GeneQuery™ Human NF-kB Signaling Pathway qPCR Array Kit
(GQH-NFKB)
Catalog #GK142

Product Description

ScienCell's GeneQuery™ NF-kB qPCR array kit (GQH-NFKB) profiles 88 key genes associated with the Human Nuclear Factor-kappa B (NF-kB) Signaling Pathway. The NF-kB signaling pathway is a critical regulatory pathway in human cells that plays a central role in the immune response, inflammation, cell proliferation, and survival. It is involved in the transcriptional regulation of genes that control these processes. NF-kB is a protein complex that acts as a transcription factor, meaning it controls the expression of specific genes by binding to their regulatory regions. The pathway can be triggered by various stimuli, including infection, inflammation, and cellular stress. Dysregulation of the NF-kB pathway is associated with various diseases, including chronic inflammatory disorders, autoimmune diseases, and cancer. Understanding the regulation of this pathway is of great importance for both basic research and the development of therapeutic interventions. Brief examples of how included genes may be grouped according to function are shown below:

- **Receptor:** TLR3, TLR4, IL1R1, RIPK2, TNFRSF1A, TNFRSF1B
- **Cytokine:** IL10, IL1A, IL6, IL1B, TNFSF10, TNFSF11, TNF
- **Transcription Factors:** ATF1, EGR1, JUN, STAT1, FOS, MKI67
- **Cell Cycle Regulation:** CDKN1A, CCND1, CCNE1, CDK4

GeneQuery™ qPCR array 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 is amplified. Each primer set has been validated by qPCR with melt curve analysis, and gel electrophoresis.

GeneQuery™ qPCR Array Kit Controls

Each GeneQuery™ plate contains eight controls (Figure 1).

- Five target housekeeping genes (ACTB, GAPDH, LDHA, NONO, 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	Cat #	Quantity	Storage
GeneQuery™ array plate with lyophilized primers	GK142	1	4°C or -20°C
Optical PCR plate seal	N/A	1	RT
Nuclease-free H$_2$O	GQ100-1	2	4°C

Additional Materials Required (Materials Not Included in Kit)

Component	Recommended
Reverse transcriptase	First-Strand cDNA Synthesis Master Mix, 4x (ScienCell, Cat #MB6008)
cDNA template	Customers' samples
qPCR master mix	GoldNStart TaqGreen qPCR Master Mix (ScienCell, Cat #MB6018)

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

GQH-NFKB 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 product should be stored at 4°C and is good for up to 12 months. For long-term storage (>1 year), store the product 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.

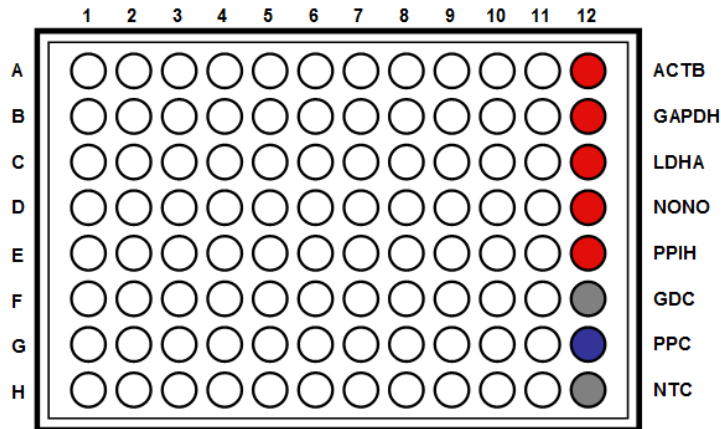Figure 1. Layout of GeneQuery™ qPCR array kit controls

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.)

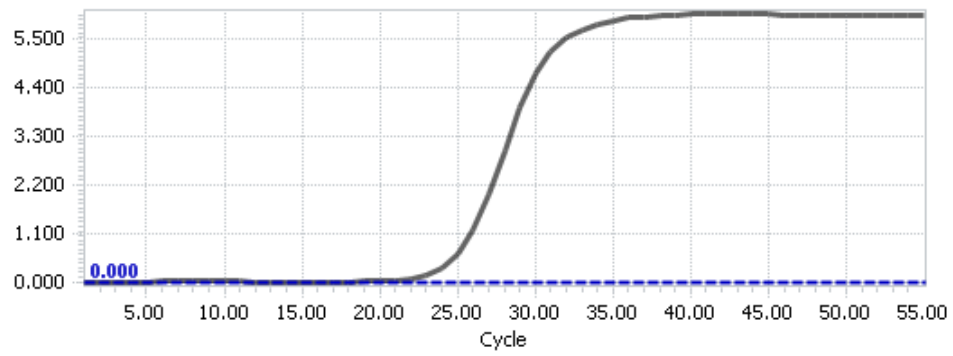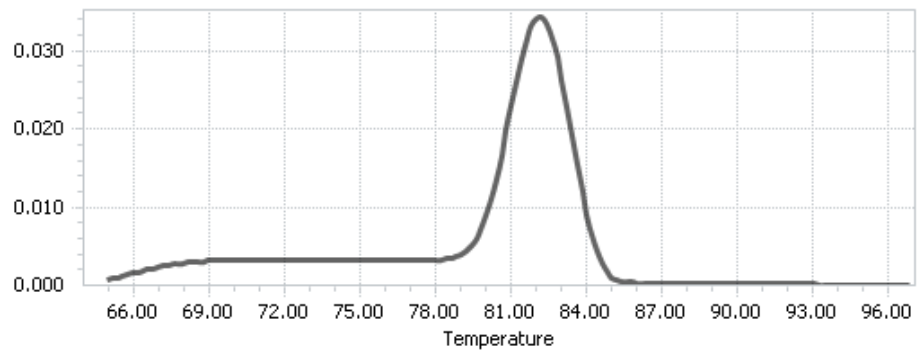Figure 2. A typical amplification curve showing the amplification of a qPCR product.

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 provide 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 5 housekeeping genes included in this kit: ACTB, GAPDH, LDHA, NONO, 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.

   $$\Delta Cq \text{ (ref)} = Cq \text{ (HKG, experimental sample)} - Cq \text{ (HKG, control sample)}$$

   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.

   $$\Delta Cq \text{ (ref)} = \text{average } (\Delta Cq \text{ (HKG1)}, \Delta Cq \text{ (HKG2)},\ldots\ldots, \Delta Cq \text{ (HKG n)})$$ (n is the number of housekeeping genes selected)

   If using all 5 housekeeping genes included in this kit (ACTB, GAPDH, LDHA, NONO, and PPIH) use the following formula:

   $$\Delta Cq \text{ (ref)} = (\Delta Cq(ACTB)+\Delta Cq(GAPDH)+\Delta Cq(LDHA)+\Delta Cq(NONO)+\Delta Cq(PPIH))/5$$

   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),
   $$\Delta Cq \text{ (GOI)} = Cq \text{ (GOI, experimental sample)} - Cq \text{ (GOI, control sample)}$$

   $$\Delta\Delta Cq = \Delta Cq \text{ (GOI)} - \Delta Cq \text{ (ref)}$$

   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 5 housekeeping genes obtained for experimental and control samples.

	Genes of Interest		Housekeeping Genes				
Samples	GOI1	GOI2	*ACTB*	*GAPDH*	*LDHA*	*NONO*	*PPIH*
Experimental	21.61	22.19	17.16	17.84	20.12	19.64	26.40
Control	33.13	26.47	18.20	18.48	20.57	19.50	26.55

$$\Delta Cq \ (ref) = (\Delta Cq(ACTB)+\Delta Cq(GAPDH)+\Delta Cq(LDHA)+\Delta Cq(NONO)+\Delta Cq(PPIH))/5$$
$$= ((17.16\text{-}18.20)+(17.84\text{-}18.48)+(20.12\text{-}20.57)+(19.64\text{-}19.50)+(26.40\text{-}26.55))/5$$
$$= -0.43$$

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

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

$$\Delta\Delta Cq \ (GOI1) = \Delta Cq \ (GOI1) - \Delta Cq \ (ref)$$
$$= -11.52 - (-0.43)$$
$$= -11.09$$

$$\Delta\Delta Cq \ (GOI2) = \Delta Cq \ (GOI2) - \Delta Cq \ (ref)$$
$$= -4.28 - (-0.43)$$
$$= -3.85$$

$$\text{Normalized GOI1 expression level fold change} = 2^{-\Delta\Delta Cq \ (GOI1)}$$
$$= 2^{11.09}$$
$$= 2180$$

$$\text{Normalized GOI2 expression level fold change} = 2^{-\Delta\Delta Cq \ (GOI2)}$$
$$= 2^{3.85}$$
$$= 14.4$$

Conclusion: Upon treatment, expression level of GOI1 increased 2,180 fold, and expression level of GOI2 increased 14.4 fold.

ScienCell™
Research Laboratories

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GeneQuery™ qPCR Array Plate Layout*
(*8 controls* in Bold and Italic)

	1	2	3	4	5	6	7	8	9	10	11	12
A	ATF1	BTK	CDK2	EGR1	IKBKB	IRAK2	MYD88	PIK3C2A	RELB	TLR3	TNFSF10	*ACTB*
B	ATM	CASP3	CDK4	ELK1	IKBKG	IRF1	NFKB1	PIK3CD	RIPK1	TLR4	TNFSF11	*GAPDH*
C	ATR	CASP8	CDKN1A	FADD	IL10	JUN	NFKB2	PIK3R5	RIPK2	TLR7	TP53	*LDHA*
D	BAX	CASP9	CHEK1	FAS	IL1A	LY86	NFKBIA	PPARA	SFN	TNF	TRADD	*NONO*
E	BCL2	CCND1	CHEK2	FOS	IL1B	MAP3K1	NKIRAS1	PTEN	STAT1	TNFRSF10B	TRAF1	*PPIH*
F	BIRC2	CCNE1	CHUK	GSK3B	IL1R1	MAP3K7	NKIRAS2	PTGS2	TBK1	TNFRSF18	UBE2N	*GDC*
G	BMP2	CD40	CTNNBL1	HMGB1	IL6	MDM2	NOD1	REL	THBS1	TNFRSF1A	WNT4	*PPC*
H	BMP7	CDK1	EGFR	HRAS	IRAK1	MKI67	NOS2	RELA	TLR2	TNFRSF1B	WNT5A	*NTC*