MASSEY UNIVERSITY
COLLEGE OF SCIENCES
TE WĀHANGA PŪTAIAO

MASSEY GENOME SERVICE

Sanger Sequencing and Genotyping using Life Technologies 3500XL capillary instrumentation
Operational since 2003

SERVICE OUTLINE AND PRICE LIST
March 2026

SERVICE INCLUDES

Sanger sequencing and genotyping data delivery
Fast turnaround times
Free Courier Service within New Zealand

Enquiries regarding service outline and pricing contact:
Xiaoxiao Lin – Laboratory Manager (Phone: +64 6 951 9080)

MASSEY GENOME SERVICE

Sanger Sequencing & Genotyping using Life Technologies 3500XL Capillary Instrumentation

SERVICE OUTLINE & PRICE LIST

Effective 1st March 2026
Prices in New Zealand dollars and excludes G.S.T

SERVICE TYPE	PRICES (excluding G.S.T)	TURNAROUND TIME (From Receipt of Sample/s)
Sequencing		
Full Sequencing Service (Plasmids/PCR Products)	$13.00	2 working days
Full Sequencing Service (Cosmids, fosmids and BACs)	$19.00	2 working days
Full Sequencing Service (Bacterial Genomic DNA)	$33.00	2 working days
Capillary Separation Sequencing Service ①	$9.00	2 working days
Capillary Separation 96-well Plate Sequencing Service ①	$630.00 per plate	2 working days
Capillary Separation with reaction cleanup Sequencing Service ①	$10.50	2 working days
96-well Plate Service with reaction cleanup Sequencing Service ①	$780.00 per plate	2 working days
Genotyping		
Capillary Separation Service (when ≥12 samples are submitted) ②	$11.00 (a **processing fee** will apply for **less than 12 samples** per request) ②	2 working days
Plate Service	$800.00 per plate	2 working days

CONSUMABLES	PRICES (excluding G.S.T)
BigDye® Terminator v3.1 – 80µl vial ①	$240.00
BigDye® Terminator v3.1 – 800µl vial ①	$2400.00
Overnight courier with dry ice ③	Please email for availability and pricing
Overnight courier with ice pack ④	$75.00

Please note:

① Customers using the "**Capillary Separation Sequencing Service**", "**Capillary Separation 96-well Plate Sequencing Service**", "**Capillary Separation with reaction cleanup Sequencing Service**", and "**96-well Plate Service with reaction cleanup Sequencing Service**" can purchase BigDye® Terminator v3.1 or its direct drop-in substitutes from the Massey Genome Service. Please contact our service for purchasing.

② MGS will be charging an extra processing fee for less than 12 samples per request. **For 1 to 3 samples, there is a $25.00 fee; for 4 to 7 samples, there is a $20.00 fee; for 8-11 samples, there is a $15.00 fee**.

③ There is limited access to dry ice, please email x.x.lin@massey.ac.nz for availability and prices for shipping reagents on dry ice using New Zealand Couriers.

④ Charges apply to customers who require consumables to be delivered using overnight courier. Please make sure a purchase order for the courier service is sent with the sequencing request.

To send samples in PCR tubes or plates

The Massey Genome Service requires customers who are using the Full Sequencing Service to send the template and primers premixed in 0.2ml individual PCR tubes or 0.2ml strip tubes.

For the Sequencing Capillary Separation Service and Sequencing Capillary Separation Service with reaction cleanup please send the sequencing reactions in 0.2ml individual PCR tubes or 0.2ml strip tubes.

For the Sequencing Plate Service and Sequencing Plate Service with reaction cleanup, please send the sequencing reactions in a 96 well plate, sealed with strip tubes, plastic seal or foil seal. The strip tubes provide the best result.

Template and primer concentration requirements

Template type	Template total quantity (in final volume)	Primer total quantity* (in final volume)	Final volume required #
PCR product: 100-200bp 200-500bp 500-1000bp 1000-2000bp >2000bp Rule: For PCR products use **4ng** of template for every 100bp.	Quantity: **4-8ng** **8-20ng** **20-40ng** **40-80ng** **80-200ng**	4pmol	20ul if using your own primer, 19ul if using MGS primer
Single-stranded plasmid	**100-200ng**	4pmol	20ul if using your own primer, 19ul if using MGS primer
Double-stranded plasmid	**400-1000ng**	4pmol	20ul if using your own primer, 19ul if using MGS primer
Cosmid, BAC DNA, Lambda DNA	**1-2µg**	6.4pmol	20ul if using your own primer, 18ul if using MGS primer
Bacterial genomic DNA	**4-6µg**	6.4pmol	20ul if using your own primer, 18ul if using MGS primer

* Make sure only one primer is added to the template/primer premix

Make the template/primer premix up to the final volume with filtered molecular grade water.

Example of requirements

You have a 500bp PCR product at a concentration of 7ng/µL and your primer is at a concentration of 2pmol/µL.

For PCR products use **4ng** of template for every 100bp. So, for a 500bp product you will need to add 20ng to the template/primer premix. At a concentration of 7ng/µL you will need to add 3µL template to the premix to get 21ng for your PCR template.

For the primer you need 4pmol total amount in the template/primer premix. So, at a concentration of 2 pmol/µL you will need to add 2 µL primer to the premix. You then need to make the premix up to a final volume of 20 µL by adding 15 µL of filtered molecular grade water to the premix to get the final volume of 20 µL.

Using spectrophotometer or fluorometer for quantification

Relying solely on spectrophotometer readings (e.g. NanoDrop) for quantification can be misleading if contaminants are present. Either too little or too much DNA template can cause sequencing failure. I recommend quantifying the sample using a Qubit fluorometer to get more accurate concentration readings if you have access to one. Also check the OD 260/280 and 260/230 ratios on the NanoDrop. For high-quality DNA, a Nanodrop 260/280 ratio should be between 1.8 and 2.0 to indicate low protein contamination, while the 260/230 ratio should be in the 1.8–2.2 range to show low contamination from other organic compounds like phenol. A 260/280 ratio lower than 1.8 suggests protein or phenol contamination, and a 260/230 ratio below 1.8 indicates the presence of other contaminants that could interfere with downstream applications.

MGS recommend using a fluorometer (e.g. Qubit) if you have access to one. Qubit will generate a more accurate concentration reading.