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Demystifying the genomics
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*Improving efficiency,**

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*performance and flexibility
of targeted sequencing, by
Emily Leproust A Sample to
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*NEBNext Ultra II DNA Library
Prep Protocol How to reduce
your test turnaround for
large panels in molecular
oncology Hematological
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are intended for molecular
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for the diagnosis,
prevention, or treatment of

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QIASEQ Targeted Methyl Panels offer a single-day solution capable of targeting thousands of CpG sites in the genome. As with targeted DNA panels, QIASEQ solutions are based on single-primer extension (SPE) technology that provides a sensitive and specific solution for detecting regions all across the genome.

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According to the QIASEQ Targeted DNA panel Handbook

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and protocol, and depending on the input DNA for the library preparation, the ideal value for Average reads per group should be 2 to 4, with 4 being the best value for the highest DNA input (i.e., 40ng).

~~Quality Control for the
Identify QIAseq DNA Variants
workflow~~

QIAseq Pan-cancer Multimodal Panel for comprehensive genomic profiling of solid tumors and heme malignancies . Unlock insights into multiple cancers with just 10 ng total nucleic acid input. Go to product page Experience our innovative, single-day sample to

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simultaneous enrichment and
profiling of 605 relevant
DNA variant and RNA fusion
biomarkers found across
multiple ...

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panel 33 QIAseq Targeted DNA
Panels delivered
consistently high sequencing
specificity and coverage

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uniformity with different
DNA inputs. 94,0 94,7 90,5
99,5 99,6 99,9 97,7 99,2
97,8 99,4 97,4 99,8 0 20 40
60 80 100 120 101Z-1 ng
101Z-10 ng 101Z-20 ...

~~Targeted RNA and DNA
sequencing in disease
prediction ...~~

Massively Parallel
Sequencing (MPS) allows to
sequence the total
mitochondrial DNA (mtDNA)
through specific panels.
Human Mitochondria Panel is
one of the QIAseq Targeted
DNA panels developed by
QIAGEN for MPS, which have
an optimized chemistry based
on the integration of unique
molecular indices (UMIs).

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QIAseq 16S/ITS Panel
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analysis Sequencing is
performed on an Illumina
MiSeq NGS system using a v2
kit with 251 x 2 paired end
run or a v3 kit with 276 x 2
paired end run. It is highly
recommended to perform
sequencing data analysis

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with the CLC Genomics
Workbench with Microbial
Genomics Module and QIAseq
16S Panel Analysis.

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throughput ...~~

QIAseq Targeted NGS for
Cancer Research, 10.10.2016

- Offers specificity that beats capture-based approaches
- Lets you use sequencing capacity on regions targeted by the panel, with minimal off-target sequencing
- Lets you achieve more uniform enrichment for more sequencing efficiency
- It delivers unmatched specificity and uniformity

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(compared to capture-based methods)

~~Digital DNA-seq Technology:
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