GeneQuery™ Human VIM-VIM2P Pseudogene Transcription Analysis qPCR Kit (GQP-VIM2P)

Catalog #GK814

Product Description

Pseudogenes are DNA segments introduced into the genome by gene duplication or RNA retrotransposition. The majority of pseudogenes bear high sequence similarity to their corresponding functional genes, but have lost some or all of the functionality. ScienCell's GeneQuery™ Human VIM-VIM2P Pseudogene Transcription Analysis qPCR Kit (GQP-VIM2P) is designed to facilitate the transcript quantification of pseudogene VIM2P and its highly related gene, VIM. Human VIM2P pseudogene and VIM gene are located on chromosome 6 and 10, respectively. GQP-VIM2P guarantees that each primer set only amplifies the designated gene or pseudogene without non-specific amplification for precise quantification.

GeneQuery™ pseudogene transcription analysis qPCR kits are qPCR ready in a 96-well plate format, with each well containing one primer set that can specifically recognize and efficiently amplify a target gene's cDNA. The carefully designed primers ensure that: (i) the optimal annealing temperature in qPCR analysis is 65°C (with 2 mM Mg^{2+}, and no DMSO); (ii) the primer set recognizes all known transcript variants of target gene, unless otherwise indicated; and (iii) only one gene or pseudogene is amplified. Each primer set has been validated by qPCR with melt curve analysis and gel electrophoresis.

Note: all gene and pseudogene names follow their official symbols by the Human Genome Organization Gene Nomenclature Committee (HGNC).

GeneQuery™ Pseudogene Transcription Analysis qPCR Controls

Each Pseudogene Transcription Analysis qPCR plate contains six controls (Figure 1).

- Three target housekeeping genes (ACTB, LDHA and PPIH), which enable normalization of data.
- The Genomic DNA (gDNA) Control (GDC) detects possible gDNA contamination in the cDNA samples. It contains a primer set targeting a non-transcribed region of the genome.
- Positive PCR Control (PPC) tests whether samples contain inhibitors or other factors that may negatively affect gene expression results. The PPC consists of a predispensed synthetic DNA template and a primer set that can amplify it. The sequence of the DNA template is not present in the human genome, and thus tests the efficiency of the polymerase chain reaction itself.
- The No Template Control (NTC) is strongly recommended, and can be used to monitor the DNA contamination introduced during the workflow such as reagents, tips, and the lab bench.

Kit Components

Component	Quantity	Storage

GeneQuery™ plate with lyophilized primers	1	4°C or -20°C
Optical PCR plate seal	1	RT
Nuclease-free H_2O	2 mL	4°C

Additional Materials Required (Materials Not Included in Kit)

Component	Recommended
Reverse transcriptase	MultiScribe Reverse Transcriptase (Life Tech, Cat. #4311235)
cDNA template	Customers' samples
qPCR master mix	FastStart Essential DNA Green Master (Roche, Cat. #06402712001)

Quality Control

All the primer sets are validated by qPCR with melt curve analysis. The PCR products are analyzed by gel electrophoresis. Single band amplification is confirmed for each set of primers.

Product Use

GQP-VIM2P is for research use only. It is not approved for human or animal use, or for application in clinical or *in vitro* diagnostic procedures.

Shipping and Storage

The product is shipped at ambient temperature. Upon receipt, the plate should be stored at 4°C and is good for up to 12 months. For long-term storage (>1 year), store the plate at -20°C in a manual defrost freezer.

Procedures

Note: The primers in each well are lyophilized.

1. Prior to use, allow plates to warm to room temperature.
2. Briefly centrifuge at 1,500x g for 1 minute before slowly peeling off the seal.
3. Prepare 20 µl PCR reactions for one well as shown in Table 1.

Table 1

cDNA template	**0.2 – 250 ng**
2x qPCR master mix	10 µl
Nuclease-free H_2O	variable
Total volume	***20 µl***

Important: **Only** use polymerases with hot-start capability to prevent possible primer-dimer formation. **Only** use nuclease-free reagents in PCR amplification.

4. Add the mixture of 2x qPCR master mix, cDNA template, and nuclease-free H_2O to each well containing the lyophilized primers. Seal the plate with the provided optical PCR plate seal.

   Important: In NTC control well, do NOT add cDNA template. Add 2x qPCR master mix and nuclease-free H2O only.

5. Briefly centrifuge the plates at 1,500x g for 1 minute at room temperature. For maximum reliability, replicates are strongly recommended (minimum of 3).
6. For PCR program setup, please refer to the instructions of the master mix of the user's choice. We recommend a typical 3-step qPCR protocol for a 200nt amplicon:

Three-step cycling protocol

Step	**Temperature**	**Time**	**Number of cycles**
Initial denaturation	95°C	10 min	1
Denaturation	95°C	20 sec	40
Annealing	65°C	20 sec	
Extension	72°C	20 sec	
Data acquisition	Plate read		
Recommended	*Melting curve analysis*		1
Hold	4°C	Indefinite	1

7. ***(Optional)*** Load the PCR products on 1.5% agarose gel and perform electrophoresis to confirm the single band amplification in each well.

Figure 1. Layout of GeneQuery™ qPCR array kit.

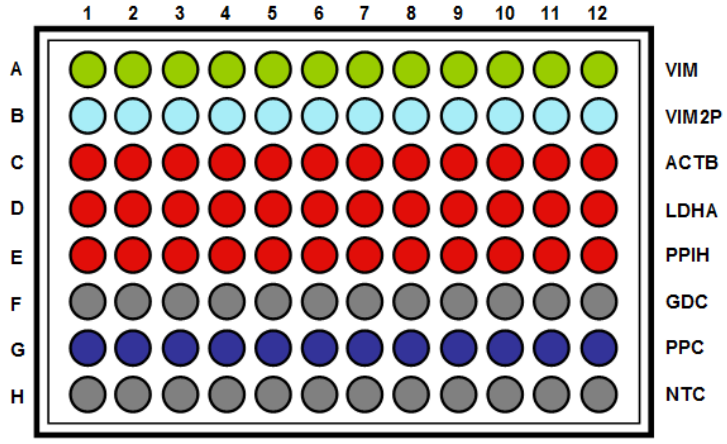


Table 2. Interpretation of control results:

Controls	***Results***	***Interpretation***	***Suggestions***
Housekeeping gene controls	Variability of a housekeeping gene's Cq value	The expression of the housekeeping gene is variable in samples; cycling program is incorrect	Choose a constantly expressed target, or analyze expression levels of multiple housekeeping genes; use correct cycling program and make sure that all cycle parameters have been correctly entered
gDNA Control (GDC)	Cq ≥ 35	No gDNA detected	N/A
	Cq < 35	The sample is contaminated with gDNA	Perform DNase digestion during RNA purification step
Positive PCR Control (PPC)	Cq > 30; or The Cq variations > 2 between qPCR Arrays.	Poor PCR performance; possible PCR inhibitor in reactions; cycling program incorrect	Eliminate inhibitor by purifying samples; use correct cycling program and make sure that all cycle parameters have been correctly entered
No Template Control (NTC)	Positive	DNA contamination in workflow	Eliminate sources of DNA contamination (reagents, plastics, etc.)

Figure 2. A typical amplification curve showing the amplification of a qPCR product.

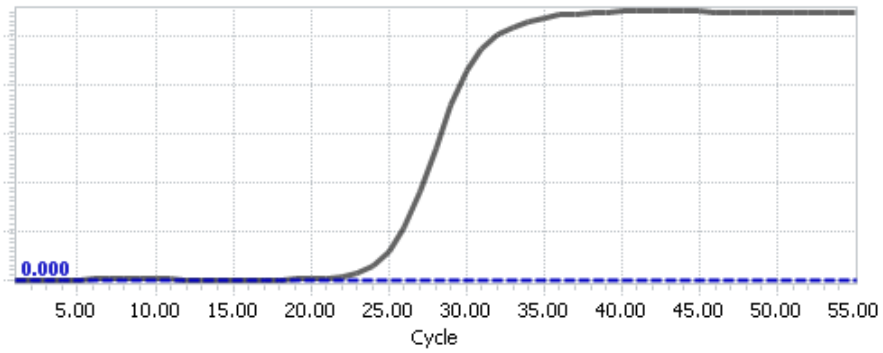
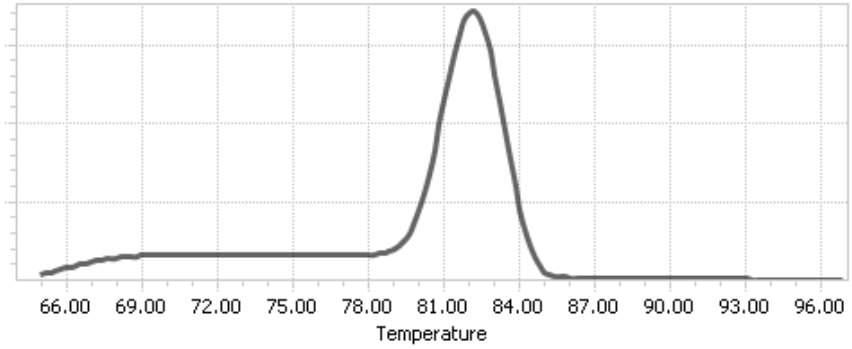


Figure 3. A typical melting peak of a qPCR product.



Quantification Method: Comparative ΔΔCq (Quantification Cycle Value) Method

1. ***Note:*** Please refer to your qPCR instrument's data analysis software for data analysis. The method provided here serves as guidance for quick manual calculations.

   You can use one or more housekeeping genes as a reference to normalize samples.

   Important: We highly recommend using all 3 housekeeping genes included in this kit, ACTB, LDHA and PPIH.

2. For a single housekeeping gene, ΔCq (ref) is the quantification cycle number change for that housekeeping gene (HKG) between an experimental sample and control sample.

   ΔCq (ref) = Cq (HKG, experimental sample) - Cq (HKG, control sample)

   When using multiple housekeeping genes as a reference, we recommend normalizing using the geometric mean [1] of the expression level change, which is the same as normalizing using the arithmetic mean of ΔCq of the selected housekeeping genes.

   ΔCq (ref) = average (ΔCq (HKG1), ΔCq (HKG2),....., ΔCq (HKG n)) (n is the number of housekeeping genes selected)

   If using all 3 housekeeping genes included in this kit, ACTB, LDHA and PPIH, use the following formula:

   ΔCq (ref) = (ΔCq(ACTB)+ΔCq(LDHA)+ΔCq(PPIH)) /3

   Note: ΔCq (HKG) = Cq (HKG, experimental sample) - Cq (HKG, control sample), and ΔCq (HKG) value can be positive, 0, or negative.

3. For any of your genes of interest (GOI),

   ΔCq (GOI) = Cq (GOI, experimental sample) - Cq (GOI, control sample)

   ΔΔCq = ΔCq (GOI) - ΔCq (ref)

   Normalized GOI expression level fold change = $2^{-\Delta\Delta Cq}$

References

[1] Vandesompele J, De Preter K, Pattyn F, Poppe B, Van Roy N, De Paepe A, Speleman F. (2002) "Accurate normalization of real-time quantitative RT-PCR data by geometric averaging of multiple internal control genes." *Genome Biol.* 3(7): 1-12.

Example: Comparative ΔΔCq (Quantification Cycle Value) Method

Table 3. Cq (Quantification Cycle) values of 2 genes-of-interest and 3 housekeeping genes obtained for experimental and control samples.

	Genes of Interest		Housekeeping Genes		
Samples	**GOI1**	**GOI2**	***ACTB***	***LDHA***	***PPIH***
Experimental	21.61	22.19	17.16	20.12	26.40
Control	33.13	26.47	18.20	20.57	26.55

$\Delta Cq\ (ref) = (\Delta Cq(ACTB)+\Delta Cq(LDHA)+\Delta Cq(PPIH))\ /3$
$= ((17.16-18.20)+(20.12-20.57)+(26.40-26.55))/3$
$= -0.55$

$\Delta Cq\ (GOI1) = 21.61 - 33.13$
$= -11.52$

$\Delta Cq\ (GOI2) = 22.19 - 26.47$
$= -4.28$

$\Delta\Delta Cq\ (GOI1) = \Delta Cq\ (GOI1) - \Delta Cq\ (ref)$
$= -11.52 - (-0.55)$
$= -10.97$

$\Delta\Delta Cq\ (GOI2) = \Delta Cq\ (GOI2) - \Delta Cq\ (ref)$
$= -4.28 - (-0.55)$
$= -3.73$

Normalized GOI1 expression level fold change $= 2^{-\Delta\Delta Cq\ (GOI1)}$
$= 2^{10.97}$
$= 2006$

Normalized GOI2 expression level fold change $= 2^{-\Delta\Delta Cq\ (GOI2)}$
$= 2^{3.73}$
$= 13.3$

Conclusion: Upon treatment, expression level of GOI1 increased 2,006 fold, and expression level of GOI2 increased 13.3 fold.

Appendix. Plate type choice chart.

Plate type A

Brand	Model	kit catalog #
ABI / Life Tech	ABI 5700	GK814-A
	ABI 7000	GK814-A
	ABI 7300	GK814-A
	ABI 7500	GK814-A
	ABI 7700	GK814-A
	ABI 7900 HT	GK814-A
	QuantStudio	GK814-A
	ViiA 7	GK814-A
Bio-Rad	Chromo4	GK814-A
	iCycler	GK814-A
	iQ5	GK814-A
	MyiQ	GK814-A
	MyiQ2	GK814-A
Eppendorf / Life Tech	Matercycler ep realplex 2	GK814-A
	Matercycler ep realplex 4	GK814-A
Stratagene	MX3000P	GK814-A
	MX3005P	GK814-A

Plate type B

Brand	Model	kit catalog #
ABI / Life Tech	ABI 7500 Fast	GK814-B
	ABI 7900 HT Fast	GK814-B
	QuantStudio Fast	GK814-B
	StepOnePlus	GK814-B
	ViiA 7 Fast	GK814-B
Bio-Rad	CFX Connect	GK814-B
	CFX96	GK814-B
	DNA Engine Opticon 2	GK814-B
Stratagene	MX4000	GK814-B

Plate type C

Brand	Model	kit catalog #
Roche	Lightcycler 96	GK814-C
	Lightcycler 480 (96-well)	GK814-C