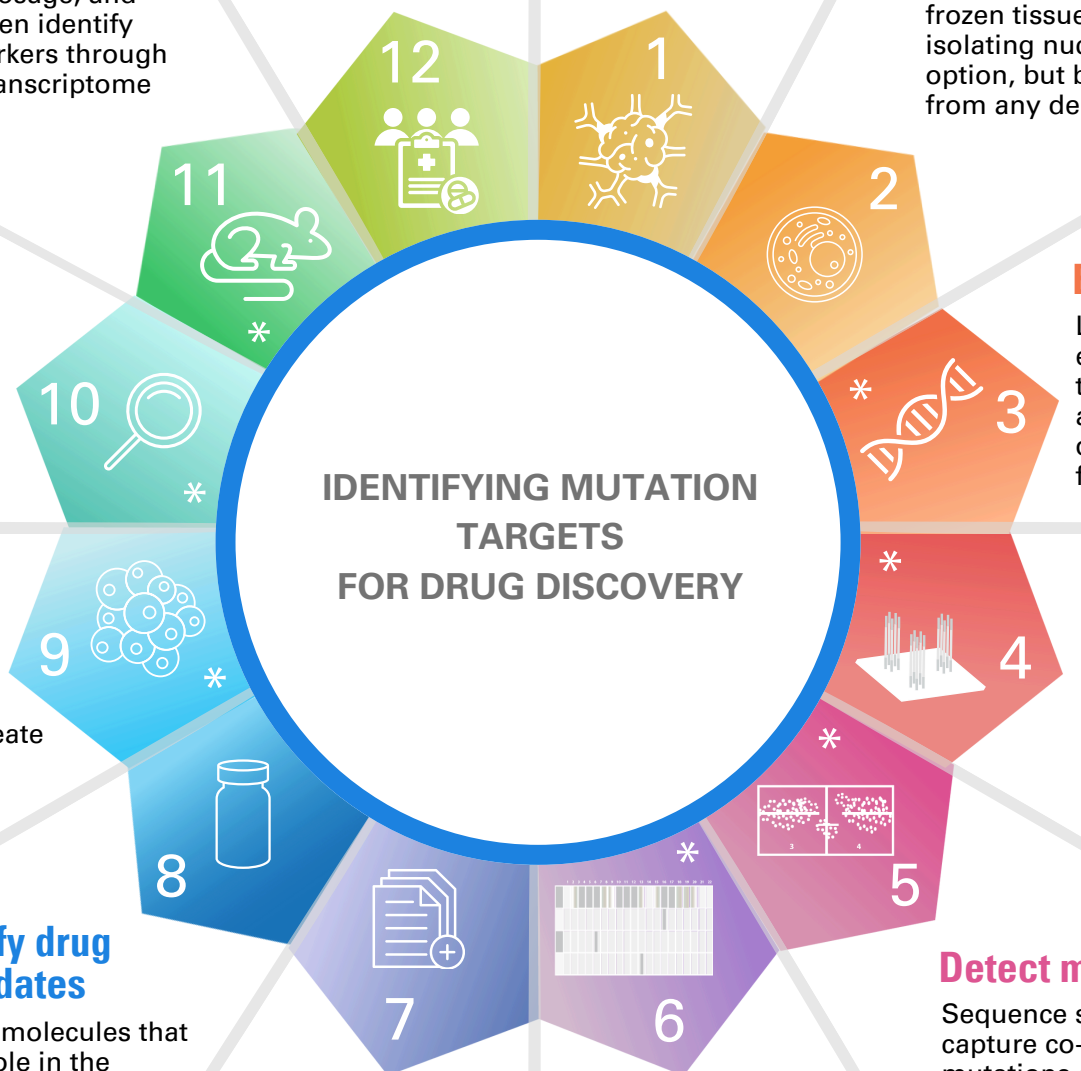

Acquire tissue samples from tumor banks

Freezing tissues preserves high-quality nucleic acids, so samples will be more reliable for downstream NGS or other molecular profiling.

Isolate whole cells or nuclei

Isolating high-quality whole cells from frozen tissue can be challenging, so isolating nuclei instead is a good option, but be sure your sample is free from any debris and contamination.

Extract nucleic acids

Lyse cells sufficiently to expose nucleic acids, but take care not to over-lyse, as this can compromise the quality of your nucleic acids for downstream reactions.

Prep your NGS library

Apply whole-genome sequencing to detect CNVs and SNVs to identify tumor-driving mutations.

Detect mutation events

Sequence single cells to capture co-occuring mutations and the clonal lineage missed with bulk sequencing.

Identify tumor subclones

Detect rare subclones using high-throughput single-cell analysis.

Study sequencing data

Conduct retrospective analysis of previous sequencing data as a reference set for further validation.

Identify drug candidates

Identify molecules that play a role in the molecular pathway of the tumor-driving mutations detected.

Establish in vitro model

Choose a cell line appropriate to your disease of interest and create an in vitro model using cloning and gene-editing tools.

Apply treatment

Screen your drug candidates in vitro to identify the safest and most effective leads for in vivo testing.

Establish in vivo model

Study pharmacodynamics and pharmacokinetics to understand the method of administration, dosage, and toxicity in vivo then identify additional biomarkers through changes in the transcriptome posttreatment.

Begin the next phase of trials

Advance the biomarkers and drug candidates demonstrating efficacy and safety for further study.

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* Takara Bio has innovative tools to foster success in this step.

NGS=next-generation sequencing.
CNV=copy number variation.
SNV=single nucleotide variant.