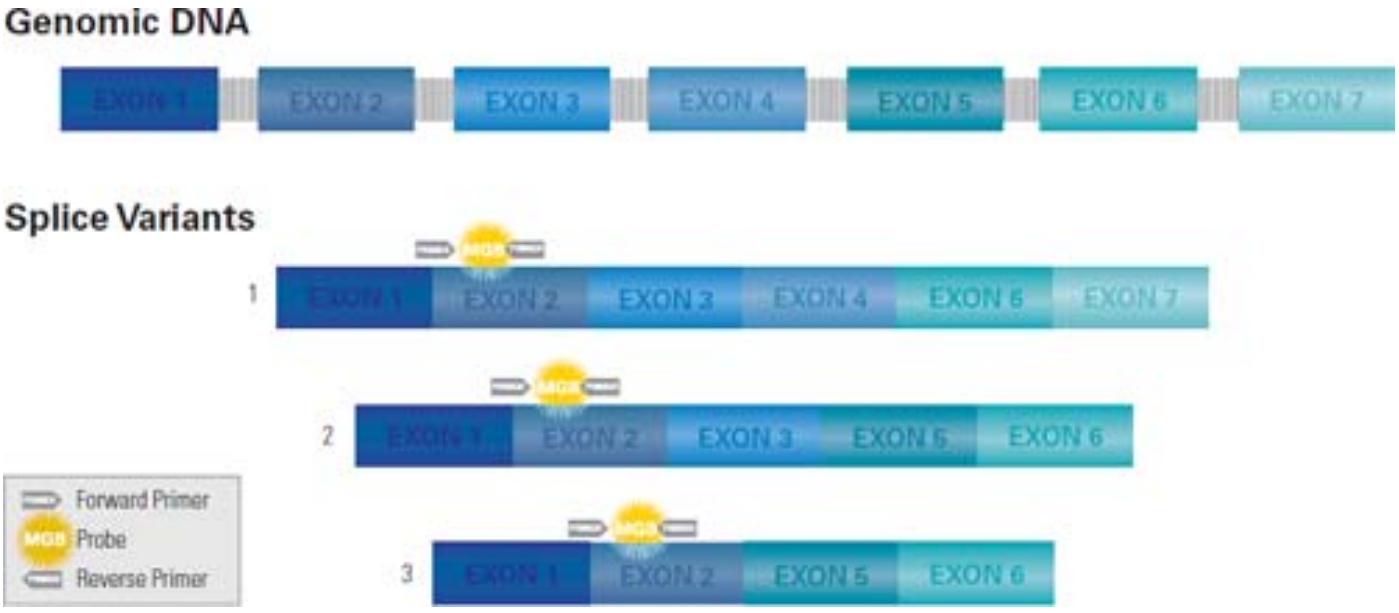
The Power of Solaris Design

Our bioinformatics experts have developed a robust algorithm that identifies genomic assays based on optimal functionality, specificity, and splice variant coverage. The result is a single recommended, high performing assay for your gene expression experiments. The algorithm includes:

- Multiple stringent probe and primer parameters for optimal assay performance
- Selective placement of Superbases and use of MGB™ moiety for increased design flexibility
- Identification of consensus sequence for splice variant coverage
- Exon junction spanning design to avoid genomic DNA amplification
- BLAST analysis for assay specificity

Details of Solaris Design

1. When designing a functional assay, numerous design parameters are applied with high stringency, including: overall GC content, optimal sequence length, melting temperature (Tm), stretches of homogenous nucleotides (i.e. GGGG).
2. The algorithm adjusts the Tm and enables universal cycling conditions by incorporating the MGB™ moiety and by selective placement of Superbases.
3. When there is more than one splice variant for a target gene, a consensus (or common) sequence is identified, representing design space where assays will detect all known splice variants (See figure below).
4. BLAST analysis is a critical component of any comprehensive qPCR assay design protocol and BLAST analysis has been integrated into the Solaris design algorithm. The algorithm utilizes transcript and pseudogene databases to identify and eliminate sequences that are more likely to lead to erroneous priming and detection (i.e. off-target effects).
5. To mitigate the potential for genomic DNA amplification, the design algorithm, whenever possible, will place one of the assay components (probe or primer) or amplicon over an exon junction boundary.



Detect all known splice variants of your target gene for comprehensive target analysis.