Probe Name: Unique identifier of the probe

Gene Symbol: Gene symbol

Transcript Name: Ensembl ID of the transcript

Species

Exon intron: Region targeted by the probe (exon, intron or exon junction)

Binding Score: 50% of the score is determined by the melting temperature (Tm) of the probe arm with the highest Tm. 25% of the score is based on the percentage of the probe sequence located within a coding sequence (CDS). 25% of the score is defined by whether the probe spans an exon junction.

Specificity Score: The score is determined by the length of the longest exact sequence match to another gene, its binding localization (intron, exon), its orientation (sense, antisense) and the number of genes targeted.

Crosses Exon Junction: Indicates whether the probe spans an exon junction

CDS Overlap Percentage: Indicates the % of the probe overlapping with a CDS region

5p Exon%: If TRUE in **Crosses Exon Junction,** which proportion of the probe is on the 5' of the exon junction

3p Exon%: If TRUE in **Crosses Exon Junction,** which proportion of the probe is on the 3' of the exon junction

Full Probe Sequence: Sequence of the Padlock probe. The notation '**/5Phos/**' indicates phosphorylation at the 5' end.

RCA Primer Sequence: Sequence of the RCA primer to amplify the Padlock probe. The asterisk (*****) in the RCA primer sequence denotes a phosphorothioate bond.

Detection Probe ID : Fluorescent probe ID to detect the amplified probes (See Fluorescent Probe List)

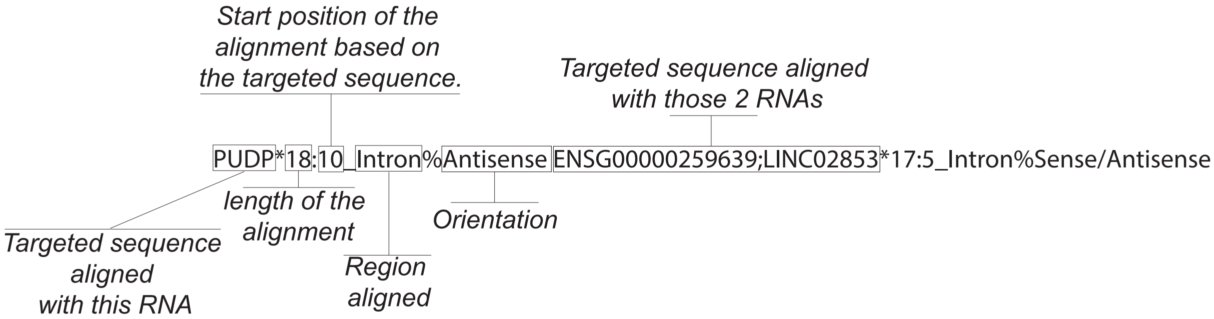
Fluorescent Probe Sequence: Fluorescent probe sequence to detect the amplified probes

Targeted Sequence: Sequence targeted by the probe

Perfect Match Genes: Other gene(s) with sequences that are 100% reverse-complementary to the probe arms.

One Mismatch Genes: Other gene(s) with sequences that have a single mismatch in reverse complementarity to the probe arms.

Longest exact match: Specifies potential binding to other gene(s), with the length of the exact match indicated following the asterisk (*), the starting position of the alignment within the targeted sequence following the colon (:), the region targeted following the underscore (_) and the orientation following the percentage sign (%). When the aligned region corresponds to more than one gene, the names of all targeted genes are separated by a semicolon (;).



Ensembl Gene Name: Ensembl ID of the genomic region

Genome Assembly: Reference genomes

Genome Annotations: Genome annotations

5p Arm : Sequence of the 5’ arm of the probe

Fluorescent Probe Binding: Region of the probe binding to the fluorescent oligo used during detection rounds

RCA Primer Binding: Region of the probe binding to the RCA primer

Spacer: Spacer sequence

3p Arm : Sequence of the 3’ arm of the probe