

General guidelines for sample dimensions and scan time for Micro-CT 100 scanning at the Centre for High-Throughput Phenogenomics

Sample Holder Diameter (mm)	Sample Holder Length (mm)	Field of View (mm)	High Resolution Voxel Size (µm)	Scan Time per Detector Position (min)	Detector Position Length (mm)	Medium Resolution Voxel Size (µm)	Scan Time per Detector Position (min)	Detector Position Length (mm)
9.0	78.0	10.2	5.0	*min = 14.0, **max = 51.6	1.000	10.0	*min = 7.2, **max = 26.4	1.000
		15.2	7.4	*min = 14.0, **max = 51.6	1.495	14.8	*min = 7.2, **max = 26.4	1.495
		20.5	10.0	*min = 14.0, **max = 51.6	2.040	20.0	*min = 7.2, **max = 26.4	2.040
		35.2	17.2	*min = 14.0, **max = 51.6	3.492	34.4	*min = 7.2, **max = 26.4	3.492
		50.4	24.6	*min = 14.0, **max = 51.6	5.018	49.2	*min = 7.2, **max = 26.4	5.018
		75.4	36.8	*min = 14.0, **max = 51.6	7.507	73.6	*min = 7.2, **max = 26.4	7.507
		90.1	44.0	*min = 14.0, **max = 51.6	8.976	88.0	*min = 7.2, **max = 26.4	8.976
		105.1	51.3	*min = 14.0, **max = 51.6	10.465	102.6	*min = 7.2, **max = 26.4	10.465
14.0	92.0	10.2	5.0	*min = 14.0, **max = 51.6	1.000	10.0	*min = 7.2, **max = 26.4	1.000
		15.2	7.4	*min = 14.0, **max = 51.6	1.495	14.8	*min = 7.2, **max = 26.4	1.495
		20.5	10.0	*min = 14.0, **max = 51.6	2.040	20.0	*min = 7.2, **max = 26.4	2.040
		35.2	17.2	*min = 14.0, **max = 51.6	3.492	34.4	*min = 7.2, **max = 26.4	3.492
		50.4	24.6	*min = 14.0, **max = 51.6	5.018	49.2	*min = 7.2, **max = 26.4	5.018
		75.4	36.8	*min = 14.0, **max = 51.6	7.507	73.6	*min = 7.2, **max = 26.4	7.507
		90.1	44.0	*min = 14.0, **max = 51.6	8.976	88.0	*min = 7.2, **max = 26.4	8.976
		105.1	51.3	*min = 14.0, **max = 51.6	10.465	102.6	*min = 7.2, **max = 26.4	10.465
19.0	84.0	10.2	5.0	*min = 14.0, **max = 51.6	1.000	10.0	*min = 7.2, **max = 26.4	1.000
		15.2	7.4	*min = 14.0, **max = 51.6	1.495	14.8	*min = 7.2, **max = 26.4	1.495
		20.5	10.0	*min = 14.0, **max = 51.6	2.040	20.0	*min = 7.2, **max = 26.4	2.040
		35.2	17.2	*min = 14.0, **max = 51.6	3.492	34.4	*min = 7.2, **max = 26.4	3.492
		50.4	24.6	*min = 14.0, **max = 51.6	5.018	49.2	*min = 7.2, **max = 26.4	5.018
		75.4	36.8	*min = 14.0, **max = 51.6	7.507	73.6	*min = 7.2, **max = 26.4	7.507
		90.1	44.0	*min = 14.0, **max = 51.6	8.976	88.0	*min = 7.2, **max = 26.4	8.976
		105.1	51.3	*min = 14.0, **max = 51.6	10.465	102.6	*min = 7.2, **max = 26.4	10.465
34.0	110.0	10.2	5.0	*min = 14.0, **max = 51.6	1.000	10.0	*min = 7.2, **max = 26.4	1.000
		15.2	7.4	*min = 14.0, **max = 51.6	1.495	14.8	*min = 7.2, **max = 26.4	1.495
		20.5	10.0	*min = 14.0, **max = 51.6	2.040	20.0	*min = 7.2, **max = 26.4	2.040
		35.2	17.2	*min = 14.0, **max = 51.6	3.492	34.4	*min = 7.2, **max = 26.4	3.492
		50.4	24.6	*min = 14.0, **max = 51.6	5.018	49.2	*min = 7.2, **max = 26.4	5.018
		75.4	36.8	*min = 14.0, **max = 51.6	7.507	73.6	*min = 7.2, **max = 26.4	7.507
		90.1	44.0	*min = 14.0, **max = 51.6	8.976	88.0	*min = 7.2, **max = 26.4	8.976
		105.1	51.3	*min = 14.0, **max = 51.6	10.465	102.6	*min = 7.2, **max = 26.4	10.465
48.0	110.0	10.2	5.0	*min = 14.0, **max = 51.6	1.000	10.0	*min = 7.2, **max = 26.4	1.000
		15.2	7.4	*min = 14.0, **max = 51.6	1.495	14.8	*min = 7.2, **max = 26.4	1.495
		20.5	10.0	*min = 14.0, **max = 51.6	2.040	20.0	*min = 7.2, **max = 26.4	2.040
		35.2	17.2	*min = 14.0, **max = 51.6	3.492	34.4	*min = 7.2, **max = 26.4	3.492
		50.4	24.6	*min = 14.0, **max = 51.6	5.018	49.2	*min = 7.2, **max = 26.4	5.018
		75.4	36.8	*min = 14.0, **max = 51.6	7.507	73.6	*min = 7.2, **max = 26.4	7.507
		90.1	44.0	*min = 14.0, **max = 51.6	8.976	88.0	*min = 7.2, **max = 26.4	8.976
		105.1	51.3	*min = 14.0, **max = 51.6	10.465	102.6	*min = 7.2, **max = 26.4	10.465
73.0	130.0	10.2	5.0	*min = 14.0, **max = 51.6	1.000	10.0	*min = 7.2, **max = 26.4	1.000
		15.2	7.4	*min = 14.0, **max = 51.6	1.495	14.8	*min = 7.2, **max = 26.4	1.495
		20.5	10.0	*min = 14.0, **max = 51.6	2.040	20.0	*min = 7.2, **max = 26.4	2.040
		35.2	17.2	*min = 14.0, **max = 51.6	3.492	34.4	*min = 7.2, **max = 26.4	3.492
		50.4	24.6	*min = 14.0, **max = 51.6	5.018	49.2	*min = 7.2, **max = 26.4	5.018
		75.4	36.8	*min = 14.0, **max = 51.6	7.507	73.6	*min = 7.2, **max = 26.4	7.507
		90.1	44.0	*min = 14.0, **max = 51.6	8.976	88.0	*min = 7.2, **max = 26.4	8.976
		105.1	51.3	*min = 14.0, **max = 51.6	10.465	102.6	*min = 7.2, **max = 26.4	10.465
88.0	130.0	10.2	5.0	*min = 14.0, **max = 51.6	1.000	10.0	*min = 7.2, **max = 26.4	1.000
		15.2	7.4	*min = 14.0, **max = 51.6	1.495	14.8	*min = 7.2, **max = 26.4	1.495
		20.5	10.0	*min = 14.0, **max = 51.6	2.040	20.0	*min = 7.2, **max = 26.4	2.040
		35.2	17.2	*min = 14.0, **max = 51.6	3.492	34.4	*min = 7.2, **max = 26.4	3.492
		50.4	24.6	*min = 14.0, **max = 51.6	5.018	49.2	*min = 7.2, **max = 26.4	5.018
		75.4	36.8	*min = 14.0, **max = 51.6	7.507	73.6	*min = 7.2, **max = 26.4	7.507
		90.1	44.0	*min = 14.0, **max = 51.6	8.976	88.0	*min = 7.2, **max = 26.4	8.976
		105.1	51.3	*min = 14.0, **max = 51.6	10.465	102.6	*min = 7.2, **max = 26.4	10.465
103.0	130.0	10.2	5.0	*min = 14.0, **max = 51.6	1.000	10.0	*min = 7.2, **max = 26.4	1.000
		15.2	7.4	*min = 14.0, **max = 51.6	1.495	14.8	*min = 7.2, **max = 26.4	1.495
		20.5	10.0	*min = 14.0, **max = 51.6	2.040	20.0	*min = 7.2, **max = 26.4	2.040
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		50.4	24.6	*min = 14.0, **max = 51.6	5.018	49.2	*min = 7.2, **max = 26.4	5.018
		75.4	36.8	*min = 14.0, **max = 51.6	7.507	73.6	*min = 7.2, **max = 26.4	7.507
		90.1	44.0	*min = 14.0, **max = 51.6	8.976	88.0	*min = 7.2, **max = 26.4	8.976
		105.1	51.3	*min = 14.0, **max = 51.6	10.465	102.6	*min = 7.2, **max = 26.4	10.465

* Minimum scan time is based on 0.5mm Al filter ('medium'), 90 kVp (the highest energy setting), and 300 ms integration time (the highest integration time for 0.5 Al and 90kVp). Actual scan times may be higher or lower than those provided in the chart. Therefore, this chart is meant to serve as a guideline for general expectations prior to visiting the Centre for High-Throughput Phenogenomics. The exact scan time for your particular sample can be provided prior to submitting the actual scan.

* Maximum scan time is based on 0.5mm Al filter ('medium'), 45 kVp (the lowest energy setting), and 1400 ms integration time (the highest integration time for 0.5 Al and 45kVp). Actual scan times may be higher or lower than those provided in the chart. Therefore, this chart is meant to serve as a guideline for general expectations prior to visiting the Centre for High-Throughput Phenogenomics. The exact scan time for your particular sample can be provided prior to submitting the actual scan.

Voxel size not possible with this sample holder
 Voxel size only possible with decreased field of view

Note: High Resolution settings are based on 1.5x binning, 2048 samples, and 1000 projections/180°
 Note: Medium Resolution settings are based on 3.0x binning, 1024 samples, and 500 projections/180°