Enhanced whole genome sequencing: simplifying the path from DNA to data

A next-generation enhanced whole genome (eWGS) workflow powered by upgraded xGen™ NGS chemistries—delivering exceptionally high-quality libraries, easier hybridization capture, and flexible coverage tuning in a single, unified workflow. Achieve higher-confidence data with fewer steps, less variability and a faster path from sample to sequencer.

A single, unified eWGS workflow

Whole genome and targeted libraries constructed together in one tube and workflow. No splitting, recombining, or additional normalization of samples.

Built in sequencing coverage tunabilty

Simple, reagent-based adjustments support desired panel-to-genome coverage ratios. Scales seamlessly across small, medium and large target sizes.

Built on upgraded xGen chemistries

Advanced fragmentase generates high quality libraries with minimal artifacts and chimeras. xGen Hyb and Wash v3 kit improvements streamline handling while supporting robust enrichment.

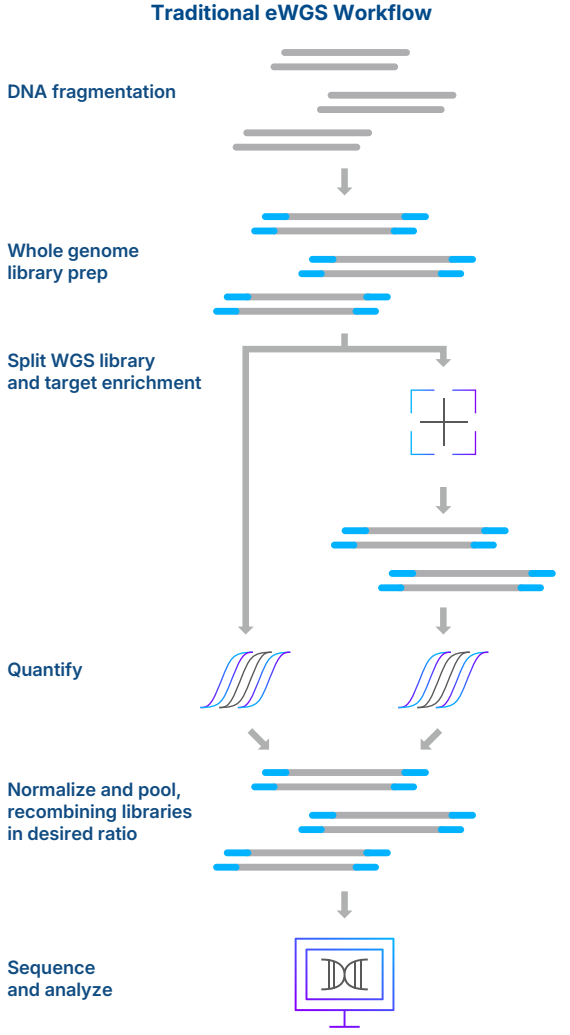

Figure 1. Comparison of traditional eWGS workflow an d the streamlined xGen eWGS workflow. The traditional eWGS workflow (left) requires multiple steps, including splitting libraries, separate target enrichment, and normalization/pooling before sequencing. In contrast, the xGen eWGS workflow (right) integrates whole genome and target enrichment into a single streamlined process, eliminating library splitting and complex pooling steps. This simplified approach reduces hands-on time and workflow complexity, enabling faster progression from sample to sequencing and analysis.

Data highlights: Single-workstream enhanced whole genome sequencing

The unified eWGS architecture reduces workflow complexity and eliminates steps that typically require splitting, recombining, or additional normalization of libraries. This simplification not only decreases hands on time but also reduces opportunities for user-introduced variability and sample swapping. The result is a faster, more convenient path from DNA to interpretable data. Coverage depth can be scaled across small, medium and large capture panels using one simple, reagent-based adjustment during library prep—no additional workflow or QC steps, and no additional PCR or cleanup steps on targeted libraries like would be necessary in a traditional eWGS workflow. Coverage depth can be right sized to meet study goals without redesigning workflows or making major library prep adjustments, accelerating study design and maximizing sequencer efficiency.

Predictable, tunable target enrichment coverage

With a single reagent-based adjustment during library preparation, coverage across any capture panel size scales smoothly and reliably. This approach preserves consistent panel-to-genome coverage ratios without requiring protocol modifications, added QC, or separate handling of samples destined for both whole-genome and targeted sequencing. The result is a highly flexible system that can tailor depth to the needs of oncology, population genomics, or translational studies—optimizing both sequencing efficiency and study sensitivity.

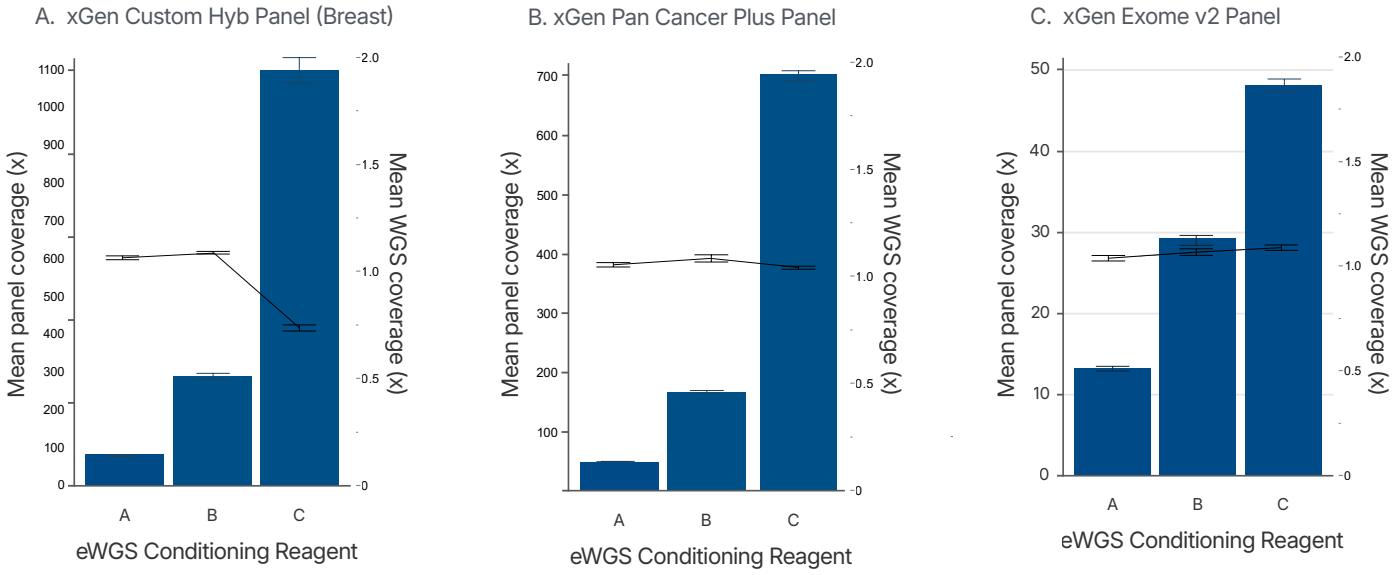

Figure 2 A-C: Tunable panel coverage across a wide range of hybrid-capture panel sizes. Libraries were prepared from Coriell NA12878 gDNA, xGen DNA Library Prep EZ v2 (EAP) and eWGS Conditioning Reagent A, B and C, followed by hybrid capture using an xGen Hyb Cap Panel: **A** Custom Hyb Breast Panel (~8 k probes), **B** Pan Cancer Plus Panel (~50 k probes), or **C** Exome v2 Panel (~415 k probes) using xGen Hyb & Wash Reagents v3 .

Coverage was normalized to 1× WGS (±0.3×) to illustrate proportional scaling of panel to genome coverage. Bars represent mean panel coverage (left axis); line series represent mean WGS coverage (right axis) (±SD). The consistent lowpass WGS signal with adjustable target enrichment depth demonstrates robust tunability across panel sizes, enabling flexible optimization for diverse study designs.

Become an early access collaborator—start shaping the next generation of eWGS!

Learn more about our early access program here.