

PrimePCR™ Assay Validation Report

Gene Information

Gene Name	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2
Gene Symbol	B3GALT2
Organism	Human
Gene Summary	<p>This gene is a member of the beta-13-galactosyltransferase (beta3GalT) gene family. This family encodes type II membrane-bound glycoproteins with diverse enzymatic functions using different donor substrates (UDP-galactose and UDP-N-acetylglucosamine) and different acceptor sugars (N-acetylglucosamine galactose N-acetylgalactosamine). The beta3GalT genes are distantly related to the Drosophila Brainiac gene and have the protein coding sequence contained in a single exon. The beta3GalT proteins also contain conserved sequences not found in the beta4GalT or alpha3GalT proteins. The carbohydrate chains synthesized by these enzymes are designated as type 1 whereas beta4GalT enzymes synthesize type 2 carbohydrate chains. The ratio of type 1:type 2 chains changes during embryogenesis. By sequence similarity the beta3GalT genes fall into at least two groups: beta3GalT4 and 4 other beta3GalT genes (beta3GalT1-3 beta3GalT5). This gene encodes a protein that functions in N-linked glycoprotein glycosylation and shows strict donor substrate specificity for UDP-galactose.</p>
Gene Aliases	BETA3GALT2, GLCT2, beta3Gal-T2
RefSeq Accession No.	NC_000001.10, NG_012691.1, NT_004487.19
UniGene ID	Hs.518834
Ensembl Gene ID	ENSG00000162630
Entrez Gene ID	8707

Assay Information

Unique Assay ID	qHsaCIP0033793
Assay Type	Probe - Validation information is for the primer pair using SYBR® Green detection
Detected Coding Transcript(s)	ENST00000367434
Amplicon Context Sequence	CTATTCTTTGGCAATCATTTTCTAATTCAGTCACATTGTCTCTCTTGTAGTCATTCT TCCTTGGTCAGGCCATTTATGTGAAGAGGATTATGCCCACTGAAAATACTTTTGG CACGCCATCACTTCAGCAAAAAAGATGCTATCGAACATGCGCACATCCCC
Amplicon Length (bp)	132
Chromosome Location	1:193150758-193155255
Assay Design	Intron-spanning
Purification	Desalted

Validation Results

Efficiency (%)	99
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R²	0.9992
cDNA Cq	30.13
cDNA Tm (Celsius)	82
gDNA Cq	
Specificity (%)	100

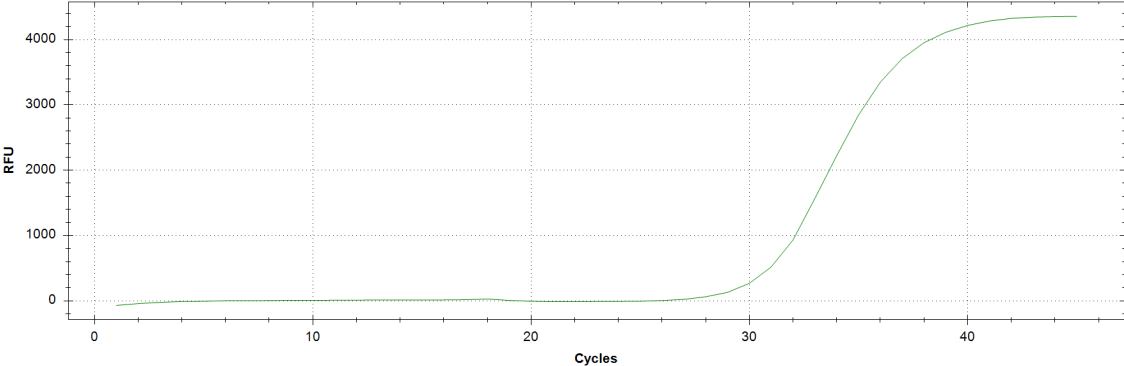
Information to assist with data interpretation is provided at the end of this report.

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B3GALT2, Human

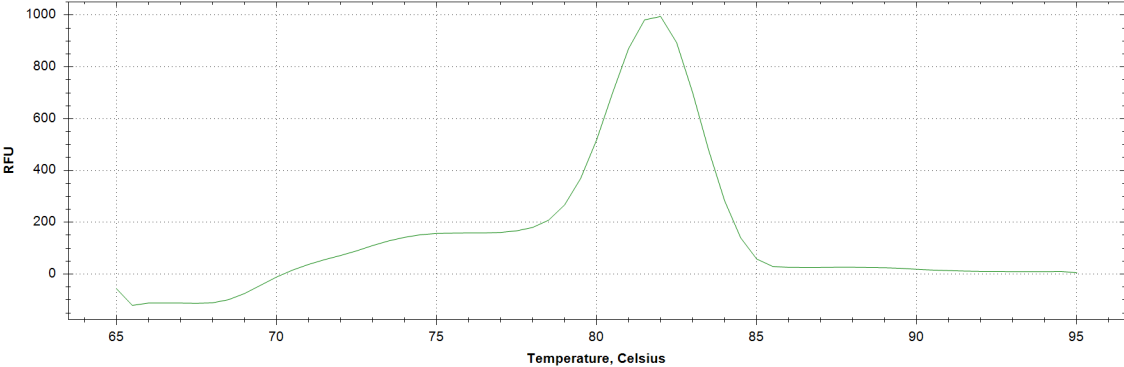
Amplification Plot

Amplification of cDNA generated from 25 ng of universal reference RNA



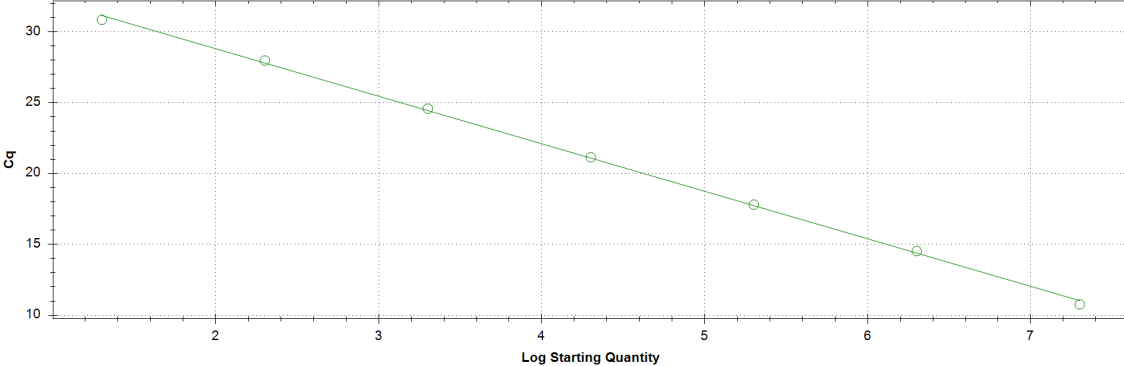
Melt Peak

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	<p>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.</p> <p>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.</p> <p>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.</p> <p>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.</p>
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.
R²	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	<p>Cq value obtained from 25ng of cDNA transcribed from universal RNA when performing wet-lab validation of the assay.</p> <p>Note: Not all genes will be expressed at a detectable level in the universal RNA sample.</p>
cDNA Tm	<p>Melting temperature of the amplicon when running a melt curve analysis.</p>
gDNA Cq	<p>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.</p> <p>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.</p>
Specificity	<p>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.</p> <p>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.</p>