# Genetics is complex.
Sample prep shouldn't be.

Research geneticists understand that the elegance behind Mendel's work was its simplicity; we now understand, it wasn't a complete story. Traits can be complex and be modified by factors, such as randomness. And, the current intricacies of a bench-to-bedside strategy for personalized medicine research only adds to the complexity.

Sample prep should be simple.

| Sample homogenization	DNA/RNA extraction	Automated NGS library prep
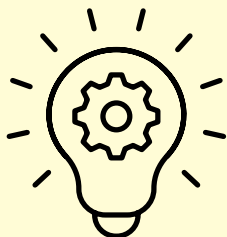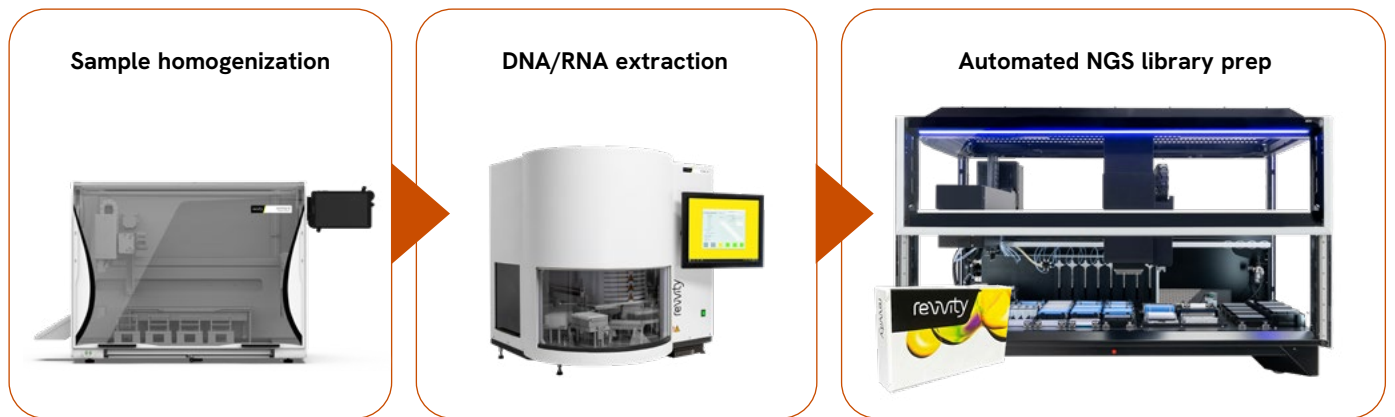
When did you last consider pre-analytical automation?

- Pre- or extra-analytical processes can bring additional sources of potential error into workflows, different to those of analytical/post-analytical technologies.
- Determining sample size and/or biological relevance is already challenging, without needing to calculate in a risk of manual error in the prep.

Getting all you can from your NGS?

- Expand into proteogenomics with BioLegend oligo-conjugated antibodies, hashtags, and cocktails.

- Revvity has developed over 130 vendor-qualified library prep protocols, including our NEXTFLEX™ chemistries.

NGS library prep automated workstation solutions
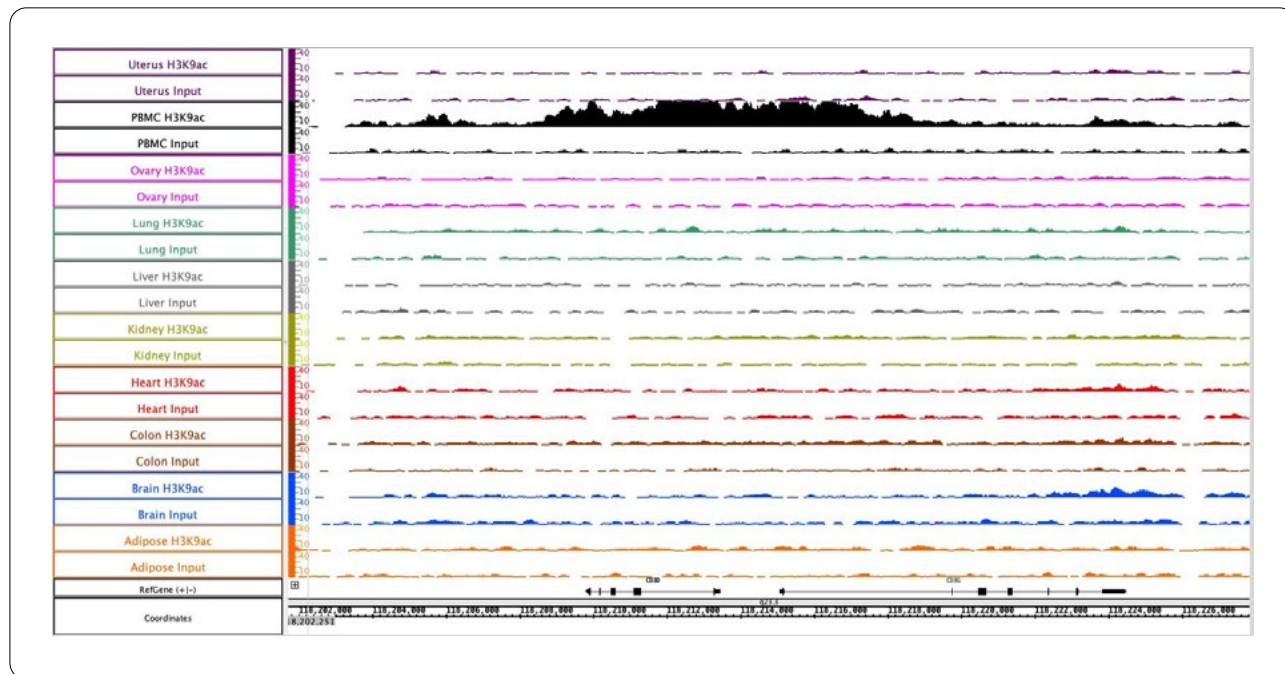
Genome browser tracks at CD3 locus, marking T-cells, using ChIP-seq from fixed human research biospecimen via multiple-sample bead milling and multi-sample sonication. Strong H3K9 acetylation is observed throughout the gene body in the PBMC population.

POSTER

Leverage our cryo-cooling with the mid-throughput Omni Bead Ruptor Elite bead mill (Cat # 19-042E) for temperature-sensitive analytes.

APP NOTE

DepleteX® and TotalSeq™ technologies combine to boost low-abundance transcript detection.

APP NOTE

A ChIP-Seq analysis workflow from various tissues using the Omni Bead Ruptor Elite™ and PIXUL™ MultiSample Sonicator.