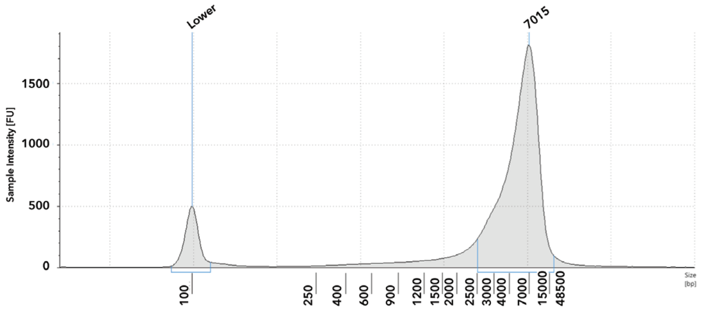
powered by MEDGENOME

Whole Genome/ Exome Sequencing QC Report

QC Report for Whole Genome Sequencing Libraries from high quality DNA

Sample QC

A



B **Sample Table**

Well	DIN	Conc. [ng/ µl]	Sample ID	Alert	Observations
C1	6.2	79.8			Issue with ladder peak detection (too many peaks detected)

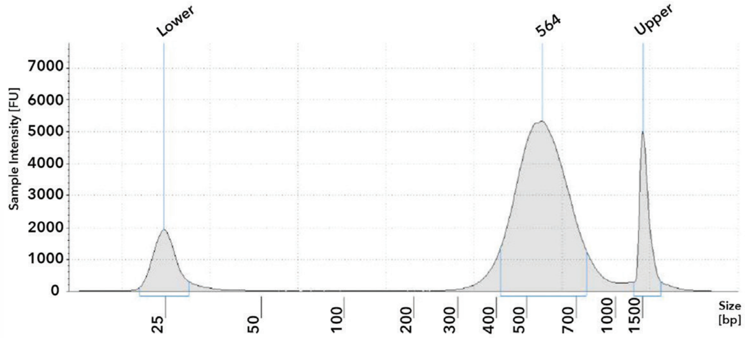
C **Peak Table**

Size [bp]	Calibrated Conc. [ng/ µl]	Assigned Conc. [ng/ µl]	% Integrated Area	From [bp]	To [bp]	Peak Comment	Observations
100	8.50	8.50	-	86	114		Lower Marker
7015	66.3	-	100.00	2512	17783		
2947	12.9	-	83.63	1970	7494		
-	-	-	-	-	-		Sample Well

Figure 1 : A) Representative Electropherogram generated from TapeStation shows profile of input DNA. B) Table shows quantification of the DNA in the sample. C) Shows quantification of the major peaks detected in the electropherogram.

Library QC

A



B **Sample Table**

Well	Conc. [ng/ µl]	Sample ID	Alert	Observations
D1	36.5			

C **Peak Table**

Size [bp]	Calibrated Conc. [ng/ µl]	Assigned Conc. [ng/ µl]	Peak Molarity [nmol/l]	% Integrated Area	Peak Comment	Observations
25	6.00	-	369	-		Lower Marker
564	36.5	-	99.7	100.00		
1500	6.50	6.50	6.67	-		Upper Marker

Figure 2 : A) Representative electropherogram obtained from TapeStation shows the profile of the finished library for whole genome sequencing. B) Table shows quantification of the library generated. C) Table shows quantification of the peak in the library.

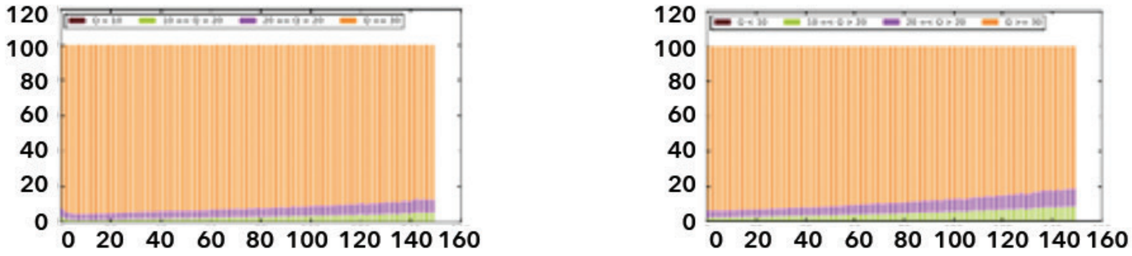
Sequencing QC

1.1 Read orientation-R1

1.2 Read orientation-R2

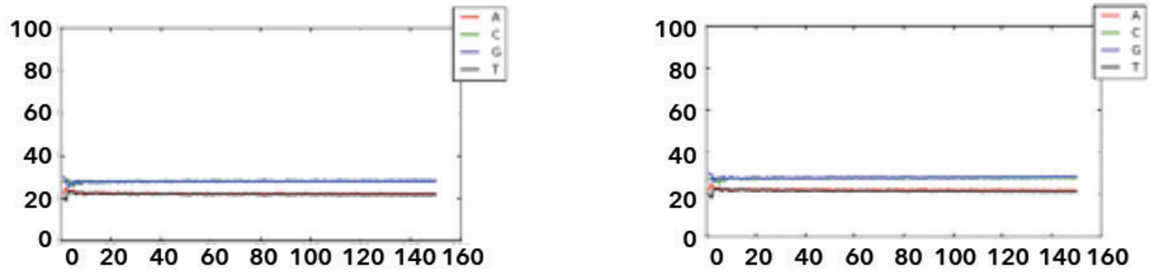
1.1.1 Quality distribution

1.2.1 Quality distribution



1.1.2 Base distribution

1.2.2 Base distribution



1.1.3 GC distribution

1.2.3 GC distribution

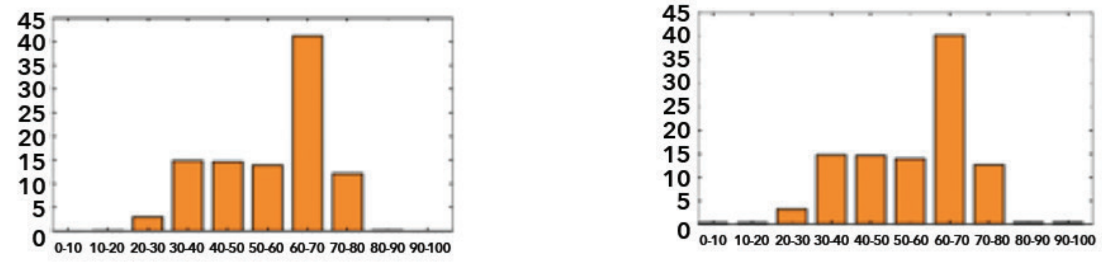
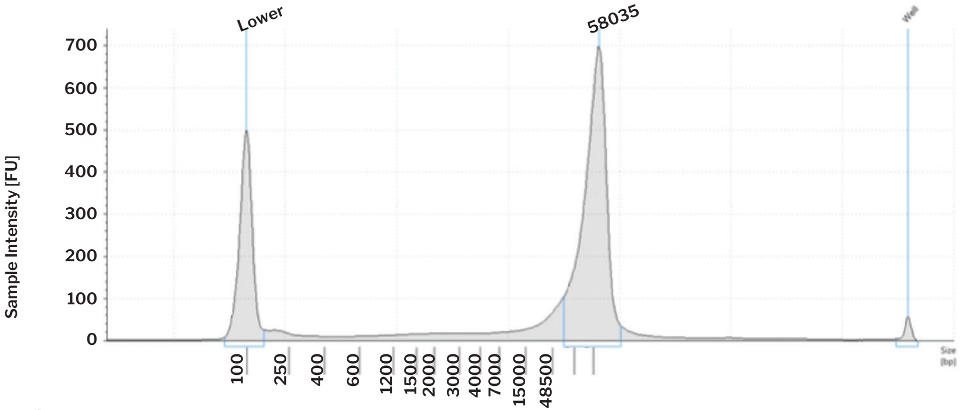


Figure 3 : Representative FastQC report showing quality of reads obtained from the sequencing run.

QC Report for Whole Exome Sequencing Libraries from high quality DNA

A



B Sample Table

Well	DIN	Conc. [ng/ µl]	Sample ID	Alert	Observations
B1	8.2	28.9			

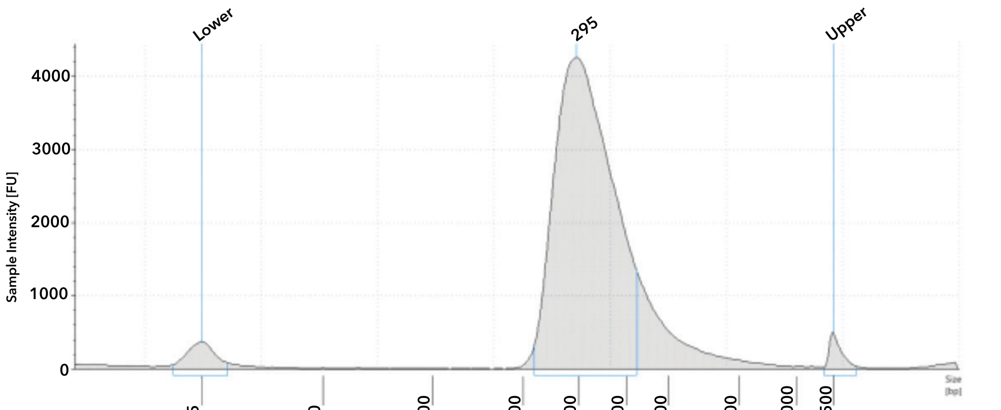
C Peak Table

Size [bp]	Calibrated Conc. [ng/ µl]	Assigned Conc. [ng/ µl]	% Integrated Area	From [bp]	To [bp]	Peak Comment	Observations
100	8.50	8.50	-	62	147		Lower Marker
58035	20.5	-	97.65	10378	>60000		
-	-	-	-	-	-		Sample Well

Figure 4 : A) Representative Electropherogram generated from TapeStation shows profile of input DNA. B) Table shows quantification of the DNA in the sample. C) Shows quantification of the major peaks detected in the electropherogram.

Library QC

A



B Sample Table

Well	Conc. [ng/ µl]	Sample ID	Alert	Observations
D1	10400			

C Peak Table

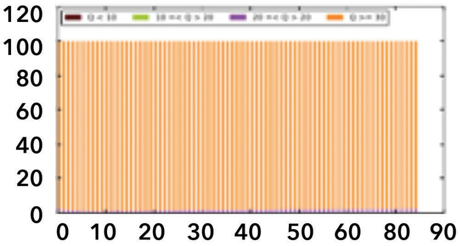
Size [bp]	Calibrated Conc. [ng/ µl]	Assigned Conc. [ng/ µl]	Peak Molarity [nmol/l]	% Integrated Area	Peak Comment	Observations
25	434	-	26700	-		Lower Marker
295	10400	-	54100	100.00		
1500	250	250	256	-		Upper Marker

Figure 5 : A) Representative electropherogram obtained from TapeStation shows the profile of the finished library for whole exome sequencing . B) Table shows quantification of the library generated. C) Table shows quantification of the peak in the library.

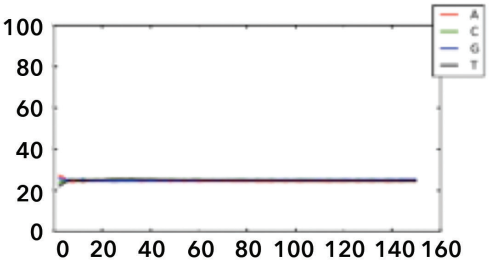
Sequencing QC

1.1 Read orientation-R1

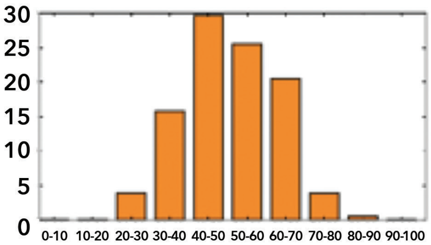
1.1.1 Quality distribution



1.1.2 Base distribution

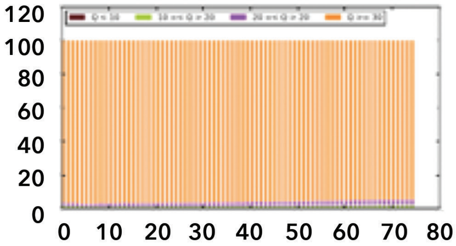


1.1.3 GC distribution

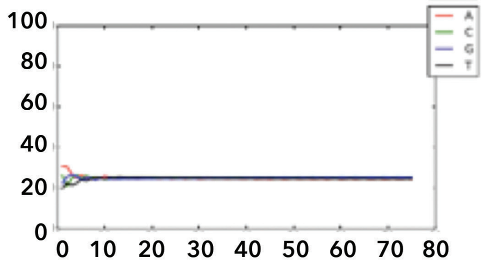


1.2 Read orientation-R2

1.2.1 Quality distribution



1.2.2 Base distribution



1.2.3 GC distribution

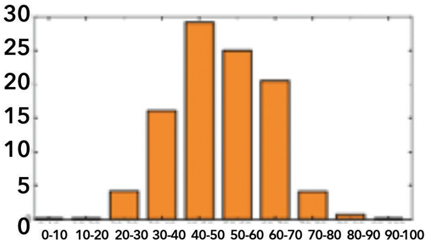
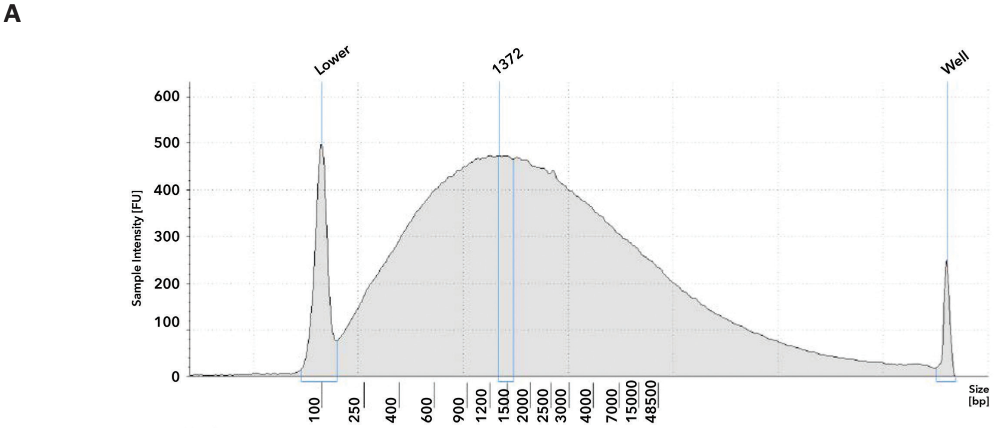


Figure 6 : Representative FastQC report showing quality of reads obtained from the sequencing run.

QC Report for Whole Exome Sequencing Libraries from FFPE tissue sourced DNA

Sample QC



B

Sample Table

Well	DIN	Conc. [ng/ µl]	Sample ID	Alert	Observations
B1	2.7	151			Sample concentration outside recommended range

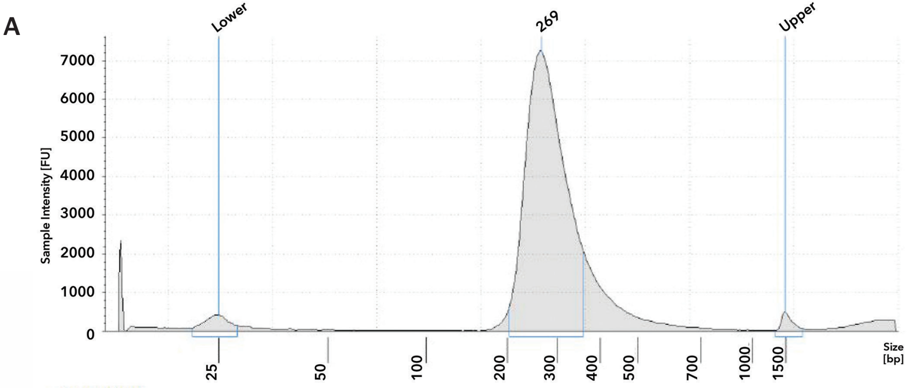
C

Peak Table

Size [bp]	Calibrated Conc. [ng/ µl]	Assigned Conc. [ng/ µl]	% Integrated Area	Peak Comment	Observations	Peak Comment	Observations
100	8.50	8.50	-	64	138		Lower Marker
1372	8.25	-	80.89	1347	1623		
-	-	-	-	-	-		Sample Well

Figure 7 : A) Representative Electrophoregram generated from TapeStation shows profile of input DNA. B) Table shows quantification of the DNA in the sample and C) shows quantification of the major peaks detected in the electropherogram.

Library QC



B

Sample Table

Well	Conc. [ng/ µl]	Sample ID	Alert	Observations
C1	14200			

C

Peak Table

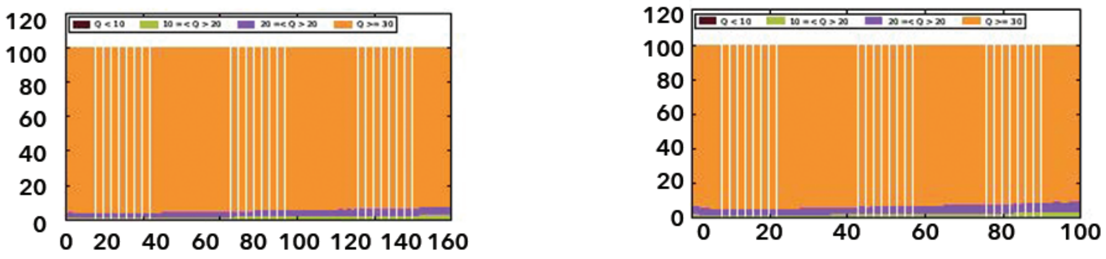
Size [bp]	Calibrated Conc. [ng/ µl]	Assigned Conc. [ng/ µl]	Peak Molarity [pmol/l]	% Integrated Area	Peak Comment	Observations
25	496	-	30500	-		Lower Marker
269	14200	-	81000	100.00		
1500	250	250	256	-		Sample Well

Figure 8 : A) Representative electropherogram generated from TapeStation shows profile of WES library. B) Table shows overall concentration of the library. C) Table shows quantification of the major peak detected in the library.

Sequencing QC

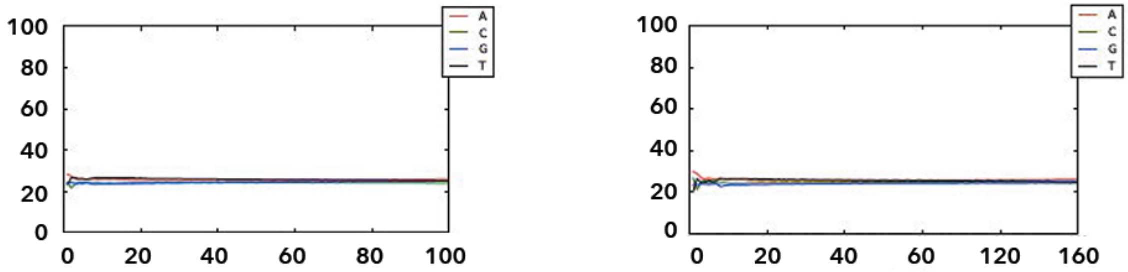
3.1 Read orientation-R1

3.2 Read orientation-R2



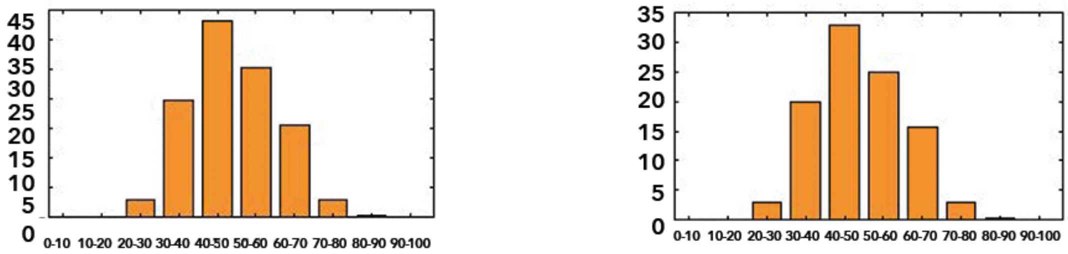
3.1.1 Quality distribution

3.2.1 Quality distribution



3.1.2 Base distribution

3.2.2 Base distribution



3.1.3 GC distribution

3.2.3 GC distribution

Figure 9 : Representative FastQC report showing quality of reads obtained from the sequencing run.