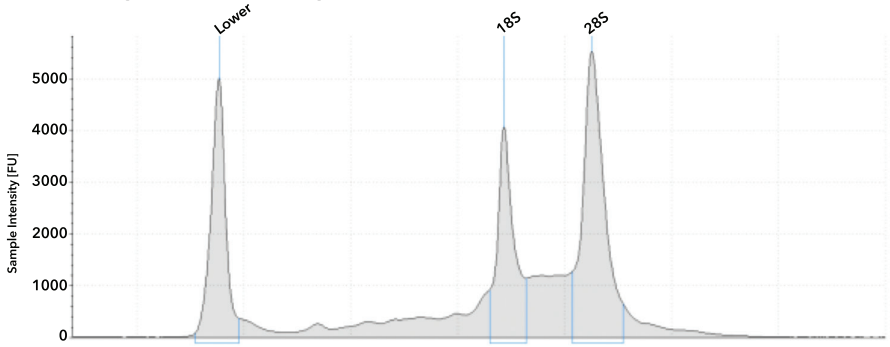
MEDGENOME

Whole Transcriptome Analysis QC Report

QC Report for RNA-Seq Libraries generated using Micro-dissected Tissue



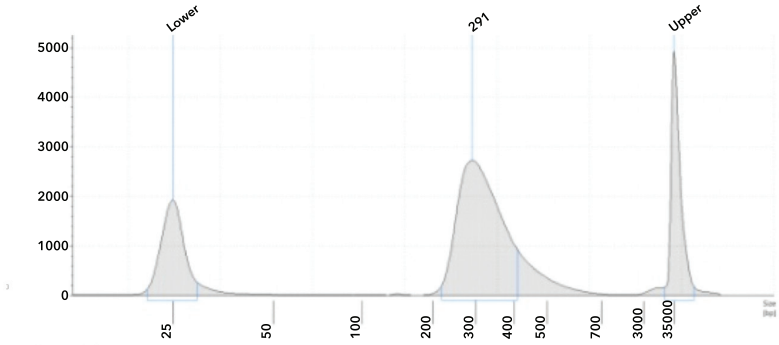
Sample Table

Well	RINe	28s/18S (Area)	Conc. [ng/ µl]	Sample ID	Alert	Observations
B1	8.7	1.8	105			

Peak Table

Size [nt]	Calibrated Conc. [ng/ µl]	Assigned Conc. [ng/ µl]	Peak Molarity [nmol/1]	% Integrated Area	Peak Comment	Observations
-	40.0	40.0	-	-		Lower Marker
-	22.2	-	-	35.94		18S
-	39.6	-	-	64.06		28S

Figure 1: *A) Representative Electrophoregram generated from TapeStation shows profile of RNA input from micro-dissected tissue. B) Table shows quantification of the sample input and quality of RNA is reported by RIN. C) Table shows quantification of the peaks in the sample.*



Sample Table

Well	Conc. [ng/ µl]	Sample ID	Alert	Sample ID	Observations
C1	16.4		105		

Peak Table

Size [bp]	Calibrated Conc. [ng/ µl]	Assigned Conc. [ng/ µl]	Peak Molarity [nmol/1]	% Integrated Area	Peak Comment	Observations
25	6.17	-	379	-		Lower Marker
291	16.4	-	86.6	100.00		
1500	6.50	6.50	6.67	-		Upper Marker

Figure 2: *A) Representative Electrophoregram generated from TapeStation shows profile of NGS library generated using the RNA isolated from fresh-frozen tissue. B) Table shows quantification of the library. C) Table shows the quantification of the peaks in the library.*

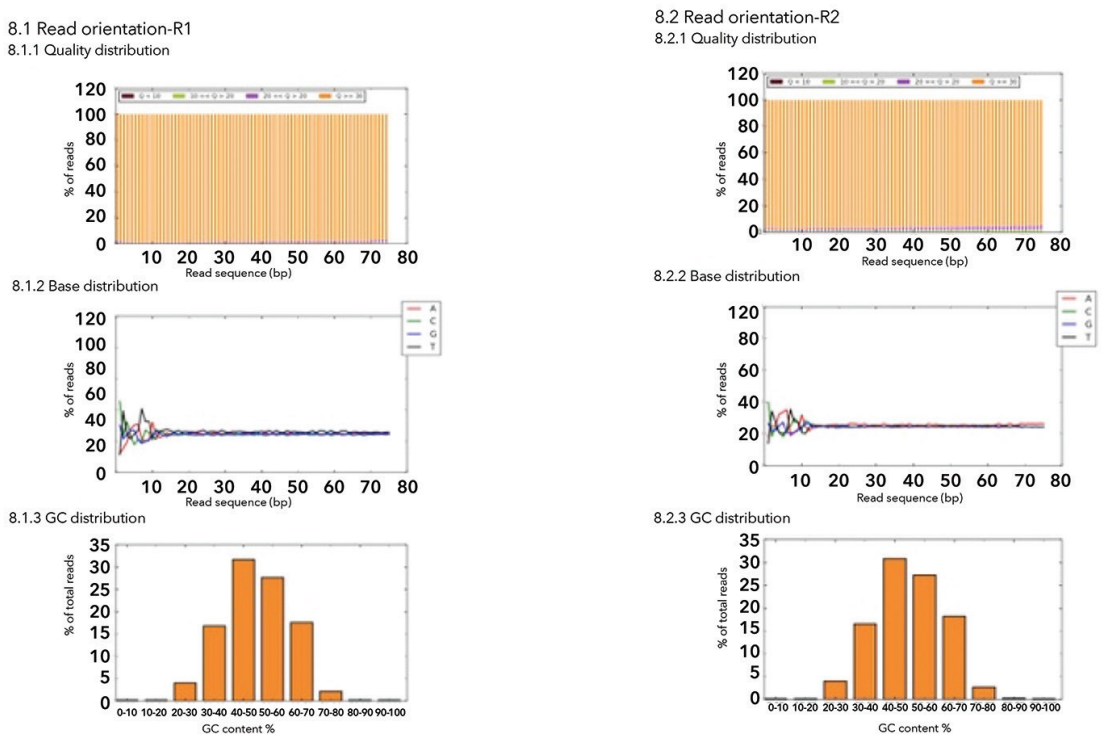
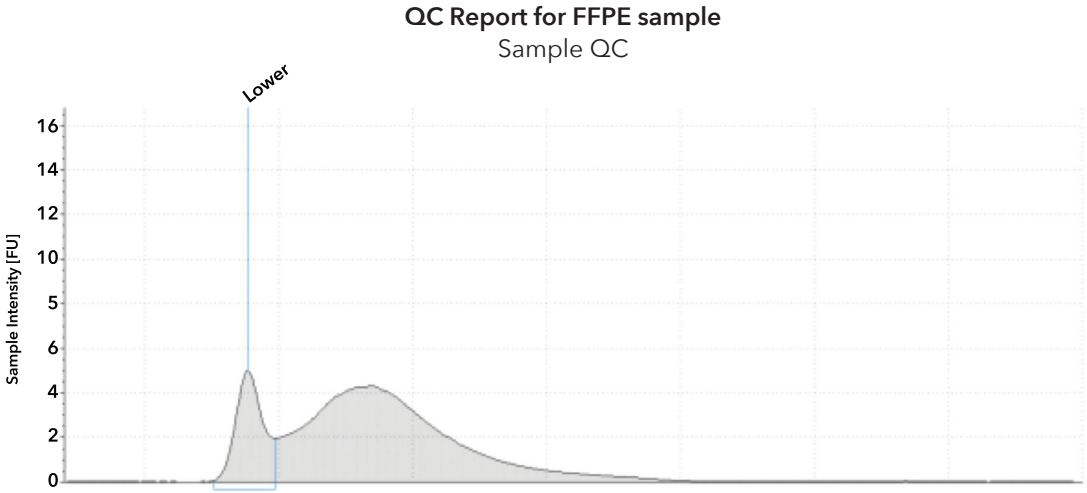


Figure 3: *Representative FastQC report showing quality of reads obtained from the sequencing run.*



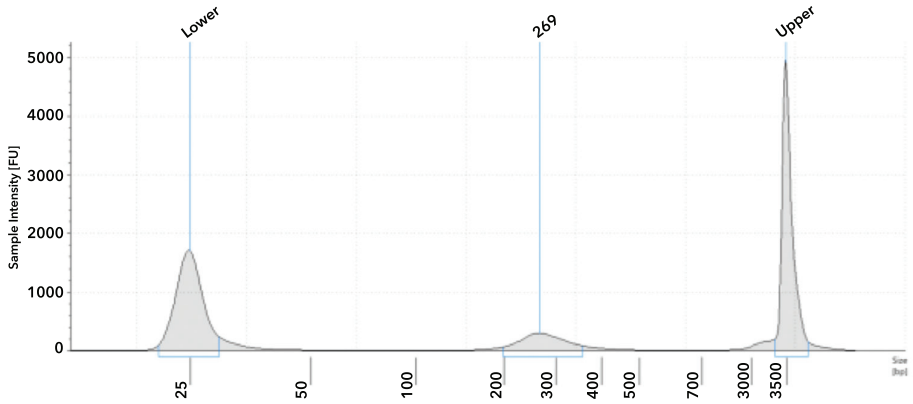
B **Sample Table**

Well	DV200	28s/18S (Area)	Conc. [ng/ µl]	Sample ID	Alert	Observations
B1	58%	-	99.5			

C **Peak Table**

Size [nt]	Calibrated Conc. [ng/ µl]	Assigned Conc. [ng/ µl]	Peak Molarity [nmol/l]	% Integrated Area	Peak Comment	Observations
-	40.0	40.0	-	-		Lower Marker

Figure 4: *A) Representative Electrophoregram generated from TapeStation shows profile of RNA input from FFPE-curl. B) Table shows quantification of the sample input and quality of RNA is reported by DV200. C) Table shows quantification of the peaks in the sample.*



Sample Table

Well	Conc. [ng/ µl]	Sample ID	Alert	Observations
B1	1.70		105	

Peak Table

Size [bp]	Calibrated Conc. [ng/ µl]	Assigned Conc. [ng/ µl]	Peak Molarity [nmol/1]	% Integrated Area	Peak Comment	Observations
25	6.03	-	371	-		Lower Marker
269	1.70	-	9.71	100.00		
1500	6.50	6.50	6.67	-		Upper Marker

Figure 5: *A) Representative Electrophoregram generated from TapeStation shows profile of NGS library generated using the RNA isolated from fresh-frozen tissue. B) Table shows quantification of the library. C) Table shows the quantification of the peaks in the library.*

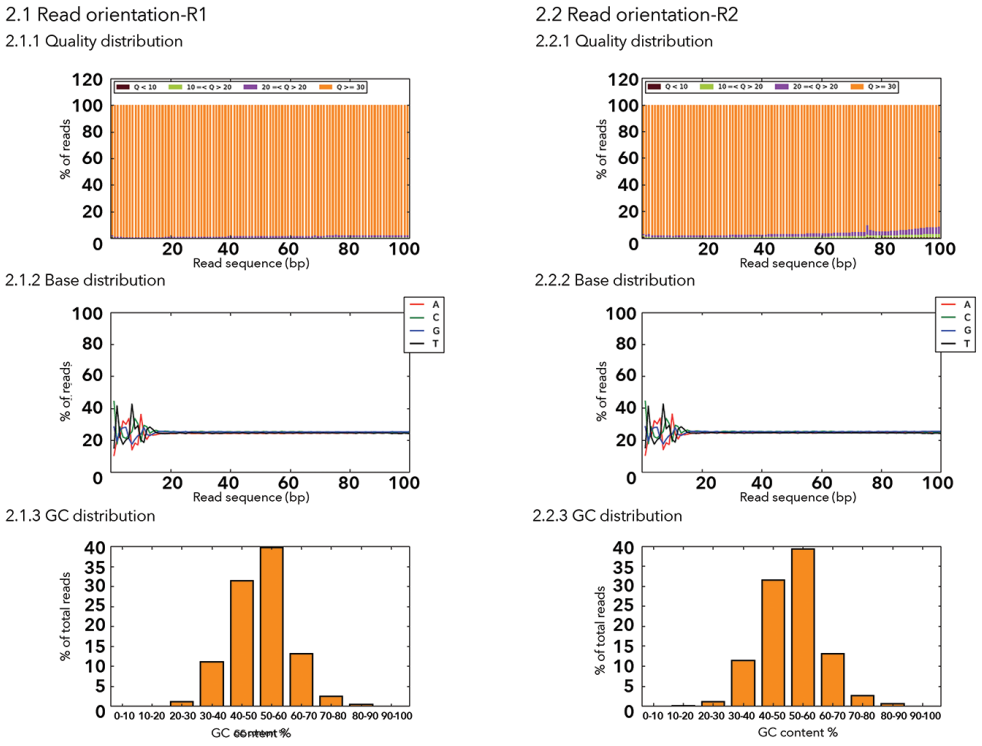
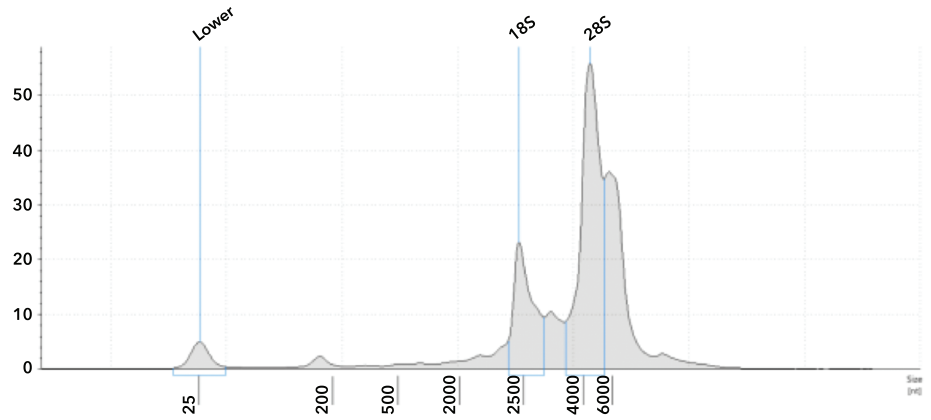


Figure 6: *Representative FastQC report showing quality of reads obtained from the sequencing run.*



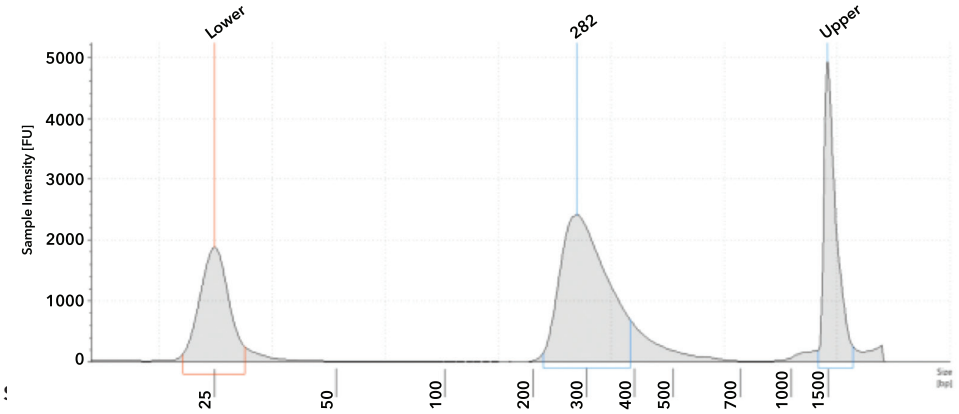
Sample Table

Well	RINe	28s/18S (Area)	Conc. [ng/ µl]	Sample ID	Alert	Observations
B1	9.3	2.5	638		⚠	RNA concent ration outside recommended range for RINe

Peak Table

Size [nt]	Calibrated Conc. [ng/ µl]	Assigned Conc. [ng/ µl]	Peak Molarity [nmol/1]	% Integrated Area	Peak Comment	Observations
25	40.0	40.0	4710	-		Lower Marker
1892	104	-	161	28.91		18S
4352	255	-	172	71.09		28S

Figure 7: *A) Representative Electrophoregram generated from TapeStation shows profile of RNA input from dissociated cells . B) Table shows quantification of the sample input and quality of RNA is reported by RIN. C) Table shows quantification of the peaks in the sample.*



Well	Conc. [ng/ µl]	Sample ID	Alert	Sample ID	Observations
B1	12.3				

Peak Table

Size [bp]	Calibrated Conc. [ng/ µl]	Assigned Conc. [ng/ µl]	Peak Molarity [nmol/1]	% Integrated Area	Peak Comment	Observations
25	5.92	-	364	-		Lower Marker
282	12.3	-	67.3	100.00		
1500	6.50	6.50	6.67	-		Upper Marker

Figure 8: *A) Representative Electrophoregram generated from TapeStation shows profile of NGS library generated using the RNA isolated from fresh-frozen tissue. B) Table shows quantification of the library. C) Table shows the quantification of the peaks in the library.*

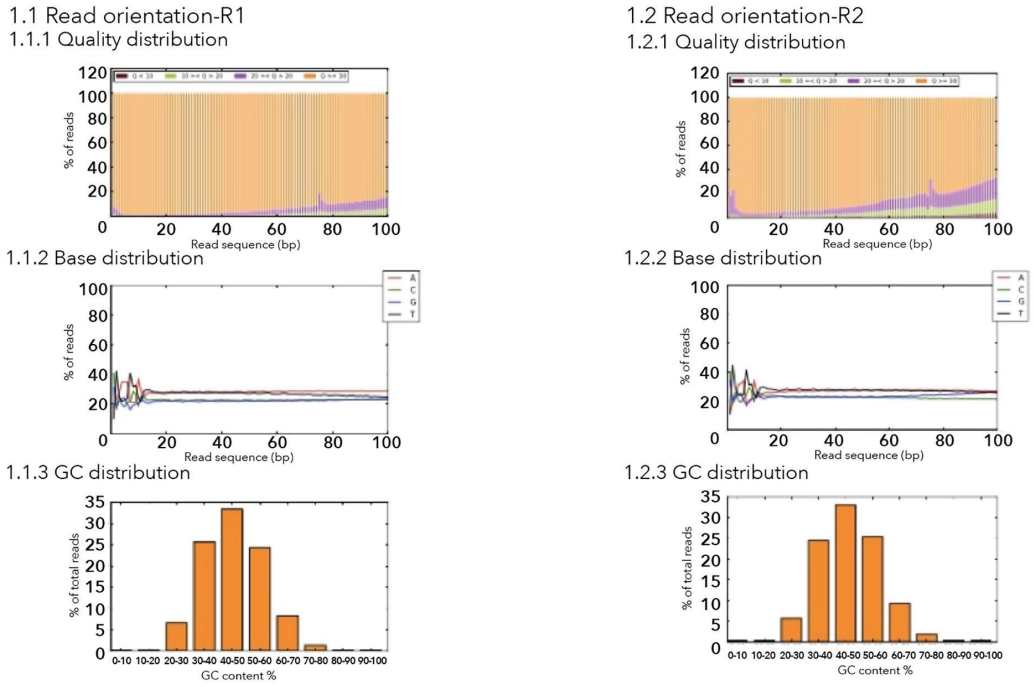
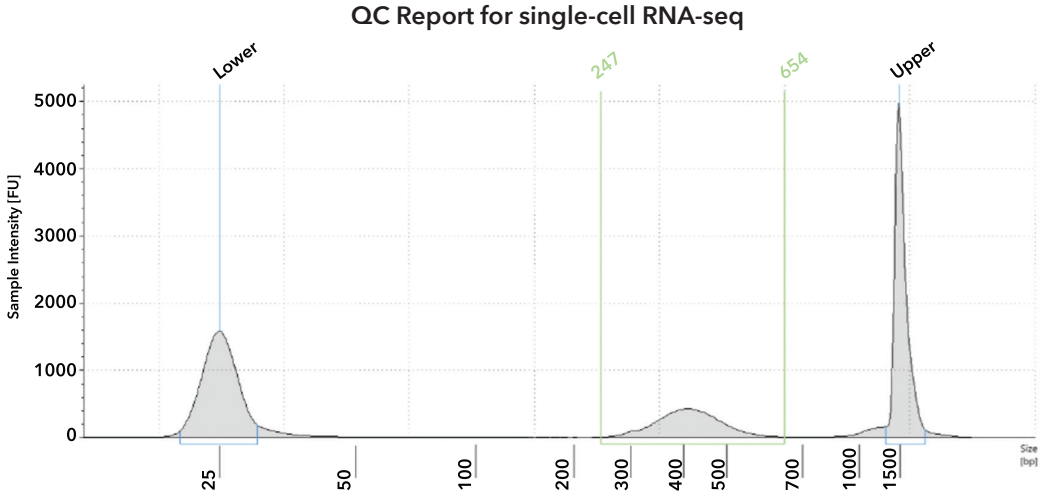


Figure 9: *Representative FastQC report showing quality of reads obtained from the sequencing run.*



Region Table

From [bp]	To [bp]	Average Size [bp]	Region Molarity [nmol/l]	Conc. [ng/ µl]	% of Total	Region Comment	Color
247	654	417	3.22	12.2	73.74		

Figure 10: *A) Representative electropherogram of gene expression libraries generated from single-cells using the 10X Gene Expression Analysis Kit. B) The table below shows quantification of the library.*

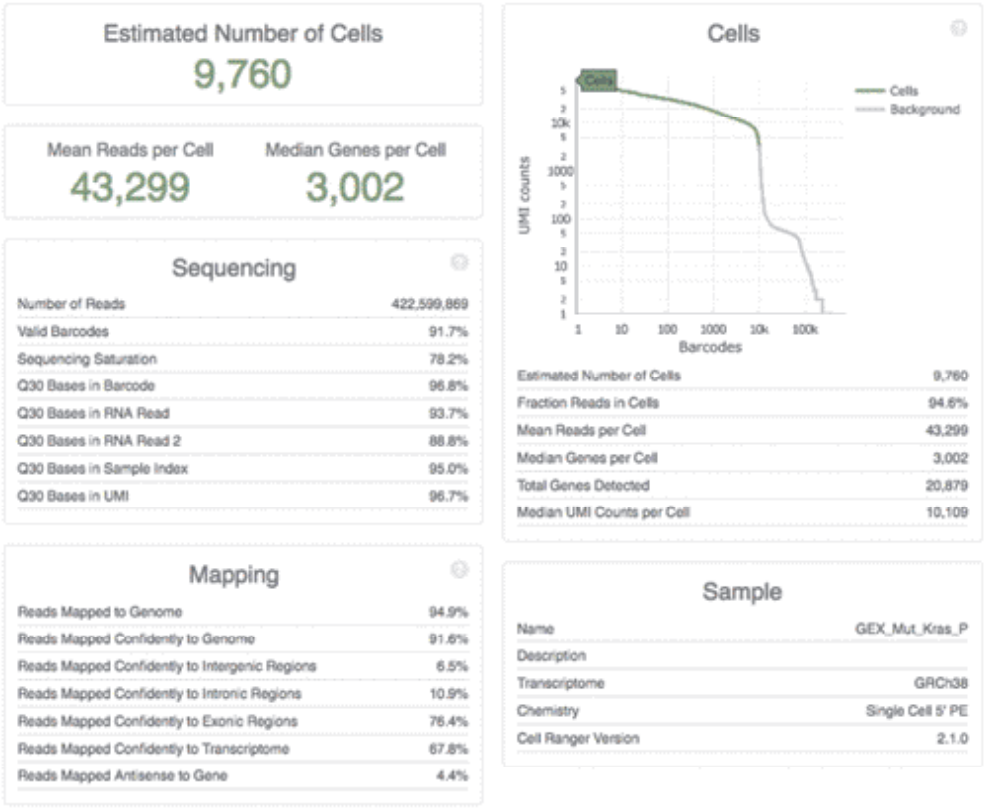


Figure 11: *Sample representation of output from a 10X cell-ranger software of the summary of the reads obtained from a gene expression run with a 10X 3'-gene expression profiling kit.*

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