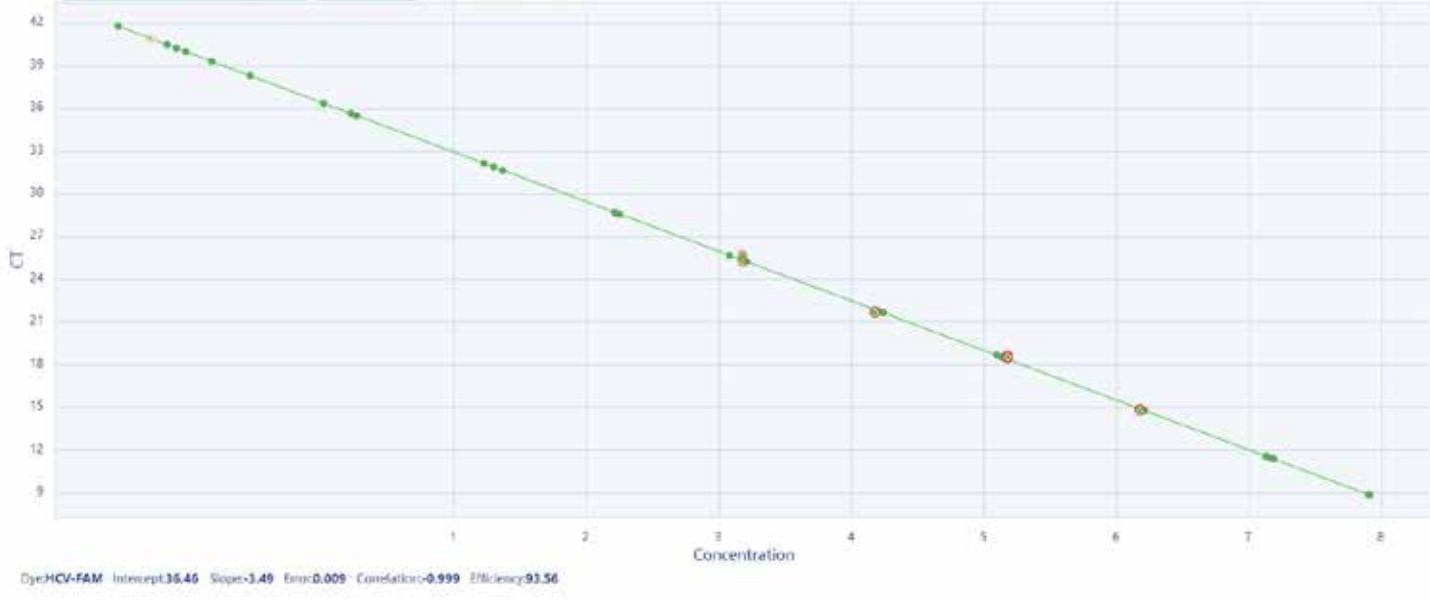
Analysis procedures supported by Insta-Q Series software



Absolute Quantification

- Absolute quantification is achieved by comparing the Ct values of the test samples to a standard curve.
- The result of the analysis is quantity of nucleic acid (copy number, unit mass) per given amount of sample (per cell, per ng of total RNA).
- Absolute quantitation uses serially diluted standards of known concentrations to generate a standard curve.
- Standard curve produces a linear relationship between Ct and initial amounts of total DNA or cDNA from RNA of the Gene of interest (GOI), allowing the determination of the concentration of unknowns based on their Ct values.
- The linearity is denoted by the R squared (r^2) value (r is Pearson Correlation Coefficient) and should be very close to 1 (> 0.985).
- The efficiency of both the standard curve and sample reactions should be between 90 and 110%.
- The instrument can also be used to quantify ready to load NGS libraries using standard SYBR based assays allowing for accurate library quantification and precise loading into Illumina sequencing machines.

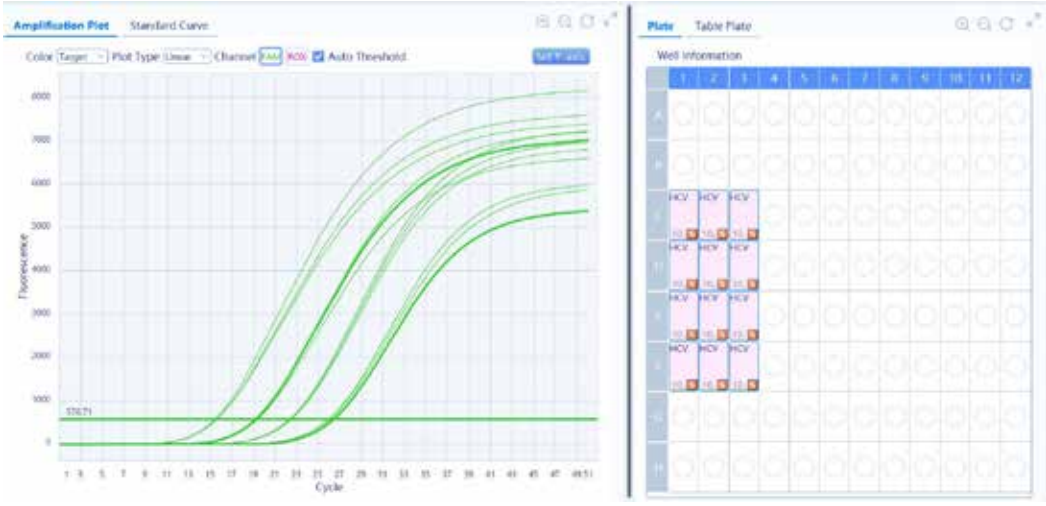
Standard Quantification Assay



Plotting a Standard Curve

- In absolute quantification, the quantity (e.g., copy number or unit mass) of the unknown sample is interpolated from a range of standards of known quantity.
- To construct a standard curve, a template with known concentration is required.
- Dilution of this template is then performed and these dilutions serve as the standards. The unknown test samples are assayed with the standards in the same experimental run.
- The standard curve constructed from the diluted standard template can then be used to determine the target quantity in the unknown sample by interpolation, similarly to using molecular size standards to determine the molecular size of an unknown DNA band on an agarose gel.
- Standard curve can be imported from previous run experiments. It can be imported only in standard curve assays. Hence standards need not be run every time.

Software Analysis Interface



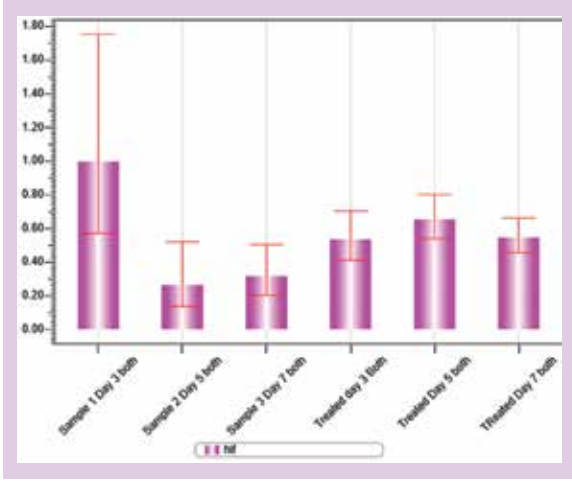
Relative Quantification

- Let's get the nomenclature settled.
  - The gene of interest whose expression is getting determined is the target gene.
  - The housekeeping gene whose expression is unregulated is called the reference gene.
  - The sample (or group of samples) being used as a control is the calibrator sample.
  - Finally, the sample (or group) that is being treated or tested for differences is the test sample.
  - The ratio of the target gene expression in the test sample over the calibrator sample is interchangeably called the expression fold change or relative gene expression.
- Amplification efficiency of the reaction is an important consideration when performing relative quantitation.
- Past methods of calculating gene expression have assumed the amplification efficiency of the reaction is ideal, or 1.
- Actual amplification efficiency values for a particular reaction can be established via a standard curve measurement during assay design, and multiple standard curves should be run to verify that this efficiency measurement is reproducible.
- Although absolute quantification can be useful in determining absolute quantities of target, the majority of scientific questions regarding gene expression can be accurately and reproducibly answered by measuring the relative concentration of the GOI in unknown samples.
- Differences in Ct value between an unknown sample and reference sample are expressed as fold- changes (i.e., up- or down- regulated) relative to the reference sample and thereby the results are expressed as a target/reference ratio.

Features

- Automated calculation of ΔCt and ΔΔCt values by software.
- Exact and final RQ values provided by software at the end of the assay.
- Easy and hassle free transfer of data to Excel or Word format on a Single Click.
- Option to import Standard curves run from other experiments in RQ assays as well.
- Normalization to multiple endogenous controls.

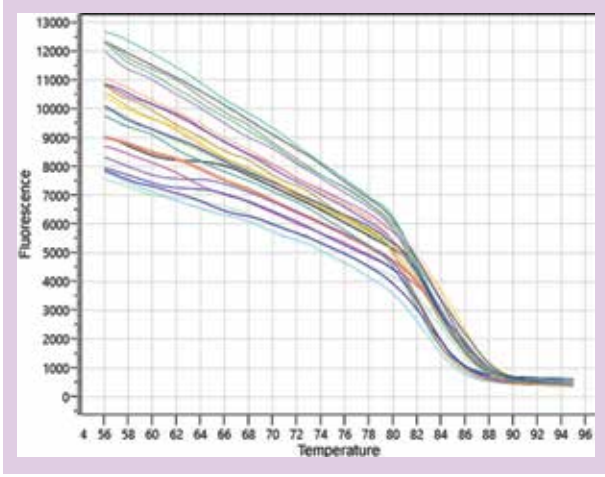
Relative Quantification



High-Resolution Melt Analysis

- The principle of HRM is the same as a Low-Resolution Melt curve, except that the temperature difference between each fluorescence reading is reduced.
- During a Low-Resolution Melt curve analysis, the temperature increases are typically in 0.5 °C steps, but for HRM this is reduced to 0.008 - 0.2 °C increments.
- This allows a much more detailed analysis of the melting behaviour.
- HRM sensitivity and reliability has been improved with the use of a variety of new dsDNA intercalating dyes viz., - LCGreen (R), SYTO9, EvaGreen (R), Chromofy and BEBO.

HRM data



Features

- HRM assays can be run using the same software. Saves the trouble of learning and procurring a new software.
- No external calibration required for running HRM assays.

- Cost effective compared to other genotyping technologies such as sequencing and TaqMan SNP typing.
- Fast and able to accurately genotype huge numbers of samples in rapid time.
- Fast and high-throughput analysis of post-PCR of genetic mutations or variance in nucleic acid sequences.
- With a good quality, HRM assay powerful genotyping can be performed by non-geneticists in any laboratory with access to an HRM capable Real-Time PCR machine.

HRM has renewed interest in the utility of DNA melting for a wide range of uses, including:

- Mutation discovery (gene scanning)
- Species identification
- Screening for loss of heterozygosity
- Somatic acquired mutation ratios
- DNA fingerprinting
- HLA compatibility typing
- SNP genotyping
- Association (case/control) studies
- Characterization of haplotype blocks
- Allelic prevalence in a population
- DNA methylation analysis
- Identification of candidate predisposition genes
- DNA mapping

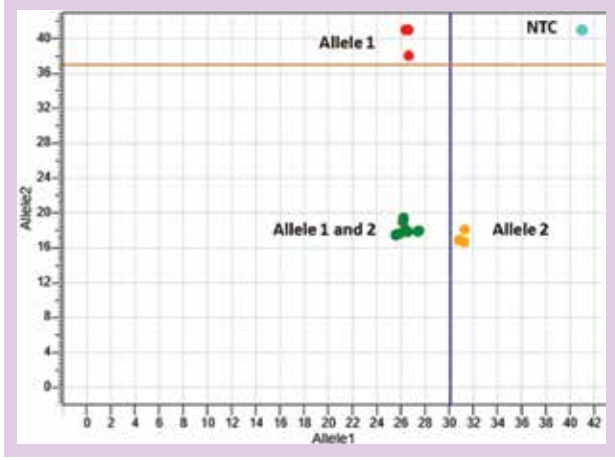
Single Nucleotide Polymorphism (SNP)

- A Single Nucleotide Polymorphism or SNP is a DNA sequence variation occurring when a single nucleotide in the genome differs between members of a species or two allele of a gene.
- Probe based SNP Genotyping Assays provide a highly flexible technology for detection of polymorphisms within any genome.
- Probe Assays have a simple workflow and provide a quick way to generate genotyping data.

Features

- Auto Call and Manual call options
- Easy and colour coded Scatter plot based on SNP assay analysis

SNP



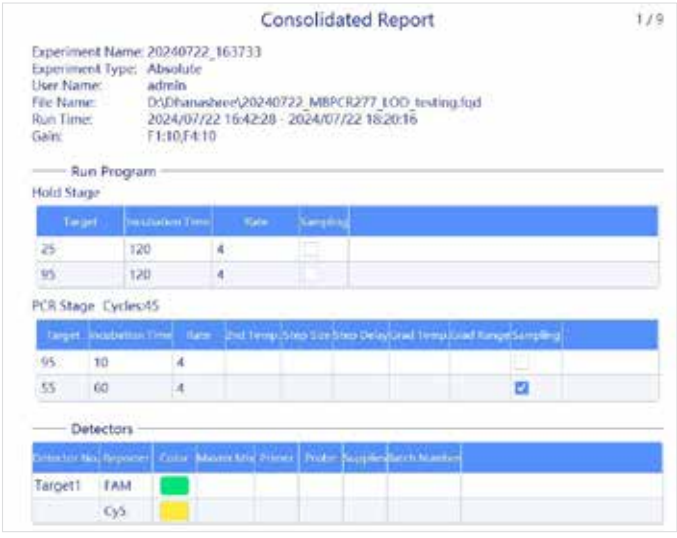
Gene Studies

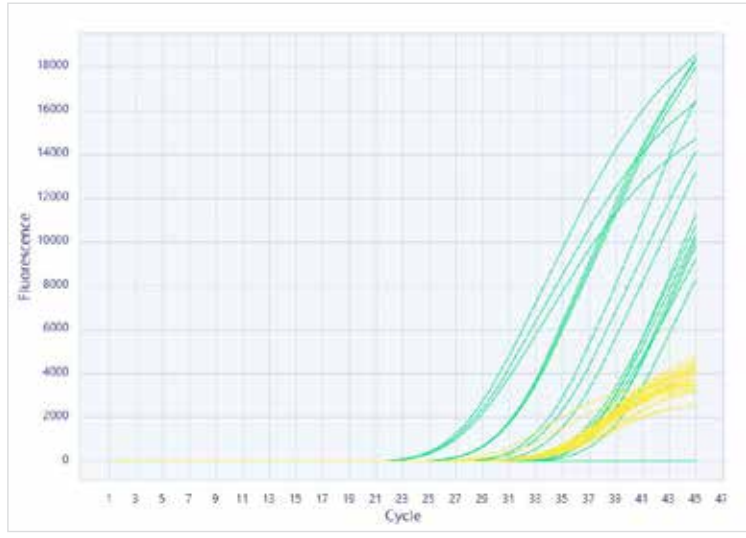
- Multiple plates combined into one expenment with the Gene Study Feature.
- Software has a reference Gene Selector Tool displaying gene stability for selection of ideal reference genes.
- Up to 5,000 Cq values from different data files will be compared for gene expression analysis.

Report Generation

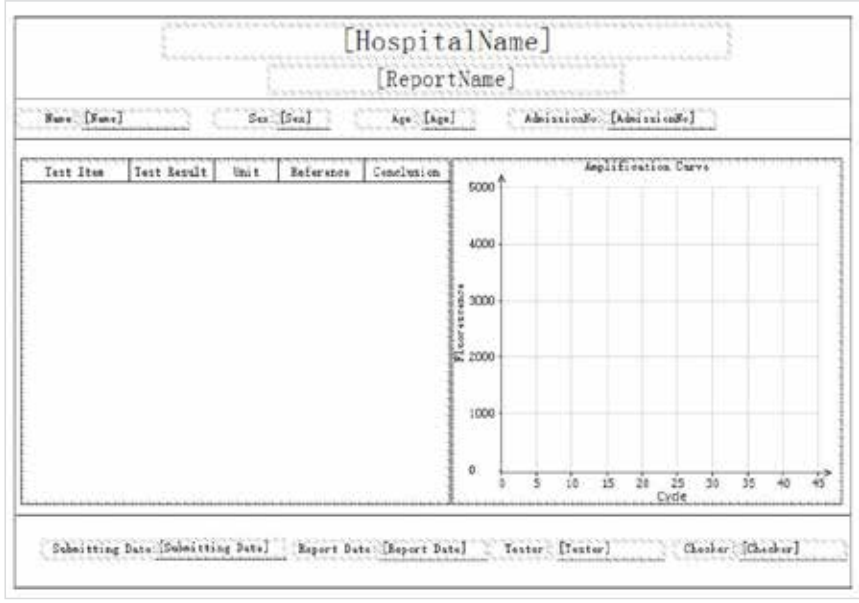
- Generate automatic assay reports at the end of PCR run.
- Customize assay reports as per requirement using built in report editor
- All in one consolidated report for
  - Accurate & concised experimental details
  - Basic experiment information
  - Experiment process
  - Plate diagram
  - Amplification curve
  - Result table with Ct values

Consolidated Report / QC Report





Report Template



Technical Specifications

Product Name	Insta-Q96® AG	Insta-Q96® AG 6.0
Product Code	MBLA027	MBLA028
Sample capacity	96 well (0.2ml tubes, strips & plate), 12x8 (0.2 mL) Strips	
Detection Channel	5 channels	6 channels
No. of Multiplexing	5 channels	6 channels
Reaction Volume	5-100 µL	
Dynamic Range	1~10^{10} Copies	
Excitation Wavelength	300-800nm	
Emission Wavelength	500-800nm	
Dyes	F1: FAM, SYBR Green I F2: VIC, HEX, TET, JOE F3: ROX, TEXAS -RED F4: Cy5, Quasar -670 F5: Cy5.5, Quasar -705	F1: FAM, SYBR Green I F2: VIC, HEX, TET, JOE F3: ROX, TEXAS -RED F4: Cy5, Quasar -670 F5: Cy5.5, Quasar -705 F6: TAMRA
Operating temp range	4°C-100°C	
Heating rate	6°C/s	
Cooling rate	5.5°C/s	
Avg Ramp rate	3.7°C/s	
Hot Lid temperature	105°C±5°C	
Temperature control accuracy	± 0.1°C	
Temperature uniformity	± 0.3°C	
Temp. Control Mode	Standard / Fast	
Gradient Temp. Range	1-36 °C (Zone to Zone , 6 Zones , ± 6°C Max)	
Mode of operation	Continuous operation	
Scan Period	3 seconds for one channel	
Feature Function	• Absolute Quantification • Automatic Data Analysis • Melt Curve • Genotyping • Gradient • Customized Parameters	• Relative Quantification • Multi-Channel Crosstalk Correction • HRM • SNP Analysis • Background • No passive reference dye required
Communication Interface	2 USB, WiFi, Ethernet	
Integrated memory	100 GB	
Data Export Format	Pdf, text, jpeg, excel, RDML, CSV	
Secure System Function	Secure user log in, Audit trails and electronic records , LIMS enabled	
Input power	100-240V~ 50Hz 1000VA	
Overall dimensions	490mm × 290mm × 391mm	
Weight	28 kg	
Certification	CE, IVDR	

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