Duplex Sequencing is an ultra-high accuracy sequencing method that overcomes the limitations of Next-Generation Sequencing by independently tracking both strands of individual DNA molecules. The paired sequences are compared to eliminate errors.

**Duplex Sequencing Reveals True Mutations**

- > 10,000-fold increase in accuracy over standard NGS
- Eliminates virtually all background errors, revealing ultra-low frequency variants
- Compatible with any Illumina® sequencer
- Easy to adopt with no special equipment needed

The same gene sequenced by standard Illumina® Sequencing (left) and with Duplex Sequencing (right). With conventional methods, every position in the gene appears mutated in 0.1-1% of molecules sequenced. Duplex Sequencing eliminates the background noise, revealing the previously hidden true mutation.

**Duplex Sequencing Eliminates Technical Noise**

Duplex Sequencing capitalizes on the naturally-occurring complementarity between strands of the DNA double-helix.

Each strand of each original molecule is uniquely labelled such that both can be tracked throughout amplification and sequencing for subsequent error correction.
Duplex Sequencing solves genetic needle-in-a-haystack challenges. Duplex Sequencing is a fundamentally enabling platform technology for rare variant detection with many and diverse applications (above). A need for ultra-high accuracy in DNA sequencing is the common thread tying these applications together. TwinStrand has purpose-built solutions for mutagenesis and AML MRD available now with more applications currently in development.