

## Real Time PCR protocol

### **Reverse Transcription for Standard RNA (AB Taqman)**

Total RNA (best from liver) (2.0 µg)	Xµl
10X Buffer	10.0µl
25mM MgCl <sub>2</sub>	22.0µl
dNTP Mixed (10mM)	20.0µl
Oligo dT or Random Hexamer (50µM)	5.0µl
RNase Inhibitor (20U/µl)	2.0µl
Reverse Transcriptase (50U/µl)	2.5µl
RNase free H <sub>2</sub> O	(38.5-X)µl

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**Total Volume** **100 µl**

**Note:** A 100µl RT reaction efficiently converts a maximum of 2.0µg total RNA to cDNA. Multiple RT reactions should be performed if more than 2.0µg total RNA is used.

Incubate @ 25°C for 10 min

RT @ 48°C for 30 min

Inactivate @ 95°C for 5 min

**Note:**

1. The incubation step is necessary to maximize primer-RNA template binding.
  2. Store all cDNA samples at -15 to -25°C
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### **Make Standard Curve**

**Note:**

1. The ideal standard curve range is between  $10^2$ ~ $10^7$  copy of cDNA.
2. average:  $2.28 \times 10^8$  copy = 1ng cDNA

Use **SPECTRAmax PLUS** plate reader to read the cDNA concentration.

Use the following protocol: Under menu → Assays → Nucleic Acids → Pre-read Plates with Dilutions

**Note:** At least do duplicates, usually do triplicates.

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1. Add 98 $\mu$ l of H<sub>2</sub>O to each well
2. Read plates
3. Add 2 $\mu$ l of cDNA prepared by previous RT reaction.
4. Read plates.

**Note:** Make sure dilution factor is 50. The concentration unit is in  $\mu$ g/mL.

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From the reading concentration (usually several hundred  $\mu\text{g}/\text{mL}$  or  $\text{ng}/\mu\text{l}$ ), try to dilute down the concentration to  $1 \times 10^7$  copy of cDNA/ $\mu\text{l}$ . That is, if in  $100\mu\text{l}$  of final volume,  $4.39\text{ng}$  of cDNA should be added. Make a serial dilution to achieve this concentration instead of one simple dilution (less accurate because of small volume pipeting).

Calculations: (eg.  $550\text{ng}/\mu\text{l} \rightarrow (10\mu\text{l in } 90\mu\text{l}) \rightarrow 55\text{ng}/\mu\text{l} \rightarrow (10\mu\text{l in } 90\mu\text{l}) \rightarrow 5.5\text{ng}/\mu\text{l} \rightarrow (10\mu\text{l in } 45\mu\text{l}) \rightarrow 1\text{ ng}/\mu\text{l} \rightarrow (4.39\mu\text{l in } 95.61\mu\text{l}) \rightarrow 10^7\text{ copy}/\mu\text{l}$ )

Once  $1 \times 10^7$  copy of cDNA was made. Make a serial dilution range from  $1 \times 10^2 \sim 1 \times 10^7$  (6 different concentrations). These will be used as a standard curve purpose in later real time PCR reactions.

**Note:** *It might be more accurate to make 2-fold standard curve instead of 10-fold. But for totally unknown sample, make 10-fold standard curve usually is the case.*

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### ***Real time PCR Reactions (SYBR Green 2x Master from AB)***

1. Normalize the primer concentrations and mix gene-specific forward and reverse primer pair. Each primer concentration in the mixture is 0.4 pmol/ $\mu$ l.
2. Make the following mixture/reaction.

SYBR Green Mix (2x)	12.5 $\mu$ l
Sample cDNA or 10-fold dilutions standard cDNA	1 $\mu$ l
Primer pair mix (0.4 $\mu$ M)	1 $\mu$ l
H <sub>2</sub> O	up to 25 $\mu$ l

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**Total volume** **25 $\mu$ l**

**Note:** *Make triplicates for all samples and standard cDNA!*

3. The conditions for the amplification were as follows:

1. 50°C	2 min
2. 95°C	10 min
3. 95°C	15 sec
4. 60°C	30 sec
5. 72°C	30 sec
5. go to step 3 for 39 times	
6. 72°C	10 min

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4. After PCR is finished, remove the tubes from the machine. The PCR specificity can be examined by 3% agarose gel using 5 $\mu$ l from each reaction.
5. Analyze the data.

**Note:** Each primer set needs to have each standard curve. A control primer set is usually required.

**Tips:** Small volume pipeting: Always pipet small volume on the plate first, then pipet the large amount. Here, try pipet 1 $\mu$ l of cDNA sample in each 96-well first, then add the reaction mixture on top of it.

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### Real-time PCR Run

1. Use the white 96-well plates (located in the drawer of realtime PCR machine); caps in the same drawer. Do not try to recycle the plate, as potential mistakes can be made.
2. Open the opticon program, select user, load the main protocol that has same cycles as described earlier but also included a melting curve calculation following the final protocol: 65 $^{\circ}$ C to 95 $^{\circ}$ C in 0.2 $^{\circ}$ C increments with data acquisition at each increment for 0.1 s.
3. The entire plates will be read no matter how the plate setup were looked like, therefore, it's not critical to have plate setup right at the beginning. However, it is highly recommended to use the template attached to this protocol to plan ahead the plate.

**Note:** To enter the number greater than 10<sup>6</sup>, use scientific citation, such as 10<sup>7</sup> = 1e7.

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