

Whole Genome/ Exome Sequencing QC Report

QC Report for Whole Genome Sequencing Libraries from high quality DNA

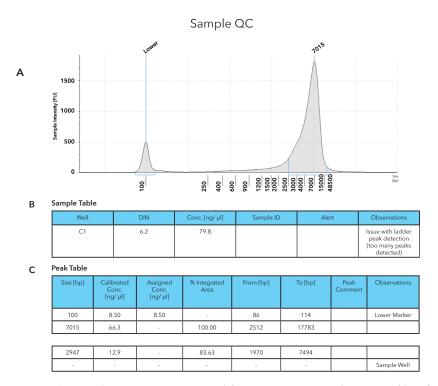


Figure 1: A) Representative Electropherogram generated from TapeStation shows profile of input DNA. B) Table shows quantification of the DNA in the sample .C) Shows quantification of the major peaks detected in the electropherogram.

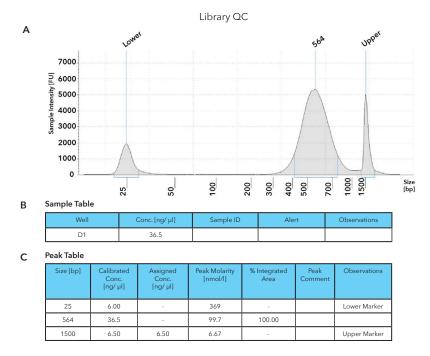


Figure 2: A) Representative electropherogram obtained from TapeStation shows the profile of the finished library for whole genome sequencing. B) Table shows quantification of the library generated. C) Table shows quantification of the peak in the library.

Sequencing QC

1.1 Read orientation-R1 1.2 Read orientation-R2 1.1.1 Quality distribution 1.2.1 Quality distribution 120 7 120 = 100 100 80 80 60 60 40 40 20 20 20 40 60 80 100 120 140 160 20 40 60 80 100 120 140 160 1.2.2 Base distribution 1.1.2 Base distribution 100 100 80 80 60 60 40 40 20 20 60 80 100 120 140 160 60 80 100 120 140 160 1.1.3 GC distribution 1.2.3 GC distribution 45 40 35 30 25 20 15 45 40 35 30 25 20 15 10 0 0-10 10-20 20-30 30-40 40-50 50-60 60-70 70-80 80-90 90-100 0 0.10 10-20 20-30 30-40 40-50 50-60 60-70 70-80 80-90 90-100

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

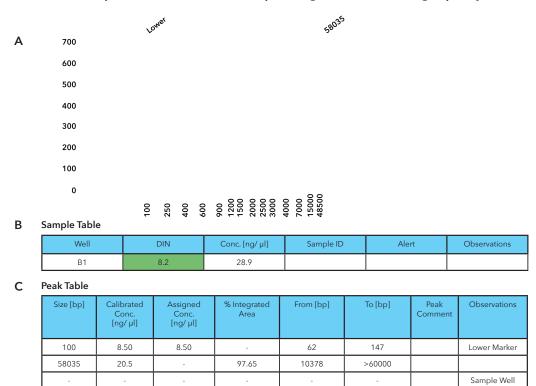


Figure 4: A) Representative Electropherogram generated from TapeStation shows profile of input DNA. B) Table shows quantification of the DNA in the sample .C) Shows quantification of the major peaks detected in the electropherogram.

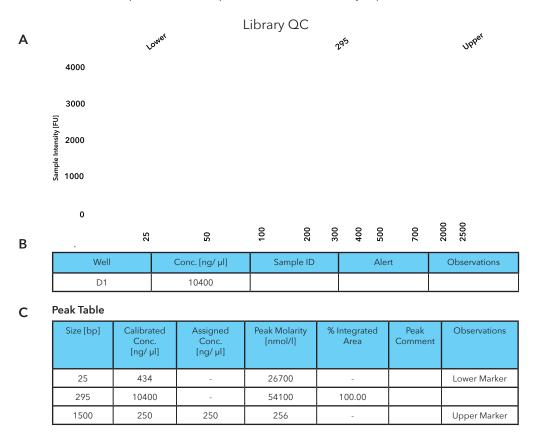


Figure 5: A) Representative electropherogram obtained from TapeStation shows the profile of the finished library for whole exome sequencing. B) Table shows quantification of the library generated. C) Table shows quantification of the peak in the library.

Sequencing QC

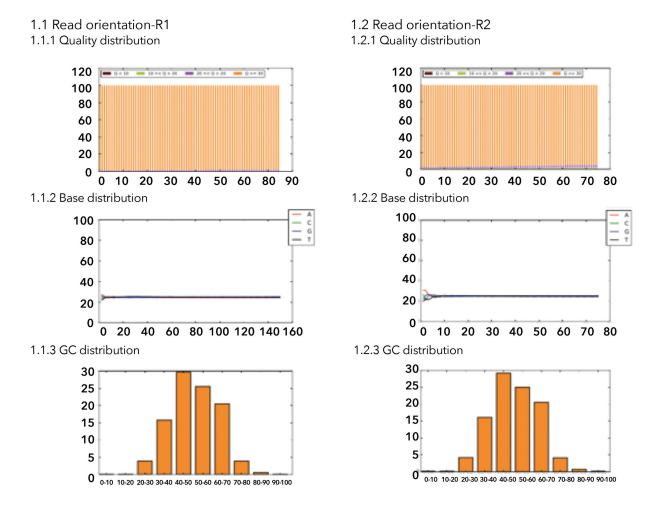
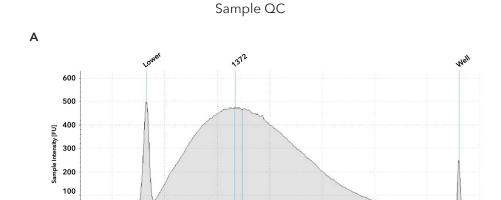


Figure 6: Representative FastQC report showing quality of reads obtained from the sequencing run.

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



B Sample Table

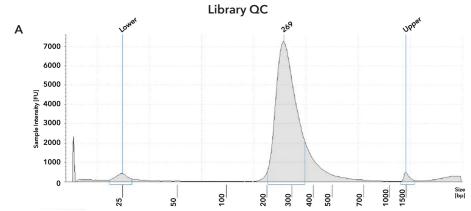
Well	DIN	Conc. [ng/ μl]	Sample ID	Alert	Observations
B1	2.7	151			Sample concentra- tion outside recommened range

900 1200 2000 2500 3000 4000 15000 48500

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.



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.

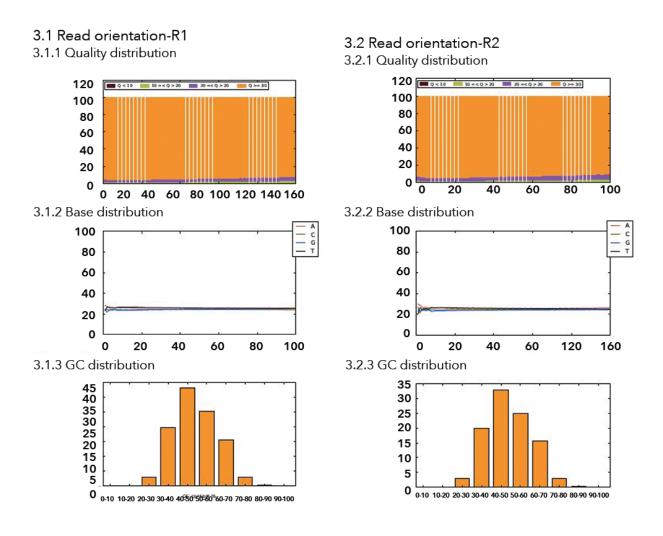


Figure 9: Representative FastQC report showing quality of reads obtained from the sequencing run.

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