

mtDNA WI-08 Cycle Sequencing

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Document ID: 966

Revision: 1

Effective Date: 8/15/2014

Status: Published

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Isopropyl wipe: 2 Pipettors (p2, p10), 02.mL rack(s), 1.5mL rack

Take out: tube of Big Dye

Primers (including C stretch primers if necessary)

Allow to warm up to room temperature

Label: 0.2mL tubes **per primer**- NC, RB, Q/K, HL60

dilution tubes for each region- Q/K, HL60

(Remember extra tubes for C stretches)

Make Cocktail: Dispense 8μL of Big Dye into each tube

Followed by 5μL of the appropriate primer

Lastly add 7μL* of sample in the order of NC's, RB's, Q/K, HL60

*NC's/ RB's take straight 7μL

*For Samples/ Positive target ~8ng

Formula: $\frac{\text{Target Sequencing Amount}}{\text{CE Concentration}} = \text{Amount of Sample Needed}$

Ex. CE concentration K1 HV1 = 42.20ng/μL

$\frac{8\text{ng}}{42.20\text{ng}/\mu\text{L}} = 0.18\mu\text{L} = 0.2\mu\text{L}$

42.20ng/μL

Total amount= 7μL

0.2μL sample + 6.8μL dH₂O

Dilution for both primers (2X)= 14μL

0.4μL sample + 13.6μL dH₂O

Vortex dilution tubes

Add 7μL into A1 tube and 7μL into B1 tube

Repeat for K1 HV2

Lastly make your dilutions for HL60 and add to the appropriate labeled tubes

Spin down tubes and place into Thermal cycler

Determine total ng Sequenced:

$$\text{Ex. } 42.20\text{ng}/\mu\text{L} \times 0.2\mu\text{L} = 8.44\text{ng} = 8.4\text{ng}$$

Remember:

With C-stretches- count up all peaks for CE Concentration

Knowns- A4, B4 for HV1 C-stretch

- D2 for HV2 C-stretch

*Extra dilution tubes, may need to add water to NC's/RB's for HV1

Q's- A4 for HV1B, B4 for HV1A

- Proceed as usual for HV2 C-stretch (D2 takes care of it, however C4 can additionally be used)

*Extra dilution tubes