

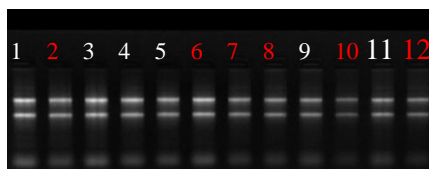
## Cloud-Seq RNA QC Report

### 1. Total RNA QC Report

#### 1. RNA Quantification and Quality Assurance by NanoDrop ND-1000

| Sample ID | Sample Name | OD260/280<br>Ratio | Conc.<br>(ng/ $\mu$ l) | Volume<br>( $\mu$ l) | Quantity<br>(ug) | QC result |
|-----------|-------------|--------------------|------------------------|----------------------|------------------|-----------|
| 2         | Control1    | 1.82               | 264.67                 | 18                   | 4.76             | pass      |
| 6         | Control2    | 1.82               | 127.21                 | 18                   | 2.29             | pass      |
| 7         | Control3    | 1.85               | 152.72                 | 18                   | 2.75             | pass      |
| 8         | Patient1    | 1.81               | 64.99                  | 18                   | 1.17             | pass      |
| 10        | Patient2    | 1.80               | 60.23                  | 18                   | 1.08             | pass      |
| 12        | Patient3    | 1.86               | 130.96                 | 18                   | 2.36             | pass      |

### 2. RNA Integrity and gDNA contamination test by Denaturing Agarose Gel Electrophoresis



\*For spectrophotometer, the O.D. A260 /A280 ratio should be close to 2.0 for pure RNA (ratios between 1.8 and 2.1 are acceptable). The O.D. A260/A230 ratio should be more than 1.8.

### Library QC Report

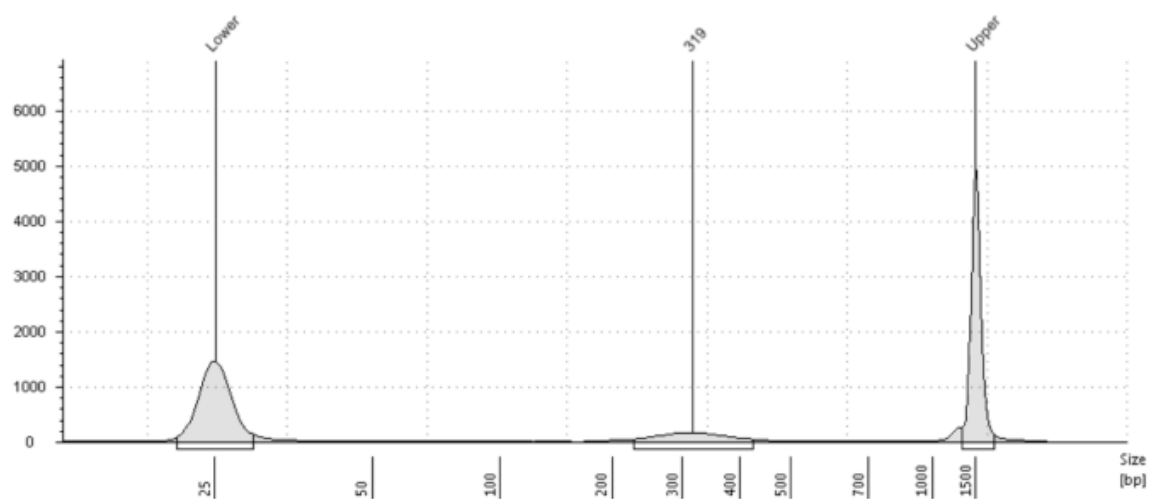
#### Quality Assessment of Sequencing Library

Sequencing library was determined by Agilent 2100 Bioanalyzer using the Agilent DNA 1000 chip kit (Agilent, part # 5067-1504)

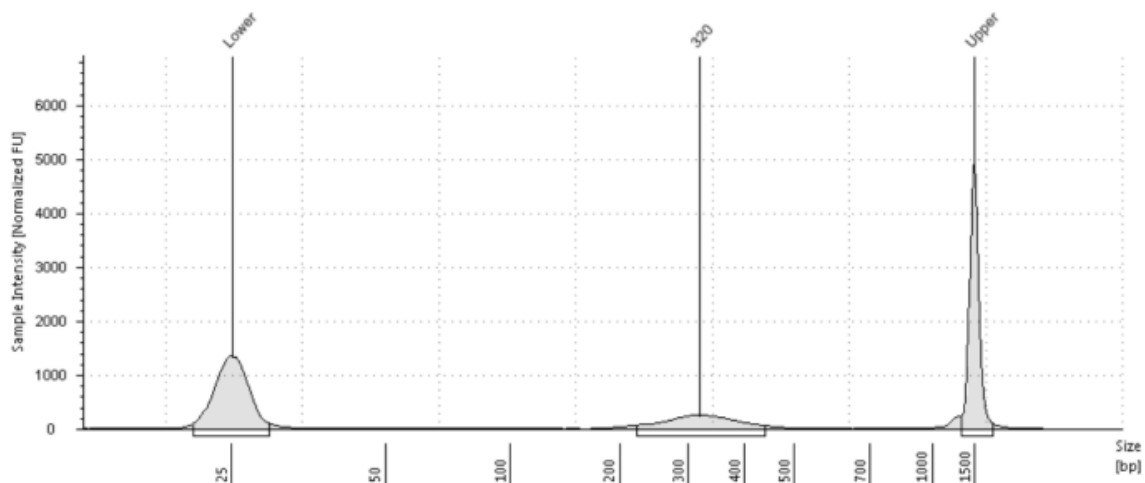
| Sample Name | Size (bp) | Conc. (ng/μl) | Conc. (nmol/L) | Volume (μl)* | Total Amount (ng) |
|-------------|-----------|---------------|----------------|--------------|-------------------|
| Patient1    | 319       | 1.52          | 7.32           | 10           | 15.2              |
| Patient2    | 320       | 2.51          | 12.0           | 10           | 25.1              |
| Patient3    | 310       | 3.16          | 15.7           | 10           | 31.6              |
| Control1    | 321       | 1.57          | 7.53           | 10           | 15.7              |
| Control2    | 307       | 2.99          | 15.0           | 10           | 29.9              |
| Control3    | 320       | 1.80          | 8.68           | 10           | 18                |

\*The libraries were adjusted to 10nM before cluster generation.

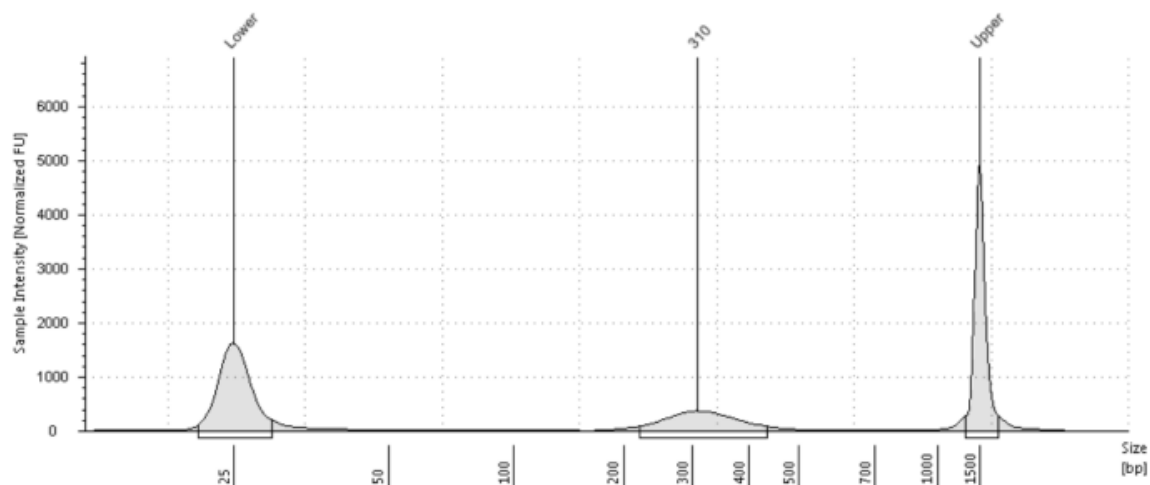
Patient1



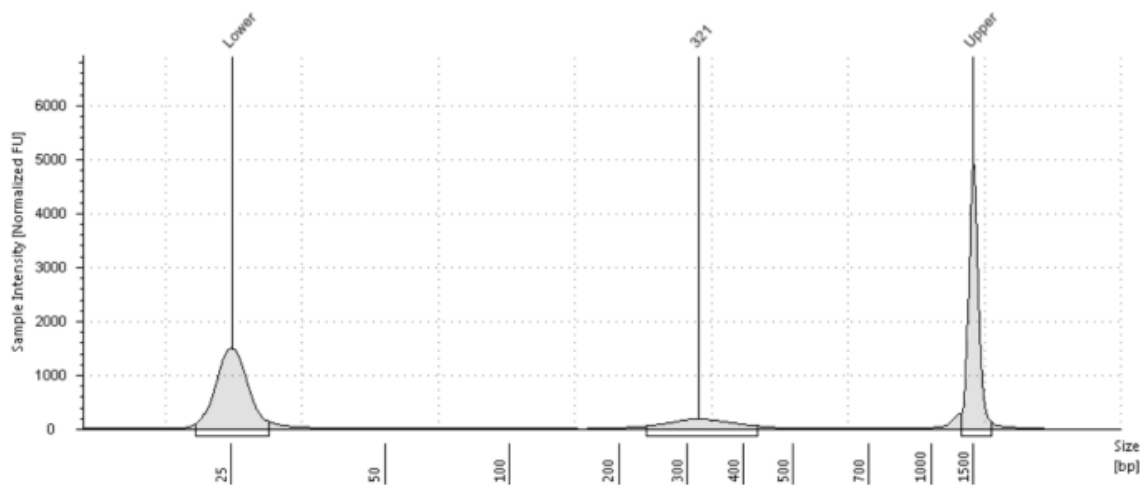
Patient2



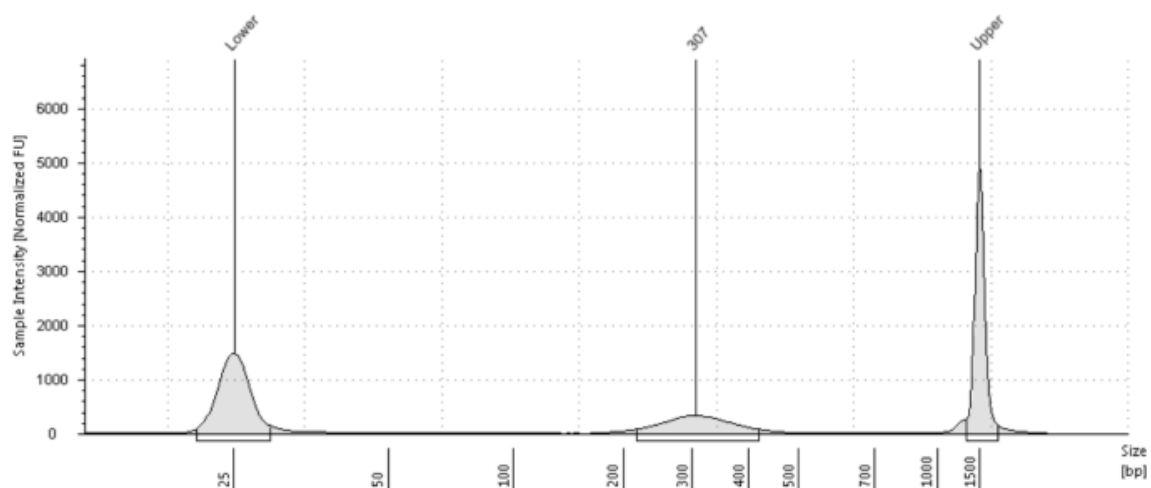
Patient3



Control1



Control2



Control3

