



GeneQuery™ Human Mesenchymal to Epithelial Transition qPCR Array Kit (GQH-MET) Catalog #GK095

Product Description

ScienCell's GeneQuery™ Human Mesenchymal To Epithelial Transition qPCR Array Kit (GQH-MET) is designed to facilitate gene expression profiling of 88 key genes involved in reversible mesenchymal to epithelial transition (MET). MET and the reverse process, epithelial to mesenchymal transition (EMT), are involved in embryogenesis, cancer metastasis, and stem cell reprogramming. Brief examples of how genes may be grouped are shown below:

- **EMT markers:** CDH1, CDH2, VIM, FN1, CDH11, SDC1, S100A4, ACTA2, CTNNB1, LEF1, ETS1, FOXC2, GSC, PDGFD
- **EMT-MET transition:** PAX2, WT1, BMP7, TWIST1, PRRX1
- **Proliferation and morphogenesis control:** AKT1, BMP1, BMP7, EGFR, FGFBP1, IGFBP4, JAG1, PDGFRB, SNAI1, SOX10, VCAN, WNT5A, WNT11, ZEB1
- **Differentiation control:** BMP2, COL3A1, ERBB3, F11R, FZD7, GSC, JAG1, KRT14, NODAL, SMAD2, SOX10, WNT5B
- **Transcription factors regulating MET:** CTNNB1, ESR1, FOXC2, NOTCH1, SMAD2, SNAI1/2/3, STAT3, TCF3, TCF4, TWIST1, ZEB2
- **Signaling pathways involved in MET**
 - **Estrogen receptor:** CAV2, ESR1, KRT19, TGFB3
 - **GPCR:** AKT1, FZD7, GNG11, RAC1, RGS2
 - **PI3K/AKT:** AKT1, AKT2, PIK3CA, PIK3CD, PIK3CG, PIK3R1, PIK3R3, PIK3R5

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 Mg²⁺, 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 (β -actin, 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 predisposed 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™ array plate with lyophilized primers	1	4°C or -20°C
Optical PCR plate seal	1	RT
Nuclease-free H ₂ O	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

GQH-MET 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 μ l PCR reactions for one well as shown in Table 1.

Table 1

cDNA template	0.2 – 250 ng
2x qPCR master mix	10 μ l
Nuclease-free H ₂ O	variable
<i>Total volume</i>	<i>20 μl</i>

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 H₂O 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		
<i>Recommended</i>	<i>Melting curve analysis</i>		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.

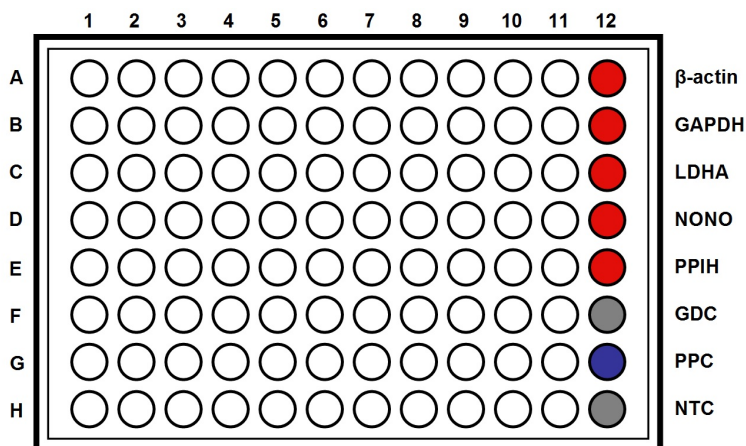


Table 2. Interpretation of control results:

<i>Controls</i>	<i>Results</i>	<i>Interpretation</i>	<i>Suggestions</i>
Housekeeping gene controls	Variability of a housekeeping gene's C _q 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)	C _q ≥ 35	No gDNA detected	N/A
	C _q < 35	The sample is contaminated with gDNA	Perform DNase digestion during RNA purification step
Positive PCR Control (PPC)	C _q > 30; or The C _q 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 $\Delta\Delta Cq$ (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 5 housekeeping genes included in this kit, β -actin, 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.

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

If using all 5 housekeeping genes included in this kit, β -actin, GAPDH, LDHA, NONO, and PPIH, use the following formula:

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

Note: $\Delta Cq \text{ (HKG)} = Cq \text{ (HKG, experimental sample)} - Cq \text{ (HKG, control sample)}$, and $\Delta Cq \text{ (HKG)}$ value can be positive, 0, or negative.

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

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

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

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

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 $\Delta\Delta Cq$ (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.

Samples	Genes of Interest		Housekeeping Genes				
	GOI1	GOI2	<i>β-actin</i>	<i>GAPDH</i>	<i>LDHA</i>	<i>NONO</i>	<i>PPIH</i>
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

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

$$\begin{aligned}\Delta Cq(\text{GOI1}) &= 21.61 - 33.13 \\ &= -11.52\end{aligned}$$

$$\begin{aligned}\Delta Cq(\text{GOI2}) &= 22.19 - 26.47 \\ &= -4.28\end{aligned}$$

$$\begin{aligned}\Delta\Delta Cq(\text{GOI1}) &= \Delta Cq(\text{GOI1}) - \Delta Cq(\text{ref}) \\ &= -11.52 - (-0.43) \\ &= -11.09\end{aligned}$$

$$\begin{aligned}\Delta\Delta Cq(\text{GOI2}) &= \Delta Cq(\text{GOI2}) - \Delta Cq(\text{ref}) \\ &= -4.28 - (-0.43) \\ &= -3.85\end{aligned}$$

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

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

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



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GeneQuery™ Human Mesenchymal To Epithelial Transition qPCR Array Plate Layout*
(*8 controls* in Bold and Italic)

	1	2	3	4	5	6	7	8	9	10	11	12
A	ACTA2	CAV2	COL3A1	F11R	IGFBP4	MUC1	PIK3CG	RGS2	SNAI3	TGFB2	VCAN	<i>β-actin</i>
B	AKT1	CDH1	COL5A2	FGFBP1	ILK	NODAL	PIK3R1	RPS27A	SOX10	TGFB3	VIM	<i>GAPDH</i>
C	AKT2	CDH11	CTNNB1	FN1	JAG1	NOTCH1	PIK3R3	S100A4	SPINT2	TGFBR1	WNT11	<i>LDHA</i>
D	ARHGEF18	CDH2	DSP	FOXC2	KRT14	PAX2	PIK3R5	SDC1	STAT3	TGFBR2	WNT5A	<i>NONO</i>
E	AXL	CDKN2A	EGFR	FZD7	KRT19	PDGFD	PRKCZ	SMAD2	STK11	TIMP1	WNT5B	<i>PPIH</i>
F	BMP1	CDKN2B	ERBB3	GNG11	LEF1	PDGFRB	PRRX1	SMURF1	TCF3	TRIM28	WT1	<i>GDC</i>
G	BMP2	CLDN4	ESR1	GSC	MMP2	PIK3CA	RAB25	SNAI1	TCF4	TWIST1	ZEB1	<i>PPC</i>
H	BMP7	CLDN7	ETS1	HNRNPAB	MST1R	PIK3CD	RAC1	SNAI2	TGFB1	UBA52	ZEB2	<i>NTC</i>

* gene selection may be updated based on new research and development

Appendix. Plate type choice chart.

Plate type A

Brand	Model	kit catalog #
ABI / Life Tech	ABI 5700	GK095-A
	ABI 7000	GK095-A
	ABI 7300	GK095-A
	ABI 7500	GK095-A
	ABI 7700	GK095-A
	ABI 7900 HT	GK095-A
	QuantStudio	GK095-A
	ViiA 7	GK095-A
Bio-Rad	Chromo4	GK095-A
	iCycler	GK095-A
	iQ5	GK095-A
	MyiQ	GK095-A
	MyiQ2	GK095-A
Eppendorf / Life Tech	Matercyler ep realplex 2	GK095-A
	Matercyler ep realplex 4	GK095-A
Stratagene	MX3000P	GK095-A
	MX3005P	GK095-A

Plate type B

Brand	Model	kit catalog #
ABI / Life Tech	ABI 7500 Fast	GK095-B
	ABI 7900 HT Fast	GK095-B
	QuantStudio Fast	GK095-B
	StepOnePlus	GK095-B
	ViiA 7 Fast	GK095-B
Bio-Rad	CFX Connect	GK095-B
	CFX96	GK095-B
	DNA Engine Opticon 2	GK095-B
Stratagene	MX4000	GK095-B

Plate type C

Brand	Model	kit catalog #
Roche	Lightcycler 96	GK095-C
	Lightcycler 480 (96-well)	GK095-C