# PrimePCR™ Assay Validation Report

## Gene Information

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|---|---|
| **Gene Name** | aldehyde dehydrogenase 16 family, member A1 |
| **Gene Symbol** | ALDH16A1 |
| **Organism** | Human |
| **Gene Summary** | This gene encodes a member of the aldehyde dehydrogenase superfamily. The family members act on aldehyde substrates and use nicotinamide adenine dinucleotide phosphate (NADP) as a cofactor. This gene is conserved in chimpanzee dog cow mouse rat and zebrafish. The protein encoded by this gene interacts with maspardin a protein that when truncated is responsible for Mast syndrome. Alternatively spliced transcript variants encoding different isoforms have been found for this gene. |
| **Gene Aliases** | MGC10204 |
| **RefSeq Accession No.** | NC_000019.9, NT_011109.16, NG_012747.1 |
| **UniGene ID** | Hs.719998 |
| **Ensembl Gene ID** | ENSG00000161618 |
| **Entrez Gene ID** | 126133 |

## Assay Information

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|---|---|
| **Unique Assay ID** | qHsaCIP0028729 |
| **Assay Type** | Probe - Validation information is for the primer pair using SYBR® Green detection |
| **Detected Coding Transcript(s)** | ENST00000293350, ENST00000455361, ENST00000433981 |
| **Amplicon Context Sequence** | ACGTCCAGCTGGCCCAGCAGCTGCTCCACTACCATGCAATCCAGGCATCCACCCAGGAGGAGGCACTGGCAGGCTGGGAGCCCATGGGAGTAATTGGCCTCATCCTGCCACCCACATTCTCCTTCCTTGAGATGATGTGGAGGATTTGCC |
| **Amplicon Length (bp)** | 120 |
| **Chromosome Location** | 19:49963019-49964141 |
| **Assay Design** | Intron-spanning |
| **Purification** | Desalted |

## Validation Results

| | |
|---|---|
| **Efficiency (%)** | 103 |
| **$R^2$** | 0.9999 |
| **cDNA Cq** | 22.66 |
| **cDNA Tm (Celsius)** | 86 |

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| **gDNA Cq** | |
| **Specificity (%)** | 100 |

Information to assist with data interpretation is provided at the end of this report.

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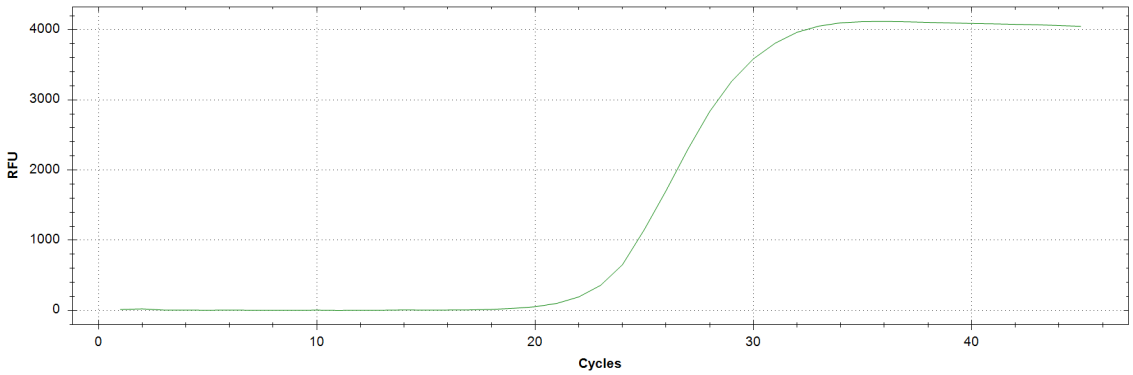
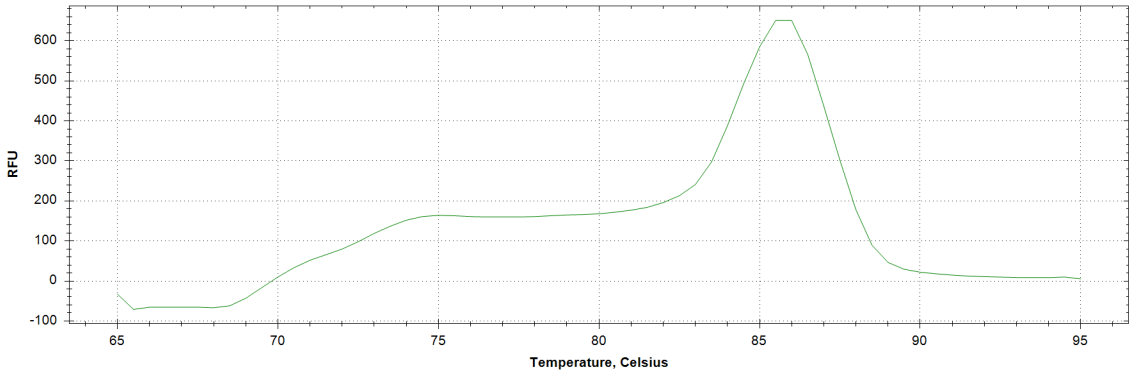
ALDH16A1, Human

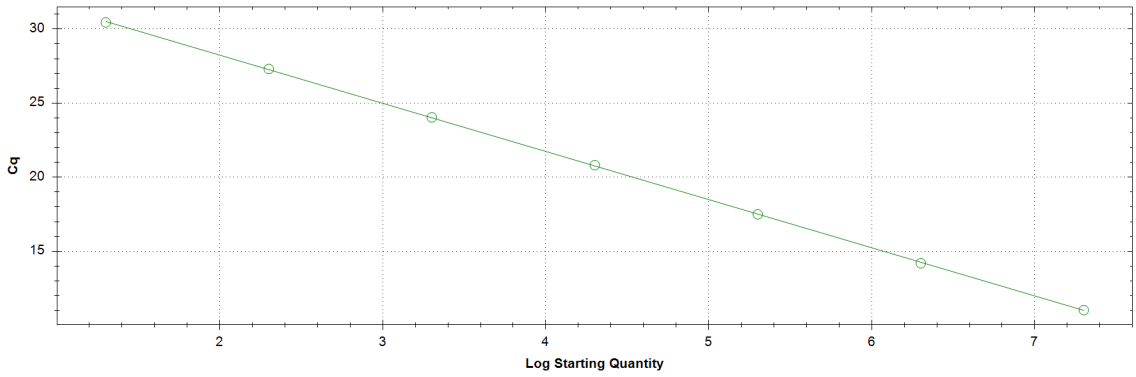
**Amplification Plot**
Amplification of cDNA generated from 25 ng of universal reference RNA




**Melt Peak**
Melt curve analysis of above amplification




**Standard Curve**
Standard curve generated using 20 million copies of template diluted 10-fold to 20 copies



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## Products used to generate validation data

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|---|---|
| **Real-Time PCR Instrument** | CFX384 Real-Time PCR Detection System |
| **Reverse Transcription Reagent** | iScript™ Advanced cDNA Synthesis Kit for RT-qPCR |
| **Real-Time PCR Supermix** | SsoAdvanced™ SYBR® Green Supermix |
| **Experimental Sample** | qPCR Human Reference Total RNA |

## Data Interpretation

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|---|---|
| **Unique Assay ID** | This is a unique identifier that can be used to identify the assay in the literature and online. |
| **Detected Coding Transcript(s)** | This is a list of the Ensembl transcript ID(s) that this assay will detect. Details for each transcript can be found on the Ensembl website at www.ensembl.org. |
| **Amplicon Context Sequence** | This is the amplicon sequence with additional base pairs added to the beginning and/or end of the sequence. This is in accordance with the minimum information for the publication of real-time quantitative PCR experiments (MIQE) guidelines. For details, please refer to the following publication, "Primer Sequence Disclosure: A Clarification of the MIQE Guidelines" (Bustin et al 2011). |
| **Chromosome Location** | This is the chromosomal location of the amplicon context sequence within the genome. |
| **Assay Design** | Exonic: Primers sit within the same exon in the mRNA transcript and can potentially co-amplify genomic DNA. If performing gene expression analysis, it is suggested that the samples be treated with a DNase to eliminate potential unwanted signal from contaminating genomic DNA.<br><br>Exon-exon junction: One primer sits on an exon-exon junction in mRNA. When performing gene expression analysis, this design approach will prevent unwanted signal from contaminating genomic DNA.<br><br>Intron-spanning: Primers sit within different exons while spanning a large intron in the mRNA (intron is greater than 750bp). When performing gene expression analysis, this design approach should limit potential unwanted signal from contaminating genomic DNA.<br><br>Small intron-spanning: Primers sit within different exons with a short intron in between (intron is smaller than 750bp). Small introns may not prevent unwanted signal from contaminating genomic DNA. |
| **Efficiency** | Assay efficiency was determined using a seven-point standard curve from 20 copies to 20 million copies. While an efficiency of 100% represents a perfect doubling of template at every cycle and is ideal, typical ranges of good assay efficiency are between 90-110%. For difficult targets, assay efficiency outside of this range are accepted and reported accordingly. |
| **$R^2$** | The $R^2$ represents the linearity of the standard curve and how well the standard curve data points fit the linear regression line. Acceptable values are >0.98. |

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| **cDNA Cq** | Cq value obtained from 25ng of cDNA transcribed from universal RNA when performing wet-lab validation of the assay.<br><br>Note: Not all genes will be expressed at a detectable level in the universal RNA sample. |
| **cDNA Tm** | Melting temperature of the amplicon when running a melt curve analysis. |
| **gDNA Cq** | Cq value obtained when running the assay with 2.5ng of genomic DNA. This is more than a moderate level of genomic DNA contamination. Intron-spanning and exon-exon junction assay designs can minimize or eliminate genomic DNA detection.<br><br>Note: Genomic DNA contamination is often present at variable levels. If concerned about genomic DNA contamination, the genomic DNA contamination control assay is recommended to run with your sample to determine if genomic DNA levels are sufficient to negatively impact results. |
| **Specificity** | This value is the percent of specific amplicon reads as measured by next generation sequencing (NGS). While 100% specificity is desirable, small decreases in specificity (<1%) can be due to NGS read errors. More significant reductions are likely due to co-amplification of homologous regions.<br><br>Note: Since gene expression can be cell type and condition specific, the exact level and impact of co-amplification in a given sample is impossible to predict. If co-amplification is detected, it should be taken into consideration and reported when analyzing gene expression results. |