Starting with our July 20 run (SA11031) we noticed shorter-than-expected read lengths. This resulted in extensive trouble shooting, fixes to hardware, and ultimately realization that a particular sequencing kit lot was also not optimal.

Typical example size distributions from a ~500-600 bp amplicon library are shown here:
1) UT instrument, sample CCHIP, kit lot #93833820, before hardware was fixed, run SA11031:
2) Non-UT instrument, sample CCHIP, kit lot #93833620, run SA11037:
3) UT instrument, sample CCHIP, kit lot #93833620, after hardware was fixed, run SA11042:
4) UT instrument, sample CCHIP, kit lot #93846120, after hardware was fixed, run SA11045:

![Graph of frequency vs. f](image.png)
Another example, genomic DNA fragment sample:

1) Non-UT instrument, old lot (93833620):

![Graph of JA11152_HFLAV_RL20.fna with frequency on the y-axis and $f$ on the x-axis.](image-url)
2) UT instrument, after hardware fixes, new lot (93846120):

![Graph](JA11152_HFLAV_RL20.fna)