



## Relative Human Telomere Length Quantification qPCR Assay Kit (RHTLQ)

Catalog #8908

100 reactions

### Product Description

Telomeres are repetitive nucleotide elements at the ends of chromosomes that protect chromosomes from degradation and genetic information loss. Normal diploid cells lose telomeres with each cell cycle. Telomere length, therefore, decreases over time and may predict lifespan. Telomere shortening has negative effects on health conditions and has been linked to many health issues including aging and cancer. Accurate and consistent quantification of telomere length is important in many aspects of cell biology such as chromosomal instability, DNA repair, senescence, apoptosis, cell dysfunctions, and oncogenesis.

Sciencell's Relative Human Telomere Length Quantification qPCR Assay Kit (RHTLQ) is designed to directly compare the average telomere length of the samples. The telomere primer set recognizes and amplifies telomere sequences. The single copy reference (SCR) primer set recognizes and amplifies a 100 bp-long region on human chromosome 17, and serves as reference for data normalization. The carefully designed primers ensure: (i) high efficiency for trustworthy quantification; and (ii) no non-specific amplification. Each primer set has been validated by qPCR with melt curve analysis and gel electrophoresis for amplification specificity and by template serial dilution for amplification efficiency.

### Kit Components

Cat #	Component	Quantity	Storage
MB6018a-1	2X GoldNStart TaqGreen qPCR master mix, 1 mL	2 vials	-20°C
8908a	Telomere primer set, lyophilized	1 vial	-20°C
8908b	Single copy reference (SCR) primer set, lyophilized	1 vial	-20°C
8908c	Nuclease-free H <sub>2</sub> O	4 mL	4°C

### Additional Materials Required (Materials Not Included in Kit)

Component	Recommended
genomic DNA template	Customers' samples
qPCR plate or tube	

### Quality Control

The specificity of the primer sets is validated by qPCR with melt curve analysis. The PCR products are analyzed by gel electrophoresis. The efficiency of the primer sets is validated by template serial dilution (See **Appendix**).

### Product Use

RHTLQ 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 on dry ice. Upon receipt, store the GoldNStart TaqGreen qPCR master mix (Cat #MB6018a-1) in the dark at -20°C in a manual defrost freezer, the primers (Cat #8908a and 8908b) at -20°C in a manual defrost freezer, and the nuclease-free H<sub>2</sub>O (Cat #8908c) at 4°C. Once thawed, do NOT refreeze GoldNStart TaqGreen qPCR master mix (Cat #MB6018a-1), and keep in the dark at 4°C or on ice at all times.

## Procedures

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

1. Prior to use, allow vials (Cat #8908a and #8908b) to warm to room temperature.
2. Centrifuge the vials at 1,500x g for 1 minute.
3. Add 200  $\mu$ l nuclease-free H<sub>2</sub>O (Cat #8908c) to telomere primer set (lyophilized, Cat #8908a) to make telomere primer stock solution. Aliquot as needed. Store at -20°C in a manual defrost freezer. Avoid repeated freeze-and-thaw cycles.
4. Add 200  $\mu$ l nuclease-free H<sub>2</sub>O (Cat #8908c) to SCR primer set (lyophilized, Cat #8908b) to make SCR primer stock solution. Aliquot as needed. Store at -20°C in a manual defrost freezer. Avoid repeated freeze-and-thaw cycles.
5. For each genomic DNA sample, prepare two qPCR reactions, one with telomere primer stock solution, and one with SCR primer stock solution. Prepare 20  $\mu$ l qPCR reactions for one well as shown in Table 1.

**Table 1.**

Reference genomic DNA sample	1 $\mu$ l
Primer stock solution (Telomere or SCR)	2 $\mu$ l
2X GoldNStart TaqGreen qPCR master mix (Cat #MB6018a-1)	10 $\mu$ l
Nuclease-free H <sub>2</sub> O (Cat #8908c)	7 $\mu$ l
<b>Total volume</b>	<b>20 <math>\mu</math>l</b>

6. Seal the qPCR reaction wells. Centrifuge the plates or tubes at 1,500x g for 15 seconds. For maximum reliability, replicates are highly recommended (minimum of 3).
7. Refer to Table 2 for qPCR program setup. The 2X GoldNStart TaqGreen qPCR master mix (Cat #MB6018a-1) does not contain a ROX passive reference dye. If the qPCR instrument being used has a "ROX passive reference dye" option, please deselect this option.

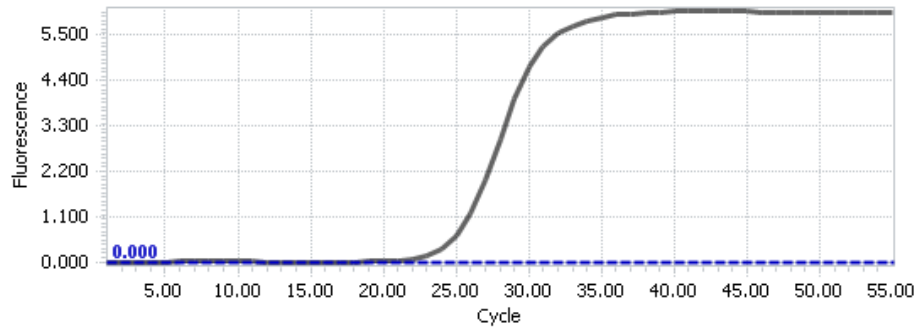
**Note:** The primary factors that determine optimal annealing temperature are the primer length and primer composition. Based on the properties of telomere and SCR primer sets (Cat #8908a and #8908b), we highly recommend an annealing temperature of 52°C as shown in Table 2:

**Table 2.**

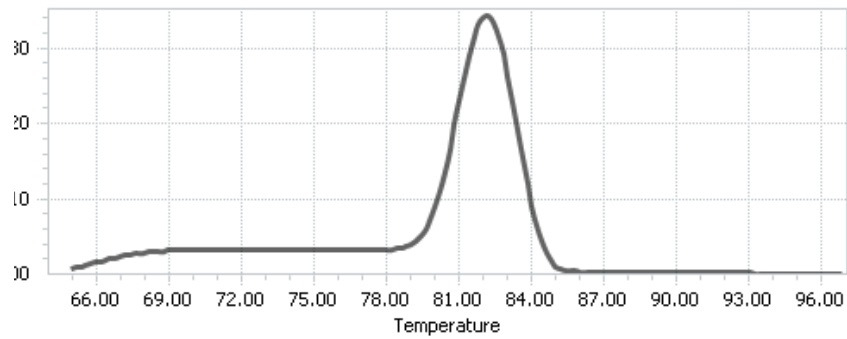
Step	Temperature	Time	Number of cycles
Initial denaturation	95°C	10 min	1
Denaturation	95°C	20 sec	32
Annealing	52°C	20 sec	
Extension	72°C	45 sec	

Data acquisition	Plate read		
<i>Optional</i>	<i>Melting curve analysis</i>		1
Hold	20°C	Indefinite	1

**Figure 1.** A typical amplification curve showing the amplification of a qPCR product.



**Figure 2.** A typical melting peak of a qPCR product.



### **Quantification Method: Comparative $\Delta\Delta Cq$ (Quantification Cycle Value) Method**

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**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.

1. For telomere (TEL),  $\Delta Cq$  (TEL) is the quantification cycle number difference of TEL between two genomic DNA samples.

$$\Delta Cq \text{ (TEL)} = Cq \text{ (TEL, sample 2)} - Cq \text{ (TEL, sample 1)}$$

**Note:** the value of  $\Delta Cq$  (TEL) can be positive, 0, or negative.

2. For single copy reference (SCR),  $\Delta Cq$  (SCR) is the quantification cycle number difference of SCR between two genomic DNA samples.

$$\Delta Cq \text{ (SCR)} = Cq \text{ (SCR, sample 2)} - Cq \text{ (SCR, sample 1)}$$

**Note:** the value of  $\Delta Cq$  (SCR) can be positive, 0, or negative.

3.  $\Delta\Delta Cq = \Delta Cq \text{ (TEL)} - \Delta Cq \text{ (SCR)}$

4. Relative telomere length of sample 2 to sample 1 (fold) =  $2^{-\Delta\Delta Cq}$

### **Example Calculations: Comparative $\Delta\Delta Cq$ (Quantification Cycle Value) Method**

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**Table 3.**  $Cq$  (Quantification Cycle) values of telomere qPCR (TEL) and single copy reference qPCR (SCR) obtained for two genomic DNA samples.

<i>Primer set</i>	<i>Sample 1</i>	<i>Sample 2</i>
TEL	16.84	14.16
SCR	26.43	25.20

$$\begin{aligned}\Delta Cq \text{ (SCR)} &= Cq \text{ (SCR, sample 2)} - Cq \text{ (SCR, sample 1)} \\ &= 25.20 - 26.43 \\ &= -1.23\end{aligned}$$

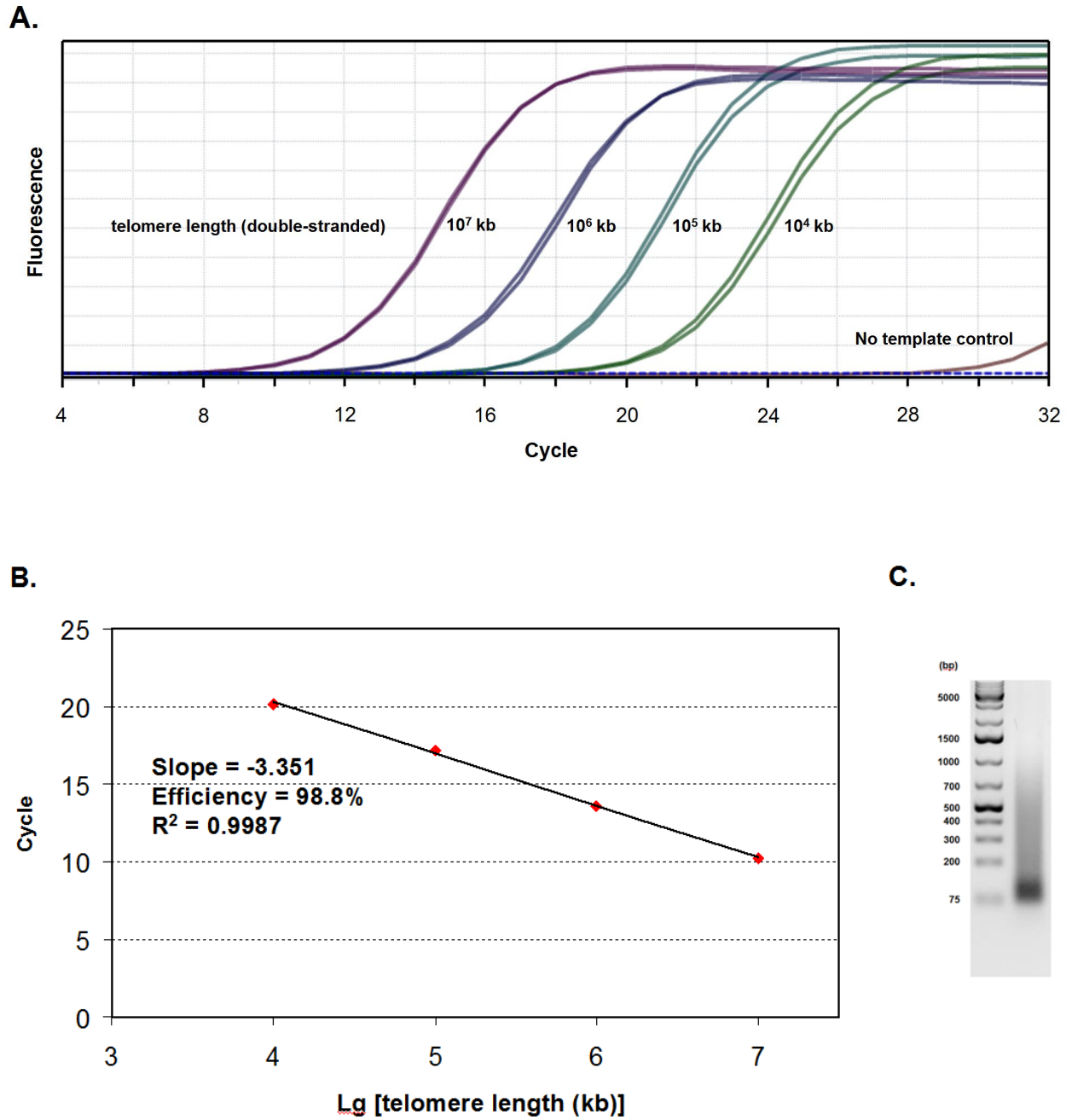
$$\begin{aligned}\Delta Cq \text{ (TEL)} &= Cq \text{ (TEL, sample 2)} - Cq \text{ (TEL, sample 1)} \\ &= 14.16 - 16.84 \\ &= -2.68\end{aligned}$$

$$\begin{aligned}\Delta\Delta Cq &= \Delta Cq \text{ (TEL)} - \Delta Cq \text{ (SCR)} \\ &= -2.68 - (-1.23) \\ &= -1.45\end{aligned}$$

$$\begin{aligned}\text{Relative telomere length of sample 2 to sample 1 (fold)} &= 2^{-\Delta\Delta Cq} \\ &= 2^{1.45} \\ &= 2.73\end{aligned}$$

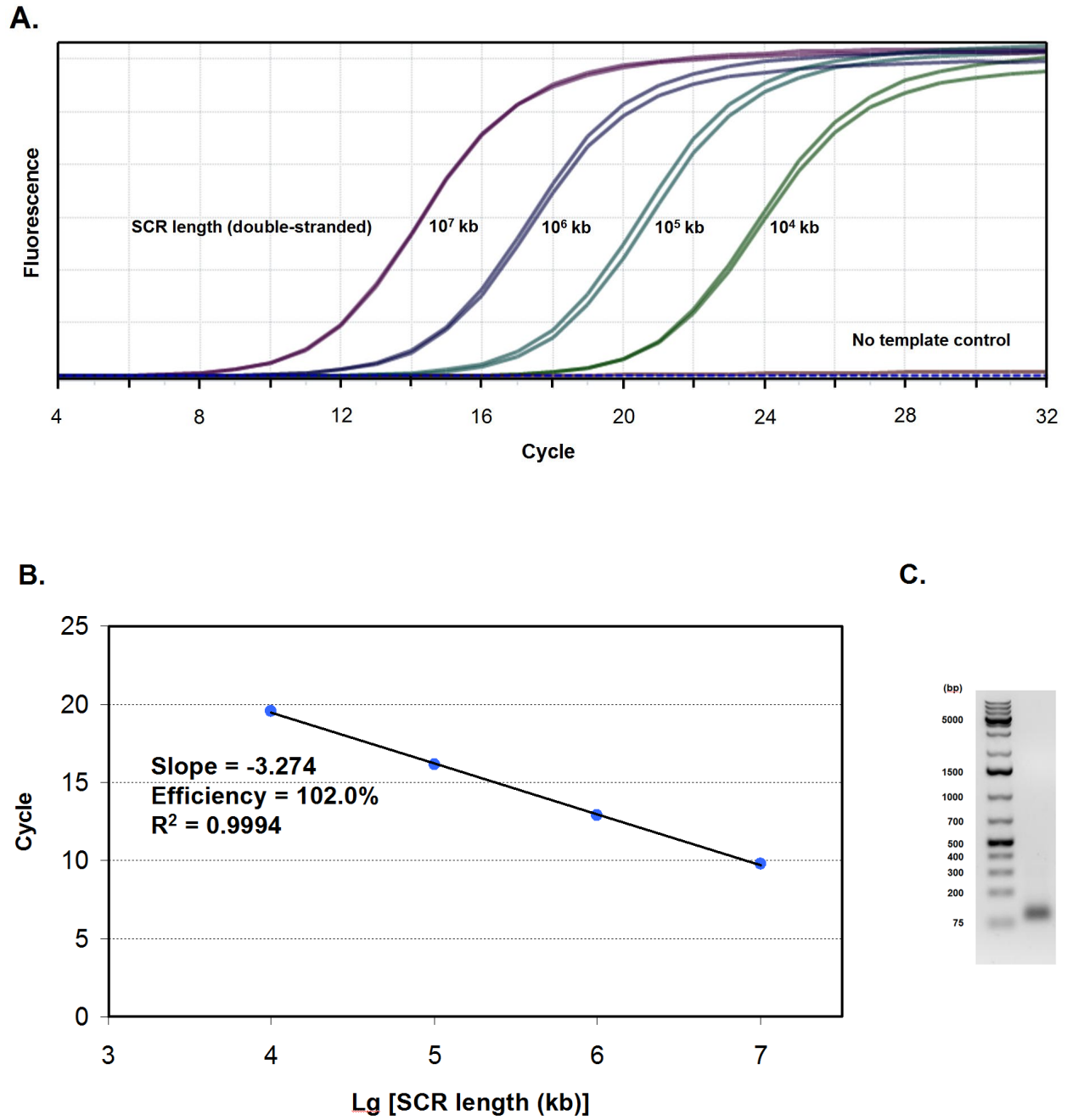
***Example Conclusions:*** The average telomere length of sample 2 is 2.73 fold longer than that of sample 1.

Appendix: Quality assessment of Telomere and SCR primer sets



**Figure 3. Quality assessment of Telomere primer set.** (A) qPCR amplification curves using serially diluted telomere repeats as template. (B) Derivation of qPCR efficiency of Telomere primer set. (C) Separation of Telomere qPCR product by gel electrophoresis. A smeared band is observed as expected.

Appendix: Quality assessment of Telomere and SCR primer sets



**Figure 4. Quality assessment of Single copy reference (SCR) primer set. (A)** qPCR amplification curves using serially diluted SCR template. **(B)** Derivation of qPCR efficiency of SCR primer set. **(C)** Separation of SCR qPCR product by gel electrophoresis.