

A universal targeted sequencing system for any high-throughput sequencing platform

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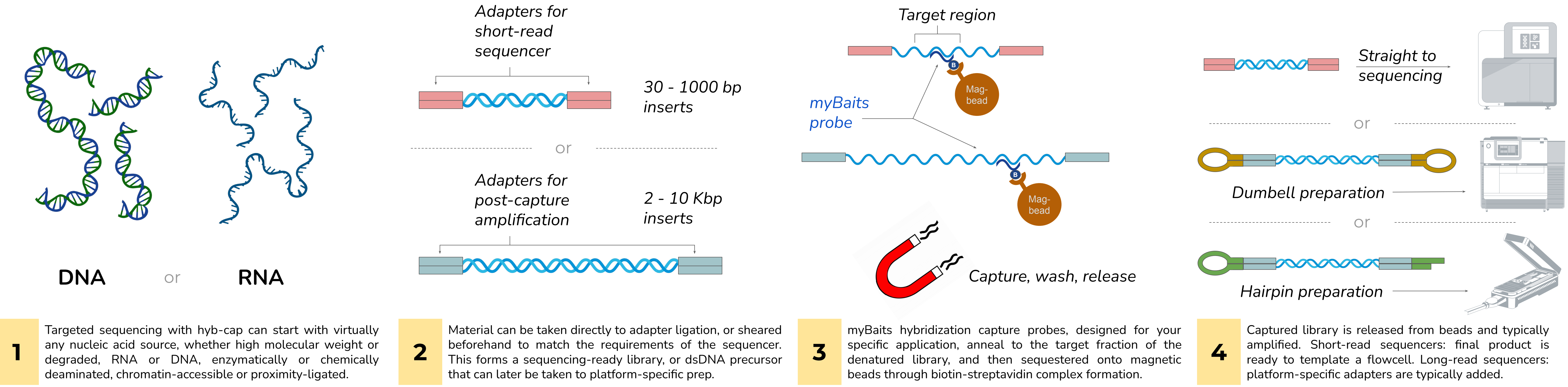
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With the recent launch of multiple novel high-throughput sequencing (HTS) platforms, the landscape of HTS workflow options is richer than ever before. Choosing a targeted sequencing solution that is compatible with sequencing on any current or future HTS platform is important for maximizing the utility of a given assay. The myBaits® hybridization capture system from Daicel Arbor Biosciences is by design universally compatible with virtually any HTS workflow, whether short- or long-read. With highly versatile custom probe design algorithms and platform-agnostic protocol options, myBaits is a robust solution for achieving any DNA or RNA targeted sequencing need for any species or sample type. In this poster, we highlight the technical features of myBaits that permit its unique versatility in the modern HTS landscape, including data examples demonstrating its universal application with both short- and long-read HTS platforms relevant to the plant and animal genomics community.

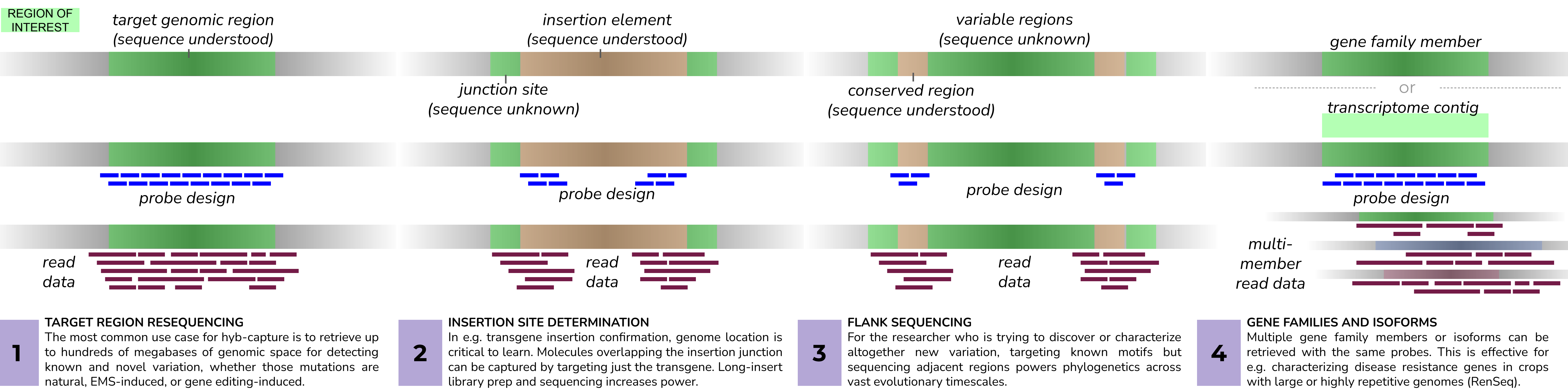
Short or long, DNA or RNA

myBaits hybridization capture (hyb-cap) is compatible with virtually any nucleic acid substrate and any style of sequencing. Whether genomic (DNA) or transcriptomic (RNA) material, of short (50-1000 bp) or long (2,000-10,000 bp) fragments, hyb-cap can retrieve and reconstruct the initial molecular frequency and sequence composition of a substrate. Probe sets initially designed for one or another substrate are also generally compatible with alternative substrates, because most probe designs are tiled across targets and can tolerate moderate levels of sequence mismatch.



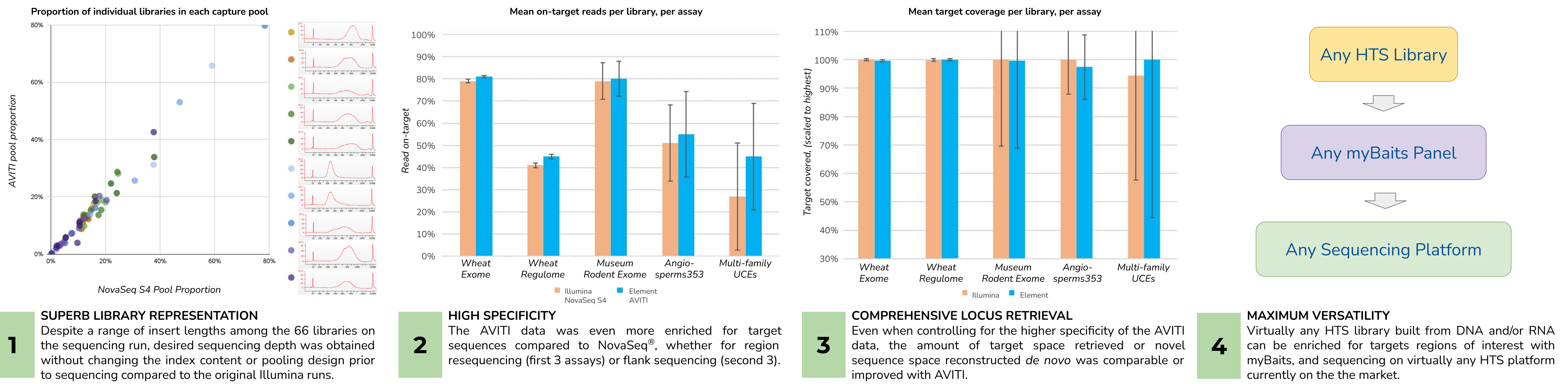
A multitude of target types

Hybridization capture with myBaits relies solely on a single probe hybridization to a target, which contrasts from PCR which requires at least two hybridization events in close proximity. This extremely simple system, combined with inherently high tolerance of nucleic acid hybridization of moderate levels of sequence mismatch, makes hyb-cap among the most versatile targeted sequencing tools. Whether you need to detect natural or artificially-induced single mutations, resolve the location of a novel element or junction event, or discover altogether new genomic regions, hyb-cap probe and experimental design can adapt - thanks to the extensive experience of the myBaits design team at Arbor.



Ready for new sequencers

In 2022, several new short-read sequencers and chemistries were announced, released, and/or made available to new regional markets. These include new systems from Element Biosciences®, Singular Genomics®, Ultima Genomics®, and PacBio®, new chemistry from Illumina®, and broader availability of platforms from MGI®. Each of these remains fundamentally compatible with hybridization capture as a pre-sequencing complexity reduction technology. We recently tested the new Element AVITI® system with several of our most popular myBaits hybridization capture panels (e.g., Wheat Exome, Wheat Regulome, Angiosperms-353, and others). In each case, the conversion to Element sequencing was seamless and returned excellent performance.



References

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