NGS FUNCTIONAL TEST REPORT

The xGen™ Custom Hyb Panel was tested using the **xGen hybridization capture of DNA libraries for NGS target enrichment** protocol and xGen cfDNA & FFPE DNA Library Prep Kit using 100 ng of Coriell genomic DNA (gDNA). Illumina® sequencing was carried out using a 2 x 150 bp paired-end run. The Picard suite of analysis tools (Broad Institute) was used to report NGS statistics as an average across experimental replicates. The analysis was conducted using your probe BED file to serve as both the probes and targets when calculating coverage statistics.

Statistic	Definitions	NA24385	NA12878
Probe count	The number of probes contained in the design. Each probe is designed to capture a sequence of interest.	104,461	104,461
Bait territory	The number of unique bases covered by the probes.	126,721	126,721
Total sampled reads	The total number of reads used in the analysis.	1,006,160	1,006,160
Mean insert size	The average length of the insert sequenced.	157	153
Mean target coverage	The mean coverage (number of reads) for all bases in the targeted region.	438	442
Target percent bases >30X	The percent of all target bases with 30X or greater coverage.	99.8%	99.7%
Target percent bases >100X	The percent of all target bases with 100X or greater coverage.	99.5%	99.6%
Percent selected bases	The on-target rate, calculated as the percent of sequenced bases that are located within the flanked probe regions (+250 bp on either side). Flanking accounts for the capture of libraries that contain genomic regions that naturally extend beyond the targeted sequence.	82.8%	82.7%
Percent duplication	Percent of mapped reads that are duplicates. This metric also depends on the total sequencing depth.	4.6%	4.7%
Fold-80 base penalty	The fold over-coverage needed to raise 80% of target bases to mean coverage. For example, fold-80 value of 1.5 means 1.5-fold sequencing depth is needed to achieve this.	1.62	1.23
Target percent bases 0–0.1X mean	The percent of target bases with ≤0.1X mean coverage.	0.2%	0.3%
Target percent bases 0.1–0.2X mean	The percent of target bases with >0.1X but ≤0.2X mean coverage.	0.1%	0.0%
Target percent bases 0.2–0.5X mean	The percent of target bases with >0.2X but ≤0.5X mean coverage.	10.2%	3.2%
Target percent bases 0.5–1.5X mean	The percent of target bases with >0.5X but ≤1.5X mean coverage.	89.1%	96.4%
Target percent bases 1.5–2.5X mean	The percent of target bases with >1.5X but ≤2.5X mean coverage.	0.5%	0.5%
Target percent bases >2.5X mean	The percent of target bases with >2.5X mean coverage.	0.1%	0.1%
AT dropout	Estimate of the undercoverage of targeted AT-rich regions (≤50% GC) relative to the mean. AT dropout of 5% means that 5% of total reads that we expect to have mapped to the AT-rich regions mapped elsewhere.	2.4%	3.1%
GC dropout	Estimate of the undercoverage of targeted GC-rich regions (≥50% GC) relative to the mean. GC dropout of 5% means that 5% of total reads that we expect to have mapped to the GC-rich regions mapped elsewhere.	5.3%	2.0%

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