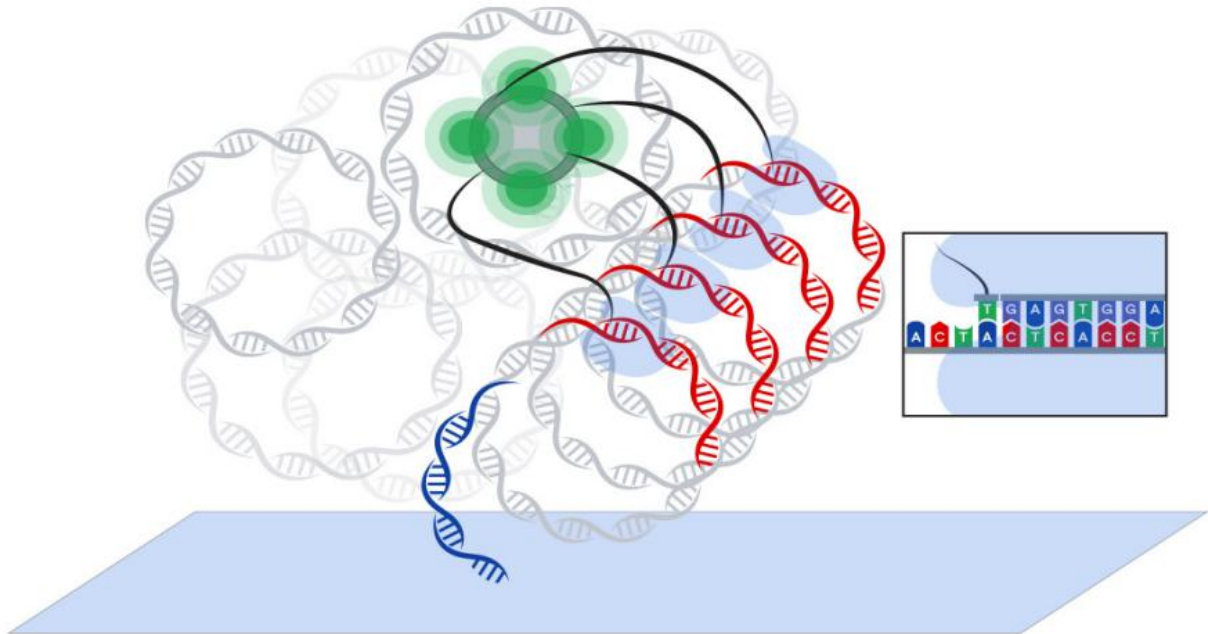


## Introducing the Element AVITI™ Sequencing System

The [Element AVITI System](#) reimagines the core components of NGS to offer a benchtop platform that grants access to the genomics ecosystem. Delivering flexible throughput at exceptionally low cost, AVITI saves time and resources without the need to batch or accept lesser quality. Avidity base chemistry (ABC) forms the core of a disruptive design that readily adapts to any application, offering methods that scale from amplicon to whole genomes.

### Novel ABC sequencing

The fundamentals of ABC technology leverage the unique properties of avidites to execute an efficient sequencing reaction and yield highly accurate data. A strong signal-to-noise ratio that persists through high polony densities drives this accuracy. When a run starts, the library hybridizes to surface primers coating the flow cell. Amplification polymerase then binds to the library and primer duplexes, catalyzing rolling circle amplification (RCA) and generating long DNA strands that include copies of the original library (Figure 2). Each strand forms a polony that contains hundreds of copies of the original library. The polonies hybridize to read-specific sequencing primers. For each cycle, a sequencing polymerase binds an avidite to a polony and primer duplex, and traps a base-specific avidite to the polony. The result forms an extremely tight complex that enables a 100-fold reduction in reagent concentration compared to sequencing-by-synthesis (SBS).<sup>1</sup> AVITI and ABC reset expectations on quality scores (Q scores), delivering exceptional Q30 accuracy for 2 x 150 sequencing at 1 90% and 1 85% for 2 x 300 sequencing. AVITI demonstrated higher accuracy compared to legacy sequencing technology. Data showed fewer soft-clipped reads in difficult homopolymer and repeat regions, among other clear advantages.

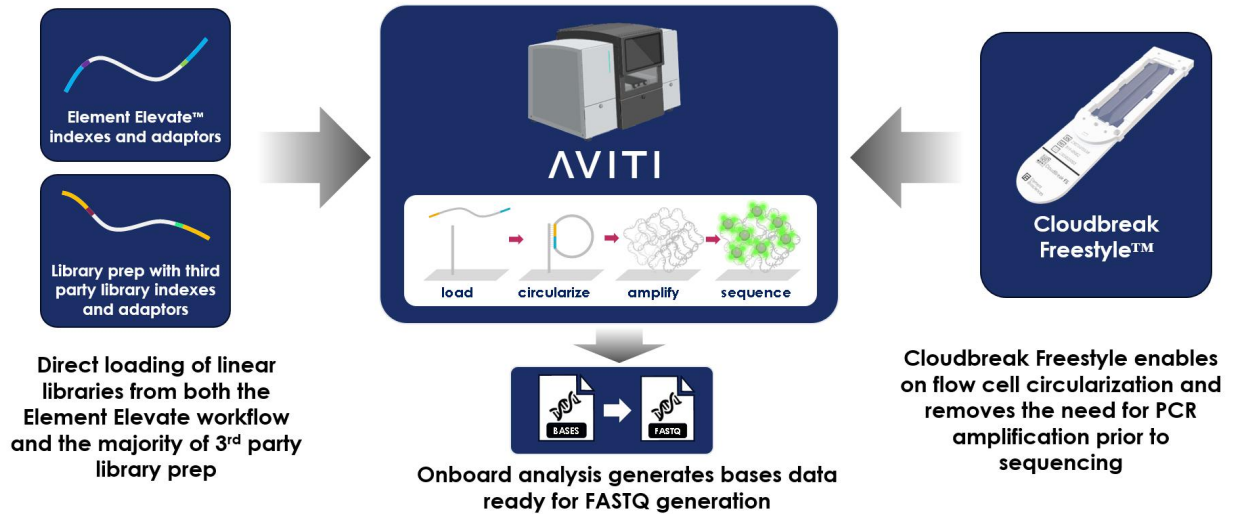


*Polymerase binds avidites at the interrogation site. The avidite arms connect to a core that provides a fluorescent signal for detection.*

[Download the infographic](#) to learn more about Avidite Base Chemistry

## **Broad compatibility with Library types**

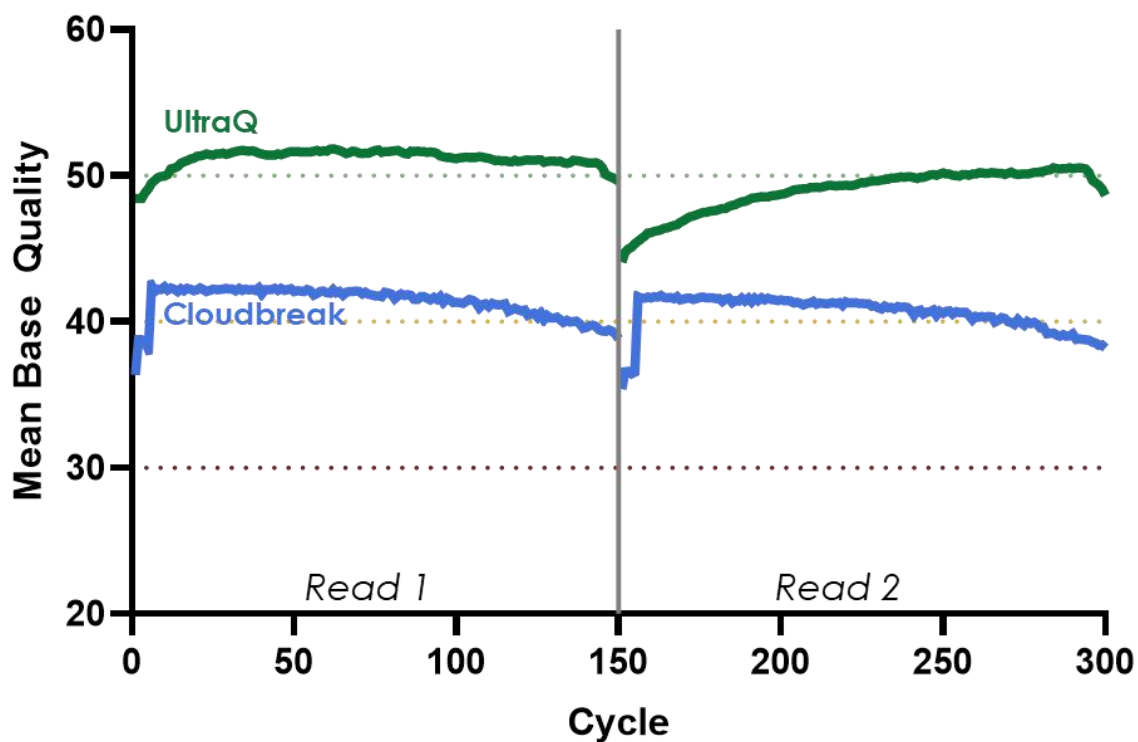
Cloudbreak Freestyle™ sequencing kits make operating the AVITI System even easier. Directly compatible with most linear third-party libraries, Cloudbreak Freestyle kits eliminate the library conversion step and save valuable preparation time. Most libraries compatible with other sequencing platforms are able to seamlessly be loaded and sequenced on the AVITI System.



Watch the [animated video](#) to learn more about Cloudbreak Freestyle

## Highest accuracy sequencing

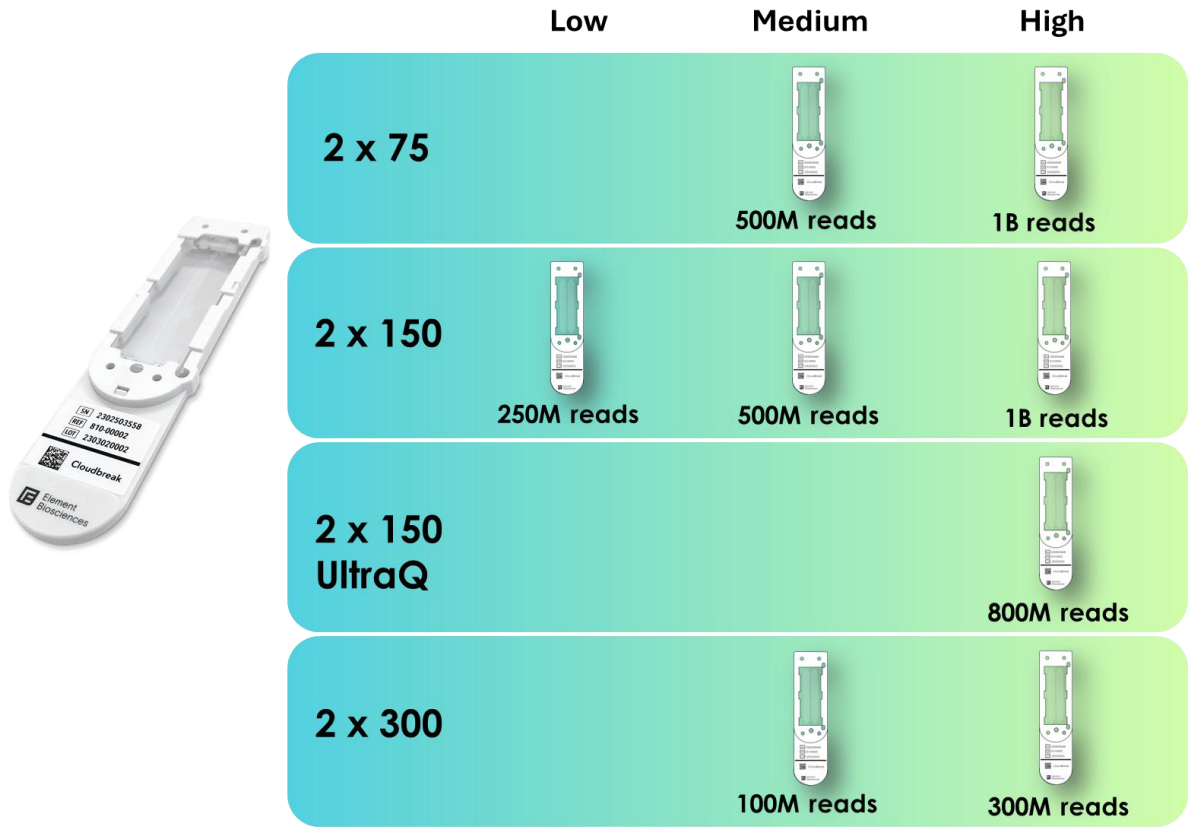
Standard Cloudbreak sequencing kits consistently generate greater than 90% bases at Q40 (estimated error rates 1 in 10,000). For applications requiring even higher accuracy such as high complexity mixed populations, high-polished genome sequencing, or ultra-rare allele detection, Cloudbreak UltraQ™ sequencing kits can be used to yield 180% of bases at Q50 (estimated error rates 1 in 100,000).



*Base quality of Cloudbreak and Cloudbreak UltraQ chemistry from 2x150 sequencing*

### **Flexible read-lengths and throughput**

Sequencing kits for the AVITI platform range from 2x75, ideal for tag-counting applications such as scRNAseq, 2x300 kits for applications that require longer reads including metagenomics and amplicon sequencing. Run throughput can be adjusted by selecting flow cells from 300M reads (2x300 medium) to greater than 1B reads (2x150 high) on each flowcell. By processing 2 independent flow cells, runs can be staggered to enable faster turnaround times and multiple configurations simultaneously.



Available flow cell configurations on the AVITI™ Platform