

Sequencing set-up for Quantitative analysis.

Quantitative Analysis

- 1 Proven Pyrosequencing technology for real-time, sequence-based detection and quantification for genetic testing and epigenetic methylation analysis in the most economical way.
- 2 System should be dedicated for short read lengths and should be able to read 80-100 bp length.
- 3 Should be capable of running 1 – 24 with analysis in as little as 15 – 60 minutes.
- 4 The system should be unique enough to combine reliable quantification and sequencing results in minutes.
- 5 Reliable quantification of allele representation and methylation status for short read-lengths.
- 6 Sequence information should be able to discover rare mutations.
- 7 Methylation analysis should be able to be combined with SNP typing in one assay. Exact reliable percentage of methylation at a particular spot should be reportable.
- 8 The system should be suited for the discovery and analysis of di-, tri- or tetra allelic mutations as well as analysis and quantification of consecutive CpG sites.
- 9 The system should provide a sequencing instrument, sample preparation workstation, and reagents and controls.
- 10 System should come with comprehensive and flexible analysis software for assay designing and analysis.
- 11 It should allow to standardize primers and probes and a dedicated software with all possible combinations with hit ratio should be available to enable the user to choose the most optimized set of primers and sequencing primer.
- 12 It should be open to standardize sequence information and vendor should provide all the reagents and consumables to support standardization.
- 13 System should be backed up with the publication for all applications it claims to perform.
- 14 Special application for cancer research and other epigenetic studies with supporting articles and published material from reputed journals.