

PrimePCR™ Assay Validation Report

Gene Information

Gene Name	ataxin 1
Gene Symbol	ATXN1
Organism	Human
Gene Summary	<p>The autosomal dominant cerebellar ataxias (ADCA) are a heterogeneous group of neurodegenerative disorders characterized by progressive degeneration of the cerebellum brain stem and spinal cord. Clinically ADCA has been divided into three groups: ADCA types I-III. ADCA I is genetically heterogeneous with five genetic loci designated spinocerebellar ataxia (SCA) 1 2 3 4 and 6 being assigned to five different chromosomes. ADCA II which always presents with retinal degeneration (SCA7) and ADCA III often referred to as the 'pure' cerebellar syndrome (SCA5) are most likely homogeneous disorders. Several SCA genes have been cloned and shown to contain CAG repeats in their coding regions. ADCA is caused by the expansion of the CAG repeats producing an elongated polyglutamine tract in the corresponding protein. The expanded repeats are variable in size and unstable usually increasing in size when transmitted to successive generations. The function of the ataxins is not known. This locus has been mapped to chromosome 6 and it has been determined that the diseased allele contains 41-81 CAG repeats compared to 6-39 in the normal allele and is associated with spinocerebellar ataxia type 1 (SCA1). At least two transcript variants encoding the same protein have been found for this gene.</p>
Gene Aliases	ATX1, D6S504E, SCA1
RefSeq Accession No.	NC_000006.11, NG_011571.1, NT_007592.15
UniGene ID	Hs.434961
Ensembl Gene ID	ENSG00000124788
Entrez Gene ID	6310

Assay Information

Unique Assay ID	qHsaCED0004240
Assay Type	SYBR® Green
Detected Coding Transcript(s)	ENST00000244769, ENST00000450222, ENST00000436367
Amplicon Context Sequence	AGATCCTATCATCAGTAAGGTAACGTATTTGAAGCGAGGTCATCTATGTA AAAAGA AATCTCAGCTCCGGAGTAGAGGTGTGCAAGTTGTTGGAGTTTCCCTATGCCAG AAACACAACACTGTCCGTGGAAAAGAGAGGAAACCAACCCAACACAATAGCAGA TGCATGTG
Amplicon Length (bp)	141
Chromosome Location	6:16301540-16301710
Assay Design	Exonic
Purification	Desalted

Validation Results

Efficiency (%)	98
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R²	0.9997
cDNA Cq	20.82
cDNA Tm (Celsius)	82.5
gDNA Cq	23
Specificity (%)	100

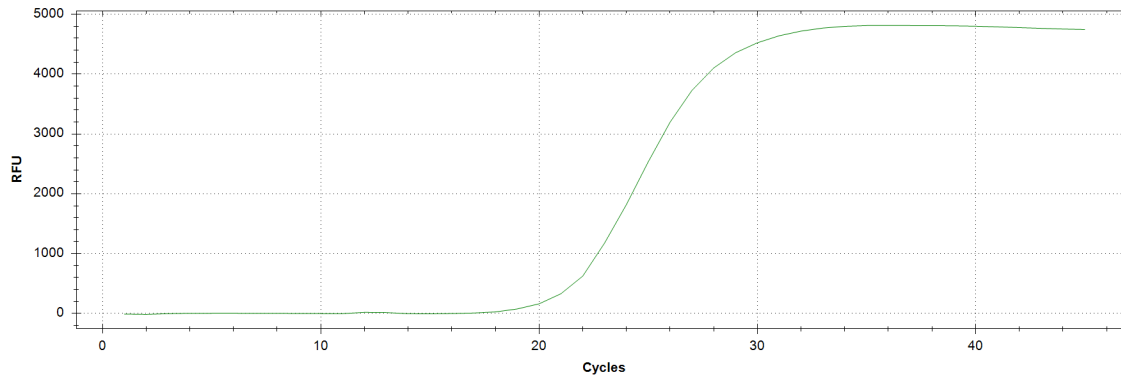
Information to assist with data interpretation is provided at the end of this report.

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ATXN1, Human

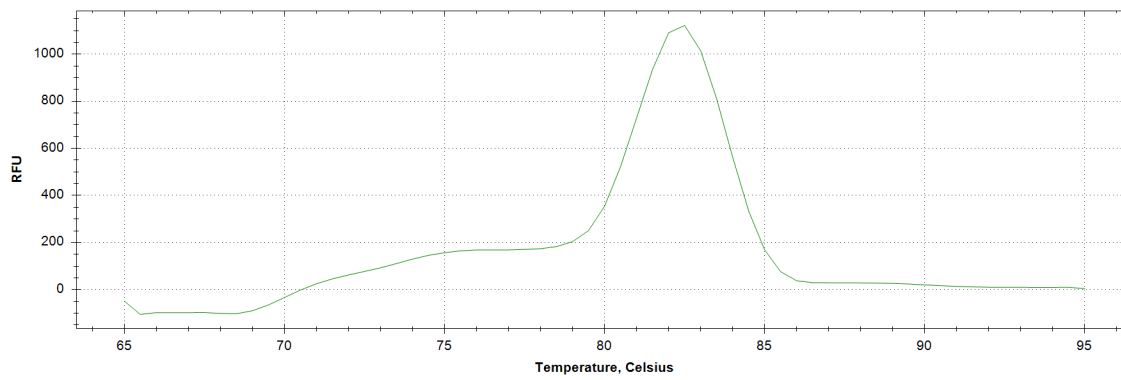
Amplification Plot

Amplification of cDNA generated from 25 ng of universal reference RNA



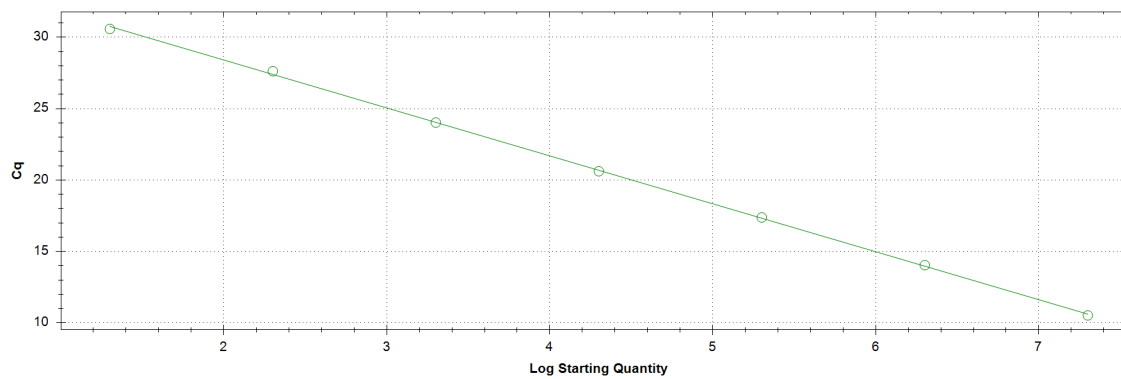
Melt Peak

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>