

Whole Genome/ Exome Sequencing QC Report

QC Report for Whole Genome Sequencing Libraries from high quality DNA

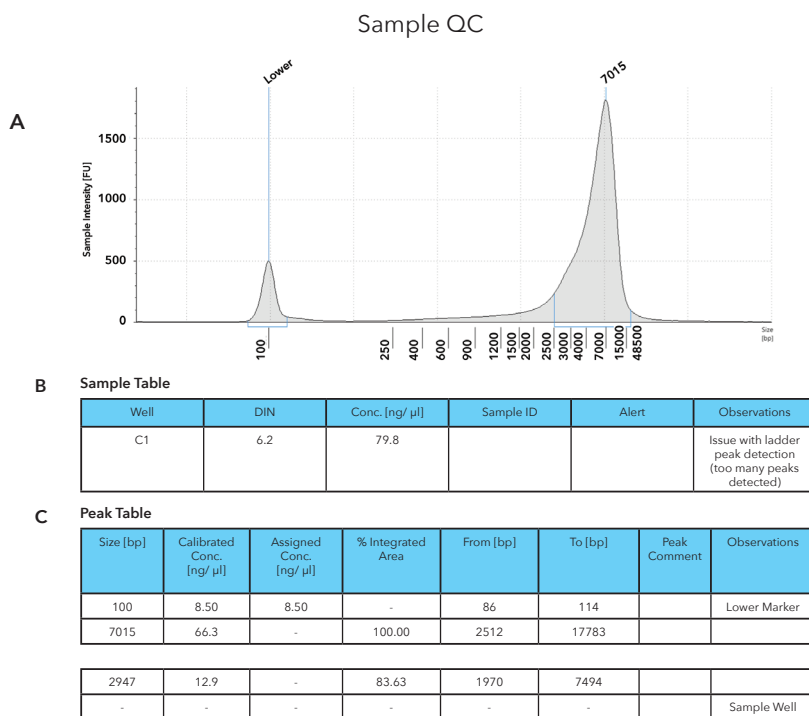


Figure 1: A) Representative Electropherogram generated from TapeStation shows profile of input DNA. B) Table shows quantification of the DNA in the sample. C) Shows quantification of the major peaks detected in the electropherogram.

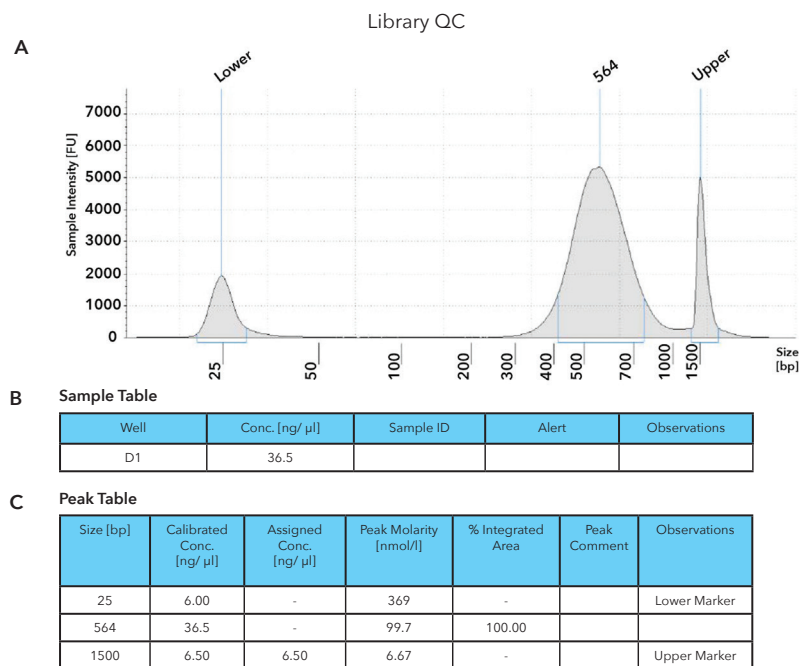
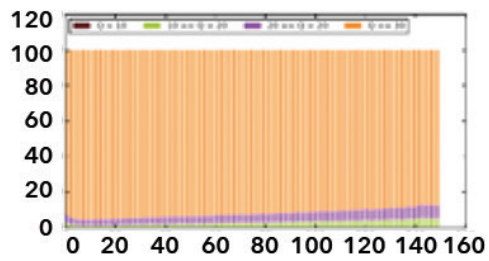


Figure 2: A) Representative electropherogram obtained from TapeStation shows the profile of the finished library for whole genome sequencing. B) Table shows quantification of the library generated. C) Table shows quantification of the peak in the library.

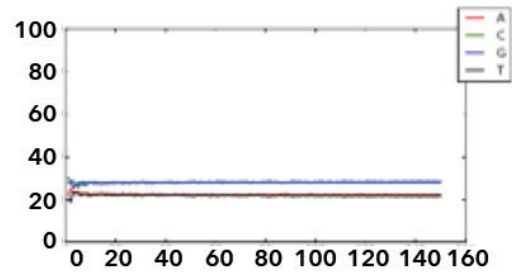
Sequencing QC

1.1 Read orientation-R1

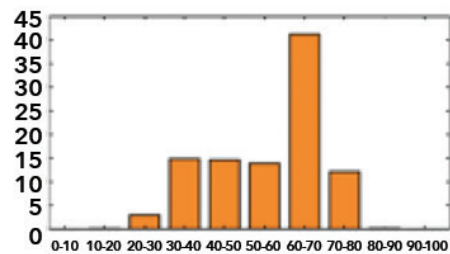
1.1.1 Quality distribution



1.1.2 Base distribution

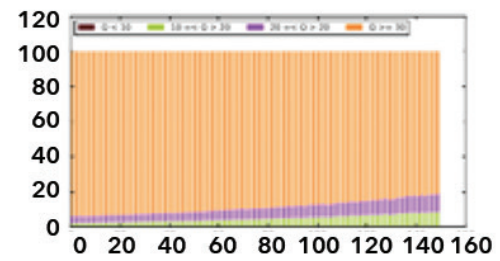


1.1.3 GC distribution

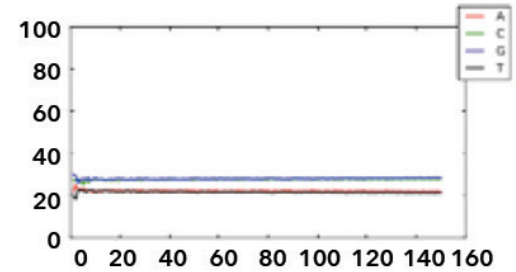


1.2 Read orientation-R2

1.2.1 Quality distribution



1.2.2 Base distribution



1.2.3 GC distribution

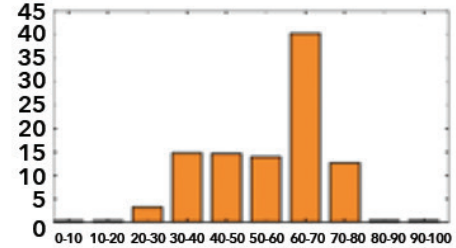


Figure 3: Representative FastQC report showing quality of reads obtained from the sequencing run.

QC Report for Whole Exome Sequencing Libraries from high quality DNA

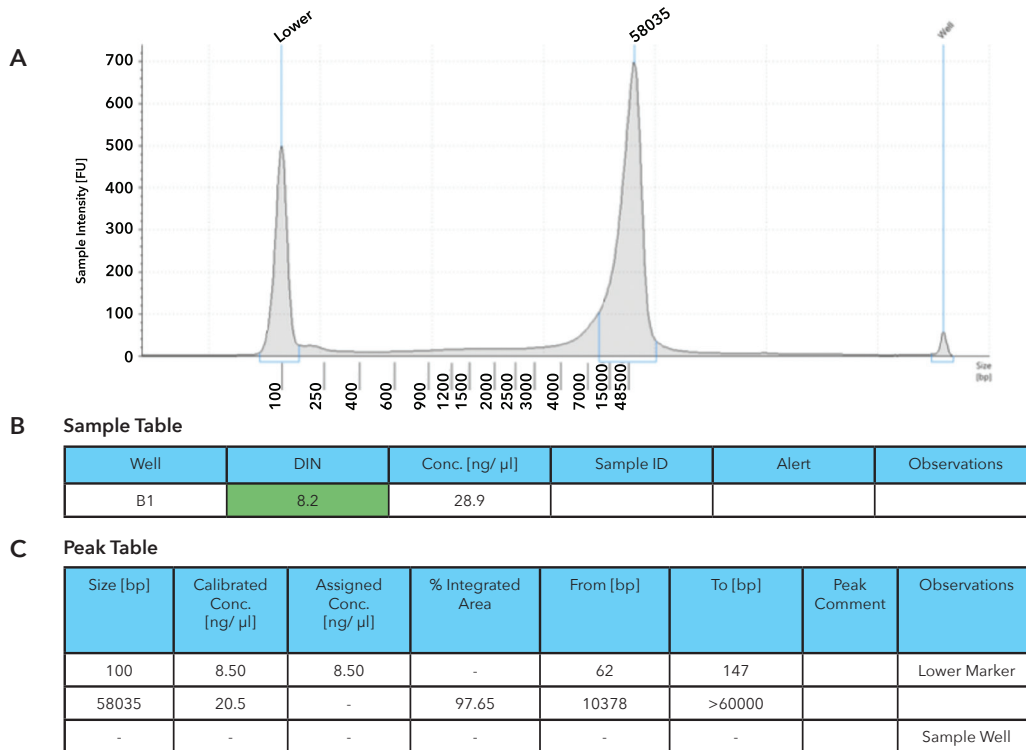


Figure 4 : A) Representative Electropherogram generated from TapeStation shows profile of input DNA. B) Table shows quantification of the DNA in the sample .C) Shows quantification of the major peaks detected in the electropherogram.

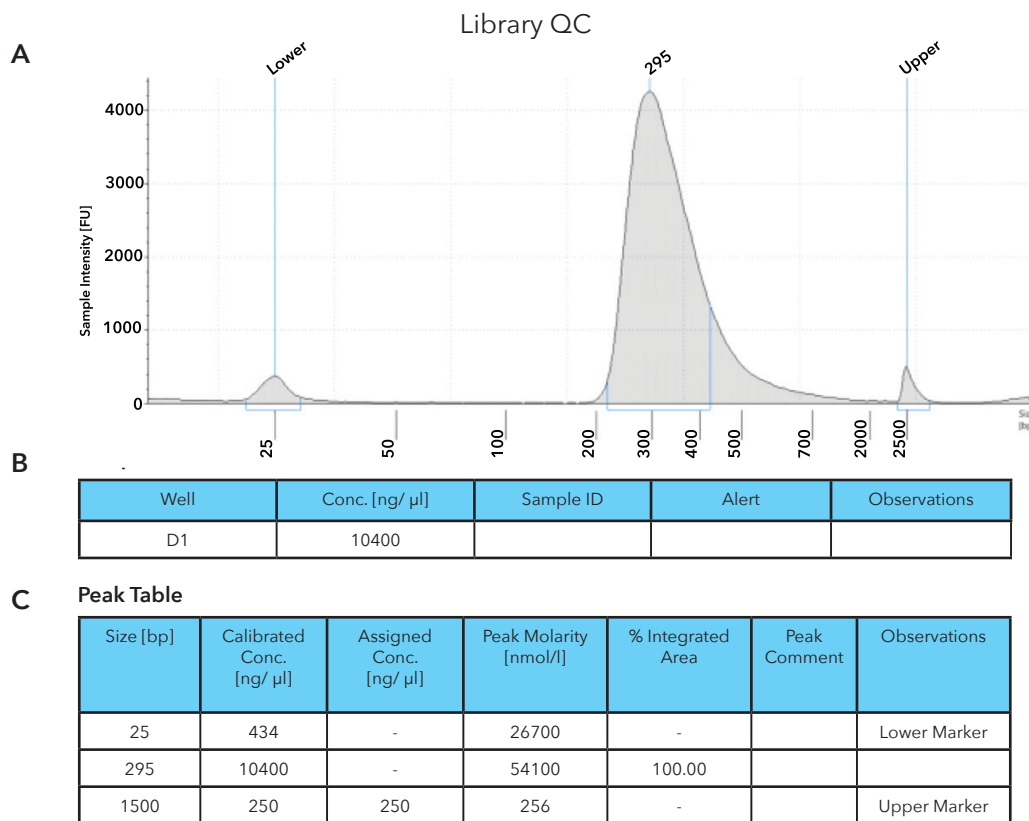
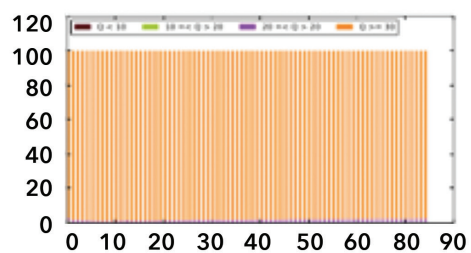


Figure 5 : A) Representative electropherogram obtained from TapeStation shows the profile of the finished library for whole exome sequencing . B) Table shows quantification of the library generated. C) Table shows quantification of the peak in the library.

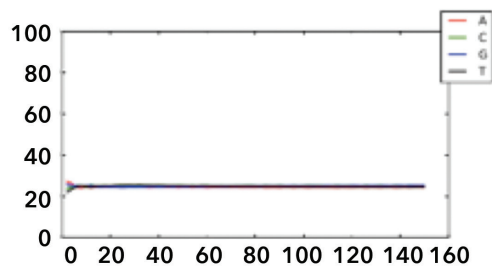
Sequencing QC

1.1 Read orientation-R1

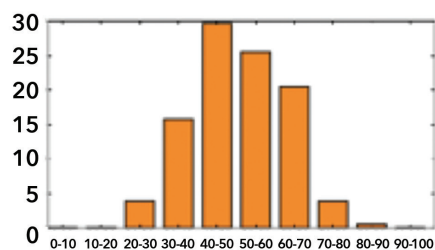
1.1.1 Quality distribution



1.1.2 Base distribution

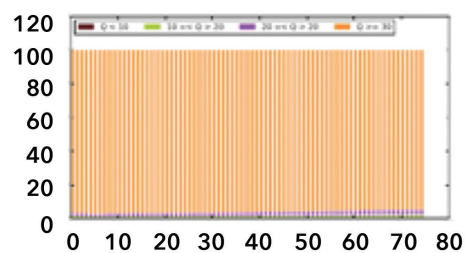


1.1.3 GC distribution

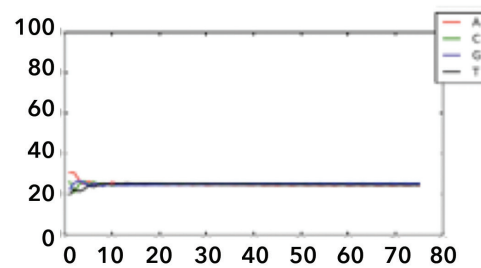


1.2 Read orientation-R2

1.2.1 Quality distribution



1.2.2 Base distribution



1.2.3 GC distribution

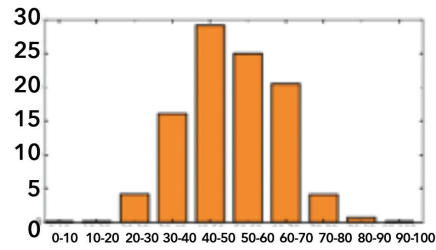


Figure 6 : Representative FastQC report showing quality of reads obtained from the sequencing run.

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

Sample QC

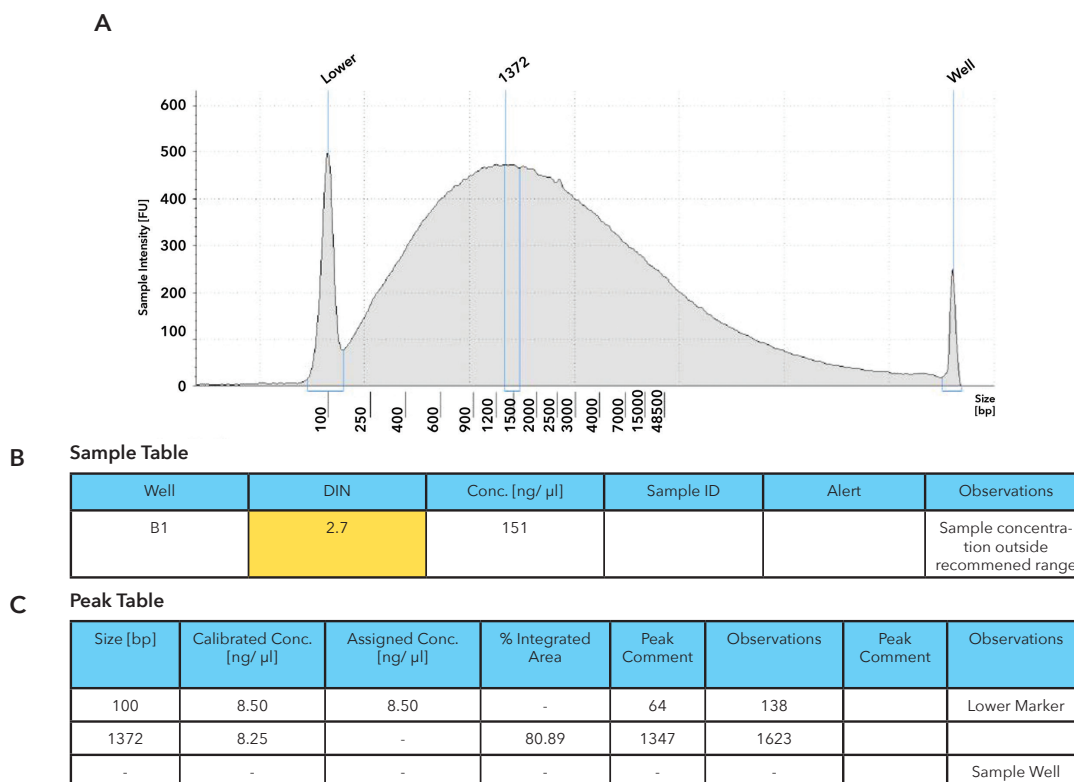


Figure 7 : A) Representative Electropherogram generated from TapeStation shows profile of input DNA. B) Table shows quantification of the DNA in the sample and C) shows quantification of the major peaks detected in the electropherogram.

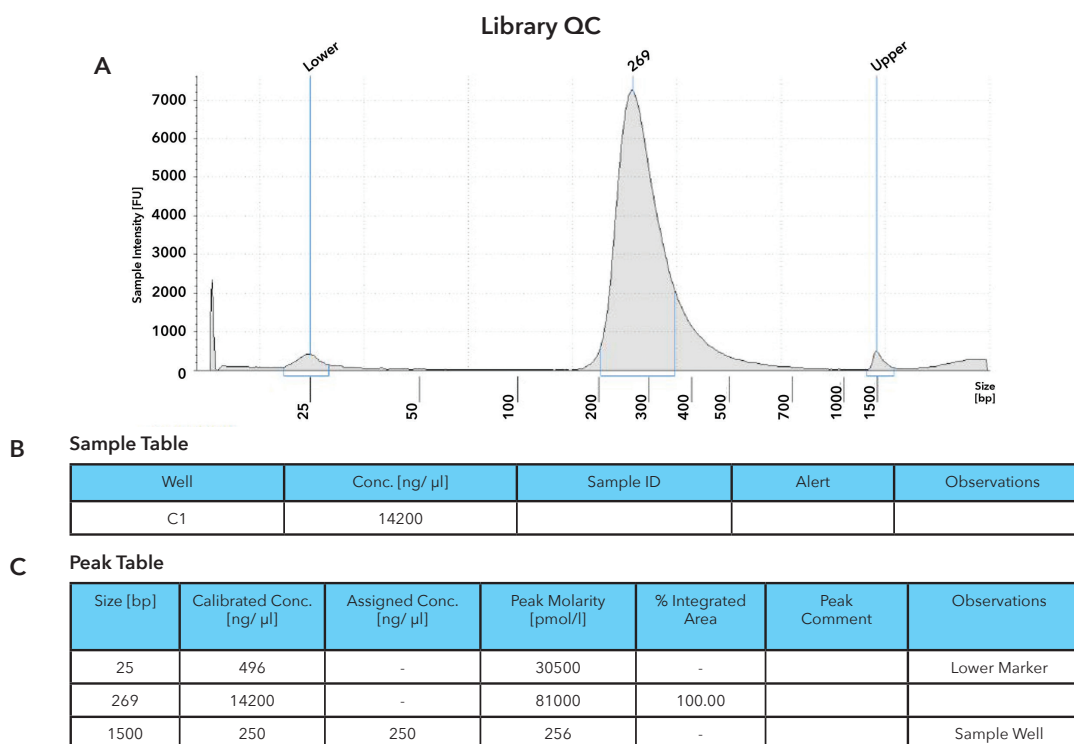
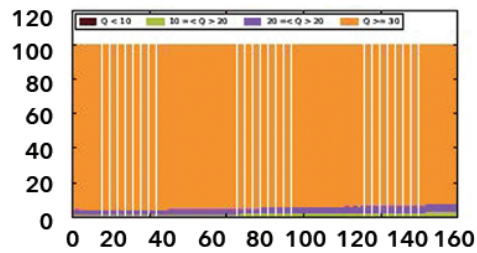


Figure 8 : A) Representative electropherogram generated from TapeStation shows profile of WES library. B) Table shows overall concentration of the library. C) Table shows quantification of the major peak detected in the library.

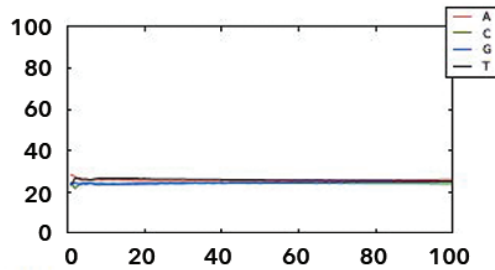
Sequencing QC

3.1 Read orientation-R1

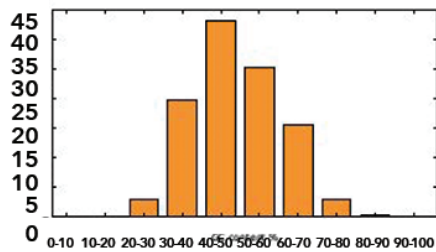
3.1.1 Quality distribution



3.1.2 Base distribution

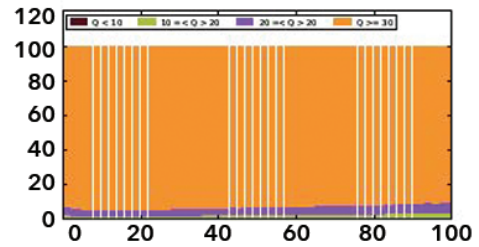


3.1.3 GC distribution

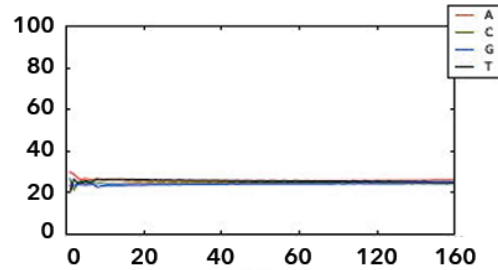


3.2 Read orientation-R2

3.2.1 Quality distribution



3.2.2 Base distribution



3.2.3 GC distribution

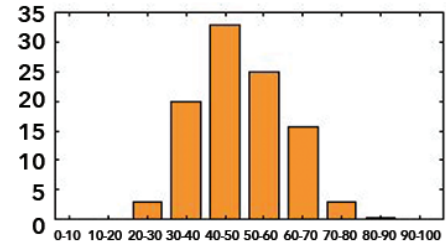


Figure 9 : Representative FastQC report showing quality of reads obtained from the sequencing run.