What is Primer Extension Target Enrichment (PETE)?

PETE is a novel NGS hybridization capture technology designed to employ primer extension reactions to specifically capture and release target library molecules for sequencing.

What's different about PETE?

Other target enrichment technologies offer either uniform, high-quality data (via probe hybridization) *or* fast, simple workflows (via amplicon-based enrichment). PETE brings together the benefits of *both* workflows–combining speed and simplicity with deep, uniform, high-quality coverage.

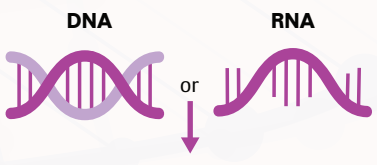
Perform fewer manual steps in a streamlined, versatile, end-to-end solution for somatic variant analysis

Save valuable time with an efficient, single-day, automatable workflow

Achieve superior performance and coverage uniformity

Here's how PETE works...

Start
with DNA or RNA

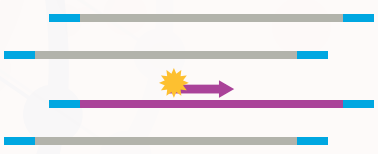


1 Prepare indexed libraries
Prepare libraries with KAPA DNA or RNA Library Prep Kits and truncated, universal adapters (▬) with or without UMIs.

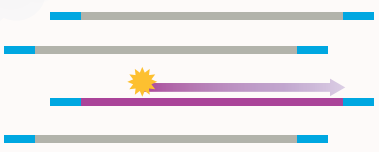
*Library molecule containing **target sequences***

*Library molecule containing **off-target sequences***

2 Anneal target-specific capture primers
Heat-denature libraries and hybridize to biotinylated target-specific capture primers (➞); for simplicity, only one strand of each denatured library molecule is shown.



3 Perform capture primer extension
Library molecules containing target sequences will form biotin-labeled capture-ready extension products, while off target library molecules will not.

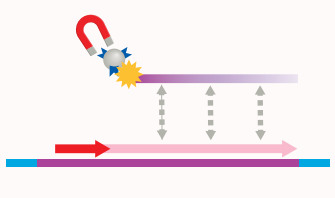


4 Capture and wash target library molecules
Use paramagnetic streptavidin beads ( ) and a magnet ( ) to capture and immobilize target molecules, and then wash away off-target molecules. The remaining library will be greatly enriched for target sequences.

5 Anneal target-specific release primers
Hybridize captured library molecules to target-specific release primers (➞); the binding sites for these primers are upstream of the capture primer sites.

6 Perform release primer extension
Primer extension releases the target molecules into the supernatant to be collected for amplification; the biotin-labeled molecules remain behind on immobilized beads.

***Target molecules** released into supernatant for amplification*



7 Amplify target library molecules
Use universal library amplification primers (➞) to amplify the released, target-enriched library molecules, and then perform cleanup.

Result
a sequencing-ready, target-enriched library

The **single-day PETE workflow** can detect all major somatic variant types—including SNVs, short indels, CNVs, MSI, and fusion transcripts—from a wide variety of sample types, including degraded DNA and RNA. To learn more about PETE technology and Roche's KAPA HyperPETE portfolio, visit **go.roche.com/KAPAHyperPETE**.

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