PrimePCR™ Assay Validation Report

Gene Information

Gene Name	LIM domain binding 3
Gene Symbol	LDB3
Organism	Human
Gene Summary	This gene encodes a PDZ domain-containing protein. PDZ motifs are modular protein-protein interaction domains consisting of 80-120 amino acid residues. PDZ domain-containing proteins interact with each other in cytoskeletal assembly or with other proteins involved in targeting and clustering of membrane proteins. The protein encoded by this gene interacts with alpha-actinin-2 through its N-terminal PDZ domain and with protein kinase C via its C-terminal LIM domains. The LIM domain is a cysteine-rich motif defined by 50-60 amino acids containing two zinc-binding modules. This protein also interacts with all three members of the myozenin family. Mutations in this gene have been associated with myofibrillar myopathy and dilated cardiomyopathy. Alternatively spliced transcript variants encoding different isoforms have been identified; all isoforms have N-terminal PDZ domains while only longer isoforms (1 2 and 5) have C-terminal LIM domains.
Gene Aliases	CMD1C, CYPHER, FLJ35865, KIAA01613, KIAA0613, LDB3Z1, LDB3Z4, LVNC3, ORACLE, PDLIM6, ZASP
RefSeq Accession No.	NC_000010.10, NT_030059.13, NG_008876.1
UniGene ID	Hs.657271
Ensembl Gene ID	ENSG00000122367
Entrez Gene ID	11155

Assay Information

Unique Assay ID	qHsaCIP0058534
Assay Type	Probe - Validation information is for the primer pair using SYBR® Green detection
Detected Coding Transcript(s)	ENST00000372066, ENST00000361373, ENST00000429277, ENST00000458213, ENST00000352360, ENST00000263066, ENST00000372056, ENST00000310944, ENST00000542786
Amplicon Context Sequence	AGCACCAGCATGTCTTACAGTGTGACCCTGACTGGGCCCGGGCCCTGGGGCTT CCGTCTGCAGGGGGGCAAGGACTTCAACATGCCCCTCACTATCTCCCGGATCAC ACCAGGCAGCAAGGCAGCCCAGTCCCAGCTCAGCCAGGGTGACCTCGTGGTGG CCATTGACGGCGTCAACACAGACACCATGACCCACCTGGAAGCCCAGA
Amplicon Length (bp)	178
Chromosome Location	10:88428440-88439229
Assay Design	Intron-spanning
Purification	Desalted

Validation Results

Efficiency (%)	98

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R^2	0.9989
cDNA Cq	27.24
cDNA Tm (Celsius)	89
gDNA Cq	32.03
Specificity (%)	100

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

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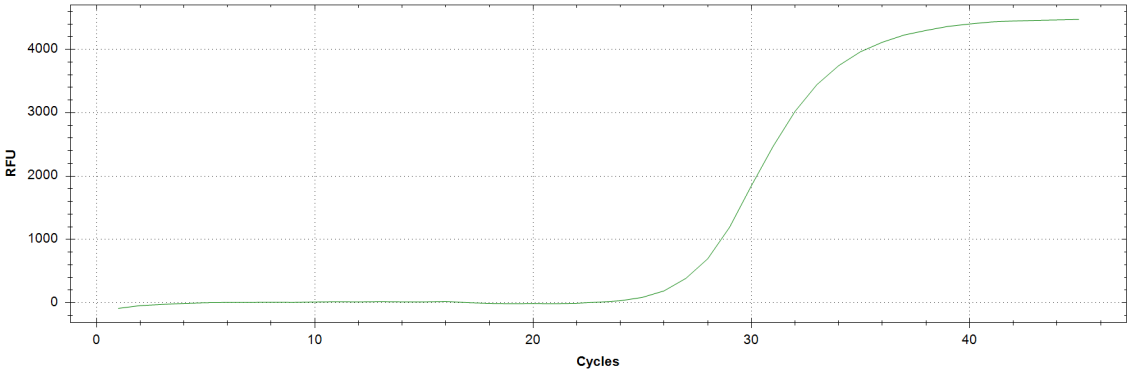
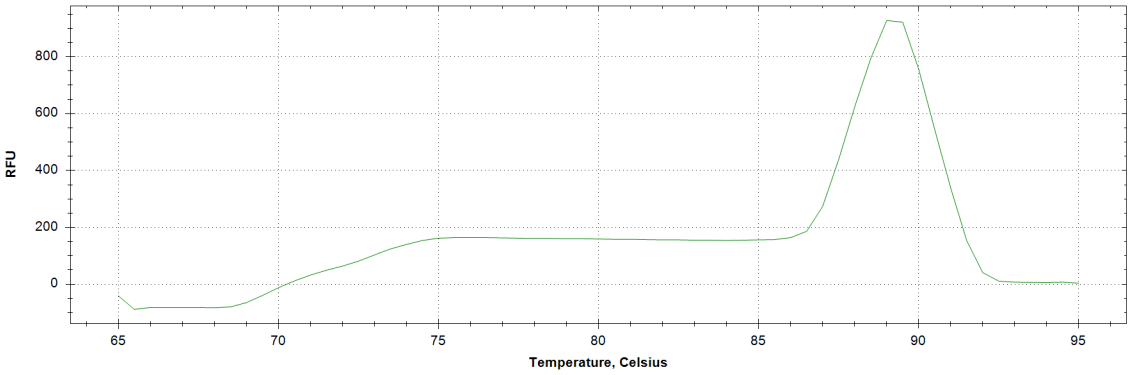
LDB3, Human

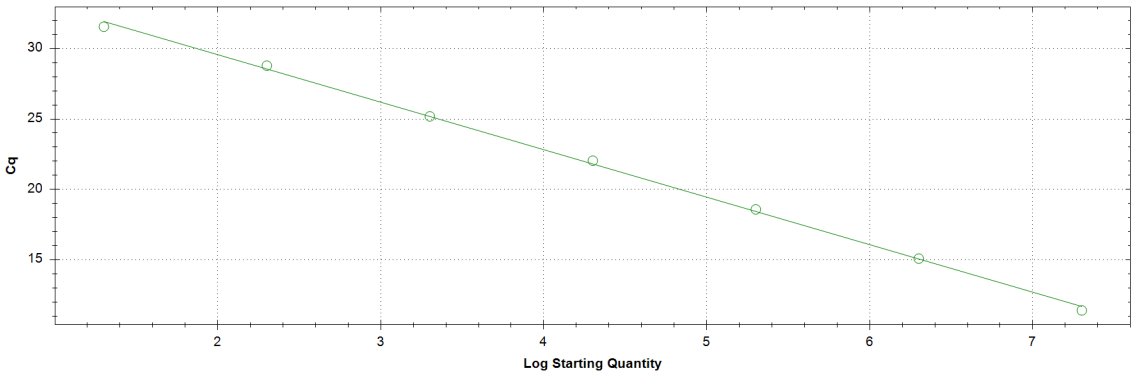
Amplification Plot
Amplification of cDNA generated from 25 ng of universal reference RNA



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

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

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. 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. 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. 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.

cDNA Cq	Cq value obtained from 25ng of cDNA transcribed from universal RNA when performing wet-lab validation of the assay. 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. 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. 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.