WGS, WES, or a Custom Panel?

Prepare Libraries

Extract DNA

Fragment DNA

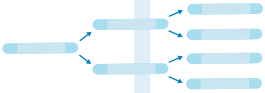
Create Library

Whole-genome sequencing (**WGS**), whole-exome sequencing (**WES**), and **custom panels** are all great options for mapping variants. However, each technique differs in cost, time, and sequencing capability, making each suitable for different research purposes.

WGS

NO HYBRIDIZATION
entire whole genome library is sequenced

AMPLIFICATION
(optional)



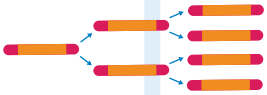
SEQUENCING
sequence spans whole genome

GGCATCAAGCCT
ATCAGGCTAGCT
AGCTCAGCATCA
GCTAGCTCAGCA

WES

HYBRIDIZATION
to **exome probes** and capture of target molecules

AMPLIFICATION



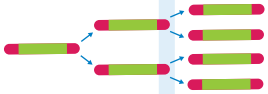
SEQUENCING
sequence enriched for exome regions

GGCATCAAGCCT
ATCAGGCTAGCT
AGCTCAGCATCA
GCTAGCTCAGCA

CUSTOM PANEL

HYBRIDIZATION
to **custom probes** and capture of target molecules

AMPLIFICATION



SEQUENCING
sequence enriched for custom target regions

GGCATCAAGCCT
ATCAGGCTAGCT
AGCTCAGCATCA
GCTAGCTCAGCA

- **comprehensive datasets that are very large**
- **requires more sequencing reagents**
- **increased time and cost for analysis**

- **cost-effective for coding regions**
- **requires fewer sequencing reagents (vs WGS)**
- **faster, simpler data analysis (vs WGS)**

- **target specific areas with greater precision**
- **requires fewer sequencing reagents (vs WGS)**
- **faster, simpler data analysis (vs WGS)**

	WGS	WES	CUSTOM PANEL
% of known disease-related mutations potentially identified	Close to ~100%	>85%	Dependent upon panel design
Sequencing results include:	~3000Mb Target Sequence Coding and noncoding regions Known and unknown variants SNPs, indels, structural variants	~40Mb Target Sequence Coding regions (typical designs; some designs include additional targets) Known and unknown variants SNPs, indels, and structural variants within target regions	100 Kb to 200 Mb Target Sequence Custom target regions Known and unknown variants SNPs, indels, and structural variants within target regions
% genome sequenced	Close to ~100%	1-5%	Dependent upon panel design
Comparative resources required	Higher cost of sequencing More time and expense for analysis Greater data storage requirements	Requires purchase of exome probe panel Additional steps for target enrichment (hybridization, etc.) Reduced sequencing costs (vs WGS) Less time and expense for analysis Smaller data storage requirements	Probe panel must be designed and purchased Additional steps for target enrichment (hybridization, etc.) Deeper coverage (with smaller panels) with much less sequencing cost compared to WES Less time and expense for analysis Smaller data storage requirements
Best suited for	Novel variant discovery, genome-wide association studies (GWAS) Analysis of regulatory and intergenic regions Identification of structural variants Sequencing of genomes that are not well annotated	Identification of variants in protein-coding regions (and with some exome panels, well-annotated regulatory regions)	Focusing on specific areas of interest to achieve greater sequencing depth (e.g., for somatic oncology) Sequencing large numbers of samples
Challenges	Very expensive to sequence the whole human genome (~3 billion bp) to the desired depths Generates an enormous amount of data that requires extensive analysis time and expertise	Misses most noncoding rearrangements Likely to miss many structural rearrangements	Requires a prior knowledge of relevant genomic regions Requires probe design expertise

Ultimately, choosing the right workflow for your research depends on your specific research questions and your available resources.

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