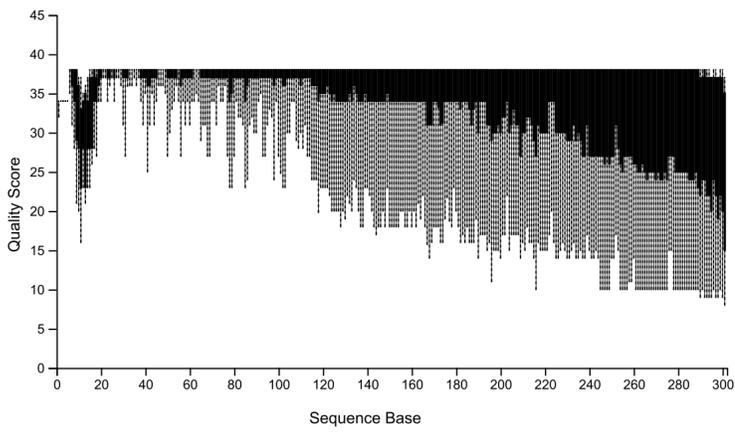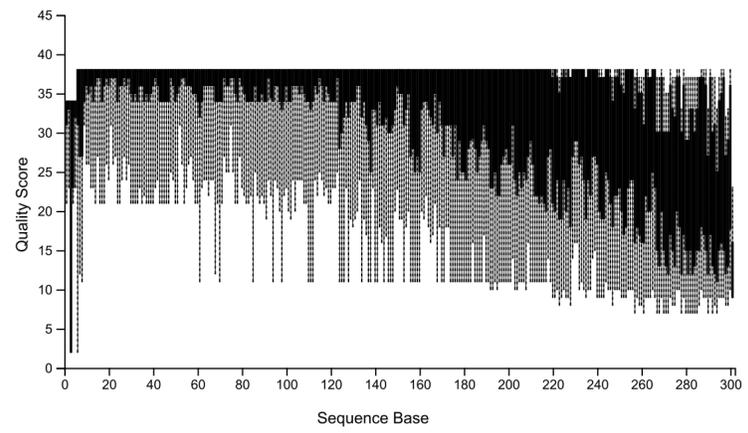![qiime2](http://qiime2.org/)

Click and drag on plot to zoom in. Double click to zoom back out to full size. Hover over a box to see the parametric seven-number summary of the quality scores at the corresponding position.

Forward Reads

Reverse Reads

These plots were generated using a random sampling of 10000 out of 6877050 sequences without replacement. The minimum sequence length identified during subsampling was 82 bases. Outlier quality scores are not shown in box plots for clarity.

Parametric seven-number summary		
Box plot feature	**Percentile**	**Quality score**
(Not shown in box plot)	2nd	...
Lower Whisker	9th	...
Bottom of Box	25th	...
Middle of Box	50th (Median)	...
Top of Box	75th	...
Upper Whisker	91st	...
(Not shown in box plot)	98th	...

Download forward parametric seven-number summaries as CSV (forward-seven-number-summaries.csv)

These plots were generated using a random sampling of 10000 out of 6877050 sequences without replacement. The minimum sequence length identified during subsampling was 82 bases. Outlier quality scores are not shown in box plots for clarity.

Parametric seven-number summary		
Box plot feature	**Percentile**	**Quality score**
(Not shown in box plot)	2nd	...
Lower Whisker	9th	...
Bottom of Box	25th	...
Middle of Box	50th (Median)	...
Top of Box	75th	...
Upper Whisker	91st	...
(Not shown in box plot)	98th	...

Download reverse parametric seven-number summaries as CSV (reverse-seven-number-summaries.csv)

Demultiplexed sequence length summary

Forward Reads

Total Sequences Sampled	10000
2%	301 nts
9%	301 nts
25%	301 nts
50% (Median)	301 nts
75%	301 nts
91%	301 nts
98%	301 nts

Reverse Reads

Total Sequences Sampled	10000
2%	300 nts
9%	300 nts
25%	300 nts
50% (Median)	300 nts
75%	300 nts
91%	301 nts
98%	301 nts